A JOINT MEETING OF THE

CANADIAN SOCIETY OF AGRONOMY
CANADIAN SOCIETY OF HORTICULTURAL SCIENCE
CANADIAN SOCIETY OF PLANT PHYSIOLOGISTS
CANADIAN BOTANICAL ASSOCIATION
CANADIAN PHYTOPATHOLOGICAL SOCIETY
CANADIAN WEED SCIENCE SOCIETY

PROCEEDINGS

JULY 17-21, 2011
SAINT MARY'S UNIVERSITY, HALIFAX
NOVA SCOTIA AGRICULTURAL COLLEGE, TRURO



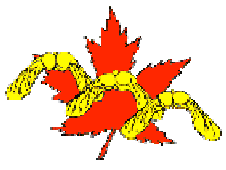

Table of Contents

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Plant Canada 2011 Program
July 16-21, 2011

Saturday, July 16		
18:00-21:00	**Canadian Phytopathological Society (CPS)** **Financial Advisory Committee meeting**	Secunda Boardroom 4th Floor, Sobey Building

Sunday, July 17		
8:30-15:00	**Canadian Phytopathological Society (CPS)** **Outgoing Board Meeting**	Secunda Boardroom 4th Floor, Sobey Building
10:00-11:30	**Canadian Journal of Plant Science Editorial Meeting**	Atrium 216
12:00-17:00	**Agricultural Institute of Canada** **(AIC) Board Meeting**	McNally Boardroom, McNally Building
13:00-15:00	**Society Executive Meetings** Canadian Society of Agronomy (CSA) (SB153) Canadian Society for Horticultural Science (CSHS) (Atrium 306) Canadian Botanical Association (CBA-ABC) (Atrium 216) Canadian Society of Plant Physiologists (CSPP) (Atrium 212) Canadian Institute of Food Science and Technology (CIFST) Atlantic Section (Atrium 217)	Sobey Building (SB) and Atrium
13:00	**Student Hospitality Room Open** Natural Sciences and Engineering Research Council of Canada (NSERC) Graduate Information Session Manon Hotte, NSERC	SB422 4th Floor, Sobey Building

13:00-19:00	**Conference Registration**	2nd Floor Lobby, Sobey Building
14:00-20:00	**Poster Setup for Poster Session #1** All student competition posters to be displayed during Poster Session #1. Please check the proceedings book for your poster number. Non-student poster presenters - please check the proceedings book for your time slot of Monday or Wednesday and your number	Loyola Conference Hall (L 290)
15:00-17:00	**NSERC News and Discovery Grant Programs** Kelly Anne Hoop, NSERC Program Officer, Ottawa	Scotia Bank Theatre Sobey Building (SB 201)
15:00-17:00	**Plant Canada Executive Meeting**	Secunda Boardroom 4th Floor, Sobey Building
17:00-19:00	**Opening Reception** Cash Bar, Hors d'oeuvres, Music	McNally Theatre Auditorium McNally Building
19:00-21:00	**Agricultural Institute of Canada - Annual General Meeting** Pizza and soft drinks	SB255, 2nd Floor, Sobey Building
19:30-20:30	**Canadian Botanical Association (CBA-ABC)** **Section Meetings:** Mycology Section, Ecology Section, Plant Development Section, Systematics and Phytogeography Section	Secunda Boardroom (SB 401), SB 415, Atrium 216, Atrium 212

Monday, July 18		
7:00	**Registration Desk Open**	2nd Floor Lobby Sobey Building
7:00	**Poster Setup for Poster Session #1** All student competition posters to be displayed during Poster Session #1. Please check the proceedings book for your poster number. Non-student poster presenters - please check the proceedings book for your time slot of Monday or Wednesday and your number	Loyola Conference Hall (L 290)
7:45-8:30	**Conference Opening** **Dr. Shahrokh Khanizadeh,** President of Plant Canada **Honorable John MacDonell,** Minister of Agriculture, Minister of Service Nova Scotia and Municipal Relations **Dr. J. Colin Dodds,** President of Saint Mary's University	McNally Theatre Auditorium McNally Building
8:30-10:00	**Plenary Session** Chair: Dr. Paul T. La Fleche, Deputy Minister of Agriculture, Nova Scotia 8:30-9:15 **"What's with the weather?"** Mr. David Phillips, Senior Climatologist, Environment Canada 9:15-10:00 **"Climate change impacts on crop production in Canada: are we heading up or down?"** Dr. Paul Bullock, Department of Soil Science, University of Manitoba	McNally Theatre Auditorium McNally Building

10:00-10:30	**Nutrition Break-** Loyola Conference Hall (L 290)

Monday, July 18						
Concurrent Session #1 10:30-12:00	**CSA** Sobey Building (SB265) **Climate change in agriculture**	**CSHS** Sobey Building (SB415) Symposium and general session	**CBA-ABC/CSPP** Sobey Building (SB260) Teaching symposium: **Evaluating student learning – How can we tell if our assignments are making a difference?**	**CSPP** Sobey Building (SB201) Symposium: **Plant responses to climate change**	**CPS** Sobey Building (SB255) Symposium: **Climate change and plant pathogens**	**CWSS** Loyola Building (L296) Symposium: **New weeds in Canada**
Session Chair	Richard Donald, Nova Scotia Agricultural College	Samir Debnath, Agriculture & Agri-Food Canada, St. John's	Cindy Ross Friedman, Thompson Rivers University	Peter Pauls, University of Guelph	Jeannie Gilbert, Agriculture and Agri-Food Canada, Winnipeg	Scott White, University of Guelph
10:30-11:00	Special topic: **Water resources and climate change** Invited speaker: Chandra Madramootoo, McGill University	**Berry production in forced culture** Invited speaker: Davide Neri, Università Politecnica delle Marche, Ancona, Italy	**BOTANY with a dash of SOTL-improving undergraduate botany curriculum using the scholarship of teaching and learning (will include a breakout session)** Invited speaker: Lyn Baldwin, Thompson Rivers University	**Mission accomplished or mission impossible: predicting biological impacts of climate change** Invited speaker: Jonathan Newman, University of Guelph	**Response of pathogenic microbes to climate change** Invited speaker: Geoffrey Dixon, University of Reading and GreenGene International, UK	**New weeds in Maritime Canada** Invited Speaker: Marian Munro, Nova Scotia Museum, Halifax
11:00-11:15						**Weed responses to climate change** Invited speaker: Mirwais Qaderi, Mount Saint Vincent University

11:15-11:30	Special topic: **Plant bio-diversity and climate change in agricultural** Invited Speaker: Robert Hijmans, University of California, Davis	**Molecular markers and antioxidant activity in berry crop diversity analysis** Samir Debnath, Agriculture and Agri-Food Canada, St. John's	Invited Speakers on theme of **Helping students write and communicate in the biological sciences** Speaker #1: **Transferring small-class assignments to a large class environment** Invited speaker: Frédérique Guinel, Wilfred Laurier University	**Adapting forest genetic resource management to climate change** Invited speaker: Sally Aitken, University of British Columbia	**Projected effects of climate change on plant diseases and how plant pathologists can prepare to meet the challenge** Invited speaker: Stella Coakley, Oregon State University	
11:30-11:45		**Molecular analysis and antioxidant activity in micropropagated berry plants acclimatized under *ex vitro* condition** Samir Debnath, Agriculture and Agri-Food Canada, St. John's				**Predicting weed invasion of Canada under climate change: measuring evolutionary potential** Invited speaker: David Clements, Trinity Western University
11:45-12:00		**Gene expression assessment of potassium phosphate foliar treatment of potato plants** Tudor Borza, Nova Scotia Agricultural College				
12:00-13:00	**Lunch** – included with registration Canadian Botanical Association (CBA-ABC) Teaching Section Meeting (SB260)					

Monday, July 18						
Concurrent Session #2 13:00-15:00	**CSA** (SB265) General Session: **Nutrient management**	**CSHS** (SB415) Student General Session	**CBA-ABC/CSPP** (SB260) 13:00-14:00 **Teaching symposium continues** 14:00-15:00 CBA General Session	**CSPP** (SB201) General Session: **Plant crop and eco-physiology**	**CPS** (SB255) Student General Session: **Molecular and physiological plant pathology**	**CWSS** (L296) General Session
Session Chair	Shabtai Bittman, Agriculture and Agri-Food Canada, Agassiz	David Percival, Nova Scotia Agricultural College	13:00-14:00 John Markham, University of Manitoba 14:00-15:00 Rodger Evans, Acadia University	Doug Campbell, Mount Allison University	Deena Errampalli, Agriculture and Agri-Food Canada, Vineland	Marie Josée Simard, Agriculture and Agri-Food Canada, Sainte-Foy
13:00-13:15	**Soybean symbiotic nitrogen fixation responses in relation to Bradyrhizobium inoculation and nitrogen use in dykeland** Panchali Katulanda, Nova Scotia Agricultural College	**Fertility management of establishing organic blackcurrants (*Ribes nigrum L.*) in Atlantic Canada** David Hobson, Organic Agricultural Centre of Canada, Truro	Open discussion teaching panel on **"Teaching and evaluating scientific writing"** Led by John Markham, University of Manitoba. John Markham will start discussion by presenting results of nationwide survey;	**Importance of residual vegetation to net carbon uptake in pine stands following mountain pine beetle attack in central British Columbia, Canada** Art Fredeen, University of Northern British Columbia	**Investigating the impact of fungal produced cytokinins on fungal development and disease progression in the *Ustilago maydis-Zea mays* pathosystem** Erin Morrison, Trent University	**Potential oilseed crops for biodiesel feedstock on the Canadian prairies** Robert Blackshaw, Agriculture and Agri-Food Canada, Lethbridge

13:15-13:30	**Belowground portioning of nitrogen in field pea and canola** Melissa Arcand, University of Saskatchewan	**Enhanced levels of phenolic compounds and antioxidant capacity *in vitro* derived lingonberry plants** Poorva Vyas, Memorial University of Newfoundland	**"Undergraduate scientific writing trends in biology Programs across Canada"** **Panelists:** Lyn Baldwin, Thompson River University Christian Lacroix, University of Prince Edward Island Jane Eddington, Dalhousie University Norm Hüner, University of Western Ontario	**Effect of water stress and temperature on growth of wild leek** Line LaPointe, Université Laval	**The effect of *Upe* expression on *Ustilago maydis* pathogenic development** Kitty Cheung, Trent University	**Determining the mechanism of resistance to glyphosate in giant ragweed *(Ambrosia trifida L.)* in Ontario** Amanda Green, University of Guelph
13:30-13:45	**Characterization of nitrogen transfer from diverse red clover populations to companion bluegrass and impact on soil nitrogen dynamics under field conditions** Malinda Thilakarathna, Dalhousie University	**Post-harvest organic carbon amendments to minimize mineral nitrogen losses in cole crop production: *in situ*** Katelyn Congreves, University of Guelph		**Mechanisms involved in the multi-metal tolerance of *Deschampsia cespitosa*: the role of metal chelators** Allison Hayward, Trent University	**SmkA MAP kinase is involved in the mycoparasitism of the plant fungal pathogen *Rhizoctonia solani*** Rony Chamoun, McGill University	**Environmental conditions, growth stages and fungicides affect herbicide tolerance of winter wheat** Melody De Jong, University of Guelph
13:45-14:00	**Nitrogen released from legume crop residues during two succeeding non-legume crops** Newton Lupwayi, Agriculture and Agri-Food Canada, Lethbridge	**Reduced-stature Rosa species through in vitro mutagenesis** Mirza Muhammad Qadeer Baig, McGill University		**Using nitrogen isotopes at natural abundance to measure genetic variation in nitrogen-use traits and source preference in *Populus balsamifera* L.,** Lee Kalcsits, University of British Columbia	**18S rDNA Phylogenies:All that glitters may not be gold** Vincent Huang, University of Guelph	**Cumulative stress occurs between hail damage and in-crop herbicide applications in tomato and sweet corn** Darren Robinson, University of Guelph

14:00-14:15	**Nitrous oxide emissions from crop nitrogen applications in eastern Canada** Tom Bruulsema, International Plant Nutrition Institute, Guelph	**Development of a prototype variable rate sprayer using digital color cameras for spot-specific application of agrochemicals in wild blueberry** Travis Esau, Nova Scotia Agricultural College	**Do mitochondria play a role in remodeling lace plant leaves during programmed cell death?** Christina Lord, Dalhousie University	**Ferric reductase activity of iron-limited cells is both promoted and inhibited by ferric chelators** Harold Weger, University of Regina	**Characterization of a virulence gene responsive to nitrogen stress in *Fusarium graminearum*** Sean Walkowiak, Carleton University	**A historical perspective on overcoming weed concerns in conservation tillage systems on the Canadian prairies** Robert Blackshaw, Agriculture and Agri-Food Canada, Lethbridge
14:15-14:30	**Comparative performance of urea and ESN in winter wheat in northern Ontario** Tarlok Sahota, Agriculture and Agri-Food Canada, Thunder Bay	**Mapping soil properties using electromagnetic induction methods in wild blueberry** Fahad Khan, Nova Scotia Agricultural College	**The role of ethylene, ethylene receptors and caspase-like genes in lace plant programmed cell death during leaf morphogenesis** Gaolathe Rantong, Dalhousie University	**Characterization and physiological importance of complex oscillations of photosynthesis induced by changing light** Guy Samson, Université du Québec à Trois-Rivières	**Chelated copper induces disease resistance in *Agrostis stolonifera L.*** Brady Nash, University of Guelph	
14:30-14:45	**Winter wheat response to nitrogen fertilizer rate and application: and no-tillage comparison** Stephen Guy, Washington State University	**Characterize and quantify soil variability to delineate management zones for variable rate fertilization in wild blueberry fields** Aitazaz Farooque, Nova Scotia Agricultural College	**Mutation-mediated disruption of cellulose synthesis in *Arabidopsis thaliana*** Moira Galway, St. Francis Xavier University	**Down regulation of Glutamine synthetase is correlated to ammonium accumulation and chlorosis in "SR7200" velvet bentgrass (*Agrostis canina* L.)** Eric Lyons, University of Guelph	**Extreme resistance induced against tomato bush stunt virus requires an active RNA silencing pathway** Raphael Sansregret, Universite de Sherbrooke	**The decline of diffuse knapweed in British Columbia** Brian Wallace, Nova Scotia Agricultural College

14:45-15:00	**Wood ash assessment for use in agriculture** Mehdi Sharifi, Nova Scotia Agricultural College		**Quantifying spatial and temporal growth patterns of developing leaves in 3D** Lauren Remmler, University of Ottawa	**The glycolytic and antioxidant H_2O_2 scavenging capacity of germinating barley seeds with different levels of dormancy** Zhen Guo Ma, Memorial University of Newfoundland	**Infection biology of *Microdochium nivale*** Linda Jewell, University of Guelph	**Rolling fall rye for weed suppression in cucumber and squash** Darren Robinson, University of Guelph
15:00-15:30	**Nutrition Break (L290)**					
Monday, July 18						
Concurrent Session #3 15:30-17:00	**CSA** (SB265) General Session: **Cropping Systems**	**CSHS** (SB415) General Session	**CBA-ABC** (SB260) General Session: **Systematics and evolution**	**CSPP** (SB201) General Session: **Plant stress and plant development**	**CPS** (SB255) Student General Session (continued): 15:30-16:00 **Ecology, epidemiology and management** 16:00-17:00 General Session **Pathogen detection, identification and taxonomy**	**CWSS**

Session Chair	Rigas Karamanos, Viterra, Calgary	Kris Pruski, Nova Scotia Agricultural College	Hugo Cota-Sanchez, University of Saskatchewan	Sophia Stone, Dalhousie University	Rick Peters, Agriculture and Agri-Food Canada, Charlottetown	
15:30-15:45	**Invited presentation by the recipient of the "Best Paper in Agronomy Award": An in silico study of the genes for the isoflavonoid pathway enzymes in soybean reveals novel expressed homologues** Martina Strömvik, McGill University	**Effect of acidification on quality and shelf-life of carrot juice** Li Juan Yu, Nova Scotia Agricultural College	**Biogeographic and phylogenetic patterns in the pantropical genus Bauhinia s.l. (Leguminosae)** Carole Sinou, University of Montreal	**Effect of abiotic stress on cytoskeleton and chloroplast arrangement** Sarah Schoor, University of Waterloo	**Biological soil disinfestations: analyzing the process and its bacterial community structure** Subrata Mowlick, Yamagata University, Japan	
15:45-16:00		**Mundulla Yellows: a 30 year problem solved** William Paton, Brandon University	**Phylogenetic relationships within the hyper-diverse Cariceae/Scirpeae s.s./Dulicheae clade (Cyperaceae) with emphasis on the circumscription of Eriophorum and Scirpus s.s.** Claire Gilmour, Canadian Museum of Nature, Ottawa	**Adaptation and acclimation of Alnus ruba in a changing climate** Brendan Porter, University of Victoria	**Efficacy of Serenade and Prestop against clubroot is affected by soil type** Hema Kasinathan, University of Guelph	
16:00-16:15	**Assessment of the environmental risks of genetically modified canola applying GC/MS metabolomics** Konstantinos Aliferis,	**Seasonal growth dynamics and carbon partitioning of the wild blueberry plant (Vaccinium angustifolium Ait.)** Jatinder Kaur,	**Genetic diversity in Coelogyne nervosa R. Rich., an endemic orchid from Southern India** Shaik Mahammad Khasim,	**Alternative oxidases of non-angiosperm plants** Karina Neimanis, Wilfred Laurier University	**Molecular aerobiology: the contribution of new spore quantification methods** Danielle Morissette, Phytodata Inc.,	

	McGill University	Nova Scotia Agricultural College	Acharya Nagarjuna University, India		Sherrington, QC	
16:15-16:30	**Examining reduced tillage on organic cropping systems** Clare Sullivan, University of Saskatchewan	**Chlorophyll fluorescence for in vivo stress detection in horticultural crops** John DeLong, Agriculture and Agri-Food Canada, Kentville		**Changes in mesophyll conductance and plant hydraulic properties during a drought–rewatering cycle in hybrid poplars with contrasting water stress tolerance** Guillaume Théroux Rancourt, Université Laval	**Genetic diversity of potato virus Y (PVY) in seed-lot potatoes in New Brunswick** Upeksha Nanayakkara, Agriculture and Agri-Food Canada, Fredericton	

16:30-16:45	**Frequency of field pea in long-term rotations impacts biological nitrogen fixation** Diane Knight, University of Saskatchewan	**Genomics of plants' responses and adaptation to global climate change** Om Rajora, University of New Brunswick		**Gibberellin metabolism and transport during germination and young seedling growth of pea (Pisum sativum L.)** Belay Ayele, University of Manitoba	**Specificity and sensitivity of a TaqMan real-time PCR assay for detection of several pathovars of Pseudomonas syringae** James Tambong, Agriculture and Agri-Food Canada, Ottawa	
16:45-17:00	**Carbon footprint of durum wheat is reduced through diversification of cropping systems** Yantai Gan, Agriculture and Agri-Food Canada, Swift Current	**Anatomical traits for efficient soil exploration and stress tolerance** Kathleen Brown, Penn State University		**Exploring two ethylene biosynthetic enzymes as potential targets of Arabidopsis RING E3 ligases, XBAT32, during lateral root production** Wendy Lyzenga, Dalhousie University		
17:00-19:30	**Poster Session #1** **(student competition posters to be displayed at this session)** Wine and Cheese Loyola Conference Hall (L290) (Poster takedown immediately following session)					
	Supper on Your Own					
19:30-21:00	**Student Barbeque –Gorsebrook Lounge**					
21:00-23:00	**Student Post Barbeque Event - Gorsebrook Lounge**					

Tuesday, July 19		
	Departure	**Tour** (All tours arrive in Truro for the Barbeque at 17:00)
7:00	**Westin Hotel**	**North Shore Tour**
7:15	**Loyola Building, Saint Mary's University**	
8:15	**Westin Hotel**	**Agronomy and Horticulture Tour of Annapolis Valley**
8:30	**Loyola Building, Saint Mary's University**	
8:45	**Westin Hotel**	**Coastal Barrens and Peggy`s Cove**
9:00	**Loyola Building, Saint Mary's University**	
8:45	**Westin Hotel**	**Algal Biodiesel Field Excursion, NRC Research Facility at Sandy Cove**
9:00	**Loyola Building, Saint Mary's University**	
17:00-19:30	**Barbeque NSAC, Truro (CBA fund raiser – Botanical Auction)**	
19:30-20:45	**Buses return to the Westin and Loyola Building, Saint Mary's University**	
21:30-23:00	**Student Social Gorsebrook Lounge, Saint Mary's University, Halifax**	

Wednesday, July 20						
7:00-10:00	**Poster setup for Poster Session #2 (Loyola Conference Hall L290)** Please check the Proceedings book for your poster number**.**					
Concurrent Session #4 8:30-10:00	**CSA** (SB265) General session: **Food, fuel and crop adaptation**	**CSHS** (SB415) Symposium	**CBA-ABC** (SB260) Ecology Symposium: **Climate change: Canada's plants on the run!**	**CSPP** (SB201) Symposium: **Plant adaptations to stress**	**CPS** (SB255) Symposium: **Mycotoxins in grain: an accumulating problem**	**CWSS** (L296) Symposium: **New crops as new weeds in Canada** **&** **Mitigating threats posed by new weeds in Canada**
Session Chair	Malcolm Morrison, Agriculture and Agri-Food Canada, Ottawa	Peter Hicklenton, Agriculture & Agri-Food Canada, Kentville	8:30-9:00 Liette Vasseur, Brock University 9:00-10:00 Art Fredeen, University of Northern British Columbia	Peter Constabel, University of Victoria	James Menzies, Agriculture and Agri-Food Canada, Winnipeg	8:30-9:15 Robert Blackshaw, Agriculture and Agri-Food Canada, Lethbridge 9:15-10:00 David Clements, Trinity Western University

8:30-8:45	Special topic: **Phytochemical antioxidants in healthy Canadian crops-the good, the better, & the best** Invited speaker: Rong Tsao, Agriculture and Agri-Food Canada, Guelph	**Agro-ecosystem approach to understanding environmental stress in fruit and vegetable production** Invited speaker: Jean-Pierre Privé, Agriculture and Agri-Food Canada, Bouctouche	**Vulnerability of plant communities in coastal British Columbia to past and future environmental change** Invited Speaker: David Clements, Trinity Western University	**Role of calcium in signaling plant stress response** Invited speaker: Wayne Snedden, Queen's University	**An overview of Ochratoxin A in Canadian grains** Invited speaker: Sheryl Tittlemier Canadian Grain Commission, Winnipeg	8:30-8:50 **New crops and crops with new traits: are they weedy or invasive?** Invited speaker: Linda Hall, University of Alberta
8:45-9:00						
9:00-9:15			**Treeline ecology: fast changing, slow growing and a little disturbing** Invited speaker: Andrew Trant, Memorial University		**Trichothecenes and other secondary metabolites from *Fusarium graminearum*-Is it just about DON?** Invited speaker: Barbara Blackwell, Agriculture and Agri-Food Canada, Ottawa	8:50-9:15 **The role and impact of volunteer and feral crop plants in the era of novel traits** Invited speaker: Rene Van Acker, University of Guelph
9:15-9:30	Special topic: **Roots of the second green revolution** Invited speaker: Jonathan Lynch, Penn State University	**CSHS/OACC Joint Session Organic agriculture: contributions to sustainable horticulture** Invited speaker: Ralph Martin, Organic Agriculture Centre of Canada, Founding Director, Nova Scotia Agricultural College		**Forest pathology in the era of genomics** Invited speaker: Armand Seguin, Laurentian Forestry Centre, St. Foy, QC		9:15-9:35 **Preventing new introductions: A federal response to emerging weed and invasive plant threats in Canada** Invited Speaker: Claire Wilson O'Driscoll, Canadian Food Inspection Agency, Dartmouth

9:30-9:45			**Assessing climate change impacts on traditional plants and species at risk in coastal regions** Invited speaker: Liette Vasseur, Brock University		**Panel Discussion**	**9:35-9:55 History of the detection of a new weed in Canada: The wooly cupgrass (*Eriochloa villosa)* case** Invited speaker: Marie Josée Simard, Agriculture and Agri-Food Canada, Sainte-Foy
9:45-10:00						
10:00-10:30	Nutrition Break (L290)					
Wednesday, July 20						
Concurrent Session #5 10:30-12:00	**CSA (SB265)** General session **Food, fuel and crop adaptation** (continued)	**CSHS/OACC (SB415)** Joint Session (continued): **Organic agriculture: contributions to sustainable horticulture**	**CBA-ABC (SB260)** General Session: **Ecology and phytogeography**	**CSPP (SB201)** **Norman Hüner symposium**	**CPS (SB255)** General Session: **Ecology, epidemiology and management**	
Session Chair	Patricia Juskiw, Agriculture and Rural Development, Alberta	Jean-Pierre Privé, Agriculture and Agri-Food Canada, Bouctouche	Paul Catling, Agriculture and Agri-Food Canada, Ottawa	Carl Douglas, University of British Columbia	Tom Hsiang, University of Guelph	

10:30-10:45	Special Topic: **Crop-based biofuel feedstock potential in Atlantic Canada - Nova Scotia model** Invited speaker: Kevin Vessey, Saint Mary's University	**Seasonal contribution of nitrogen from compost in application year and subsequent years to broccoli in a long term organic rotations experiment** Josée Owen, Agriculture and Agri-Food Canada, Bouctouche	**Traditional knowledge and botanical collections help to study climate change effects in the southern Arctic**. Laurie Consaul, Canadian Museum of Nature	10:30-11:10 **CSPP gold medal address - Shedding some light on plant adaptation and acclimation** Norman Hüner, University of Western Ontario	**Ratio of 3-ADON and 15-ADON isolated of *Fusarium graminearum* recovered from wheat plants inoculated and incubated at various temperatures** Jeannie Gilbert, Agriculture and Agri-Food Canada, Winnipeg
10:45-11:00		**Strong partnerships achieve big successes: ten years of partnership between the Canadian Society for Horticultural Science (CSHS) and the Ghana Institute of Horticulturists (GhIH) in Ghana's impoverished Upper West Region** Josée Owen, Agriculture and Agri-Food Canada, Bouctouche	**Timing it right: implications of climate variation on a mixed mating, early-flowering plant.** Hazel Cameron-Inglis, Thompson Rivers University		**Metabolic profiles of barley genotypes inoculated with trichothecene producing and nonproducing isolates of *Fusarium graminearum*** Aijamada Kushalappa, McGill University
11:00-11:15	**Isolation and biological characterization of fungal and bacterial endophytes of switchgrass** François Gagné-Bourque, McGill University	**Organic agriculture project in Nepal: an international twinning partnership program** Samir Debnath, Agriculture and Agri-Food Canada, St. John's	**Impacts of landscape disturbance on plant reproductive success: are there general trends and patterns?** Irene McKechnie, University of Ottawa		**Effect of methyl jasmonate for suppression of postharvest Botrytis in different grape cultivars** Deena Errampalli, Agriculture and Agri-Food Canada, Vineland

11:15-11:30	**Seaweed extract from *Ascophyllum nodosum* improves early establishment and stress resistance in vegetable transplants** William Neily, Acadian Seaplants Ltd, Dartmouth, Nova Scotia	**Best Management practices for organic blackcurrant production** Karen Nelson, Organic Agriculture Centre of Canada, Nova Scotia Agricultural College	**Rate and form of native and exotic plant recolonization after disturbance of forest communities in southern Ontario** Andrew Browne, Brock University	11:10-11:35 **From stress sensing to cell death in Chlamydomonas** Denis Maxwell, University of Western Ontario	***Trichoderma* spp.: antagonistic effects to *Phytophthora ramorum* growth and spore germination *in vitro*** Elisa Becker, Canadian Forest Service, BC
11:30-11:45	**Variations in isoflavone profiles of field grown red clover cultivars** Yousef Papadopoulos, Agriculture and Agri-Food Canada, Truro	**Screening of salt tolerant plants for prompting greenery in Saudi Arabia** Ali Aljaloud , KACST, Riyadh, Saudi Arabia	**Forest structure, understorey composition and bryophyte abundance across bog and lakeshore forest edges in southwest Nova Scotia** Karen Harper, Dalhousie University	11:35-12:00 **How will climate change affect conifer forests?** Ingo Ensminger, University of Toronto	**Species susceptibility and biocontrol of Fusarium wilt of *Hiemalis begonias* in Canada** Xiuling Tian, University of Guelph
11:45-12:00	**Improving the antioxidant capacity of field crops by increasing selenoprotien content** Kaushik Ghose, Agriculture and Agri-Food Canada, Charlottetown	**New sainfoin keeps pace with alfalfa for safe grazing** Surya Acharya, Agriculture and Agri-Food Canada, Lethbridge	**Invasion of *Rosa rugosa* into coastal plant communities of Brier Island, Nova Scotia** David Garbary, St. Francis Xavier University		**An innovative, high throughput screening technology for identification and optimization of effective anti-biofilm fungicides** Michael Harding, Innovotech Inc, Brooks, AB

12:00-14:00	**Working Lunch (bag lunch provided) – Society AGM's, Awards** Canadian Phytopathological Society (CPS) (SB255) Canadian Society of Agronomy (CSA) (SB265) Canadian Society for Horticultural Science (CSHS) (SB415) Canadian Botanical Association (CBA-ABC) (SB260) Canadian Society of Plant Physiologists (CSPP) (SB201) Canadian Weed Science Society (CWSS) (L296)			
Wednesday, July 20				
Concurrent Session #6 14:00-15:30	**CSA (SB265)** 14:30-15:30 General Session: **Cropping systems and breeding**	**CBA-ABC (SB260)** Symposium: **Effects of environmental change on fungal diversity & General session**	**CSPP (SB201)** General Session: **Gene regulation and molecular biology**	**CPS (SB255)** General Session: **Molecular and physiological plant pathology**
Session Chair	Balakrishnan Prithiviraj, Nova Scotia Agricultural College	Michele Piercey-Normore, University of Manitoba	Tamara Western, McGill University	Solke De Boer, Canadian Food Inspection Agency, Charlottetown

14:00-14:15	Special Topic: **Arbuscular mycorrhiza in a sustainable world** Invited speaker: Chantal Hamel, Agriculture and Agri-Food Canada, Swift Current	**Lichens and allied fungi of old wet cedar (*Thuja occidentalis*) forests in Northeastern North America: Indicators of environmental change** Invited speaker: Stephen Clayden, New Brunswick Museum, Saint John	**Regulation of secondary cell wall biosynthesis in Arabidopsis by a KNAT7 transcription factor repression complex** Carl Douglas, University of British Columbia	**Effect of temperature on cortical infection and disease severity by *Plasmodiophora brassicae* on Shanghai pak choy** Kalpana Sharma, University of Guelph
14:15-14:30		**Decomposition of moss by filamentous fungi and its potential role in arctic/alpine pedogenesis** Invited speaker: Melissa Day, University of Alberta	**Characteristics of fibres from soybean stem residue: gene identification and quantitative trait loci (QTL) mapping** Peter Pauls, University of Guelph	**Effect of host resistance on infection by *Plasmodiophora brassicae* in canola** Abhinandan Deora, Agriculture and Agri-Food Canada, Saskatoon
14:30-14:45	**Recombinant expression if plant diacylglycerol acyltransferases from tissue that accumulate saturated fatty acids** Ying Zhang, University of Alberta	**The blue-stain fungi of Manitoba and NW Ontario** Invited speaker: Georg Hausner, University of Manitoba	**What causes the pointed first leaf phenotype in Arabidopsis thaliana ribosomal protein mutants?** Chad Stewart, University of Saskatchewan	**Susceptibility of potato and other hosts to late blight caused by Canadian genotypes of *Phytophthora infestans*** Rick Peters, Agriculture and Agri-Food Canada, Charlottetown
14:45-15:00	**Integration of marker assisted selection for scald resistance into the FCDC breeding program** Patricia Juskiw, Agriculture and Rural Development, Alberta	**Monitoring ecological integrity and air quality with lichens at Kejimkujik national park and national historic site** Invited speaker: Troy McMullin, University of Guelph	**Characterization of a transcriptional circuit involving the transcription factor, AtMYB61** Michael Prouse, University of Toronto	**A new class of gene expression control molecules in *Ustilago maydis*** Barry Saville, Trent University

15:00-15:15	**Genotype and environment influence GABA concentration in short-season soybean** Malcolm Morrison, Agriculture and Agri-Food Canada, Ottawa	**Effects of environmental change on lichen fungi** Invited speaker: Brinda Timsina and Dr. Michele Piercey-Normore, University of Manitoba	**Towards identifying candidates for a major resistance gene to common bacterial blight in OAC Rex (*Phaseolus vulgaris*)** Denise Cooper, University of Guelph	**Sequencing and assembly of a fungal genome** Tom Hsiang, University of Guelph
15:15-15:30	**Lack of hybrid seeding rate interactions for corn growth silage yield and quality** William Cox, Cornell University	**The distribution, structure and ecophysiology of *Peltigera hydrothyria*, 'The Water Fan', a rare and endangered macrolichen that grows under water** David Richardson, Saint Mary's University	**Extracellular glycosidases of *Pythium irregular*** Dimitre Ivanov, University of Western Ontario	**CPS Education Award winning video "A Legend in Crisis" –** The Canadian Chestnut Council
15:30-17:30	**Poster Session #2** Coffee, Tea and Juice Loyola Conference Hall (L290) (Poster take down immediately following session)			
16:30-17:30	**Plant Canada Executive Meeting** Secunda Boardroom, 4th Floor of Sobey Building			
18:30-20:30	**Closing Banquet** Westin Hotel Commonwealth Ballroom and the Atlantic Ballroom			

Thursday, July 21					
7:30-8:30	Canadian Phytopathological Society (CPS) Incoming Board meeting Secunda Boardroom, 4th Floor, Sobey Building				
Concurrent Session #7 8:30-10:00	**CSA/CSHS/OACC (SB255)** Joint Session: **Organic and sustainable agriculture**	**CSA (SB265)** 2011 CSA Borlaug Symposium: **Crop physiology and abiotic stresses**	**CBA-ABC (SB260)** General Session: **Ecology**	**CSPP (SB201)** General Session **Biochemical process and biotechnology**	**CIFST/CSHS (SB415)** Session **Fruits: bioactives and health benefits**
Session Chair	Andrew Hammermeister Organic Agriculture Centre of Canada, Nova Scotia Agricultural College	9:30-10:00 Gavin Humphreys, Agriculture and Agri-Food Canada, Winnipeg	Hugues Massicotte, University Northern British Columbia	Chris Todd, University of Saskatchewan	Vasantha Rupasinghe, Nova Scotia Agricultural College
8:30-8:45	**Sustainability and integrity of organic farming in a global food chains perspective** Invited speaker: Niels Halberg Director ICROFS, Tjele, Denmark			**Biochemical and molecular characterization three cell wall-localized purple acid phosphatase isozymes upregulated by phosphate-starved *Arabidopsis thaliana*** Hernan Del Vecchio, Queen's University	8:30-8:55 **Blueberries and human health** Wilhelmina Kalt, Agriculture and Agri-Food Canada, Kentville
8:45-9:00			**Plant resurrection on the rocks: drought tolerance strategies in granite outcrop species of southwest Western**	**The secreted purple acid phosphatase isozymes AtPAP12 and AtPAP26 play a pivotal role in extracellular phosphate-**	

			Australia Michael Shane, University of Western Australia	**scavenging by *Arabidopsis thaliana*** Whitney Robinson, Queen's University	
9:00-9:15			**Are endophytic fungi hosted by the lodgepole pine dwarf mistletoe (*Arceuthobium americanum*)?** Cindy Ross-Friedman, Thompson Rivers University	**Tissue-specific expression, phosphorylation, and monoubiquitination of phosphoenolpyruvate carboxylase isozymes of the castor oil plant, *Ricinus communis* L** Brendan O'Leary, Queen's University	8:55-9:15 **Antihypertensive properties of selected fruit bioactives** Nileeka Balasuriya and Vasantha Rupasinghe, Nova Scotia Agricultural College
9:15-9:30	**Are organic farms different? A Canadian perspective** Invited speaker: Derek Lynch, Nova Scotia Agricultural College		**Distribution of arboreal lichens in a dry Douglas-fir forest of southern British Columbia** André Arsenault, Natural Resources Canada	**Engineering Tolerance to Multiple Fungal Pathogens in *Brassica napus* canola** Nat Kav, University of Alberta	9:15–9:35 **Inhibition of LDL oxidation *in vitro* and regulation of cholesterol metabolism in hamsters by apple skin bioactives** Surangi Thilakarathna, Vasantha Rupasinghe and Yanwen Wang, Nova Scotia Agricultural College

9:30-9:45		**Crop adaptation to abiotic stress** Invited speaker: Rosalind Bueckert, University of Saskatchewan	**Boreal forest moss-associated nitrogen fixation in a changing climate** John Markham, University of Manitoba	**Cytosolic NADPH-dependent glyoxylate reductase from Arabidopsis: crystal structure and kinetic characterization of active site mutants provide evidence for β-HAD family membership** Vikramjit Bajwa, University of Guelph	9:35-10 :00 **Latest research on health benefits of cranberry** Amy Howell, Rutgers University
9:45-10:00			**Sensitivity of green roof functioning to plant type and diversity** Jeremy Lundholm, Saint Mary's University	***In vitro* expression of transposase promotes reactivation of Ds transposons.** Surinder Singh, McGill University	
10:00-10:30	Nutrition Break				
Thursday, July 21					
Concurrent Session #8 10:30-12:00	**CSA/OACC (SB255)** Joint Session: **Organic and sustainable agriculture**	**CSA (SB265)** **2011 Borlaug Symposium Continues**	**CIFST/CSA (SB415)** Session : **Malting barley: progress from grain to glass**	**CBA-ABC (SB260)** **Mycology section**	**CSPP (SB201)** General Session: **Breeding and production**
Session Chair	Derek Lynch, Nova Scotia Agricultural College	Gavin Humphreys, Agriculture and Agri-Food Canada, Winnipeg	Alex Speers, Dalhousie University	Hugues Massicotte, University of Northern British Columbia	Gale Bozzo, University of Guelph

10:30-10:45	**The effects of pea, faba bean and lupin on two years of subsequent crops** Jane King, University of Alberta	**The implication of climate change for the Canadian seed industry** Invited speaker: Todd Hyra, SeCan, Morden, MB	10:30-10:55 **Developing brewing value selection tools for malting barley breeding** Invited speaker: Brian Rossnagel. University of Saskatchewan	**Weresub Memorial Lecture:** **"Research on aquatic hyphomycetes in a changing world".** Invited speaker: Felix Baerlocher, Mount Allison University	**Sequencing the bean genome: the applied bean genomics and bioproducts project** Gregory Perry, University of Guelph
10:45-11:00	**Measuring botanical diversity and adaptation in pastures** Julien Winter, Cobourg, ON				**Quantitative trait loci for water-use efficiency in barley (*Hordeum vulgare* L.) under rain-fed conditions on the Canadian Prairies** Anthony Anyia, 2 Alberta Innovates - Technology Futures
11:00-11:15	**Active ingredient analysis in *in vitro* propagation and conservation of selected Himalayan medicinal herbs for sustainable utilization and conservation** Shyamal Nandi, Plant Institute of Himalayan Environment and Development, India	**Role of plant breeding in adaptation of plants to the changing environment – canola model** Invited speaker: Igor Falak, Pioneer Hi-Bred Production LP, Caledon, ON	10:55-11:15 **Association mapping of malting quality traits in barley** Invited speaker: Aaron Beattie, University of Saskatchewan		**Identification and quantification of anthocyanins and flavonols in saskatoon fruits (*Amelanchier alnifolia* Nutt.) during development and at maturity** Jocelyn Ozga, University of Alberta
11:15-11:30	**Phosphorus availability in organic dairy farm soils: a closer look at the role of soil biology** Paul Voroney, University of Guelph		11:15-11:35 **Starch degrading enzymes and their role in brewing fermentation** Invited speaker: Michael J. Edney, Canadian Grain Commission, Winnipeg		**Is glutamate decarboxylase-derived γ-aminobutyrate involved in physiological disorders of apples during controlled atmosphere storage** Chris Trobacher, University of Guelph

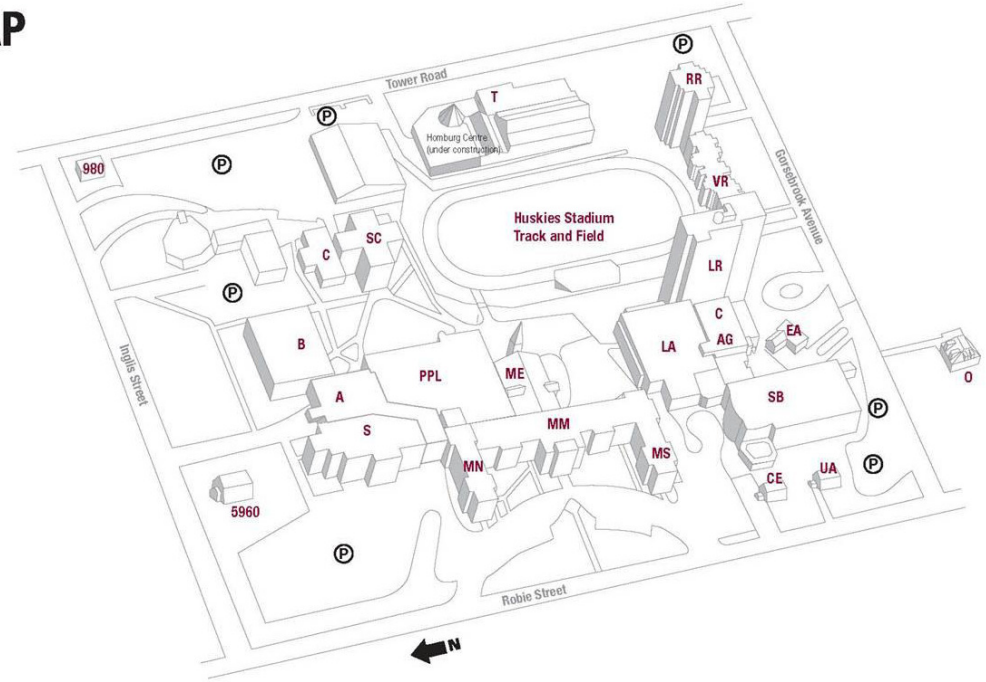
11:30-11:45	**Fertility management for organic cereal production** Andrew Hammermeister, Organic Agriculture Centre of Canada, Nova Scotia Agricultural College	**Recent advances in the development of crop cultivar for adaptation to changing environmental conditions** Invited speaker: Yousef Papadopoulos, Agriculture and Agri-Food Canada, Truro	11:35-11:55 **The influence of malting barley on beer fermentability** Invited speaker: Alex Speers, Dalhousie University		**SPAD chlorophyll meter as a decision-making tool to optimize recoverable white sugar in sugarbeet production** Jessica Turnbull, University of Guelph
11:45-12:00	**Crop productivity and nitrogen dynamics under extended organic vegetable rotations** Derek Lynch, Nova Scotia Agricultural College				
12:00 -12:15	**President's Awards- presentations for best CSPP student poster and talk** (SB201)				
12:15-13:30	**Society Executive Meetings** **CSHS** (SB415), **CBA** (SB260), **CSPP** (SB201)				
12:15-18:30	**Post Conference Tour of NSAC –** need to pre-register, bag lunch provided				

Conference Maps

CAMPUS MAP

SAINT MARY'S UNIVERSITY SINCE 1802

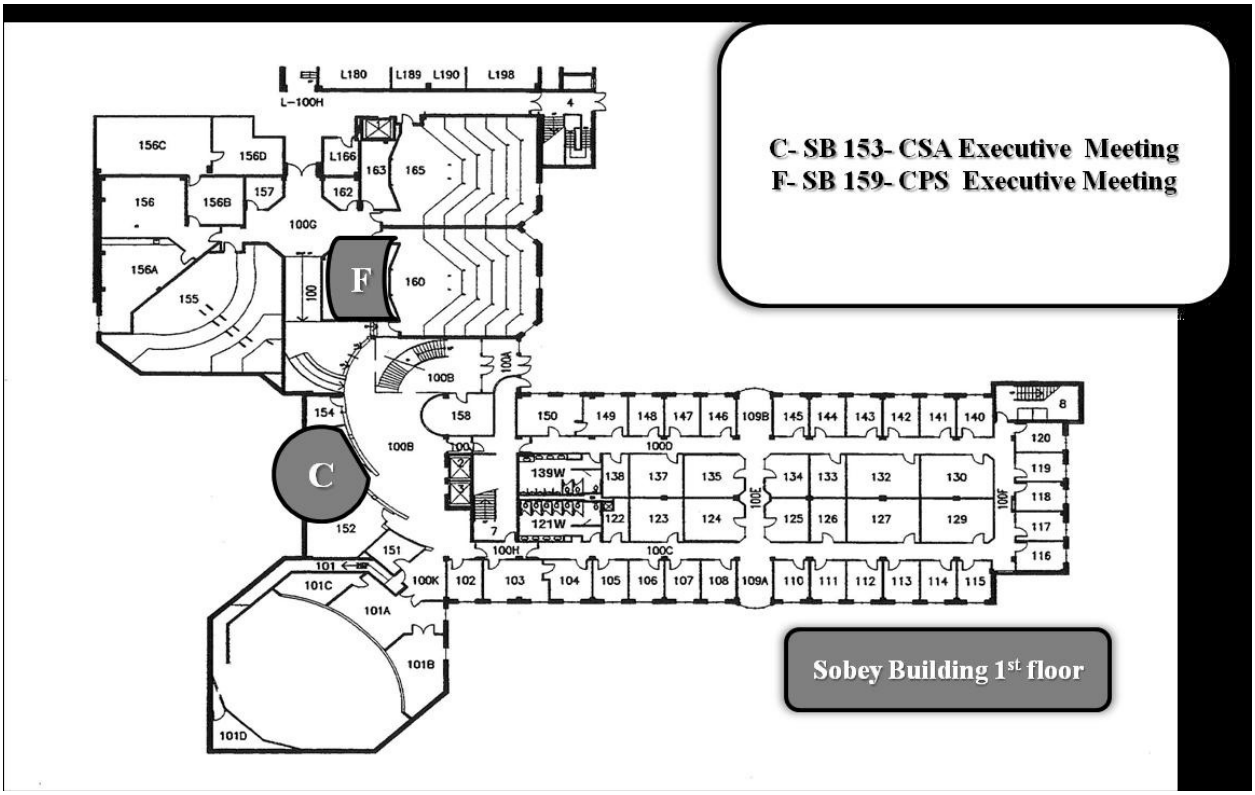
One University. One World. Yours.

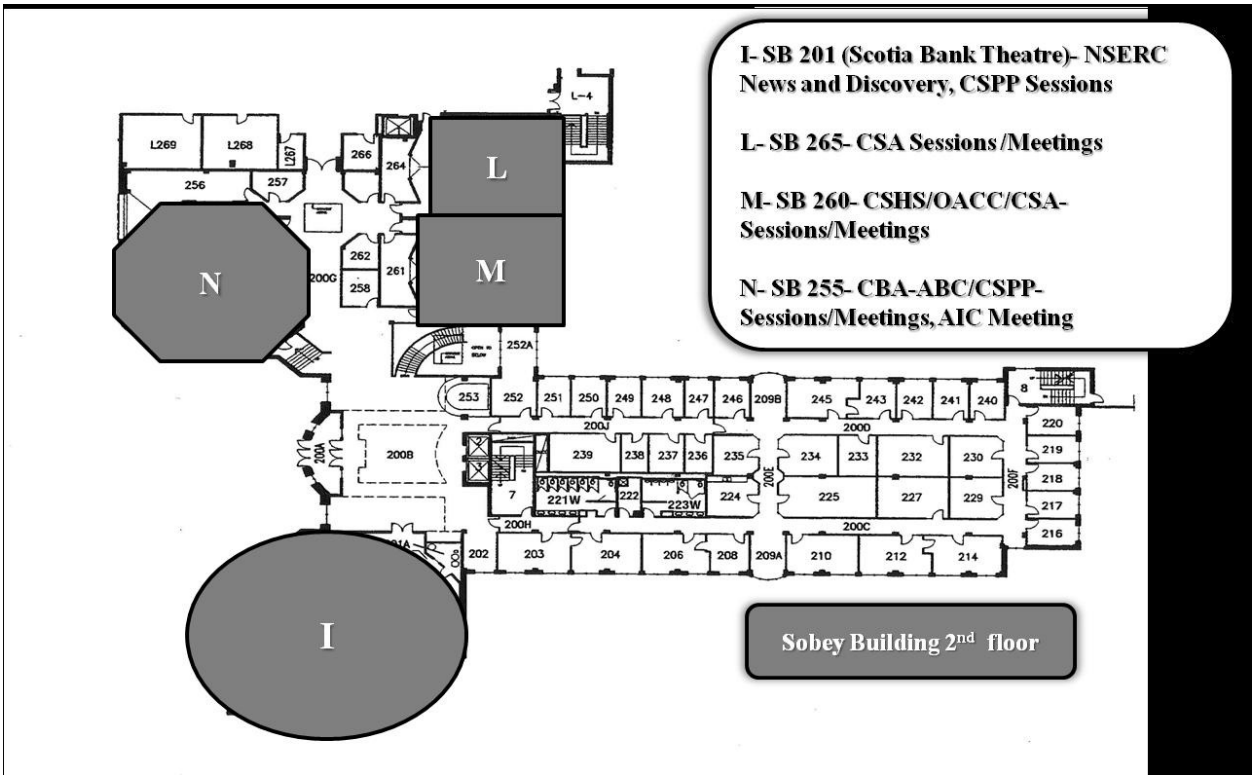


A	Atrium	**LA**	Loyola Academic Complex	Ⓟ	Parking	**T**	The Tower
AA	Alumni Arena	**LR**	Loyola Residence	**PPL**	Patrick Power Library	**UA**	Development/Alumni
AG	Art Gallery	**ME**	McNally East Wing	**RR**	Rice Residence	**VR**	Vanier Residence
B	Burke Building	**MM**	McNally Main	**S**	Science Building	**980**	TESL Centre
C	Cafeteria	**MN**	McNally North Wing	**SB**	Sobey Building	**5960**	Gorsebrook Research Institute for Atlantic Canada Studies/ CN Centre for Occupational Health & Safety
CE	Continuing Education	**MS**	McNally South Wing	**SC**	O'Donnell Hennessey Student Centre		
EA	External Affairs	**O**	The Oaks/International Activities				

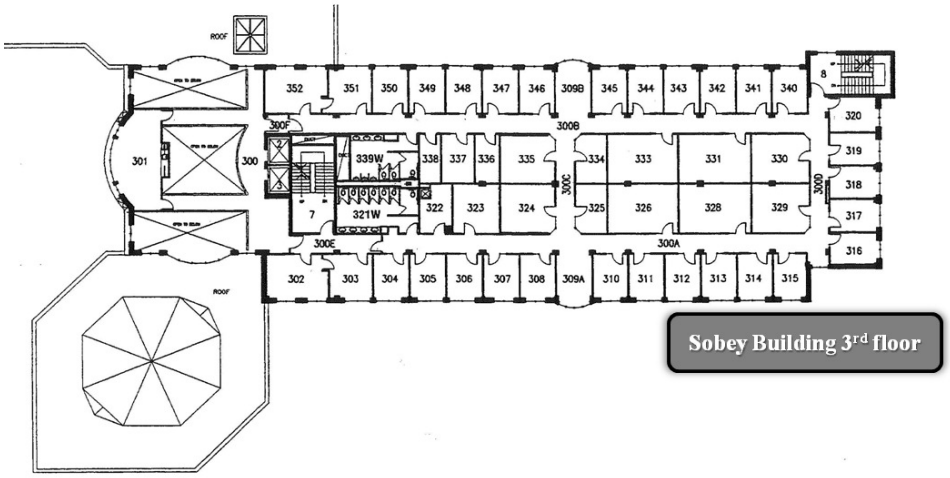
All main buildings are wheelchair accessible and most are connected by tunnels or walkways.

Conference Maps

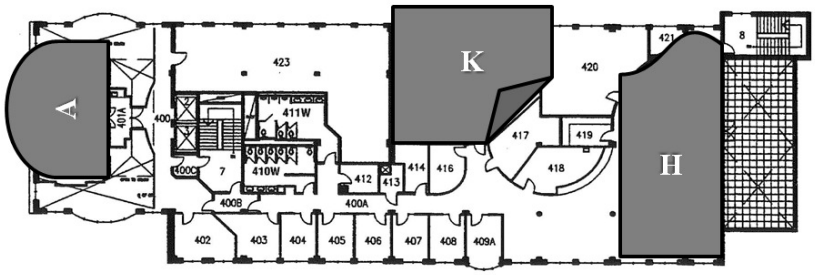




Conference Maps



Sobey Building 3rd floor



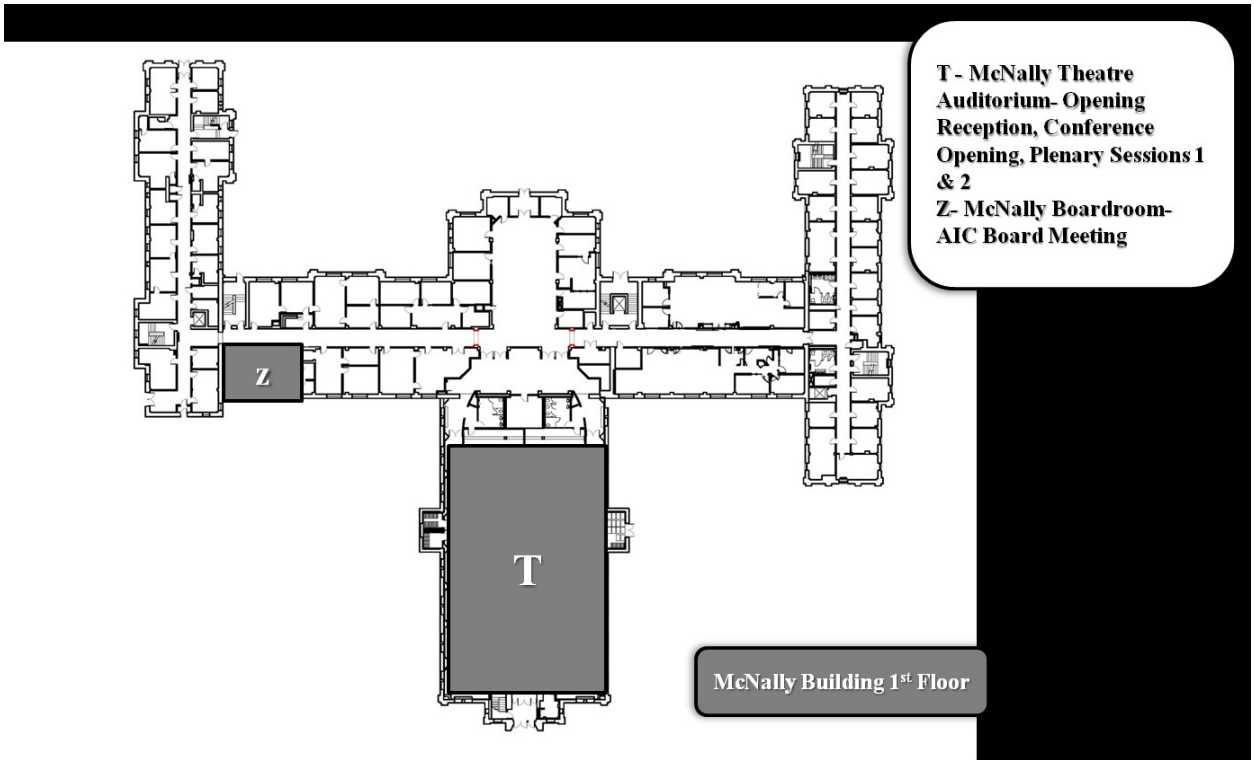
Sobey Building 4th floor

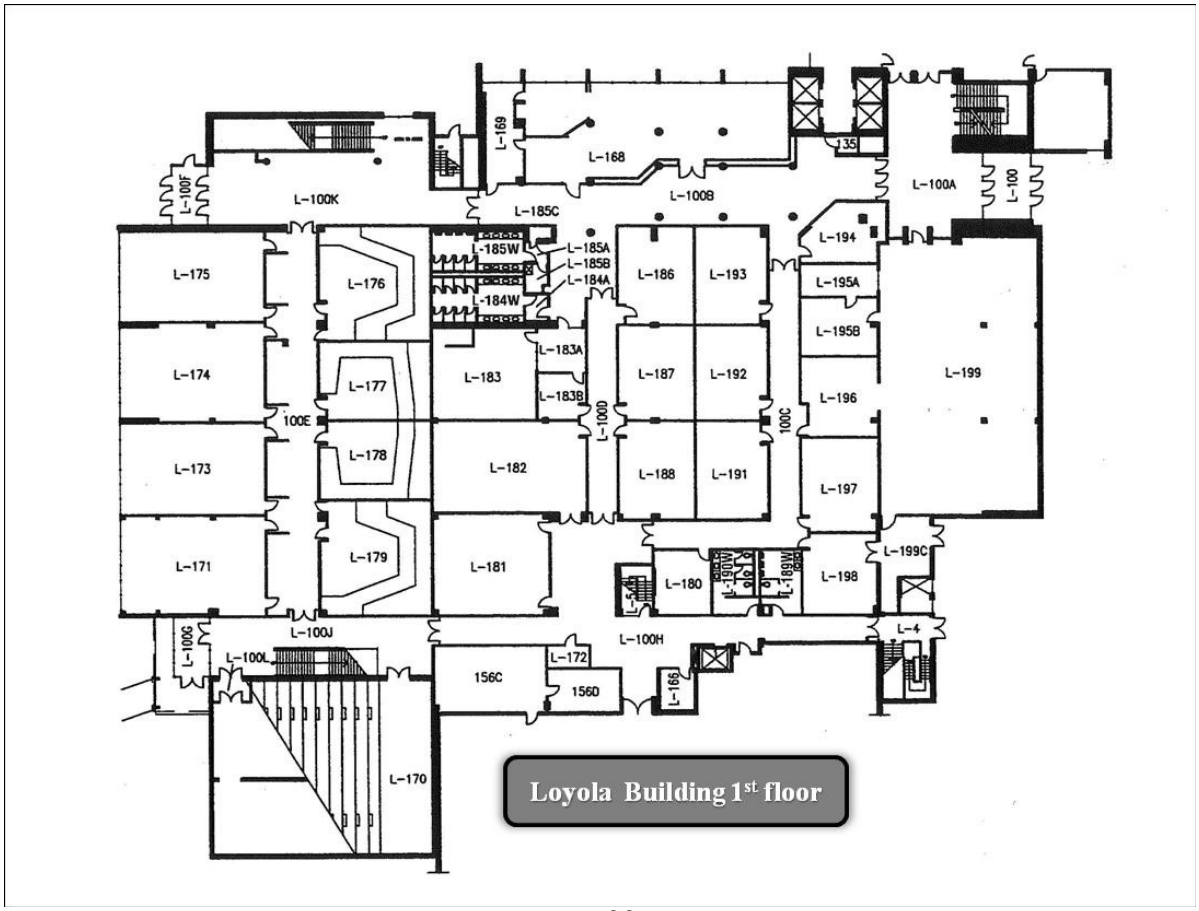
A- Secunda Boardroom- Meetings- CPS (Financial Advisory, Incoming & Outgoing) , CBA-ABC Mycology Section, AIC Executive

K- SB 415- CBA-ABC Ecology Section Meeting, CPS CIFST/CSA Sessions

H- SB 422- Graduate Student Hospitality Room & NSERC Information Session

Conference Maps





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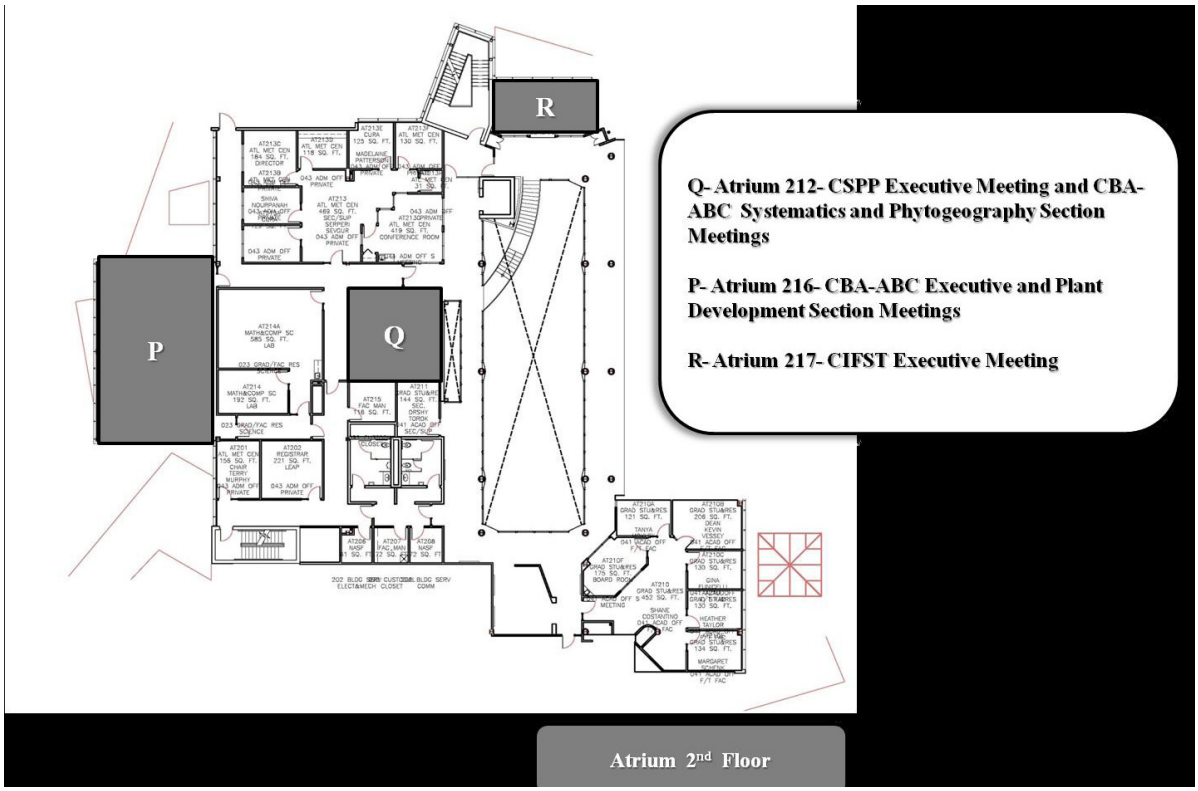
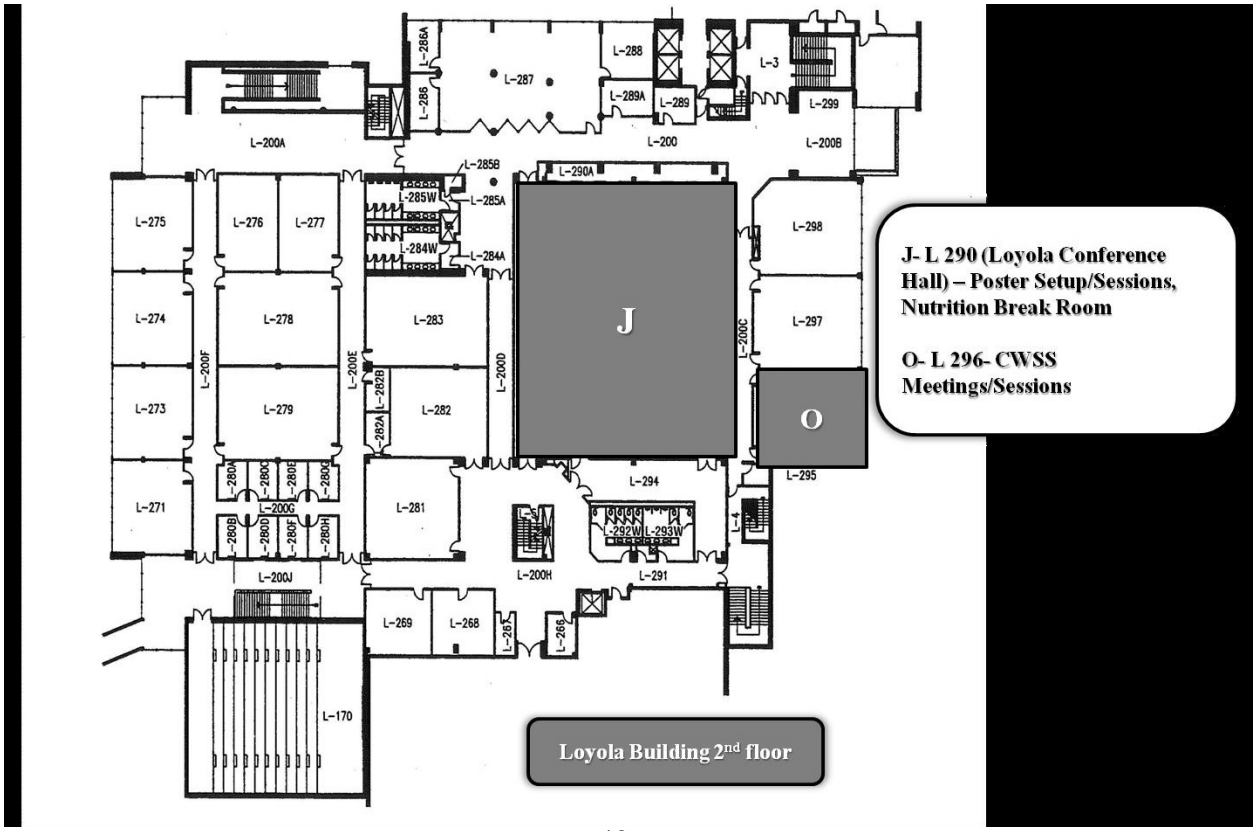
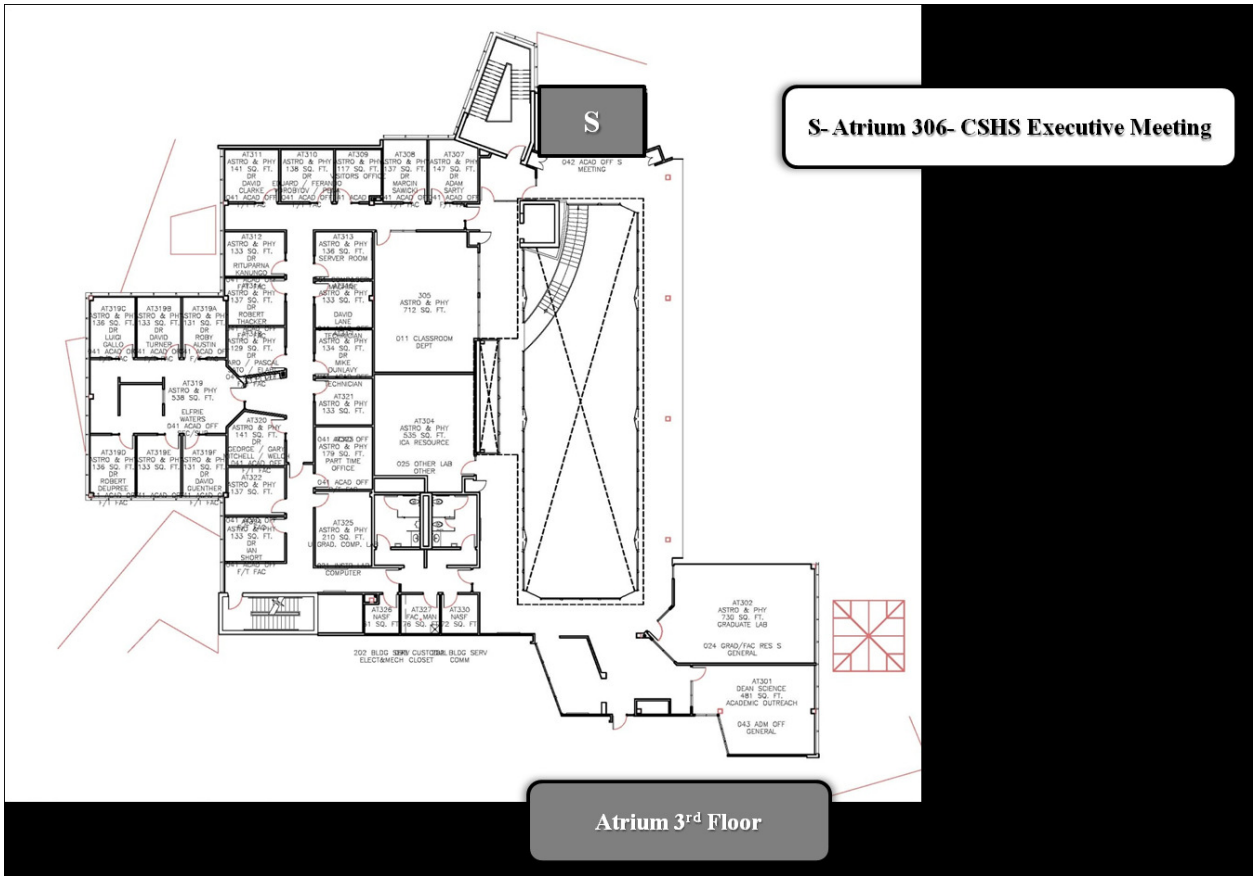




Conference Maps



Conference Opening Ceremony

Monday, July 18, 2011
0745h

McNally Theatre Auditorium
McNally Building

Honourable John MacDonell
Minister of Agriculture
Minister of Service Nova Scotia and Municipal Relations
Province of Nova Scotia

Dr. Shahrokh Khanizadeh
President
Plant Canada

Dr. J. Colin Dodds
President
Saint Mary's University

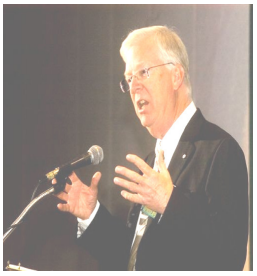
Monday, July 18, 2011 **Plenary Session**

Chair: Dr. Paul T. LaFleche
Deputy Minister of Agriculture

Time: 0830-1000
Room: McNally Theatre Aud.

0830-0915

What's With the Weather?



Dr. David Phillips
Senior Climatologist
Envirnonment Canada

People all over are asking: What's happening to the weather? It's almost as if extreme weather has become the norm - an epidemic of ferocious, killer, catastrophic weather everywhere. Further, the seasons seem to be out of whack, certainly not what our teachers and parents told us it would be like. Is the global climate going through unprecedented change? Is our weather becoming more extreme? And, if so, are people responsible or is it external forces? Or both? Some experts suggest that we may be witnessing the beginning of a profound climate change and bad weather may be proof of an overheated, out-of-control planet. There is so much we don't know about the Earth's climate system. But what has become clear is that the planet is warming and the number of weather-related disasters is on the rise. We can no longer assume that conditions in the past will apply in the future. Coping with more variable and uncertain weather will take more ingenuity and adaptability – something Canadians are good at. We also should expect more accurate, timely and credible long-lead weather forecasts.

0915-1000

Climate Change Impacts on Crop Production in Canada:
Are We Heading Up or Down?

Dr. Paul Bullock
Department of Soil Science
University of Manitoba

Climate change has been cited as a concern for future crop production but in Canada there are also some potential benefits. Do the positive impacts of climate change on crop productivity outweigh the negative impacts? Are secondary impacts of climate change more important? Is the weak link in our predictions related to our limited understanding of the interactions of all these effects? This presentation will focus on the current state of our knowledge to help us identify the gaps and better answer these critical questions.

Monday, July 18, 2011
Canadian Society of Agronomy
Session 1: ***Climate Change in Agriculture***

Oral Presentations
Time: 1030-1200h
Room: 265 Sobey Building

Chair: Dr. Richard Donald
Nova Scotia Agricutural College

1030 **Chandra Madramootoo**
McGill University, Montreal, Quebec
Water resources and climate change

1115 **Robert Hijmans**
University of California, Davis, USA
Plant biodiversity and climate change in agricultural landscapes

1030 **Chandra A. Madramootoo**
Water resources and climate change

The work of several researchers, much of which culminated in the 2008 report of the Intergovernmental Panel on Climate Change (IPCC) has pointed to the fact that precipitation intensity and variability are likely to increase the risk of flooding and droughts in several areas. While annual river runoff and water availability are expected to increase at higher altitudes, and in some wet tropical regions, many arid and semi arid areas are expected to witness increasing drought and higher temperatures. Flooding of major crop producing areas such as Australia, Pakistan, and the mid west US will lead to a reduction in the cultivation of major cereals and grains, and thus reduced food availability in both national and international markets. Of equally worrying concern are the projected droughts in regions such as Sub Saharan Africa, the Western US, and the Mediterranean Basin. Lower rainfalls and water shortages are projected in these regions. Prolonged droughts will put even more stress on limited water supplies and will increase the competition for water among all economic and environmental uses. The above impacts and severity of floods and droughts, of unprecedented magnitude, are already putting a strain on the infrastructure that is in place to cope with such disasters. It is anticipated that billions of dollars will have to be spent to upgrade water infrastructure, to cope with floods and droughts. Increased risks of both floods and droughts in many parts of the world will have an impact on food production, since both climatic extremes will limit the full potential of our food producing lands. Such impacts will force those involved in water for food production to explore methods of water management which conserve water, as well as mitigate flood damages. With irrigated agriculture producing some 40% of the world's food, and the need to double food production by the year 2050, there is going to be severe competition for limited water supplies. New irrigation techniques which make better use of advanced soil water monitoring, management and application technologies will therefore need to be developed, if food security is to be achieved. What is not as readily evident is how to flood proof, in a cost effective manner, low lying coastal and riverain food producing lands.

1115 **Robert J. Hijmans**
Plant biodiversity and climate change in agricultural landscapes

Over the past 75 years, there has been an extraordinary and steady increase in crop productivity. It has been predicted that this trend will change because of climate change, unless major research and development efforts are put in place. The use of wild and cultivated plant biodiversity for crop improvement is a key adaptation strategy. I will discuss where and what adaptation is most needed, and where crop improvement is likely to be successful based on what we know about plant physiology, past varietal change, and the management of agricultural biodiversity by farmers. I will also speak about the potential repercussions of failing to maintain stable growth in agricultural productivity for the conservation of wild and cultivated plants.

Monday, July 18, 2011 **Oral Presentations**
Canadian Society of Agronomy **Time:** 1300 – 1500h
Session 2: ***Nutrient Management*** **Room**: 265 Sobey Building

Chair: Dr. Shabtai Bittman
Agriculture & Agri-Food Canada, Agassiz

1300 **Panchali Katulanda**
Soybean symbiotic nitrogen fixation responses in relation to Bradyrhizobium inoculation and nitrogen use in dykeland

1315 **Melissa Arcand**
Belowground partitioning of nitrogen in field pea and canola

1330 **Malinda Thilakarathna**
Characterization of nitrogen transfer from diverse red clover populations to companion bluegrass and impact on soil nitrogen dynamics under field conditions

1345 **Newton Lupwayi**
Nitrogen released from legume crop residues during two succeeding non-legume crops

1400 **Tom Bruulsema**
Nitrous oxide emissions from crop nitrogen applications in Eastern Canada

1415 **Tarlok Sahota**
Comparative performance of urea and ESN in winter wheat in northern Ontario

1430 **Stephen Guy**
Winter wheat response to nitrogen fertilizer rate and application: A conventional and no tillage comparison

1445 **Mehdi Sharifi**
Wood ash assessment for use in agriculture

1300 **Soybean symbiotic nitrogen fixation responses in relation to *Bradyrhizobium* inoculation and nitrogen use in dykeland.** P. Katulanda[1*], H. Li[1] and S. Asiedu[1] [1]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, PO Box 550, Truro, NS, B2N 5E3

Soybean is a major crop grown on dykeland, yet it is not known about the soybean symbiotic nitrogen fixation performance on this unique, important land resource covering 18,000 ha areas in Nova Scotia. The objectives of this study were to examine the influence of *Bradyrhizobium* inoculation and starter N inputs on soybean symbiotic N fixation to improve soybean grain yield. A 2-site study was conducted in Habitant marsh and Wellington marsh in 2010. The treatments consisted of four rates of *B. japonicum* inoculants at 0, 1.5, 3 and 4.5 g kg^{-1}seeds (IR_0, $IR_{1.5}$, IR_3 and $IR_{4.5}$) and four rates of starter N fertilizers at 0, 10, 20, and 30 kg ha^{-1} (N_0, N_{10}, N_{20} and N_{30}), arranged with three replications in a split plot design. A genetically modified, Round-up ready soybean cultivar 'Lynx' was used in the study. The symbiotic N fixation was estimated using relative abundance of ureide-N concentrations. The inoculated plants showed significantly higher plant biomass ($P < 0.0178$), nodule number ($P < 0.0219$) and nodule weight ($P<0.0076$) than the control plants. The relative ureide-N ratio (4× Ureide-N/ (4×ureide-N+ NO3-N) ×100) were significantly higher in $IR_{4.5}$ and IR_3 (mean 50%) than in $IR_{1.5}$ and IR_0 (mean 32%) ($P<0.0316$). The daily N fixation rates during seed filling stage were 4, 3.7, 3 and 1.8 kg $ha^{-1}d^{-1}$, respectively, for the treatment $IR_{4.5}$, IR_3, $IR_{1.5}$ and IR_0. These daily N fixation rates resulted in the significant difference in cumulative N fixation among $IR_{4.5}$ (141 kg ha^{-1}), IR_3 (131 kg ha^{-1}), $IR_{1.5}$ (110 kg ha^{-1}) and IR_0 (64 kg ha^{-1}) (LSD = 64 kg ha^{-1}, $\alpha = 0.05$). The soybean grain yields were significantly higher in $IR_{4.5}$ (3666 kg ha^{-1}), IR_3 (3404 kg ha^{-1}), $IR_{1.5}$ (3164 kg ha^{-1}) compared to the IR_0 (2420 kg ha^{-1}) (LSD = 637 kg ha^{-1}, $\alpha = 0.05$). There was no significance effect from starter N application on soybean daily N absorption or grain yields. It was suggested that by increasing the rate of *Bradyrhizobium* inoculant rate (by 150% of the standard rate) could stimulate soybean symbiotic N fixation in dykeland, to improve grain yield.

1315 **Below ground partitioning of nitrogen in field pea and canola**. M. M. Arcand[1*], J. D. Knight, and R. E. Farrell. [1]Department of Soil Science, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8

The diversity of traditional cereal-based crop rotations in the Canadian prairies has increased with the inclusion of pulse and oilseed crops. Differences in quality and quantity of the residues that remain in the soil following harvest of these diverse crop species may have implications for subsequent nutrient cycling. Currently, belowground inputs of N are not adequately estimated due to difficulties in recovering roots from soil and accounting for rhizodeposition during crop growth. The purpose of this study was to quantify the partitioning of plant nitrogen in roots and rhizodeposits of field pea and canola in a controlled environment using the cotton-wick ^{15}N labelling technique. ^{15}N-enriched urea was introduced into the stem of canola and field pea plants in small pulses over a 5-week period beginning at 21 days after planting. Plants were harvested at physiological maturity and the above and belowground plant material and bulk and rhizosphere soil were analyzed for N content and ^{15}N using isotope ratio mass spectrometry. A higher proportion of the recovered ^{15}N was found in belowground components (roots, in particular) of canola compared to pea. However, a much higher proportion of ^{15}N was found in pea grain (79%) relative to canola (53%). Total N was greater for pea than for canola on a per plant basis and a higher proportion of N was allocated to grain. As a result, only about 5% of total plant N remained belowground following harvest of pea, while 20% of canola residue-N remained in the

soil. The relative distribution of belowground N as roots and rhizodeposits will also be presented and implications for N cycling will be discussed.

1330 **Characterization of nitorgen transfer from diverse red clover popoulations to companion bluegrass and impact on soil nitrogen dynamics under field conditions.** R. M. M. S. Thilakarathna[1*], Y. A. Papadopoulos[2], A. V. Rodd[3], S. A. E. Filmore[4], A. N. Gunawardena[1] and B. Prithiviraj[5]. [1]Department of Biology, Life Science Centre, Dalhousie University, 1355 Oxford Street, Halifax NS B3H 4J1 Canada; [2]Agriculture and Agri-Food Canada, Nova Scotia Agricultural College, PO Box 550, Truro, NS, Canada B2N 5E3; [3]Agriculture & Agri-Food Canada, 4016 Highway 302, Nappan, NS, Canada B0L 1C0; [4]Agriculture & Agri-Food Canada, 32 Main Street, Kentville, NS, Canada B4N 1J5; [5]Nova Scotia Agricultural College, PO Box 550, Truro, NS, Canada B2N 5E3

Research into the dynamics of nitrogen flow between legume and companion grasses may provide a management strategy for developing efficient cycling of nitrogen (N) and reduce losses of this essential nutrient in crop production systems. In the current study the ability of two diverse red clover (*Trifolium pratense* L.) cultivars ('AC Christie' - diploid and 'Tempus' - tetraploid) to transfer fixed nitrogen and the impact of these cultivars on soil nitrogen dynamics were evaluated under field conditions. Plants from each cultivar were transplanted into an established bluegrass (*Poa pratensis* L.) stand in 2008. Samples were collected from three harvests during the 2009 growing season and nitrogen transfer from the red clover cultivars to companion bluegrass was measured using the isotope dilution technique and natural abundance methods. Soil samples and soil water samples were also collected to evaluate cultivar effects on soil N dynamics. Both the red clover cultivars were shown to have high N fixing capacity across three harvests and more than 90% of the clover nitrogen was derived from biological N fixation. The proportions of bluegrass N derived from N transfer were 7, 11 and 26 % with respect to the first, second and third harvests. The soil N associated with the two red clover cultivar rhizospheres was different from each other during the growing season. In this field study the soil extractable nitrate concentration of the red clover rhizosphere was consistently higher than ammonium concentration. Soil nitrate content with 'Tempus' increased as the growing season progressed. Soil extractable nitrate of the 'Tempus' sward was higher than the 'AC Christie' stand in the top 15 cm of soil as well as at the 15-30 cm zone. The soil water nitrate content associated with the 'AC Christie' sward increased periodically but remained constant throughout the growing period for 'Tempus' which suggests that the dynamics of nitrogen cycling is distinctly different between the two cultivars. Therefore selection of appropriate legume-grass mixtures is important to increase N transfer while minimizing N leaching losses.

1345 **Nitrogen released from legume crop residues during two succeeding non-legume crops.** Newton Lupwayi[1*] and Yoong Soon[2]. Agriculture & Agri-Food Canada, [1]Box 3000, Lethbridge, Alberta, Canada T1J 4B (email: newton.lupwayin@agr.gc.ca) and [2]Box 29, Beaverlodge, Alberta, Canada T0H 0C0

We quantified N released from residues of two pea (*Pisum sativa* L.) varieties ('Camry' and '4010'), faba bean (*Vicia faba* L.) grown for seed, faba bean green manure (GM) and chickling vetch (*Lathyrus sativus* L.) GM during the first and second succeeding non-legume crops. The legumes were grown in 2007, and wheat (*Triticum aestivum* L.) and canola (*Brassica napus* L.) were grown in 2008 and 2009, respectively. The N contained in these residues at harvest was in the order: faba bean (154 kg N ha^{-1}) ≥ '4010' pea and chickling vetch GM (129 and 125 kg N ha^{-1}, respectively) ≥ faba bean GM (107 kg N ha^{-1}) > 'Camry' pea (65 kg N ha^{-1}). The average percentage of residue N released over time was: chickling vetch GM (74%) = faba bean GM (67%) > faba bean for seed (55%) > 'Camry' pea (42%) = '4010' pea (38%). The average

amounts of N released were: chickling vetch (96 kg N ha^{-1}) = faba bean for seed (83 kg N ha^{-1}) > faba bean GM (66 kg N ha^{-1}) > '4010' pea (49 kg N ha^{-1}) > 'Camry' pea (27 kg N ha^{-1}). At the last sampling time, faba bean GM residues had only 3% of their initial N remaining, chickling vetch GM 4%, '4010' pea 21%, 'Camry' pea 20%, and faba bean for seed 23%. Amounts of N that had been released by that time were 124 kg N ha^{-1} from chickling vetch residues, 118 kg N ha^{-1} from faba for seed, 104 kg N ha^{-1} from '4010' pea, and 53 kg N ha^{-1} from 'Camry' pea. The N release patterns over time were different. Green manure residues released about 80% of their N within two months of decomposition in 2007, i.e., before wheat was seeded in 2008. Faba bean grown for seed released about 50%, and pea residues released only about 20% of their N in the corresponding period. Green manure residues released the remaining N slowly thereafter, but the other residues released N at a faster rate when wheat and canola were grown in 2008 and 2009, respectively.

1400 **Nitrous oxide emissions from crop nitrogen applications in Eastern Canada.** T.W. Bruulsema[1*], O. Bergeron[2], P. Rochette[2], and B.J. Zebarth[3]. [1]International Plant Nutrition Institute, Guelph, ON N1G 1L8; [23]Agriculture and Agri-Food Canada — [2]Ste-Foy, QC; — [3]Fredericton, NB

Nitrogen fertilizer use has been shown to increase emissions of nitrous oxide, a gas implicated in climate change and stratospheric ozone depletion. However, continued nitrogen inputs are also essential for supporting foreseeable demand for agricultural crops. Management practices that reduce emissions while supporting increased yields need to be specified in protocols to qualify as offsets in carbon trading schemes, and as ecological goods and services. We used several approaches, including meta-analysis, to draw conclusions from the largest possible dataset from Eastern Canadian studies in which nitrous oxide emissions were measured in response to application of nitrogen fertilizer. The objective was to identify specific effects of source, rate, timing and placement on emissions per unit land area and per unit of crop yield. The findings are to be incorporated into the recently-approved Nitrous Oxide Emission Reduction Protocol, to meet the required standards for scientific backing of coefficients and methodology used in existing and anticipated regulatory mechanisms facilitating the trading of carbon credits.

1415 **Comparative performance of urea and ESN in winter wheat in Northern Ontario.** T. S. Sahota*[1], J. Rowsell[2], H. Dhillon[1] and J. Kobler[2*1] Thunder Bay Agricultural Research Station, 435 James St. S, Thunder Bay, Ontario, Canada P7E 6S7 (e-mail: tarloksahota@tbaytel.net), [2]New Liskeard Agricultural Research Station, University of Guelph, Armstrong St., New Liskeard, Ontario, Canada, P0J 1P0

Field experiments were conducted at Thunder Bay (2007-2010) and New Liskeard (2006-2009) to study comparative performance of urea and ESN in winter wheat. Treatments included zero N, and urea and ESN (Environmentally Smart Nitrogen, Agrium Inc.'s brand name for polymer coated urea) each @ 40, 80 and 120 kg ha^{-1} at both the locations. Interactions between the sources and rates of N were not significant. Averaged over years, application of urea @ 120 kg N ha^{-1} increased grain yield of winter wheat by > 500 kg ha^{-1} as compared to no N at Thunder Bay, where increase in grain yield by ESN @ 120 kg N ha^{-1} was ~370 kg ha^{-1}. Urea produced slightly higher grain yield than ESN at Thunder Bay, but the reverse was true at New Liskeard. The yield differences were however non significant. Straw yield followed a trend similar to the grain yield. Grain protein content with the two fertilizers matched closely at all rates of N, though increased with increasing rates of N, especially at Thunder Bay. Post harvest Nitrate N, ammoniacal N and total mineral N, at all soil depths (0-30, 30-60 and 60-90 cm) was only marginally higher with ESN than with urea at Thunder Bay; the reverse was true for New Liskeard where amounts of residual N were higher than Thunder Bay. Profile distribution of total mineral N was 52 %, 24 %

and 24 % in 0-30, 30-60 and 60-90 cm at Thunder Bay. Corresponding figures for New Liskeard were 43.5 %, 29.7 % and 26.8 %, respectively.

1430 **Winter wheat response to nitrogen fertilizer rate and application: A conventional and no tillage comparison.** S. O. Guy* and M. A. Lauver, Department of Crop and Soil Sciences, Washington State University, Pullman, Washington, USA 99164-6420 sguy@wsu.edu

No tillage (NT) systems versus conventional tillage (CT) systems can influence nitrogen availability due to lower soil temperature, higher residue, higher organic matter, higher biological activity, higher water availability, and plant growth differences. Nitrogen fertility is critical for hard red winter wheat (HRWW) production, protein level, quality, and value. This study near Genesee, Idaho, USA evaluated nitrogen fertilizer rates: 56, 84, 112, 140, 168, and 197 kg ha^{-1} and factorial application timings: 100% fall, 70% fall + 30% spring, and 60% fall + 25% spring + 15% foliar at anthesis in a NT and CT comparison. HRWW 'Boundary' followed dry pea in a three year rotation with spring wheat before pea. Between NT and CT, HRWW grain yields responded to N rates differently year to year, but were not different over years 2006-2010 averaging 5,175 kg ha^{-1}. Across years, optimum nitrogen fertilizer rates were 140 kg ha^{-1} producing 5339 kg ha^{-1} of grain in CT and 168 kg ha^{-1} producing 5493 kg ha^{-1} of grain in NT. Grain protein averaged 0.7% lower in NT than CT. Protein versus N rate regression shows protein increased at 0.122% per 10 kg ha^{-1} N in CT and 0.110% per 10 kg ha^{-1} N in NT. Protein regressions were not different in slope but were different in level between tillage treatments. Both grain density and seed weights were higher in NT than CT, decreased with N rate, and regressions were different in level but not slope. Split N applications only produced slightly higher grain density, seed weight and harvest index, but did not significantly influence other characteristics. There were more heads in NT, 656 m^{-2}, than in CT, 603 m^{-2}. Equivalent yields, higher test weights and seed weights, but lower protein show the benefits and drawbacks of HRWW in NT. Because of lower protein value, soft white winter wheat may be preferred in NT.

1445 **Wood ash assessment for use in agriculture.** M. Sharifi[1*], K. Mahoney[1] and L. Leblanc[2]. [1]Dept. of Environmental Science, Nova Scotia Agricultural College, Truro, Nova Scotia (msharifi@nsac.ca); and [2]LP Consulting Ltd., Windsor, Nova Scotia

More than 40,000t of wood ash is produced as a by-product of energy production each year in Atlantic Canada for which there is no readily available recycling outlet. Increased disposal costs caused by stricter environmental regulations and a shift towards sustainability have increased interest in using wood ash as soil amendment in agriculture. In this study, three wood ash sources in Atlantic Canada were (i) evaluated for their liming potential and reaction time, and (ii) evaluated as soil amendment to improve soil fertility. The liming potential of the ash sources was evaluated through soil incubation. Two acidic soils, with contrasting organic matter content and cation exchange capacity were amended with wood ash and commercial (Mosher & Antigonish) lime. Annual ryegrass was grown in a randomized and replicated greenhouse study to determine the fertility value of wood ash at different application rates. Treatments included control (no ash or fertilizer), synthetic fertilizers based on soil test recommendations (F), JD Irving (6, 12, 25 t/ha wet weight; DW=71%), NewPage (15, 29, 58 t/ha wet weight; DW=67%), and Brooklyn Power (7, 14, 29 t/ha wet weight; DW=96%). The lowest wood ash rate was calculated to supply half of the recommended K fertilizer for the soil (47.5 kg K/ha) with the assumption that 40% of total K in wood ash will be readily available. Nitrogen fertilizer was applied to all treatments based on general reconditions for annual ryegrass (180 kg N/ha). Liming equivalency of wood ash relative to Mosher lime (ECCE=64) was 2.4, 3.5 and 4.6 for Brooklyn, JD Irving and New Page ash after 11-wk incubation at 25°C and ~70% water-filled pore space (WFPS) moisture. All liming agents reacted within a week of application. Total dry biomass was significantly increased ($p \leq 0.001$) in

all amended treatments compared with control, by up to 300%, and was not different from fertilizer treatment. Up to 80% of total K in wood ash was plant available. Maximum allowable metal concentrations and accumulations in 45 years should be taken into consideration when wood ash is recommended for use in agriculture.

Monday, July 18, 2011
Canadian Society of Agronomy
Session 3: ***Cropping Systems***

Oral Presentations
Time: 1530 – 1700h
Room: 265 Sobey Building

Chair: Mr. Rigas Karamanos
Viterra, Calgary, Alberta

1530 **Martina Strömvik**
An in silico study of the genes for the isoflavonoid pathway enzymes in soybean reveals novel expressed homologues

1600 **Konstantinos Aliferis**
Assessment of the environmental risks of genetically modified canola applying GC/MS metabolomics

1615 **Clare Sullivan**
Examining reduced tillage in organic cropping systems

1630 **Diane Knight**
Frequency of field pea in long-term rotations impacts biological nitrogen fixation

1645 **Yantai Gan**
Carbon footprint of durum wheat is reduced through diversification of cropping systems

1530 **An in silico study of the genes for the isoflavonoid pathway enzymes in soybean reveals novel expressed homologues**. J. M. Livingstone, P. Seguin and M.V. Stromvik*. Department of Plant Science, McGill University, 21111 Lakeshore Road, Sainte-Anne- de-Bellevue, Quebec, Canada H9X 3V9 (e-mail: martina.stromvik@mcgill.ca)

Soybean [*Glycine max* (L.) Merr.], like most major crop plants, is an ancient polyploid. The soybean genome (2n=40, 975 Mb) was recently sequenced, which opened a wealth of information for genetic approaches to soybean improvement. Important genes can be located and the exact copy number can be identified. However, many predicted protein coding genes may in fact be non-functional pseudogenes, and evidence of expression is a crucial addition to genome sequence. Currently over a million (redundant) expressed sequence tags, (ESTs) from various tissues of soybean are available in public databases. These provide proof of gene expression with the benefit of also being sequence data, and they can therefore be computationally matched to the genome. An important group of genes in soybean is the enzymes of the isoflavonoid pathway. The isoflavones (e.g. daidzein, genistein and glycitein) are used by soybean in protection, defense and microbe interactions and the nutraceutical industry claim that isoflavones have several health benefits. To gain a better understanding of the extent of the isoflavonoid pathway, we identified the suite of expressed gene copies for five key enzymes (i.e., chalcone isomerase, isoflavone synthase, 2-hydroxyisoflavanone dehydratase, isoflavanone-7-O-glycosyltransferase, and isoflavone-7-O- glucoside-6''-O-malonyltransferase) in the soybean genome using bioinformatics techniques. Known gene sequences for the five enzymes were used to retrieve EST sequences from public data. Contiguous sequences (contigs) were assembled from the ESTs to represent the specific expressed genes and were subsequently matched to the chromosome-based assembly of the soybean genome. Most of the genes identified were previously known from literature, however, a novel expressed gene copy for 2-hydroxyisoflavanone dehydratase and five novel expressed gene copies of isoflavone-7-O-glucosyltransferase were discovered. In addition, three non-expressed suspected pseudogenes for isoflavone-7-O-glucosyltransferase were also identified in the genome. *In silico* expression profiles were also generated for all the genes identified in the isoflavonoid pathway.

1600 **Assessment of the environmental risks of genetically-modified canola applying GC/MS metabolomics.** K.A. Aliferis*, J. Singh and S. Jabaji. Department of Plant Science, McGill University, 21111 Lakeshore Rd., Sainte-Anne-de-Bellevue, Quebec, H9X 3V9, Canada konstantinos.aliferis@mcgill.ca (K.A.Aliferis), jaswinder.singh@mcgill.ca (J. Singh) suha.jabaji@mcgill.ca (S. Jabaji)

Since the first introduction of genetically-modified (GM) crops resistant to herbicides in mid-'90s, a number of GM crop varieties resistant to non-selective herbicides such as glyphosate, glufosinate, and triazine have been developed. FAO and WHO have recognized the potential of metabolomics as a functional genomics tool for the risk assessment of GM plants and the estimation of unintended effects, and included metabolic profiling as a complementary methodology to the already existing ones. A challenging question that needs to be answered is whether the modified GM plant's genome causes changes in its metabolome that are potentially harmful to human and non-target rhizospheric and soil fauna. In our study, gas chromatography-mass spectrometry (GC/MS) metabolomics was applied to roots of five GM canola (*Brassica napus L.*) varieties carrying genes for resistance to glyphosate (EPSPS inhibitor), glufosinate (GS inhibitor), and imazethapyr (ALS inhibition). The metabolic profiles of roots were composed of

more than 120 primary and secondary metabolites, such as amino, carboxy and lipid acids, carbohydrates, and phytosterols. Root metabolomes were monitored following treatments with the corresponding herbicides and compared to that of non-treated plants. Results confirmed the resistance of the herbicidal biochemical targets to the phytotoxic compounds as no significant alterations were detected in components of the targeted biosynthetic pathways. Additionally, although no significant alterations were observed in root metabolic profiles following the application of herbicides, changes in the levels of individual metabolites such as carboxylic acids and phytosterols, should be further investigated in order to elucidate the effects to non-targeted soil microorganisms.

1615 **Examining reduced tillage in organic cropping systems.** C. Sullivan[1]*, J. D. Knight[1], and S. J. Shirtliffe[2]. [1]Department of Soil Science, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8 (email: clare.sulivan@usask.ca); and [2]Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8

Organic grain producers commonly rely on green manures to return essential nutrients to their cropping systems. However, concerns with the use of green manures on the semiarid prairies are depletion of soil moisture and potential negatives effects associated with excessive tillage. Legume green manures supplying high amounts of N and P, and management techniques optimizing nutrient cycling and soil moisture retention are needed for successful green manure use. The objective of a two-year field study conducted in Saskatoon and Vonda, SK was to find a compromise between reducing tillage and the necessity of using tillage to maintain profitable yields in organic agriculture. The study explored the effect of termination timing and method of field pea (*Pisum sativum*) on subsequent wheat (*Triticum aestivum*) yield. Field pea was terminated at early flower, late flower and budding of 2009 by either tillage, mowing or rolling. The roller-crimper kills green manures by crimping the stems, leaving a layer of mulch on the soil surface expected to reduce surface evaporation. Green manure N uptake and soil concentrations of NO_3^-, NH_4^+ and moisture content were recorded in 2009. Green manure N uptake was significantly lower at early flower, and tended to be highest when terminated at late flower. No consistent trend was detected for soil moisture, while fall inorganic N was significantly lower for tilled treatments. In 2010 spring wheat was planted on all of the treatment plots and a subsample analyzed for N uptake three times throughout the summer. Harvest yield, grain protein content, and wheat N uptake were measured, with no consistent temporal relationship detected. The results from this study suggest reduced tillage in the green manure termination year is possible without compromising wheat yield.

1630 **Frequency of pea in long-term rotations impacts biological nitrogen fixation**. J.D. Knight1*, J. Guerin2, and M. Sather1. 1 Department of Soil Science, University of Saskatchewan,Saskatoon, SK; 2 Centre de recherche sur les grains inc., Saint-Mathieu-de-Beloeil, QC

Established plots at the Agriculture-AgriFood Canada Research Station located at Scott, Saskatchewan enabled the evaluation of the frequency with which pea (*Pisum sativum* L.*)* is included in rotation on nitrogen (N) acquisition parameters, including biological nitrogen fixation (BNF). Rotations that included pea every year (continuous pea), every second year (pea-wheat), every third year (pea-canola-wheat) and every fourth year (canola-wheat-pea-wheat) were evaluated for BNF using the enriched isotope dilution technique. Wheat microplots were established within each pea plot to serve as non-nitrogen fixing reference crops. Nitrogen from BNF in the seed and straw of the crop were determined as well as total above-ground N and additional yield parameters and soil nutrient parameters. Including pea every year or every

second year in rotation reduced the amount of BNF in pea. The most BNF acquired by pea occurred in the three or four year rotation and always in a rotation that included canola. Whether the enhancement in BNF is due to increased diversity or is specific to canola in rotation is not known. Continuous cropping of pea resulted in drastically low BNF. Percent N derived from atmosphere in the continuous pea was 15% compared to an average of approximately 55% across all other rotations in all years. While initially this was thought to be attributed to diseases compromising the continuous pea rotation this was found not to be the case. Overall yields and N acquisition in the continuous pea were comparable to the other rotations.

1645 **Carbon footprint of durum wheat is reduced through diversification of cropping systems.** Y.T. Gan [1]*, C. Liang [2], X.Y. Wang[1] and B.G. McConkey [1]. [1]Agriculture and Agri-Food Canada Research Centre, Swift Current, SK, S9H 3X2, Canada; and [2] Environment Canada, Greenhouse Gas Emission Division, 200 Sacré-Coeur, Gatineau, Québec, K1A 0H3, Canada

Greenhouse gas emissions in agriculture can be mitigated through improved crop management. This study determined the carbon footprint of durum wheat (*Triticum turgidum* L.) produced in diverse cropping systems. Durum was preceded by different combinations of oilseed, pulse, and cereal crops at five site-years in southern Saskatchewan. Total greenhouse gas emissions from the decomposition of crop residues along with various production inputs were used for the estimation of carbon footprint. On average, emissions from the decomposition of crop straw and roots accounted for 25% of the total emissions, those from the production, transportation, storage, and delivery of fertilizers and pesticides to farm gates and their applications 43%, and emissions from farming operations 32%. Durum wheat preceded by an oilseed crop (*Brassica napus* or *Brassica juncea*) the previous year had carbon footprint of 0.33 kg CO_2eq kg^{-1} of grain, or 7% lower than durum in cereal-cereal-durum system. Durum preceded by a biological N-fixing crop (*Cicer arietinum* chickpea, *Lens culinaris* lentil, or *Pisum sativum* pea) the previous year lowered its carbon footprint by 17% compared with durum preceded by a cereal crop. Durum produced in a pulse-pulse-durum system had carbon footprint 0.27 kg CO_2eq kg^{-1} of grain, 34% lower than durum grown in cereal-cereal-durum systems. Diversifying cropping systems with oilseeds and biological N-fixers significantly lowered carbon footprint of durum wheat.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society of Agronomy **Time:** 0830-1000h
Session 4: ***Food, Fuel and Crop Adaptation*** **Room**: 265 Sobey Building

Chair: Mr. Malcolm Morrison
Agriculture & Agri-Food Canada, Ottawa

0830 **Rong Tsao**
Phytochemical antioxidants in healthy Canadian crops-the good, the better, & the best

0915 **Jonathan Lynch**
Roots of the second green revolution

0830 **Phytochemical antioxidants in healthy Canadian crops – the good, the better, & the best!**
Dr. Rong Tsao, Guelph Food Research Centre, Agriculture and Agri-Food Canada

Healthy lifestyle and good dietary habit can significantly lower the risk of many chronic diseases such as cancer, cardiovascular diseases and diabetes. While essential nutrients are important in maintaining good health, in recent years, non-essential components of plant foods, i.e. phytochemicals, have been recognised as playing significant roles in preventing chronic diseases, particularly those related to oxidative stress. In this presentation, I will discuss the antioxidant phytochemicals in several unique Canadian seed crops e.g., flax, soybean and oat, and anthocyanin-rich fruits and vegetables, and how antioxidant, anti-inflammatory and anti-cancer activities can be enhanced by optimising agronomic and food processing conditions.

0915 **Roots of the Second Green Revolution**
Dr. Jonathan Lynch, Plant Nutrition, Pennsylvania State University, PA, USA

Drought and low soil fertility are primary constraints to food production in poor nations. The ‘green revolution’ of intensive fertilizer use coupled with fertilizer-responsive varieties has not reached the poorest nations, and is not an economically viable strategy for the foreseeable future. What is needed is a ‘second green revolution’ that improves crop yields without requiring intensive inputs. In recent years a number of root traits have been identified that improve crop adaptation to drought and low soil fertility. In this presentation I will review these traits, their genetic control, their use in crop breeding programs, and their agroecological and socioeconomic effects in rural communities in developing countries.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society of Agronomy **Time:** 1030-1200h
Session 5: ***Food, Fuel and Crop Adaptation*** **Room**: 265 Sobey Building

Chair: Patricia Juskiw
Agriculture and Rural Development, Alberta

1030 **Kevin Vessey**
Crop-Based biofuel feedstock potential in Atlantic Canada - Nova Scotia model

1100 **Francois Gagne-Bourque**
Isolation and biological characterization of fungal and bacterial endophytes of switchgrass

1115 **William Neily**
Seaweed extract from ascophyllum nodosum improves early establishment and stress resistance in vegetable transplants

1130 **Yousef Papadopoulos**
Variations in isoflavone profiles of field grown red clover cultivars

1145 **Kaushik Ghose**
Improving the antioxidant capacity of field crops by increasing selenoprotein content

1030 **Crop-Based Biofuel Feedstock Potential in Atlantic Canada - Nova Scotia Model.** Dr. J. Kevin Vessey, Department of Biology, Saint Mary's University, Halifax, Nova Scotia

An estimated 100,000 acres of abandoned, "inactive" farmland currently exists in Nova Scotia. This land represents a great opportunity for cultivation of biofuel feedstock crops without encountering the "food versus fuel" debate. Potential biofuel feedstock crops include biomass grasses (e.g. Switch grass, Reed Canary grass), agro-forestry crops (e.g. hybrid poplar, willow), and convention sugar (e.g. sugar beet) and oil seed crops (e.g. soybean and canola). While great potential exists for cultivation of crop-based biofuel feedstocks in the Province, forestry and marine-based feedstock has been the primary focus to date.

1100 **Isolation and biological characterization of fungal and bacterial endophytes of switchgrass (*Panicum virgatum L.*).** F. Gagne-Bourque*, P. Seguin, M. Rani and S. Jabaji. Department of Plant Science, McGill University, 21111 Lakeshore Rd., Sainte-Anne-de-Bellevue, Quebec, H9X 3V9, Canada [francois.gagne-bourque@mail.mcgill.ca> (F. Gagne-Bourque), philippe.seguin@mcgill.ca (P. Seguin), mamta.rani@mcgill.ca (M. Rani), suha.jabaji@mcgill.ca (S. Jabaji)]

Switchgrass (*Panicum vergatum* L.) is identified as a model perennial energy crop because of several attributes: efficient storage of solar energy as biomass through photosynthesis, productive long-lived perennial crop with high resource use efficiency and good adaptability to marginal soils. It has been established that perennial grasses harbour different types of endophytic bacteria and fungi. This study was conducted to explore fungal and bacterial endophyte communities inhabiting native switchgrass plants of Quebec and Ontario. The primary focus of this study is to isolate the endophytes in pure culture from surface-sterilized leaf tissues using different isolation techniques, and provide taxonomic identifications based on comparative analysis of ITS rDNA gene sequences. From these data, we evaluated the biodiversity of these potentially beneficial endosymbionts and allowed us to identify candidate endophytes for introduction into commercial switchgrass cultivars for biomass enhancement. A total of 42 endophytes (21 bacteria and 21 fungi) were isolated from whole plant samples collected at early vegetative, and full reproductive stages. Biolog technologies GP2, GN2 and FF Microplate ^{tm} were used to help group the endophytes and provide their metabolite fingerprint. The bacterial endophytes (gram positive and negative) and their culture filtrates were tested for their antimicrobial activity against commonly known pathogenic fungi among which eight were fully sequenced and were shown to belong to different bacterial orders like Bacilli, Entorobactariales, Actinobaceria. Sequence analyses of the endophytic fungi confirmed that they belong to *Chaetomium, Epicoccum, Emericella, Ascochyta, Penicillium and Alternaria* taxa, all of which have been reported as endophytes in grasses. Species-specific primers designed for selected bacterial endophytes showed that endophytes move from one switchgrass generation to the next via seeds, representing a vertical transmission mode. Similar studies are underway for the fungal endophytes. Artificial inoculations of young switchgrass seedlings with selected bacterial endophytes hold promise as a method of reinfection switchgrass seedlings. Future experiments are aimed at enhancing switchgrass yield and vigour via artificial inoculation methods.

1115 **Seaweed extract from *Ascophyllum nodosum* improves early establishment and stress resistance in vegetable transplants.** W. Neily [1]*, L. Shishkov[1], D. Titus[1] and K. Griegoschewski[11]Acadian Seaplants Ltd, Dartmouth, Nova Scotia, Canada

Many vegetable and ornamental bedding plant crops are grown in plug trays and cell packs under greenhouse conditions prior to transplanting into the field or landscape. The development of a large, healthy root system is important for young seedlings to help withstand the shock of transplanting. Seaweed extracts are known to improve root development of horticultural plants as well as to help alleviate some symptoms typically associated with abiotic stresses such as drought and soil salinity. Greenhouse experiments at the Dr. James S. Craigie Research Center in Cornwallis Nova Scotia were designed to test the effects of Acadian® seaweed extracts (a derivative from *Ascophyllum nodosum*) on root development in lettuce, melon, tomato, and pepper. Seaweed extract treatments in combination with 10-52-10 N-P-K fertilizer were applied as a drench and compared to plants which only received 10-52-10. The roots and leaves of plants from each treatment were examined with WinRhizo root and WinFolia leaf image analysis systems. Time lapse videos were also used to record results. Replicated trials showed significant improvements in root length, surface area, volume and leaf area when seaweed extract was applied in combination with fertilizer. Further studies examined the effects of seaweed extract on salinity and drought stress in pepper, lettuce, and tomato. Results showed that seaweed extract extended the time before plants began to succumb to water stress compared to fertilizer treated controls. Seaweed extract was also shown to reduce the negative effects of high soil salinity during early plant establishment. These results suggest that seaweed extract applications improve early root and shoot development and may provide some protection against water and salinity stress.

1130 **Variations in isoflavone profiles of field grown red clover cultivars**. R. Tsao[1], Y.A. Papadopoulos*[2], K.E.Glover[3], K. A. Power[1]; K. B. McRae[4], and S. A. E. Fillmore[4]. [1]Food Research Program, Agriculture & Agri-Food Canada, Guelph, ON, Canada; [2]Agriculture and Agri-Food Canada, Haley Institute, PO Box 550, Truro, N.S. Canada B2N 5E3; [2]Nova Scotia Agricultural College, Truro, N.S.; [4]Atlantic Food and Horticulture Research Centre, Agriculture and Agri-Food Canada, Kentville, NS

In addition to producing essential nutrients for animal feed, red clover (RC) also produces a variety of beneficial secondary metabolites, including isoflavones, which can be used as a natural-source estrogen replacement, and are metabolized in the digestive system to compounds that show strong antioxidant and specific anticarcinogenic activities. Genetics, growing conditions and processing conditions have been found to significantly alter the composition and concentration of the above polyphenols. Our previous studies have shown that the specific isoflavone composition of RC extracts is an important factor in activity related to effects on menopausal-related symptoms and diseases. In this study tissue samples of 13 RC cultivars grown under field conditions were taken prior to first and second harvests in two post establishment years (2004 and 2005) to determine the concentration of individual isoflavones using HPLC. Individual isoflavone concentrations and total isoflavone concentration differed significantly among and within cultivars. We found significant genetic variability for total isoflavone concentration and individual isoflavone concentrations and these differences were also related to ploidy level of cultivars. On average diploid cultivars produced slightly higher total isoflavones than tetraploid cultivars and first growth samples produced slightly higher total concentrations than samples obtained from re-growth in both years of this study. However, the concentrations of most isoflovones were substantially higher in the first growth than re-growth in both years. More interestingly the concentrations of biochanin A, formononetin, diadzein and orobol were substantially higher in 2004 while pratensein, pseudobaptigenin and prunetin were

substantially higher in 2005. The concentrations of genistein and irilone were similar in both years. These results demonstrate that the individual isoflavones concentrations were influenced by genotype, harvest date and year.

1145 **Improving the antioxidant capacity of field crops by increasing selenoprotein content.** B. Fofana[1] (Bourlaye.fofana@agr.gc.ca), D. Main[1], K. Ghose*[1,2], M. Grimmett[1], C.W. Kirby[1], J. McCallum[1], R. Peters[1], K. Drake[1], S. Locke[3], and M. Sweeney-Nixon[2]. [1]Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, C1A 4N6, PEI, Canada; [2]Biology Department, University of Prince Edward Island, 550 University Avenue, Charlottetown, C1A 4P3, PEI, Canada; and [3]Institute of Nutriscience and Health, National Research Council, 550 University Avenue, Charlottetown, C1A 4P3, PEI, Canada

The incidence of chronic human diseases such as cancers and diabetes is increasing worldwide. Despite successes in their treatment, preventative measures have become top priorities. Oxidative stress plays a role in the onset and development of many diseases, and plants are sources of polyphenolics, proteins, and mineral antioxidants, key micronutrients in human and animal diets. Plants are also a unique source for Selenium (Se), a micronutrient not required by plants but, at low doses, is essential for human and animal health. Thus, there is increasing interest in plant natural products as preventative agents in chronic diseases. Se deficiency is reported in many parts of the world due to low soil Se levels. Se is absorbed and metabolized in *planta* via sulphur assimilation pathways and is incorporated into sulphur containing amino acids and seleno-compounds such as methylselenic acid. However, studies using agronomic practices aimed at increasing Se content in the proteins of field crop are scarce. Here, we report on the increase of total Se and selenoprotein content in three major Canadian field crops: potato, soybean and flax. Sodium selenate was applied to seed prior to planting or as post emergence foliar sprays in field trials. Se levels were determined in mature seed and tubers as well as in their total protein extracts. A high level of Se translocation from planted seed or spayed leaves into new seed, tubers and their proteins was observed. The nature of some of the selenoproteins as well as the impact of increased total selenium and selenoprotein content on a field crop's antioxidant capacity will be described and discussed.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society of Agronomy **Time:** 1400-1530h
Session 6: ***Cropping Systems and Breeding*** **Room**: 265 Sobey Building

Chair: Balakrishnan Prithiviraj
Nova Scotia Agricultural College

1400 **Chantal Hamel**
Arbuscular mycorrhiza in a sustainable world

1430 **Ying Zhang**
Recombinant expression if plant diacylglycerol acyltransferases from tissue that accumulate saturated fatty acids

1445 **Patricia Juskiw**
Intergration of marker assisted selection for scald resistance into the FCDC breeding program

1500 **Malcolm Morrison**
Genotype and environment influence GABA concentration in short-season soybean

1515 **William Cox**
Lack of hybrid by seeding rate interactions for corn growth silage yield and quality

1400 **Arbuscular mycorrhiza in a sustainable world**. C. Hamel[1]*; N. Bazghaleh[1]; M. Dai[1]; E. Furrazola Gomez[2]; Y. Torres-Arias[2]; and A. K. Singh[1]. [1]Semiarid Prairie Agricultural Research Centre AAFC, Swift Current, Saskatchewan, Canada, S9H 3X2 (e-mail: hamelc@agr.gc.ca); and [2]Instituto de Ecologia y Sistematica, Carretera de Varona Km 3 1 / 2, Capdevila, Boyeros, Habana, Cuba

Sustainable cropping systems will be nutrient efficient and support the capacity of the soil resource. The management of P, a finite resource, appears as a particular challenge. The arbuscular mycorrhizal (AM) fungi will be solicited, as they contribute importantly to soil physical quality and mobilization of nutrients, in particular P. The AM hyphal networks enmesh the soil matrix providing structural stability and improving water infiltration. These hyphal networks are also an exclusive source of plant available nutrients on which crops get connected soon after germination. The AM symbiosis particularly improves the efficiency of P use by crops, as the AM hyphal networks extract and mobilize nutrients from mineral and organic substances of soils and act as a pipeline for their rapid translocation to roots. Tight cycling of N and P is one characteristic of nutrient efficient soil-plant systems that is promoted by AM hyphal networks and permits good crop yield on soils with low fertility, thus, reducing environmental losses. Effective transformation of nutrients into yield is another component of nutrient use efficiency that is enhanced by AM fungi. The AM symbiosis is well known to increase plant tolerance to disease and drought stress, thus, maximizing yield at a given level of soil fertility. Reducing crop dependence on nutrient inputs through the creation of highly effective AM symbioses in crops is a step towards sustainability. The effectiveness of crops AM symbiosis can be improved by the adoption of practices favouring their formation, for example, reduced tillage, reduced frequency of summer fallow, and inoculation with highly effective AM fungal isolates. The use of certain rotations and innocuous pesticides would also strengthen the AM symbiosis of crop plants. Plants have a large influence on their biological environment in part through the production of bioactive phytochemicals. The selection of crop genotypes with improved compatibility with the AM fungi naturally occurring in cultivated fields appears as an ecological approach to the sustainability of crop production. Alternatively, the identification and use of phytochemicals in bioproducts may have direct applications in sustainable crop production, or at least, in AM fungal inoculants production.

1430 **Recombinant expression of plant diacylglycerol acyltransferases from tissues that accumulate saturated fatty acids.** Y. Zhang[1*], R.M. Siloto[1], F. Tahira[2], P. Krishna[2] and R.J. Weselake[1], [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, T6G 2P5, [2]Department of Biology, University of Western Ontario, London, ON, Canada, N6A 5B7

Vegetable oils enriched in saturated fatty acids (SFAs) provide solid-fat functionality in food processing. They can be used as substitute ingredients for the production of margarines and shortenings to reduce the degree of hydrogenation, which generates harmful *trans* fatty acids. Previous attempts to engineer oilseeds to accumulate SFAs targeted the early stages of fatty acid metabolism. Our focus is on latter stages of storage lipid assembly with particular attention to enzymes that can preferentially incorporate SFAs in triacylglycerol (TAG). Acyl-CoA:diacylglycerol acyltransferase (DGAT, EC 2.3.1.20) catalyzes the biosynthesis of TAG and is encoded by two distinct polypeptides designated DGAT1 and DGAT2. We isolated *DGAT* cDNAs from seabuckthorn (*Hippophae rhamnoides*) pulp that accumulates palmitic acid (16:0)

and palmitoleic acid (16:1$^{cis\Delta 9}$) and cocoa (*Theobroma cacao*) beans, that are rich in SFAs, and designated them as *HrDGATs* and *TcDGATs*, respectively. Expression of *HrDGAT1, HrDGAT2, TcDGAT1* and *TcDGAT2* rescued TAG synthesis in the *Saccharomyces cerevisiae* mutant strain H1246. Measurements of *in vitro* DGAT activity with yeast microsomes showed that HrDGAT1 and TcDGAT1 can efficiently incorporate 16:0-CoA, 16:1$^{cis\Delta 9}$ -CoA, 18:0-CoA and 18:1 $^{cis\Delta 9}$-CoA to TAG. Yeast cultures expressing *DGAT1* displayed substantially higher accumulation of TAG compared to those expressing *DGAT2*. However, expression of *DGAT2* resulted in preferential synthesis of TAGs containing SFAs in yeast. Expression of *HrDGAT1* in developing seeds of *Arabidopsis thaliana* restored seed oil content to similar amounts of *A. thaliana* wild type and altered slightly the seed fatty acid profile with a significant reduction in the accumulation of eicosenoic acid (20:1$^{cis\Delta 11}$). These results suggest that *HrDGAT2* and *TcDGAT2* could be potentially be used to increase SFA incorporation in vegetable oils. Combined with auxiliary approaches, this research might lead to vegetable oils with beneficial properties to the food industry.

1445 **Integration of marker assisted selection for scald resistance into the FCDC Breeding Program.** P. Juskiw*, J. Zantinge, and K. Xi. Field Crop Development Centre, Alberta Agriculture and Rural Development, Lacombe, Alberta Canada T4L 1W8 (e-mail: patricia.juskiw@gov.ab.ca)

Selection for disease resistance in plant breeding programs can be hampered by year to year variability in disease development. This environmental dependence is especially limiting in early generations. In barley (*Hordeum vulgare* L.), markers for resistance to scald (*Rhyncosporium secalis* (Oudem.) J.J. Davis) have been identified by the group at Field Crop Development Centre (FCDC) to mark the resistance genes inherited from 'Seebe', a two-row general purpose barley released in 1992 that still shows good resistance to the scald pathogen in Alberta. Barley breeders at FCDC use a modified bulk program for the majority of their breeding efforts. In the F_6 bulk, 100 or 200 heads are selected for F_7 headrows. Leaves were sampled from these headrows for marker analysis. In 2009, a total of 700 entries from six populations were evaluated for scald resistance using the SSR marker Ebmac635 previously found linked to scald susceptibility. Of these entries, 285 had the susceptibility marker, and from the remaining 415 lines, 122 were selected based on agronomics. These lines were harvested and seed was run through the near-infrared spectroscopy (NIRS) lab for quality analyses. A total of 22 lines were advanced to first year yield tests in 2010. When these 22 lines were grown in the 2010 Lacombe scald nursery ratings based on a 0-9 scale were made: 15 lines rated as R or MR, six rated as I and only one line rated as S. The marker worked better in some populations than others. Additional scald resistance markers were identified from the 2009 populations. These markers were used in our 2010 head row nursery on another 1,300 lines from seven populations. In 2011 we will again evaluate the efficiency of the markers by comparison with reactions in the Lacombe scald nursery. We will also use them on an additional 3,100 F_7 lines from 16 populations. While the efficiency of the marker seemed very good, there is a limit on the number of lines that the lab can process during the period in June when the leaves are collected from the field and July when the headrow selections are made.

1500 **Genotype and environment influence GABA concentration in short-season soybean.** Malcolm J. Morrison*[1], Judith R. Fregeau-Reid[1], Elroy R. Cober[1], [1] Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Central Experimental Farm, K.W. Neatby Bldg. 960 Carling Ave. Ottawa, ON., K1A 0C6 Morrisonmj@agr.gc.ca

Gamma-aminobutyric acid (GABA) is a four carbon, non-protein amino acid found in most life forms on the planet. The metabolic function of GABA in plants is still under investigation. In

humans, GABA is the main inhibitory neurotransmitter in the brain but there is no evidence that its consumption can affect the brain. There is clinical proof that the consumption of GABA reduces high blood pressure in humans. It is estimated that up to 30% of the population in most countries have high blood pressure. Soy foods, such as tofu, soymilk, tempeh, natto, and miso are easily obtainable and their consumption could be a method for a portion of the population to lower their blood pressure. Our objective was to determine if there were genotypic and/or environmental influences on the concentration of GABA in short-season soybean cultivars. Sixteen cultivars, representing 71 years of short-season plant breeding progress (1934 to 2003), were grown in a randomized complete block design with 4 replications at the Central Experimental Farm, Ottawa, ON using appropriate agronomic and cultural practice. When ripe, seed was harvested, and cleaned for yield and seed weight determination. A sample retained for protein, oil, and GABA determination. Protein and oil were analysed by NIR while GABA was determined using a gas chromatograph. There were significant cultivar, year, and cultivar x year interactions for all characters examined. The year affect and cultivar x year interaction indicates that the environment influences these traits and changes the cultivar rank order to some extent. There was a 3 fold difference in GABA concentration between cultivar extremes. Plotting the year of cultivar release (YOR) against the trait showed that yield, and oil have increased with plant breeding while protein and GABA concentration have decreased. These results will form the basis of a breeding program to increase GABA concentration in food grade soybean.

1515 **Lack of hybrid by seeding rate interactions for corn growth, silage yield and quality.** W.J.Cox[1]* and J.H. Cherney. Cornell University, Dep. of Crop and Soil Sci., Ithaca, NY, 14853 (wjc3@cornell.edu)

Transgenic Bt (*Bacillus thuringiensis*) corn (*Zea mays* L.) hybrids may require higher but brown midrib (BMR) and silage-specific hybrids may require lower seeding rates than currently recommended for silage in the Northeast USA. We planted dual-purpose (three Bt and one non-Bt), two BMR, and two silage-specific hybrids to evaluate growth, dry matter (DM) yield, and quality responses to four seeding rates (61,750 to 98,800 kernels ha^{-1}). Hybrid by seeding rate interactions were not observed. At silking (R1), BMR hybrids averaged 6% lower leaf area index (LAI, 4.58) compared with dual-purpose hybrids and 7% lower biomass (1050 g m^{-2}) compared with two dual-purpose hybrids. Crop growth rates were similar from the 14th leaf (V14) stage to R1 stage between BMR and dual-purpose hybrids (34.3 to 35.8 g m^{-2} d^{-1}) so less BMR vegetative growth was associated with 10% lower LAI (3.46) and biomass (480 g m^{-2}) at the V14 stage. Biomass and LAI had linear responses to seeding rates. The BMR compared with two dual-purpose hybrids averaged 8% lower DM yield (20.7 Mg ha^{-1}) but similar predicted milk yield (37.6 Mg ha^{-1}) because of 8% higher milk Mg^{-1} values (1823 kg Mg^{-1}). Silage-specific compared with two dual-purpose hybrids averaged about 7.5% lower DM with similar milk Mg^{-1} (1685 kg Mg^{-1}), which resulted in similar milk yields. Milk and DM yields showed quadratic, and milk Mg^{-1} showed negative linear responses to seeding rates. Results indicate that Bt, BMR, and silage-specific hybrids should be seeded at about 89,000 kernels ha^{-1} for silage in New York.

Thursday, July 21, 2011 **Oral Presentations**
Canadian Society of Agronomy **Time:** 0830-1000h
Session 7: ***Organic and Sustainable Agriculture*** **Room**: 255 Sobey Building

Chair: Andrew Hammermeister
Organic Agriculture Centre of Canada
Nova Scotia Agricultural College

0830 **Niels Halberg**
Sustainability of organic farming in a global food chains perspective

0915 **Derek Lynch**
Are organic farms different? A Canadian perspective

2011 CSA Borlaug Symposium: Crop physiology and abiotic stresses **Time**: 0930-1000h
Room: 265 Sobey Building

Chair: Gavin Humphreys
Agriculture and Agri-Food Canada, Winnipeg

0930 **Rosalind Bueckert**
Crop adaptation to abiotic stress

0830 **Sustainability and integrity of organic farming in a global food chains perspective**
Dr. Niels Halberg
Director, International Centre for Organic Food Systems, Denmark

Demand for organic food has increased significantly in Europe and North America and consumers are being exposed to an increasing number of imported organic foods, some of which could be substituted by similar locally produced conventional food items. Even though demand is partly driven by altruistic motives it is difficult for consumers and traders to know what development they support if they buy "global organic food" in terms of e.g. environmental impact and possible improvements in poor farmers' livelihoods? Studies of certified cash crop production for export in Asia and Latin America show that there are environmental benefits of, for example, organic soybeans and oranges compared with conventional (reduction in emissions, absence of pesticides, biodiversity) but also that agro-ecological methods are not always used extensively and that organic ideas and principles are not always employed by the local farmers. Life cycle assessments of environmental impacts accumulated along the food chain showed that transport-related emissions contribute a significant part of climate impact of these products. Livelihood benefits for smallholder farmers becoming part of high value chains may be significant but there are important obstacles for their inclusion in global value chains.

0915 **Are organic farms different? A Canadian perspective**
Dr. Derek Lynch, Department of Plant and Animal Sciences
Nova Scotia Agricultural College, Truro, Nova Scotia

The overreaching goal of the Canadian organic standards is to develop farm enterprises that are ''sustainable and harmonious with the environment''. But do organic farms achieve these goals? Are the cropping systems and rotations, soil management practices and intensity of nutrient use, energy and pesticide use, floral and habitat diversity etc. on organic farms sufficiently distinct as to impart measurable and important environmental and/or ecological benefits? Synthesizing results of primarily Canadian research, Derek will present the case that the specific attributes of organic farms themselves should perhaps be considered as valuable to society as the agricultural products of these enterprises. Organic agriculture may thus offer an innovative and more holistic approach to the traditional concept of 'value added' in agriculture.

0930 **Crop adaptation to abiotic stress**. Rosalind Bueckert

More than half of Canada's crop production comes from western Canada, a region that experiences short growing seasons characterized by temperature and moisture stress. Historically the region was dominated by temperate cereal production, but in recent decades crops have included canola and pulses. Crops from this region have superior quality profiles, and some cultivars have become dominant in global crop exports. Here we will describe weather events and the resulting abiotic stresses that are common in prairie crop production, and show case how specific cultivars have been successfully adapted. We will also examine current strategies to improve crop performance in a warming climate.

Thursday, July 21, 2011 **Oral Presentations**
Canadian Society of Agronomy **Time:** 1030-1200h
Session 8: ***Organic and sustainable agriculture*** **Room**: 255 Sobey Building

Chair: Derek Lynch
Organic Agriculture of Canada
Nova Scotia Agricultural College

1030 **Jane King**
The effects of pea, faba bean and lupin on two years of subsequent crops

1045 **Julien Winter**
Measuring botanical diversity and adaptation in pastures

1100 **Shyamal Kumar Nandi**
Active ingredient analysis in vitro propagation and conservation of selected Himalayan medicinal herbs for sustainable utilization and conservation

1115 **Paul Voroney**
Phosphorus availability in organic dairy farm soils: A closer look at the role of soil biology

1130 **Andrew Hammermeister**
Fertility management for organic cereal production

1145 **Derek Lynch**
Crop productivity and nitrogen dynamics under extended organic vegetable rotations

Session 8: ***2011 CSA Borlaug Symposium continues*** **Room**: 265 Sobey Building

Chair: Gavin Humphreys
Agriculture and Agri-Food Canada, Winnipeg

1030 **Todd Hyra**
The implications of climate change for the Canadian seed industry

1100 **Igor Falak**
Role of plant breeding in adaptation of plants to the changing environment – canola model

1130 **Yousef Papadopoulos**
Recent advances in the development of crop cultivar for adaptation to changing environmental conditions

1030 **The effects of pea, faba bean and lupin on two years of subsequent crops.** J. R. King*, S. M. Ross, C. M. Williams. Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-10 Agriculture-Forestry Centre, Edmonton, Alberta, Canada T6G 2P5 (email: Jane.King@ales.ualberta.ca)

Optimum use of pulses in cropping sequences will improve the sustainability of cropping systems. Most studies assess the benefits of pulses on one subsequent crop, but benefits may extend beyond one year. A three year rotational study investigated the effects of pulse crops on subsequent crops at two sites in central Alberta (Barrhead and St Albert). In year 1 of the rotation (YR1), field pea, tannin-free faba bean, narrow-leafed lupin, barley (with N fertilizer or no-N), and canola (with N fertilizer or no-N) were grown. Year 2 (YR2) crops were barley, canola, flax, pea, triticale, CWRS wheat, CPS wheat and perennial ryegrass. Barley was seeded in 2010 as Year 3 (YR3) of the rotation. YR1 and YR2 treatments result in 56 crop sequence treatments. YR1 treatments had effects on YR3 barley yield and protein. Barley grain yields following YR1 faba bean and plus-N barley were higher than those following YR1 no-N barley or canola. YR3 grain yields were increased 14% by faba bean and 8% by pea compared to YR1 no-N treatments. At Barrhead, YR1 lupin and plus-N treatments had higher YR3 barley protein than no-N treatments. At St Albert, YR1 faba bean and plus-N barley had higher YR3 barley protein than no-N treatments. For a subset of 21 treatments, additional data was collected on biomass yield and N uptake. YR1 effects on YR3 barley biomass and N uptake were more significant at Barrhead, the site with lower soil organic matter and lower 2008-2010 rainfall. At Barrhead, YR1 plus-N treatments generally produced higher YR3 barley straw yields, higher N content in straw, higher N yields in dry matter at maturity and lower harvest index. The effects of YR1 pulse treatments on YR3 barley biomass and N uptake at Barrhead were generally intermediate between the YR1 plus-N and no-N treatments. Results indicated that benefits from using pulse crops in cropping systems can extend beyond a single year, and can improve the yield and quality of a second subsequent crop.

1045 **Measuring botanical diversity in pastures.** Julien P. Winter [1*], Gaëtane Carignan[1], Caroline Halde[1], Ralph Martin[2], [1]Department of Plant and Animal Sciences, [2]Organic Agriculture Centre of Canada,Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3 (winter.julien@gmail.com)

Botanical diversity in pasture is challenging to measure because of a wide range in species abundance and aggregation of individuals: all observations are affected by spatial scale. The objective of this research was to test two methods for surveying pastures: (1) transects of digital photographs to measure the spatial structure of the sward matrix, and (2) concentric nested quadrats to measure species abundance from 1 cm² to 0.08 ha. The survey was conducted on an experiment that modified management-intensive, rotational grazing (MIG) to affect the biodiversity in a 10-yr old naturalized pasture. The main treatments were (Trt-A) MIG: five cycles of grazing with dairy cows followed by mowing and harrowing, and (Trt-C) stockpiling: grazing every second cycle. In the third year of the experiment, spatially-lagged Gower's similarity index showed a reduction in sward matrix diversity in Trt-C C vs. Trt-A. In Trt-A, patch-size frequency analysis (PASFRAN) showed strong aggregation in Poa spp, moderate aggregation in Trifolium repens, and broad-leaved grasses, and low aggregation in Taraxacum officinale and Plantago major. In the fifth year, the nested quadrat survey showed that species abundance Trt-A > Trt-C for plants common at <10 m², with Trt-A having more small forbs and

legumes. However, at a >10 m² scale, species abundance of Trt-C > Trt-A, because grazing-intolerant forbs were establishing in Trt-C. To conclude, photography and nested quadrats gave a broad characterization of botanical diversity, and can provide a background context for more detailed studies on pasture biota and soil.

1100 **Active ingredient analysis, in vitro propagation and conservation of selected Himalayan medicinal herbs for sustainable utilization and conservation.** S.K. Nandi*, and L.M.S. Palni. G.B. Pant Institute of Himalayan Environment & Development, Kosi-Katarmal - 263 643, Almora, Uttarakhand, India (email: shyamal_nandi@rediffmail.com)

Due to increasing global demand for plant "naturals", many of the highly valued medicinal species of the Indian Himalayan Region (IHR) are subjected to unorganized and often illegal harvesting, well beyond their natural regeneration capacity; consequently they are listed in the Red Data Book and/or in the various threat categories of IUCN. Improper harvesting (tissue type, age, season, etc) results in uneconomical yields due to low content of active ingredients, and adversely affects their regeneration in the wild. Among the different high altitude medicinal herbs of the IHR, *Aconitum balfourii* Stapf., *A. heterophyllum* Wall. (all Ranunculaceae), *Picrorhiza kurrooa* Royle ex Benth. (Scrophulariaceae) and *Podophyllum hexandrum* Royle (Podophyllaceae) hold considerable pharmaceutical importance; since early times, the extract of plants/plant parts is constituent of Unani and Ayurvedic medicines, and currently in high demand for use in modern medicine. The active compounds which confer the medicinal properties do vary among different plant populations and within the same population. To meet such challenges, in vitro propagation (tissue culture) techniques have the recognized potential for rapid multiplication of the much needed planting material, and also to achieve conservation objectives. With these goals, studies were taken up to assess the active ingredient content of plants/plant parts collected from natural populations growing in different locations/altitudes, and to develop in vitro propagation methods for the abovementioned high value herbs. Using elite plant material, attempts were made to establish tissue cultures, induce multiple shoots, improve rooting, and subsequently develop suitable methods for hardening before field transfer. The survival and growth of in vitro raised plants was also monitored to evaluate field performance. In case of *P. kurrooa*, hairy root cultures were also raised which provided much higher amounts of active ingredients. Investigations in relation to active ingredient analyses to select elites, development of in vitro propagation protocols and subsequent field performance of these plants will be presented.

1115 **Phosphorus availability in organic dairy farm soils: A closer look at the role of soil biology.** K.D. Schneider[1], R.P. Voroney[1]*, D.H. Lynch[2], M. Main[2], K.E. Dunfield[1], C. Hamel[3], and I. O'Halloran[4]. [1]School of Environmental Sciences, University of Guelph, Guelph, ON, Canada, N1G 2W1 (email: kschne01@uoguelph.ca); [2]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, P.O. Box 550, Truro, NS, Canada B2N 5E3; [3]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, PO Box 1030, Swift Current, SK, Canada, S9H 3X2; and [4]School of Environmental Sciences, University of Guelph, Ridgetown Campus Ridgetown, ON, Canada, N0P 2C0

Recent studies exploring soil fertility on organic dairy farms in Ontario have reported low soil test phosphorus (P) values. However, soil test P values were not found to significantly correlate with yield, with some farms showing acceptable yields, despite the soil tests indicating low P availability. It has been suggested that increased soil biological activity in organically-managed systems is involved in providing the crop with P not measured by the standard soil test. The objective of this research was to explore the relationships between soil test P, arbuscular mycorrhizal fungi (AMF) root colonization, AMF community structure, phosphatase activity, and productivity of organic perennial forage cropping. Three long-term (>20 years) organically

managed dairy farms in south western Ontario were selected from an initial screening of 10 farms. These farms had forage fields showing low soil test P values, but relatively high yields. From each farm, one second or third year forage field was selected having a relatively flat topography and as close to uniform management as possible. Three conventional dairy farm fields with a long-term history of water-soluble P fertilizer application and located in close proximity to the organic sites were included in the study for comparison. Just prior to the first cut of hay (June 2009), root, plant, and soil samples were collected from each field. Additional plant samples were collected at each subsequent cut of hay to obtain a measure of total forage yield and plant P uptake. Results support that low STP values did not cause a yield reduction in organic forage fields. AMF root colonization was greater in organic systems, which may contribute to crop P nutrition. An Analysis of Similarity (ANOSIM) using data generated from Denaturing Gradient Gel Electrophoresis (DGGE) images revealed that there were significant differences in AMF community structure between farms of different management; however, differences due to geographical location were greater. It is anticipated that this research will assist in the understanding of P fertility and cycling in low-input agricultural systems.

1130 **Fertility management for organic cereal production.** A. M. Hammermeister[1*] and K. L. Nelson[1], [1]Organic Agriculture Centre of Canada, Nova Scotia Agricultural College Truro, Nova Scotia B2N 5E3 (email: ahammermeister@nsac.ca)

Organic grain producers in the Maritimes have struggled to maintain yields on land where manure is not readily available. They have been seeking options for both cultivar selection and the use of soil amendments compared with the standard practice of using a forage green manure. Red clover ploughdown was compared with a commercially available (4-1-2) granulated poultry manure as a nitrogen (N) source for organic cereal production in Prince Edward Island, Canada. The effects of Previous Crop (clover or oats) on six barley and two oat cultivars were assessed. In addition, Fertility Trials were conducted over two years in PEI to compare i) previous crop of oats ($oats_{prev}$) ii) previous crop of clover ($clover_{prev}$), iii) $oats_{prev}$+ N (poultry manure as per above at 3000 kg ha^{-1}, with an estimated 60 kg N_{avail} ha^{-1}), and iv) $clover_{prev}$ + N on three barley cultivars and one oat cultivar. In the Previous Crop Trial, average yield across all cultivars and years following clover was 54% higher than for yield following oats; however test weight was not affected. A significant cultivar effect was observed in the Previous Crop trial for the barley, but no interaction between cultivar and previous crop. For the Fertility Trials, yield of the $oats_{prev}$ treatment was typically lower than in other treatments although some differences (in AC Baton oats and CDC McGwire barley) were not always significant. No significant difference in yield was observed between the $oats_{prev}$+ N and the $clover_{prev}$ treatments indicating the clover cover crop provided equivalent nitrogen as 3000 kg ha^{-1} of granulated poultry manure; the additive effect of $clover_{prev}$+ N provided a significant yield increase for some cultivars. Compared with $oats_{prev}$, thousand kernel weight and test weight for the barley cultivars were higher for $clover_{prev}$ + N treatments although differences were not always significant. Barley protein content was increased when grown following clover, but was lower with application of the poultry manure. Oats were not responsive to the use of a green manure or the poultry manure.

1145 **Crop productivity and nitrogen dynamics under extended organic vegetable rotations**. D. H. Lynch[1]*, M. Sharifi[2], D. Burton[2] and A. Hammermeister[3]. [1]Department of Plant and Animal Sciences, Nova Scotia Agricultural College (NSAC), Truro, Nova Scotia, B2N 5E3(e-mail: dlynch@nsac.ca) [2]Dept. of Environmental Science, NSAC, Truro, NS; [3]Organic Agriculture Centre of Canada, NSAC, Truro, NS

The impact of green manure type and frequency with or without organic amendment or fertilizer on tuber yields, potato N uptake (PNU), greenhouse gas (GHG) emissions and overwinter N

losses were evaluated under various extended (5y) organic vegetable cropping rotations at NSAC from 2005-2010. Three pre-potato sequences included: C1(oats underseeded with red clover-red clover), C3 (carrots-oats/pea/vetch mixture (OPV)) and C4 (beans followed by buckwheat-OPV). Soil fertility treatments, applied to potatoes only included: non-amended (control), supplemented with inorganic P and N fertilizer (FERT), municipal food waste compost (MSW) (7 t DM ha^{-1}), or composted paper mill biosolids (PMB) (10 t DM ha^{-1}). Rotation sequences (i.e. green manure type) did not affect potato total yields or marketable size distribution in 2008 and 2010. However PNU was increased by red clover (C1). Wireworm damage was notably higher under C1 than C3 or C4. Yields for control and PMB were not different (averaging 31 Mg ha^{-1}). Tuber yields were greatest, and percent small tubers lowest, for FERT (averaging 38 Mg ha^{-1}) followed by MSW (34 Mg ha^{-1}) treatments. In 2009, bean yields were not affected by rotation while carrot yields were greatest under C1. PNU ranged from 96 to 149 kg ha^{-1} and was greatest for FERT. Crop N use efficiency (ranging from 30-38 kg N uptake per 10 t of yield) decreased as treatment combined N input increased (C1 vs C3/C4; FERT vs MSW/PMB). In 2008, N_2O emissions under potatoes ranged from 1.30 to 0.28 kg N_2O-N ha^{-1} for C1 and C3 sequences. In control potato sub-plots, emissions were 16% lower than under FERT (0.82 vs. 0.96 kg N_2O-N ha^{-1}) but two times greater than under red clover green manure. Data on soil mineral N and GHG emissions from the 2010 season will also be presented.

Session 8 (Rm SB255)

1030 **Implication of Climate Change for the Canadian Seed Industry.** T.J. Hyra*; SeCan; 94 Woodington Bay Winnipeg MB R3P 1M9; thyra@secan.com

The seed industry relies on the prosperity of Canadian farmers in order to be successful – we need to take a high-level view of what Canadian farmers need to be profitable and sustainable. What does it mean for the Canadian farmer? What do modern Canadian farmers want? What can we deliver? From a business perspective farmers want to maximize the profitability of their operation. So that is the goal of the seed industry as well – the challenge is that seed cannot do this alone. Good seed of the right variety is a great first step, but there are no magic bullets. Canola in western Canada has to be considered one of the greatest success stories in Canadian agriculture – partly because of advancements in seed technology and partly because of a committed, fully-integrated business approach for the crop. What can we learn from this example and apply to other crops in other geographies? What are some of the immediate and evolving challenges facing Canadian farmers today? How does climate fit in? How much can we solve with plant breeding? Where do we need to pull every available lever to ensure we have a healthy, competitive agricultural industry – one that will allow Canada to continue to play a key role in feeding a growing global population.

1100 **Role of plant breeding in adaptation of plants to the changing environemt – canola model**. Igor Falak, Canola R&D, Pioneer Hi-Bred Production LP, Caledon, ON

Canola is Canada's "Cinderella crop" that has emerged through extensive breeding efforts. From quality improvements and herbicide tolerance to hybrid adoption, canola has evolved into a stable, high-yielding crop. Extensive breeding work is underway to further utilize genetic variability and improve yield stability under changing environmental conditions. Wet environments and long-term population breeding were used to develop Sclerotinia resistant hybrids that reduce yield losses from this constant disease threat in western Canada. Breeding materials and experimental hybrids are being tested in a range of stressful environments occurring across the Canadian prairies, from water-logging to drought and cold, with the goal of improving stress-tolerance.

1130 **Recent advances in the development of crop cultivars for adaptation to changing environmental conditions.** Yousef A. Papadopoulos[1], G. Humphreys[2], L. Reid[3] and B. Coulman[4]. [1]Agriculture and Agri-Food Canada, 100-5 Haley Institute, PO Box 550, Truro, N.S. Canada B2N 5E3; [2]Agriculture and Agri-Food Canada, Winnipeg, MB; [3]Agriculture and Agri-Food Canada, Ottawa, ON; [4] Plant Sciences Department, University of Saskatchewan, Saskatoon, SK S7N 5A8

Increases of 2 to 6ºC in minimum air temperature and extreme fluctuations in environmental conditions have been attributed to global warming. Predicted fluctuations in air temperature during the growing season and winter are anticipated to affect the performance and sustainability of field crops in Canada. Higher annual temperatures in the northern latitudes will increased the impact of insect and pathogen species, as well as, the number of new species that would be otherwise unable to survive cooler conditions. Abiotic diseases associated with environmental extremes are also expected to increase. The most important effects of climate change on plant diseases will result from the interaction between abiotic and biotic diseases. There will be opportunities for new crops and cultivars to be introduced but effective systems must be in place to prevent new and existing pathogens from impacting the performance and sustainability of field crops in Canada. Current strategies for plant breeding programs includes: 1) developing germplasm adapted to increased length of growing season which, will affect the persistence of perennial field crops; 2) developing germplasm with increased resistance to existing insects and pathogens, as well as, to new biotic threats; and 3) developing stress tolerance in the major crops. Breeding programs for corn are centered on developing hybrids with faster kernel drydown to reduce drying costs at harvest and resistance to multiple diseases including: 1) Fusarium spps ear and stalk rots; 2) northern corn leaf blight; 3) eyespot; 4) common rust; 5) common smut; and 6) grey leaf spot, new disease rapidly spreading into Canada. Spring wheat breeding programs are focused on increasing yield stability through development of new diverse cultivars with adaptation to diverse environments. These varieties are developed through testing in multiple environments over multiple years which permits selection for adaptation to environmental change. In addition to environmental adaptation wheat breeders are selecting for: 1) resistance to *Fusarium* head blight, leaf and stem rust; orange wheat blossom midge; and 2) tolerance to drought and salinity are important. Recently, the importance of stripe rust has been upgraded in Western Canada and resistant lines have been identified. In forage crops, breeding programs are centered on: 1) increased persistence; 2) increased resistance to existing insects and pathogens; 3) identification of new threats of insects and pathogens; 4) increased tolerance to waterlogging, drought and salinity; 5) evaluation of new species which may be productive and persistent under changing environmental conditions.

Thursday, July 21, 2011
Canadian Institute of Food Science and Technology
Canadian Society of Agronomy
Session 8: Malting Barley: Progress From Grain to Glass

Oral Presentations
Time: 1030-1200h
Room: 415 Sobey Building

Chair: Alex Speers
Dalhousie University

1030 **Brian Rossnagel**
Developing brewing value selection tools for malting barley breeding

1055 **Aaron Beattie**
Association mapping of malting quality traits in barley

1115 **Michael J. Edney**
Starch degrading enzymes and their role in brewing fermentation

1135 **Alex Speers**
The influence of malting barley on beer fermentability

1030 **Developing brewing value selection tools for malting barley breeding.** Brian Rossnagel, University of Saskatchewan, Crop Development Centre, Saskatoon, SK

Malting barley breeders serve three masters the barley grower, the maltster and the brewer. From a grain quality and eventual marketing viewpoint the key customer is the brewer. Barley breeders attempt to develop and release barley varieties with improved "malting/brewing" quality to create larger, more competitive and more profitable malting barley markets to increase demand for and value of the barley produced by farmers in western Canada. Traditionally (and currently) selection for genetic improvement in malting barley quality has focused on so-called malting quality traits which are important for efficient and profitable malting, but are also purportedly "correlated' with brewing quality and thus perceived to be of value to the brewer. However, while loosely "correlated" to brewing quality, recent work has shown that when selecting among elite malting barley breeding lines many of the malting quality traits measured at considerable cost to the breeding program bear little relationship to what the brewer really desires, that being maximum and efficient fermentation. Finally like all plant breeders, malting barley breeders require very inexpensive, rapid tests which can be conducted on very small grain/malt samples annually to aid in the selection for malting quality among many thousands of breeding progeny at as early a stage in the breeding/selection process as possible.

1055 **Association mapping of malting quality traits in barley**. Aaron Beattie, University of Saskatchewan, Crop Development Centre, Saskatoon, SK

Association mapping (AM) is a tool that can identify regions within a genome (genome-wide AM), or within a gene (candidate gene AM), linked to the expression of traits. Historical datasets are a valuable resource, particularly when the data describes time-consuming and/or expensive to measure traits, that can mined by AM for potential marker-trait relationships. A collection of 91 elite two-row malting barley (*Hordeum vulgare* L.) lines entered in the Western Canadian Co-operative Two-Row Barley Trials over a 13 year period were analysed by genome-wide AM to identify markers associated with seven malting quality traits. A linear mixed-model incorporating population structure and familial relatedness identified 27 diversity array technology (DArT) markers associated with malting quality. These markers will assist selection of parents with complementary allele combinations for future crosses and help identify progeny with the desired alleles. Candidate expressed sequence tags (ESTs) responsible for marker-trait associations were identified for 19 of the 27 DArT markers and include genes important for seed storage protein accumulation, gibberellin-mediated gene expression, seed storage mobilization and dormancy. One of the genes identified by genome-wide AM to be significantly related to diastatic power (i.e. a measure of starch degrading enzyme activity) encoded the limit dextrinase (LD) enzyme. Within malting barley, LD activity is a critical component of starch mobilization because it is the only enzyme in germinating barley seed capable of cleaving (1-6)-α-glucosidic linkages. Because yeast are unable to metabolize branched dextrins produced by amylases during starch hydrolysis, the action of LD is important to maximize the availability of fermentable sugars. The LD gene was sequenced across the same set of 91 lines in a candidate gene AM study to identify single nucleotide polymorphisms (SNPs) linked to higher LD activity. Preliminary associations between SNPs and LD activity will be presented.

1115 **Starch degrading enzymes and their role in brewing fermentation**. Michael J. Edney, Applied Barley Research-Crops Section, Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB

Fermentation is the central process in a brewery where yeast convert sugars to ethanol while producing important flavour compounds for beer. Yeast growth is also essential for meeting the strict timelines of modern breweries. Efficient production of ethanol is dependent on the supply of fermentable sugars, while adequate yeast growth is dependent on a supply of all essential nutrients, The majority of sugars in barley are tied up in starch which are unavailable for yeast metabolism. Fortunately, barley produces a family of enzymes that degrade barley starch to fermentable sugars. The enzymes, beta-amylase, alpha-amylase, limit dextrinase and alpha-glucosidase, are produced or released during barley germination. Beta-amylase, the enzyme of greatest concentration in malt, is an exo-acting enzyme that cleaves maltose from non-reducing ends of starch. The enzyme accumulates during grain development but is only activated during germination. Alpha-amylase is an endo-acting enzyme that releases dextrin substrates for the other enzymes. It is synthesized de novo during barley germination. Limit-dextrinase is an endo-acting enzyme that cleaves branch points in the starch releasing dextrin substrates for the other enzymes. Alpha-glucosidase is considered insignificant. In this presentation relationships between levels of the three major enzymes and fermentation will be discussed.

1135 **The influence of malting barley on beer fermentability**. Alex Speers, Dalhousie University, Food Science Program, Halifax, NS

Brewers are increasingly concerned with degree and variability of fermentability and how this directly impacts production efficiency and profit. The Brewing and Malting Barley Research Institute (BMBRI) lists fermentability as a malt trait requiring further understanding and research. Several starch degrading enzymes influence fermentability (i.e., α & β-amylases, limit dextrinase and possibly α-glucosidase). Canadian malt varieties possess high levels of these starch degrading enzymes and it has been argued that due to these high enzyme levels, enzyme thermal stability is not an issue. However, aside from one report that Harrington contains high β-amylase activity (vs. Schooner) there is a lack of information on thermal stability of these diastatic enzymes. Also fermentability is only partially explained by wort sugar levels. Barley variety, other malt factors and yeast strains also can influence the extent to which wort ferments. After a short introduction to brewing, this presentation will review our knowledge of this important brewing metric. Developments in bench-top techniques for fermentability assessment will also be discussed.

Monday, July 18, 2011
Canadian Society for Horticultural Science
Session 1: ***Symposium & General Session***

Oral Presentations
Time: 1030-1200h
Room: 415 Sobey Building

Chair: Samir Debnath
Agriculture & Agri-Food Canada

1030 ***Symposium:*** Invited Speaker
Davide Neri
Berry production in forced culture

General Session

1115 **Samir Debnath**
Molecular markers and antioxidant activity in berry crop diversity analysis

1130 **Samir Debnath**
Molecular analysis and antioxidant activity in micropropagated berry plants acclimatized under *ex vitro* condition

1145 **Tudor Borza**
Gene expression assessment of potassium phosphate foliar treatment of potato plants

1030 **Berry production in forced culture.** D. Neri, Department of Environment and Crop Science, Università Politecnica delle Marche, 60131 Ancona, Italy

Berry forced production is increasing in Europe and especially in Italy. The most cultivated berries for fresh market are strawberry and raspberry. In the past, the forcing techniques aimed at increasing earliness of June bearing strawberry varieties. Nowadays the purpose is to have a year-round production, preserving berry against unfavourable climatic conditions. In Southern areas (Sicily in Italy, Huelva in Spain) with Mediterranean climate characterized by mild winters, the aim is to anticipate vegetative wake up during the winter to speed up blooming and ripening. The plants are forced using plastic tunnels. Fresh dug plants produced in altitude or in the North nurseries are planted in October. Rise bed systems are commonly used. Very low chilling June-bearing varieties can anticipate the picking in November-December and continue to produce during winter and spring (till June). In this case the planting date is anticipated in September or programmed plants can be used later in October. The production cycle is 6-7 month-long. In the North areas two types of protection systems are widespread. The first is finalized to preserve the plants from damages caused by rain, hail, wind or sun, with limited influence on picking earliness. The protection is set over the crop when the plants start blooming after the winter (likely in April). The planting date is in July-August and the harvest period is very short in the spring, in the case of June bearing varieties. The ever bearing varieties extend the production period along the summer and they are slowly increasing. The second protection system is finalized to have the main production in early fall planting programmed plants in the summer. The date of ripening depends on the planting date and soil less culture is increasingly used. The risk of reduced flowers/pollen fertility is high with high temperature and this can cause damages in fruits that could be misshapen and malformed. To anticipate the second picking season after the winter rest, the covering must be in January. The different forcing techniques, both in the nursery and in the green house, will be analyzed as well as their physiological effects on plant architecture and fruit quality.

1115 **Molecular markers and antioxidant activity in berry crop diversity analysis.** S. C. Debnath[1]*, Y. L. Siow[2], J. Petkau[2], D. An[1,3] and N. V. Bykova[3]. [1]Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, Bldg. 25, 308 Brookfield Road, St. John's, NL, Canada A1E 6J5, [2]Canadian Centre for Agrifood Research in Health and Medicine, Agriculture and Agri-Food Canada, 351 Tache Avenue, Winnipeg, Canada MB R2H 2A6, [3]Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL, Canada A1B 3X9

An improved understanding of the important role of dietary fruits in maintaining human health has led to a dramatic increase of the global berry crop production. Berry fruits contain relatively high levels of vitamin C, cellulose and pectin, and produce anthocyanins which have important therapeutic values, including antitumor, antiulcer, antioxidant, and antiinflammatory activities. There is a pressing need to develop reliable methods for identifying berry germplasm and for assessing genetic diversity/relatedness in berry genotypes for practical breeding purposes and proprietary-rights protection. The introduction of molecular biology techniques, such as DNA-based markers, allows direct comparison of different genetic material independent of environmental influences. This review presents the progress in-depth of various aspects of molecular diversity analyses in berry crop improvement program of Atlantic Cool Climate Crop Research Centre in collaboration with Canadian Centre for Agrifood Research in Health and Medicine, and Biology Department of the Memorial University of Newfoundland. Significant

progress has been made in diversity analysis of wild cranberry, lowbush blueberry, lingonberry, and cloudberry germplasm, and in strawberry and raspberry cultivars and advanced lines developed in Canada. Inter simple sequence repeat (ISSR) markers detected a sufficient degree of polymorphism to differentiate among berry genotypes, making this technology valuable for cultivar identification and for the more efficient choice of parents in the current berry breeding programs. The paper also discusses the issues that still need to be addressed to utilize the full potential of molecular techniques including expressed sequence tag-polymerase chain reaction (EST-PCR) analysis to develop improved berry environmental friendly cultivars suited to the changing needs of growers and consumers.

1130 **Molecular analysis and antioxidant activity in micropropagated berry plants acclimatized under *ex vitro* condition.** S. C. Debnath[1]*, P. Vyas[1,2], J. C. Goyali[1,2] and A. U. Igamberdiev[2]. [1]Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, Bldg. 25, 308 Brookfield Road, St. John's, NL, Canada A1E 6J5, [2]Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL, Canada A1B 3X9

Berry crops include, but are not limited to the members of the genera: *Fragaria* (strawberry; Rosaceae), *Rubus* (brambles: raspberry and blackberry; Rosaceae), *Vaccinium* (blueberry, cranberry and lingonberry; Ericaceae) and *Ribes* (currant and gooseberry; Grossulariaceae). While berry fruits have long been enjoyed huge popularity among consumers, tremendous progress in plant tissue culture, resulting in great advances in micropropagation, has occurred. The *in vitro* morphogenesis seems to be highly dependent on plant growth regulators and media used for culture, which is again genotype specific. Although automation of micropropagation in bioreactors has been advanced as a possible way of reducing propagation cost, optimal plant production depends upon better understanding of physiological and biochemical responses of plant to the signals of culture microenvironment and an optimization of specific physical and chemical culture conditions to control the morphogenesis of berry plants in liquid culture systems. Increased branching, vigorous vegetative growth and change in biochemical components are often noted in micropropagated plants acclimatized under *ex vitro* condition. Clonal fidelity can be a serious problem and strategies have been developed in order to reduce the variation to manageable levels. Molecular markers such as RAPDs, RFLPs, AFLPs, DAFs, SCARs, SSRs, ISSRs and EST-PCRs have been introduced in tissue culture research and can potentially be used in various facets of pertinent studies with berry crops. The paper describes the progress in-depth of various aspects of berry propagation *in vitro*, characterization of micropropagated berry plants for morphological characters, anthocyanin contents and antioxidant activity, and on the employment of molecular markers in these plants for the assessment of genetic fidelity, uniformity, stability and trueness-to-type among donor plants and tissue culture regenerants.

1145 **Gene expression assessment of potassium phosphite foliar treatment of potato plants**. T. Borza[1]*, G. Simpson[1], A. Schofield[1], S. Lim[1], R. Coffin[2], R. Peters[3], Z. Ganga[4], D. Pinto[5], K. Al-Mughrabi[6], B. Prithiviraj[1] and G. Wang-Pruski[1]. [1]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Privar Farms Inc., PEI, [3]Agriculture and Agri-Food Canada, PEI, [4]Cavendish Farms, PEI, [5]National Research Council-IMB, [6]New Brunswick Department of Agriculture, Aquaculture and Fisheries

Late blight, caused by *Phytophthora infestans*, represents one of the major pathogens of cultivated potato (*Solanum tuberosum*). Phosphites are a class of reduced risk fungicides efficient against specific species of Oomycetes (i.e. species of *Phytophthora* and *Pythium*). The toxic effect of phosphites to *P. infestans* is well documented; however, it is not clear if *P. infestans*

suppression is caused mainly by the direct action of phosphites or by the activation of specific defence mechanisms in the potato plant. In order to further investigate the molecular mechanisms by which phosphites enhance the resistance of potato plants to *P. infestans* infection, we set up to study, by quantitative RT-PCR (qPCR), the expression of several genes involved in carbohydrate metabolism and in defence pathways. Our experiment employed Confine™, a mono- and di-potassium salt formulation of phosphorous acid (Winfield Solutions, LLC, St. Paul, MN). Leaf samples of Confine-treated (sprayed with 1% Confine) and untreated (control) potato plants were collected 30 min, 2 h, 6 h, 24 h and 48 h after treatment. The expression levels of 10 genes from *S. tuberosum* were assessed by qPCR to quantify the effects of Confine application. Ten days after Confine™ treatment, untreated and Confine-treated plants were inoculated with *P. infestans* (10^4 sporangia/mL) and the severity of disease was monitored during a 4-week period. Four weeks after the infection with *P. infestans*, the percentage of foliar necrosis of untreated plants was >95 % while that of Confine-treated plants was <20%. The expression of the 10 genes was analysed in *P. infestans* infected leaves and in apparently healthy leaves from both untreated and Confine-treated plants.

Monday, July 18, 2011 **Oral Presentations**
Canadian Society for Horticultural Science **Time:** 1300-1500h
Session 2: ***Student General Session*** **Room**: 415 Sobey Building

Chair: David Percival
Nova Scotia Agricultural College

1300 **David Hobson**
Fertility management of establishing organic blackcurrants (*Ribes nigrum L.*) in Atlantic Canada

1315 **Poorva Vyas**
Enhanced levels of phenolic compounds and antioxidant capacity in *in vitro* derived lingonberry plants

1330 **Katelyn Congreves**
Post-harvest organic carbon amendments to minimize mineral nitrogen losses in cole crop production: *in situ*

1345 **Mirza Muhammad Qadeer Baig**
Reduced-stature Rosa species through *in vitro* mutagenesis

1400 **Travis Esau**
Development of a prototype variable rate sprayer using digital color cameras for spot-specific application of agrochemicals in wild blueberry

1415 **Fahad Khan**
Mapping soil properties using electromagnetic induction methods in wild blueberry

1430 **Aitazaz Farooque**
Characterize and quantify soil variability to delineate management zones for variable rate fertilization in wild blueberry fields

1300 **Fertility management of establishing organic blackcurrants (*Ribes nigrum* L.) in Atlantic Canada.** D. Hobson[1]*, A. Hammermeister[1], D. Lynch[1] and K. Pruski[2]. [1]Organic Agriculture Centre of Canada, Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

To study the effects of fertility rate and timing in Spring (SP + 0 kg ha^{-1} estimated available N (SP0), SP50, SP100, and SP150), Summer (SU150) and Split (SL50/100 and SL100/50) on vegetative growth and yield of establishing blackcurrants using organic amendments (blend of granulated poultry manure (Nutriwave®), and crabmeal), a factorial trial was established in 2009 on new plantings of cv. Titania (2 yr bare-root) at two sites in PEI. Measurements on plant growth, June and leaf nutrients (LN) collected at the end of July for 2009 and 2010, and nutrient supply rate (Plant Root Simulator (PRS®) probes) buried at 10cm for two weeks in mid-June 2010, and berry size and soluble sugar content (Brix). There were no differences in plant growth in the first year of growth. Differences in growth, yield and leaf N were greater at site 1 than site 2. In 2010, plant volume was greatest in SP150, but there were no significant differences between any of the other treatments and the control at site 1, and no differences at site 2. LN N was highest for SL50/100 while SU150 was lowest at site 1 ($p=0.043$), but site 2 had no differences ($p=0.495$). Plant available N from PRS® probes was highest in SP150 at site 2, but site 1 showed no significant differences ($p=0.296$). Yield was reduced for SP0 and SP50 at site 1; however, plants suffered raccoon damage which removed a significant quantity of berries from the bushes. Yield of SL100/50 was greatest in site 2, and lowest in the control. There were no differences in berry size or sugar content across any of the treatments. In summary, blackcurrants yields but not berry quality increased in response to organic fertility amendments, but nitrogen levels showed little differences across the treatments.

1315 **Enhanced levels of phenolic compounds and antioxidant capacity in in vitro derived lingonberry plants.** P. Vyas[12*], S.C. Debnath[2] and A.U. Igamberdiev[1], Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL Canada A1B 3X9, [2]Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, Bldg. 25, 308 Brookfield Road, St. John's, NL Canada A1E 6J5

Levels of antioxidant metabolites including total soluble phenolic content, total flavonoids, tannins, anthocyanins, as well as the total radical scavenging capacity, were quantified in leaves and fruits of lingonberry (*Vaccinium vitis-idaea* L.) cultivars Regal, Splendor and Ernteda nk. Each of these cultivars was obtained by three different propagation methods: conventional softwood cuttings, *in vitro* propagation of nodal explants and shoot regeneration from excised leaves of micropropagated shoots. The comparative study was performed to choose the most suitable cultivation method for getting high levels of antioxidants. It was determined that the *in vitro*-derived lingonberry cultivars had higher levels of total DPPH radical scavenging activity in both fruits and leaves, the highest being in the plants obtained from leaf cultures. The levels of all investigated antioxidant metabolites were much higher in leaves than in fruits. The phenolic content was the highest in the fruits of plants obtained from leaf culture, while in the leaves it was higher in the plants obtained by stem cutting.

1330 **Post-harvest organic carbon amendments to minimize mineral nitrogen losses in cole crop production: *in situ*.** K. A. Congreves [1]*, R. P. Voroney [2], I. P. O'Halloran [1] and L. L. Van Eerd [1]. [1]School of Environmental Sciences, University of Guelph, Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0, [2]Guelph, Ontario, Canada N1G 2W1

Cole crops, compared to many other vegetable crops, pose a great risk of inorganic N losses during the post-harvest period due to their high plant N content and low harvest index. A management practice of amending soil with readily decomposable organic carbon has the potential to immobilize excess N in agricultural systems. In a broccoli (*Brassica oleracea* var. *Italica* cv 'Ironman') -spring wheat (*Triticum aestivum* L.) rotation, a two-year, replicated field study (2009-2010 and 2010-2011) was conducted to determine the effects of organic carbon amendment on soil mineral N content (0-60 cm soil depth) after broccoli harvest. The experiment was a randomized complete block design with four replications, in both early and late broccoli production. Post-harvest treatments included a control (incorporated broccoli crop residue), a reference (oat (*Avena sativa* L.) cover crop), and three different broccoli crop residue + organic carbon amendments (at 5 t ha^{-1}): (i) crop residue + wheat straw (ii) crop residue + yard waste, and (iii) crop residue + used cooking oil. After broccoli harvest, crop residue was stock chopped, organic carbon amendments were hand applied, and disked twice for incorporation. In the subsequent growing season spring wheat was grown, with N fertilizer (90 kg N ha^{-1}) as a control treatment, and with no N fertilizer treatments. Preliminary results indicate that used cooking oil amendments lowered soil NO_3^--N concentrations by 16.5, 24.0, and 20.0, 15.2 mg NO_3^--N kg^{-1} soil, relative to control during the autumn after 2009 early and late harvest, and 2010 early and late harvest, respectively. Wheat straw and yard waste reduced soil NO_3^--N concentrations after early harvest 2010, yet neither after late harvest 2010, or early and late harvest 2009. There was no impact of organic carbon amendments on spring wheat yield or grain % N in the subsequent growing season in 2010. Thus, the incorporation of used cooking oil after broccoli harvest is a potential N management practice to minimize over-winter N losses in cole crop production.

1345 **Reduced-stature Rosa species through in vitro mutagenesis**. M.M.Q.Baig[1],[2*], I.A. Hafiz[1], N.A. Abbasi[1], T. Ahmad[1] and D. J. Donnelly[2], [1]Department of Horticulture, PMAS-Arid Agriculture University Rawalpindi, Pakistan, [2]Department of Plant Science, McGill University, Quebec, Canada

Plant height is one of the main attributes affecting general appeal and beauty of roses (*Rosa* spp.). Among the highly scented rose species, *R. gruss an teplitz*, *R. centifolia*, and *R. borboniana,* have great potential horticultural and commercial value. However, their large plant size detracts from recent trends towards selection of smaller plants for emerging markets and high-density plantations. This study aimed to produce reduced-stature plants through *in vitro* mutagenesis using gamma irradiation (Co_{60}). Shoot tips (4 reps of 15 shoot tips/rep for each of 13 treatments) cut from micropropagated shoots were exposed to up to 120 Gy. Irradiated shoot tips were micropropagated for one culture cycle. Surviving shoots were rooted *in vitro* then acclimatized for 2 months in a greenhouse. The shoot tip LD_{50} after gamma irradiation was species-dependent and 33- 54 Gy . In this dose range, survival during *in vitro* rooting and acclimatization was also affected; this was 64 to 24% and 34 to 14% of control values, respectively. Acclimatized transplants were 17 to 56% smaller with 16 to 51% less leaf area compared with the controls. Putative reduced-stature roses will be monitored over the next few years for vegetative and floral characteristics. This study adds to the ongoing efforts to obtain reduced-stature rose plants for horticultural purposes.

1400 **Development of a prototype variable rate sprayer using digital color cameras for spot-specific application of agrochemicals in wild blueberry.** T. J. Esau[1*], Q. U. Zaman[1], Y. K. Chang[1], A. W. Schumann[2], D. C. Percival[1], A. A. Farooque[1]. [1]Nova Scotia Agricultural College, PO Box 550, Truro, NS, B2N 5E3; and [2]Citrus Research and Educational Center, Lake Alfred, Florida

Wild blueberry yields are highly dependent upon agrochemicals for proper weed, disease and pest management. Growers apply uniform applications of herbicides for pre/post-emergence control of grasses and weeds, fungicides for fruit rot, monilinia blight, botrytis, valdensinea and rust, and insecticides for aphid, maggot and spanworm control. The repeated and excessive use of agrochemicals has increased cost of production and is harmful to the environment. The proper targeting of agrochemicals on an as needed basis has the potential to save a substantial amount of chemical. Therefore, the development of a real-time camera vision sensing and control system with a variable rate sprayer is capable of detecting and spraying required agrochemicals at various times of the year. The objective of this study was to incorporate cost effective μEye digital color cameras in front of a 20 foot boom sprayer propelled by a Yamaha rhino all-terrain vehicle. Custom image processing software that is capable of processing the images in real-time was used to detect weeds in mowed wild blueberry filelds. The software is able to send triggering information through a Labjack U3-HV device to a variable rate controller that sends a 12-volt direct current power signal to the solenoid valves opening the nozzles in the specific spot where the target has been detected. 20 foot wide test plots were selected in wild blueberry fields and the weed areas were mapped using an accurate RTK DGPS base station and rover set-up. A water and kaolin dye was applied and the targeted areas were mapped with the GPS for comparison using ArcMap 10 GIS software. Water sensitive papers were also placed at randomly selected locations in the test strips for statistical analysis purposes. The results can be used to determine the performance of applying agrochemical on a site-specific basis using a variable rate sprayer with real-time vision technology which will result in lowering the cost of production and reducing environmental contamination.

1415 **Mapping soil properties using electromagnetic induction methods in wild blueberry.** F. Khan[1*], Q. Zaman[1], A. Schumann[3], A. Madani[1], D. Percival[2], A. Farooque[1] and S. Saleem[1]. [1]Banting Building, Department of Engineering, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Cox Institute, Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [3]Citrus Research and Education Center, Department of Soil and Water Science, University of Florida, Lake Alfred, Florida, U.S.A. FL 33850

One of the fundamental deficiencies in many high value agriculture production systems is the lack of detailed, up-to-date and pertinent geo-referenced soil information. Rapid soil data are essential to ensure the optimum long-term management of fields and sustainability of agricultural systems. Detailed geo-referenced maps would be useful for site-specific management of agricultural inputs on an as needed basis. The objective of this study was to estimate and map variability in soil properties using a ground conductivity meter (DualEM, Milton, Ontario, Canada). Two wild blueberry (Vaccinium angustifolium Ait) fields were selected in central Nova Scotia. The selected fields had been under commercial management over the past decade with conventional fertilizer, weed and disease management practices. A grid pattern of sampling points was established (n=50 for field 1; n=50 for field 2) at each experimental site. Soil samples were collected from established grid points and were analyzed for soil texture, soil organic matter content, soil volumetric moisture content (Θ_v), soil pH and soil electrical conductivity. The ground conductivity was measured and recorded with DualEM-2 at the same selected grid points to calibrate the Dual EM-2 for the prediction of soil properties. Two comprehensive surveys were

conducted in those fields to measure the ground conductivity for soil moisture and organic matter estimation in real-time using DualEM and a differential global positioning system (DGPS). Linear regression analysis showed that apparent electrical conductivity (ECa) was significantly correlated with selected soil properties for the fields. The soil properties were predicted using regression equation, and the accuracy of the estimated values from ground conductivity data was calculated using root mean square error. The maps were developed for predicted soil parameters from ground conductivity survey data using Kriging interpolation in Arc GIS 9.3 (ESRI, Redlands, CA) software. The maps showed substantial variation in selected fields. This information will help to develop variable rate technologies like irrigation scheduling, drainage designing and variable rate fertilization in the field. The research results will be presented in the paper.

1430 **Characterize and quantify soil variability to delineate management zones for variable rate fertilization in wild blueberry fields.** A.A. Farooque[1]*, Q. U. Zaman[1], A. Madani[1], A.W. Schumann[2], D. C. Percival[1], T. J. Esau[1], F. S. Khan[1], S. R. Saleem[1], Y. K. Chang[1]. [1]Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Citrus Researches and Education Center, University of Florida, USA

The concept of management zones has been proposed as a solution to the problems associated with soil variability to more efficiently apply agricultural inputs on a site specific basis. Currently, crop management practices are implemented uniformly with inadequate attention being given to substantial variation in soil/plant characteristics, topographic features and fruit yield. Therefore, the objective of this study was to characterize and quantify variability in soil properties and fruit yield and develop management zones for site-specific fertilization. Two wild blueberry fields were selected and a grid pattern (15x15 m) was established at each experimental site to collect soil and fruit yield samples. These soil samples were analyzed for NH_4^+-N, NO_3^--N, pH, EC, texture and organic matter. The volumetric moisture content ($\ddot{y}_V$) and ground conductivity (HCP and PRP) were also recorded at the same grid points. The location of the sampling points were marked with a DGPS, and bare spots, weeds and grass patches were also mapped. The coefficient of variation, geostatistical range of influence and kriged maps suggested moderate to high variability of all soil properties and fruit yield except soil pH and silt. The cluster analysis grouped the soil and fruit yield data into five zones termed as 'very poor', 'poor', 'medium', 'good' and 'very good' zones without prior knowledge of productivity potential. Each zone exhibited the internal homogeneity and external heterogeneity at a similarity level of greater than 70%. The results of ANOVA suggested that fruit yield, HCP, PRP, $\ddot{y}_V$ and inorganic nitrogen were significantly different in developed management zones except poor and very poor zones. The correlation analysis showed significant relationships among the soil properties and fruit yield except silt and pH. The significant correlations of ground conductivity with soil properties and fruit yield suggested that a Dual EM can be used to develop management zones. Based on these results it is proposed to define bare spots as a separate class while delineating management zone, it would be helpful in saving significant amount s of fertilizer using a variable rate spreader. These results would also help in ameliorating the unproductive areas, soil variability characterization and identification of the soil properties responsible for yield variability to develop prescription maps for site-specific fertilization.

Monday, July 18, 2011 **Oral Presentations**
Canadian Society for Horticultural Science **Time:** 1530-1700h
Session 3: ***General Session*** **Room**: 415 Sobey Building

Chair: Kris Pruski
Nova Scotia Agricultural College

1530 **Li Juan Yu**
Effect of acidification on quality and shelf-life of carrot juice

1545 **William Paton**
Mundulla Yellows: a 30 year problem solved?

1600 **Jatinder Kaur**
Seasonal growth dynamics and carbon partitioning of the wild blueberry plant (*Vaccinium angustifolium* Ait.)

1615 **John M. DeLong**
Chlorophyll fluorescence for *in vivo* stress detection in horticultural crops

1630 **Om Rajora**
Genomics of plants' responses and adaptation to global climate change

1645 **Kathleen Brown**
Anatomical traits for efficient soil exploration and stress tolerance

1530 **Effect of acidification on quality and shelf-life of carrot juice.** L. J. Yu* and V. Rupasinghe. Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Acidification is a practical method to extend the shelf-life of fruit and vegetable juices. This study compared the effects of different acidification methods: blanching of carrot with 2 to 4 mg kg^{-1} of citric acid, 2 to 4 mg kg^{-1} of lactic acid and blending carrot juice with cranberry juice in the 80:20 and 70:30 ratios on the quality in terms of pH, TA, total soluble solids (TSS), turbidity, ferric reducing antioxidant power (FRAP) and beta-Carotene, and shelf-life of carrot juices in terms of total aerobic count (TAC). Water blanched carrot juice was selected as the control instead of untreated carrot juice because blanching is the necessary processing step for carrot juice processing. During the 21-day storage, the pH, TA, TSS and turbidity values were much more stable for all acidified juices than water blanched juices. The highest stability and value of antioxidant capacity (FRAP value) belonged to carrot-cranberry juice blends in 70:30 ratios compared with water blanched juices after the 21-day storage. For beta-Carotene results, carrot-cranberry juice blends in 80:20 ratios and water blanched juices gave the maximum stability compared with other juice samples. However, the highest beta-Carotene value on day 21 belonged to 4 mg kg^{-1} of lactic acid blanched juices. All acidification methods could effectively prolong the shelf-life of juices in terms of TAC value. Blanching with 4 mg kg^{-1} of lactic acid and 4 mg kg^{-1} of citric acid were among the most effective methods for expending the shelf-life of carrot juices.

1545 **Mundulla Yellows: a 30 year problem solved?** W. Paton*. Biology Department, Brandon University, Brandon, Manitoba, Canada

Mundulla yellows, a fatal disease of Eucalypts and other native Australian plants is characterized by progressive yellowing and dieback of branches. Death occurs over several years. First observed in South Australia in the 1970s it has spread into other states. To date the cause is not known. Observing and researching the phenomenon in Western Australia and Queensland in 2008, evidence is presented that suggests an abiotic trigger and strong parallels to tree and shrub decline on the Canadian Prairies in the 1940s-1960s and more recently in the mid-1970s until today.

1600 **Seasonal growth dynamics and carbon allocation of the wild blueberry plant (*Vaccinium angustifolium* Ait.).** J. Kaur[1], D. Percival[1]*, L. J. Hainstock[1] and J. P. Prive[2]. [1]Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Senator Hervé J. Michaud Research Farm, Agriculture and Agri-Food Canada, Bouctouche, New Brunswick, Canada

Field studies were conducted at wild blueberry research station, Debert to examine t he carbon allocation dynamics within the wild blueberry (*Vaccinium angustifolium* Ait.). This was achieved with biweekly measurements of dry weight, soluble sugar and starch levels of the rhizomes, roots, stems/leaves and berries of plants in the vegetative (VPP) and fruiting/cropping (CPP) phases of production. Non-structural carbohydrate levels were determined using high-pressure liquid chromatography (HPLC). Growth parameters included phenology, stem height, number of nodes per stem and dry weights of the above ground vegetation (stems and leaves), berries, rhizomes and roots. During most of the study, dry weight for rhizome remained higher compared to stem

and leaves. Rapid growth of the stem and root tissues occurred within depletion of rhizome dry weights as the rhizomes acted as a source of reserved carbohydrates to the meristematic tissues. Interestingly, root growth was observed prior to upright shoot emergence. The presence of the developing berry crop appeared to be a strong sink for photo-assimilates, as berries were found to import sucrose and convert it to fructose and glucose upon maturation. HPLC studies further confirmed the increasing levels of fructose and glucose with fruit maturity. Maintenance of functional leaf area had a significant impact on the carbohydrate source-sink dynamics with photo-assimilate supply late in the growing season (i.e., post harvest) resulting in increased rhizome sugar and starch levels and also dry weights. Given the phenology of the wild blueberry, the results exemplify the importance of the rhizomes as a strong carbohydrate source, especially in the early stages of a growing season when the carbohydrate production is limited.

1615 **Chlorophyll fluorescence for in vivo stress detection in horticultural crops.** J. M. DeLong*, R. K. Prange, A. H. Wright and P. A. Harrison. Atlantic Food and Horticultural Research Centre, Agriculture and Agri-Food Canada, 32 Main St., Kentville, Nova Scotia, Canada, B4N 1J5

Chlorophyll fluorescence (CF) has been termed a rich, but ambiguous signal. Since Kautsky's observations of leaf fluorescence in the 1930s, the theoretical understanding of CF has paralleled advances in understanding the mechanisms involved in the light reactions of photosynthesis. The development of pulse amplitude modulated (PAM) fluorometry in the 1980s facilitated a boom in the use of CF as standard methodology for detecting plant stresses from a variety of sources. In 2001, the CF-based HarvestWatch™ technology was introduced and employs pulse frequency modulation (PFM) of an excitation light source. This technique is now used in research and industrial applications worldwide, particularly for detecting and monitoring dynamic changes in the low oxygen (O_2) limit (LOL) in fruits or vegetables in a low-O_2 controlled atmosphere (CA) environment. In general, chlorophyll fluorescence methodology is popular because it is rapid and non-destructive, facilitates repeated observations on the same experimental unit and provides direct measurements of fundamental photosynthetic reactions. This presentation will highlight the physiology and application of CF as an in vivo stress probe for horticultural plants with emphasis on its usage in crop storage environments.

1630 **Genomics of plants' responses and adaptation to global climate change.** O. P. Rajora, Canadian Genomics and Conservation Genetics Institute, Faculty of Forestry and Environmental Management, University of New Brunswick, Fredericton, NB E3B 6C2 Canada

Rapid global climate change has become a prominent driving force of evolution in plant ecosystems, subjecting our planet's plants to significant abiotic stresses. This can affect plants' fitness, adaptation, productivity and evolutionary potential. Northern boreal and temperate forest trees/ecosystems are considered to be the most vulnerable to global climate change. There is an urgent need to understand the genomic basis of responses and adaptation of plants/forest tree to climate change in order to develop and use genetically improved plant varieties and to conserve and sustainably manage well-adapted, genetically diverse and healthy plant/forest genetic resources. We are using structural, functional and population genomics approaches to address this very important issue in economically and ecologically important North American boreal and temperate spruce (*Picea*) species. We have sequenced the transcriptomes of two spruce species grown under normal, elevated CO_2, drought and their combined conditions. Differentially expressed genes in response to elevated CO_2 and drought conditions and their relationships with physiological traits were discovered. We have identified and mapped quantitative trait loci (QTLs) for growth, biomass allocation and water-use-efficiency traits in spruce grown under normal and drought conditions. We are identifying and mapping genes and QTLs for traits related to growth and adaptation to climate change in spruce grown under ambient and elevated CO_2

conditions. I will discuss how genomics research and applications can assist in understanding plants' responses and adaptation to climate change by presenting highlights of our own spruce genomics work.

1645 **Anatomical traits for efficient soil exploration and stress tolerance.** K. M. Brown*, A. L. Burton, R. Jaramillo and J. P. Lynch**.** Department of Horticulture, Penn State University, University Park, PA 16802, USA

Crops subject to soil stresses, such as drought and nutrient deficiency, typically allocate more resources to roots to permit exploration for the limiting resource. In maize (*Zea mays* L.), the formation of lysigenous root cortical aerenchyma (RCA) liberates nutrients formerly tied up in cortical cell structures, and reduces the respiration required for cortical cell maintenance. RCA forms in the older parts of the roots and is most abundant in the crown roots. Comparisons of genotypes differing in RCA development show that more RCA is associated with reduced root respiration, but that a more important driver of respiratory differences is the remaining cortical cells, measured as living cortical area (LCA). Genotypes may vary in LCA as a result of differences in RCA formation or as a result of variation in root diameter, cortical cell size, and the number of cortical cell files. RCA is genetically independent of the other anatomical traits, and could therefore be used to select genotypes with improved tolerance to nutrient deficiency and drought. In addition, it would be possible to reduce the cost of root exploration by selecting genotypes with fewer cortical cells to support.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society for Horticultural Science **Time:** 0830-0915h
Session 4: ***Symposium*** **Room**: 415 Sobey Building

Chair: Peter Hicklenton
Agriculture and Agri-Food Canada, Kentville

0830 Symposium: Invited Speaker
Jean-Pierre Privé
Agro-ecosystem approach to understanding environmental stress in fruit and vegetable production

0915 CSHS/OACC Joint Session – Invited Speaker
Ralph Martin
Organic agriculture: contributions to sustainable horticulture

0830 **Agro-ecosystem approach to understanding environmental stress in fruit and vegetable production.** J. -P. Privé, Agriculture and Agri-Food Canada, Senator H.J. Michaud Research Farm, P. O. Box 2069, Bouctouche NB E4S 2J2, Canada

The objective of new agro-ecosystems for the production of high value horticultural field crops is to improve their growing environment, thereby reducing the various stresses and challenges from the inclement weather. A major trend in production throughout the northern hemisphere is the use of some form of physical protection for the crop and can range from temporary row covers to high tunnels. Plants and fruits produced within these new agro-ecosystems may provide a more environmentally durable ecosystem with the concomitant reduction in exposure to certain pathogens and an increase in marketable fruit and vegetable quality. An integrated, multidisciplinary systems approach to studying the effects of protected structures on the interaction of three trophic webs (plant, disease and insect) will be presented.

0915 **Organic agriculture: contributions to sustainable horticulture.** R. C. Martin, Organic Agriculture Centre of Canada, Nova Scotia Agricultural College, Truro, NS, Canada

The vision of the Organic Agriculture Centre of Canada is to have sustainable and science-based organic agricultural systems supporting healthy Canadian communities. With this direction and with input from over 600 organic producers across Canada and substantial funding commitments from industry partners, the Organic Science Cluster was proposed. First year results from these projects are based on research in organic greenhouse fertility management and energy efficiency, organic vegetable nutrition, pest control, seedling and transplant optimization and high value fruit production pest control and season extension. Organic production is assessed in the context of healthy food, profitability, resilient production units and conserving air, water, soil, N, P and biodiversity in a period of declining fossil fuels, climate change and economic instability. Consideration is given to reducing waste along the value chain, the accessibility and affordability of healthy food and appropriate diets for a healthy lifestyle. The principle of excellent agronomy and horticultural practice rather than substituting conventional inputs is also explored.The goal of eating well in sustainable communities is compared and contrasted with the goal of feeding the world.

Wednesday, July 20, 2011
Canadian Society for Horticultural Science
Session 5: ***CSHS/OACC Joint Session***
Organic agriculture: contributios to sustainable horticulture

Oral Presentations
Time: 1030-1200h
Room: 415 Sobey Building

Chair: Jean-Pierre Privé
Agriculture and Agri-Food Canada, Bouctouche

1030 **Josée Owen**
Seasonal contribution of nitrogen from compost in application year and subsequent years to broccoli in a long term organic rotations experiment

1045 **Josée Owen**
Strong partnerships achieve big successes: ten years of partnership between the Canadian Society for Horticultural Science (CSHS) and the Ghana Institute of Horticulturists (GhIH) in Ghana's impoverished Upper West Region

1100 **Samir Debnath**
Organic Agriculture project in Nepal: an international twinning partnership program

1115 **Karen Nelson**
Best Management practices for organic blackcurrant production

1130 **Ali Aljaloud**
Screening of salt tolerant plants for prompting greenery in Saudi Arabia

1145 **Surya Acharya**
New sainfoin keeps pace with alfalfa for safe grazing

1030 **Seasonal contribution of nitrogen from compost in application year and subsequent years to broccoli in a long term organic rotations experiment.** J. Owen[1*], S. LeBlanc[1] and S. Fillmore[2]. [1]Agriculture and Agri-Food Canada, Bouctouche NB E4S 2J2; [2]Agriculture and Agri-Food Canada, Kentville NS

One of the greatest challenges to producing vegetable crops in organic systems is ensuring adequate plant nutrient supply to meet the changing demands of a crop over its life-cycle. Organic fertility amendments are particularly challenging because only a small portion of the nutrient content is available immediately, while the remainder is released through mineralization, which is, in turn, mitigated by a host of factors such as soil temperature and moisture. How nutrients from compost are released to the soil in the application and subsequent years is the subject of research at a long term organic rotations experiment in Bouctouche New Brunswick, where broccoli, cereal underseeded to red clover, and red clover are grown in a three-year fully-phased latinized block design with six replicates over two sites. Fertility treatments consist of three fertility regimes (Synthetic Fertiliser or SF+, Low Rate Compost or LRC+, and High Rate Compost or HRC+) applied annually since 2001, until 2006, when plots were subdivided and half of each received no further fertility applications (SF-, LRC-, HRC-). From 2006 to 2009, yield and tissue N analysis of broccoli were measured along with fall soil bulk density and fall soil organic matter. In addition, sequential two-week burials of ion exchange membranes were used to capture the plant available ion concentrations, providing a season-long view of the contribution of fertility regime to soil fertility. Results showed that broccoli yields were relatively poor (up to 6.8 t ha^{-1}), despite sufficient tissue N levels (stems 1.1 to 4.4 % of dry matter; heads 1.9 to 5.7 % of dry matter). A pattern of greater head tissue N in "–" plots versus "+" plots emerged from 2006 to 2008, whereas head tissue N in SF- plots was always less than in SF+ plots. Among composted fertility treatments only small differences in season-long cumulative N supply were detected, suggesting that composting at low rates conferred essentially the same fertility benefits as at the rate 3 times higher.

1045 **Strong partnerships achieve big successes: ten years of partnership between the Canadian Society for Horticultural Science (CSHS) and the Ghana Institute of Horticulturists (GhIH) in Ghana's impoverished Upper West Region.** J. Owen[1], M. R. McDonald[2], M. Pritchard[3], D. Ceplis[4], A. -H. Abubakari[5], K. G. Mahunu[5], I.A. Idun[6] and P. Kumah[6]. [1]Agriculture and Agri-Food Canada, Bouctouche NB, [2]University of Guelph, Guelph ON, [3]University of Manitoba, Winnipeg MB, [4]Box 1716 Minnedosa MB, [5]University for Development Studies, Tamale, Ghana, [6]Kwame Nkrumah University of Science and Technology, Kumasi, Ghana

Increased food security, better nutrition, and more income for people in one of Ghana's poorest regions, have all resulted from ten years of partnership between the CSHS and the GhIH in a CIDA-funded International Twinning Partnership Project through the Agricultural Institute of Canada. The project had two main goals: 1) to support GhIH in the development of dry season vegetable growing in the impoverished Upper West Region of Ghana, which has 7 to 8 dry months a year, and 2) strengthen the institutional capacity of the GhIH so it could be a catalyst for change. Partnerships and the commitment of volunteers resulted in many successes, with a relatively low budget of ~$40,000 a year. The project funds were spent on education, training, organizational capacity and leveraging of resources from cooperating partners in the region, rather than delivering supplies and physical resources. Project funds allowed in-country horticulture experts from the universities to develop the programs and travel to the region to

deliver training. One strong component was the Farmer Field Schools, along with Training of the Trainer workshops, in which participants learn techniques and share their acquired knowledge. Demonstration gardens showed the benefits of techniques such as seedling transplantation, companion planting, compost making and use, seed selection, production and storage, neem production and use, and safe pesticide handling. This information was extended across the region using radio broadcasts in native languages. Emphasis was placed on participation and empowerment of women. Over 96% of participants reported higher yields and higher incomes which meant more vegetables for home consumption and the ability to pay school fees, register for the health service and purchase bicycles, animals and improvements for their houses. The CSHS-GhIH partnership has ensured the sustainability of these improvements by building lasting relationships, including the water users associations and farmer groups in villages, and involving local Ministry of Agriculture extension agents in delivering Farmer Field Schools and workshops. The GhIH itself has become a voice for the horticulture industry and professionals, advancing horticultural priorities in political and academic arenas.

1100 **Organic Agriculture project in Nepal: an international twinning partnership program** **Organic Agriculture project in Nepal: An international twinning partnership program.** R. R. Burlakoti[1], D. Lynch[2], C. Halde[3], T. Beach[4], S. Dahal[5] and S. C. Debnath[6]*. [1]Weather INnovations Incorporated, Chatham, Ontario, Canada N7L OB1, [2]Depa rtment of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [3]Organic Agriculture Centre of Canada, Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada R3T 2N2, [4]Agricultural Institute of Canada, 9 Corvus Court, Ottawa Ontario, Canada K2E 7Z4, [5]Sustainable Agriculture Development Program, Tanahu, Nepal, [6]Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, 308 Brookfield Road, St. John's, NL, Canada A1E 5Y7

Agriculture is the major occupation in Nepal contributing 32% of total gross domestic product (GDP) and 75% of the country's export. The traditional way of farming using low inputs (inorganic fertilizers and pesticides) provides opportunities to adopt organic farming for diversified crops, with potential domestic markets and export markets in Japan and Europe. With a goal of improving the livelihood of rural ethnic marginalized farmers of the mid-western hill of Nepal, an international development project has been started through a joint effort of Agricultural Institute of Canada (AIC), Sustainable Agricultural Development Program, Nepal (SADP), Canadian Society of Agronomy (CSA) and Canadian Society of Horticultural Science (CSHS). The Canadian team conducted a feasibility study in December 2009 by visiting the project area in Nepal, and interacted with beneficiaries (ethnic and marginal farmers), project partners and supportive organizations. A one-year project entitled, "Research and support to Organic Agriculture in Tanahu district of Nepal" commenced in April 2010 for research and support of organic farming in Tanahu district, Nepal. Canadian team members again visited Nepal in December 2010 and monitored the project progress. To date the project has successfully: strengthened the organizational capacity of the lead organization (SADP), conducted a baseline assessment study in the project area, assessed the potential domestic market for organic product, promoted organic farming among the ethnic marginal farmers groups (Kumal and Derai), identified and established a strong collaborative project link with the agricultural university and scientific societies of Nepal, and prepared a detail five-year project proposal for 2011 to 2016. The five-year project aims to change the subsistent traditional farming to commercial organic farming in the target area and will improve the livelihood of the farmers through better income generation from organic farming. The project will include scientific research on organic farming led by the Institute of Agriculture and Animal Science, TU, Nepal in collaboration with other scientific societies of Nepal. The Canadian team member (CSA and CSHS) will provide technical input, advice for the project, and monitor and supervise the project progress.

1115 **Best management practices for organic blackcurrant production.** K. L. Nelson* and A. M. Hammermeister. Organic Agriculture Centre of Canada, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Organic producers in Prince Edward Island are growing blackcurrants (*Ribes nigrum* L.) to diversify their operations and supply domestic and international markets. The organic management of weeds, fertility and diseases has not been well established. In 2009 trials were initiated at two sites previously planted in 2008 to examine the impacts of six treatments: (i) no fertility or weed control (Control); (ii) weed control only (Wonly); (iii) weed control + spring fertility (W+S); (iv) summer only (W+F); (v) spring and summer (W+SF); and (vi) weed control + fish fertilizer drench (W+D). In 2010, a disease management treatment was superimposed to create a split-plot design with disease control as the main plot (i.e. with or without sulphur spray) and three replicates of each fertility/weed control treatment as subplots. Fertility was supplied from a mixture (50:50, based on N content) of crabmeal (7% Ntot) and commercially available granulated poultry manure (4-1-2). Weeds were controlled using a 1m strip of black polyethylene plastic. A foliar sulphur spray was applied to half of the plants to assess its effects on the plants and disease. The disease of greatest prominence was white pine blister rust, with 90% leaf infection on most plants at both sites. The efficacy of the sulphur treatment was very low, and the treatment reduced plant growth at one site. In 2009 growth in the Control was significantly lower than in the Wonly and W+fertility treatments at site two. A significant fertility response was not observed until 2010 at the second site where W+SF significantly increased bush growth compared with the Wonly and Control treatments. Weed control significantly increased leaf tissue N content in 2009. Berry production was limited at one site due to the severity of disease; therefore berry analysis was restricted to one site. There was no interactive effect of disease control and treatment on the berry parameters, but there were treatment effects. Yield, hundred berry weight and Brix were significantly lower for the Control treatment. The use of fertility amendments again demonstrated a trend towards increased berry yields with a significant difference between the Wonly and W+SF. Under severe disease stress, plants with weed control and a long-term fertility management plan performed better than without management.

1130 **Screening of salt tolerant plants for prompting greenery in Saudi Arabia.** Ali A. Aljaloud[1]* and Ghulam Hassain[2]. [1]National Center for Agriculture Technology (NCAT), [2]National Center for Water Technology (NCWT), King Abdulaziz City for Science and Technology(KACST), P.O. Box:6086 Riyadh 11442 Saudi Arabia

A field experiment was carried out at Al-Muzahmiyia Research station, KACST, Riyadh, Saudi Arabia to determine salt tolerance of landscape trees. The experimental treatments were nine plants, one soil (sandy) and four levels of water salinity (2, 4, 8, and 12 thousand mg L^{-1}). The experiment was laid out by following "The Randomized Complete Block Design" with four replications. Mean plant yield (Kg/Plant) ranged between 8.2-11.24 kg (*Prosopis juliflora*), 0.7-1.3 kg (*Prosopis specigera*), 0.3-0.6 kg (*Prosopis tamarugo*), 2.7 - 5.8 kg (*Acacia nilotica*), 1.3-4.3 kg (*Leuceana leucocephola*), 0.2-1.7 kg (*Pithecellobium dulce*), 11.49-15.88 kg (*Atriplex halimus*), 7.7-18.6 kg (*Atriplex nummularia*) and 1.5-1.9 kg (*Conocarpus erectus*), in different water salinity treatment. Mean plant height ranged between 230-261 cm (*P. juliflora*), 134-168 cm (*P. specigera*), 103-118 cm (*P. tamarugo*), 181-206 cm (*Atriplex halimus*), 172-216 cm (*Acacia nilotica*), 137-145 cm (*Atriplex nummularia*), 109-173 cm (*Pithecellobium dulce*), 91-118 cm (*Conocarpus erectus*) and 199-246 cm (*Leuceana leucocephola*) in different water salinity treatment. The results indicated that landscape plants such as *Atriplex halimus, Atriplex nummularia* and *P. juliflora* produced more than 50% biomass as compared to the control

treatment. Overall, the experiment showed excellent potential for cultivation these plants for desert greenification under an arid environment.

1145 **New sainfoin keeps pace with alfalfa for safe grazing.** S. Acharya[1], A. Iwaasa[2], B. Coulman[3], P. Jefferson[4], T. McAllister[1] and Y. Wang[1]. [1]Agriculture and Agri-Food Canada Research Centre, Lethbridge, AB, Canada T1J 4B1, [2]Agriculture and Agri-Food Canada, Swift Current, SK, Canada S9H 3X2, [3]University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8, [4]Western Beef Development Center, Humboldt, SK, Canada S0K 2A0

Alfalfa is considered the 'Queen of Forages' in western Canada, as it is grown extensively due to its wide adaptability, high productivity and nutritional quality. However, alfalfa can cause bloat in grazing cattle while another high quality forage legume 'sainfoin' is known to be bloat free. It is known that condensed tannins (CT) present in sainfoin stems and leaves binds with protein in the rumen (~ neutral pH), slowing rumen digestibility and thus prevent bloat in grazing cattle. This protein-CT complex passes into the lower digestive tract, where the complex is broken due to low pH and the bypass protein is digested by the animal. Previous studies have shown that a 15% or more sainfoin in an alfalfa mix can eliminate the risk of bloat in grazing cattle. Although old cultivars of sainfoin are well adapted to western Canada and are of high nutritive value, they do not grow back at the same rate as alfalfa after grazing or persist in mixed alfalfa stands and so cannot be used for bloat free alfalfa grazing. They also do not produce as much biomass as alfalfa in pure stands and so have limited appeal for producers. Lethbridge forage breeding program has developed number of sainfoin populations with improved regrowth potential and persistence in mixed stands. This paper will summarize plant performance and quality data of some newly developed sainfoin populations when grown with or without alfalfa in western Canada and compare them with available sainfoin and alfalfa cultivars.

Monday, July 18, 2011
Canadian Botanical Association
Canadian Society of Plant Physiologists
Session 1: ***Teaching Symposium***
Evaluating student learning – How can we tell if our Assignments are making a difference?

Oral Presentations
Time: 1030-1200h
Room: 260 Sobey Building

Chair: Cindy Ross Friedman
Thompson Rivers University

1030 Invited Speaker:
Lyn Baldwin
BOTANY with a dash of SOTL - improving undergraduate botany curriculum using the scholarship of teaching and learning (will include a breakout session)

1115 Invited Speakers on theme of "Helping students write and communicate in the biological sciences"

Invited Speaker:
Frédérique Guinel
Transferring small-class assignments to a large class environment

1030 **BOTANY with a dash of SOTL--improving undergraduate botany curriculum using the scholarship of teaching and learning.** L. Baldwin, Department of Biological Sciences, Thompson Rivers University, 900 McGill Rd, Kamloops BC V2C 5N3 lybaldwin@tru.ca

In 1990, Ernest Boyer broadened the definition of academic work when he included the Scholarship of Teaching and Learning (SOTL) as one mode of faculty research. SOTL investigates teaching and student learning through observation, reflection, and hypothesis testing. Our understanding of SOTL and its relationship to scholarly teaching has become increasingly sophisticated over the last two decades and many university campuses have acknowledged the value of faculty involvement in SOTL. During this same time period, student interest and enrolment in traditional botany courses across North America has continued to decline resulting in widespread botanical illiteracy. While relatively few botany faculty have been trained in the specifics of SOTL, a national network of plant biologists represents a unique opportunity to collectively investigate ways to overcome our students' "plant blindness" and to reinvigorate botanical education. Effective SOTL projects require the same planning and critical thinking that our disciplinary research requires, but the actual data collection can occur in the classroom and laboratory. In this session, I will describe the current SOTL projects that I, along with my collaborators, are conducting—one on the use of drawing as a learning tool in botany laboratories and one on how to improve undergraduate writing skills—to outline the overall process of SOTL. We will discuss what research on teaching and learning has taught us about how to teach botany. In addition, participants will be invited to identify the critical questions they face in their plant biology courses and what role a national collaboration of plant biologists could play in addressing these questions.

1115 **Transferring small-class assignments to a large class environment.** F. C. Guinel, Department of Biology, Wilfrid Laurier University fguinel@wlu.ca

Contemporary Issues in Biology is a 2nd-year course where we want to promote critical-thinking skills and communication skills. Offered for the first time last year, this unconventional course allowed students to think about a single worldwide problem (e.g., agriculture) and to formulate an educated opinion. Not-so-traditional assignments evolving all around the specific topic were essential to the course: 1). reading scientific papers and writing responses every class, 2). creating and presenting a poster at a conference held at the semester's end, and 3). participating to debates on beliefs often heard in the society. To permit such assignments within a large class made of 180 students, creativity, enthusiasm, patience and time are required. Also, an excellent team of teaching assistants (TAs) and instructional assistants need to be put in place. First, the biweekly writing, which I marked with one of the TAs, made me aware that students did not necessarily know how to read in depth, understand questions, or answer these questions. Every class then I could address specific problems the students had about the questions, helping them achieve better. Second, each poster had to be the product of a team of 5 or 6 students; the teamwork was prominent in the tutorials and outside the class. Students were encouraged to exercise their critical-thinking and researching skills, as well as their creativity and presentation talents. Students' efforts were assessed by a portfolio, and by their teamwork and presentation skills. A conference environment was established through advertising the event widely, by making an abstract-book, and by using name tags. Third, the debates involved the representation of a government and an opposition side. Tutorial groups were clustered by 2 or 3 to represent one of

the two sides; teamwork was done within and outside lectures. At the end of each debate, the floor was opened for questions from the class audience. As the complete class was knowledgeable about the topic, participation was very good, much higher than anticipated. During this presentation, I will quickly outline the framework of the course, detail some assignments, and discuss the interest and participation of the students. I will also address the frustrations and benefits seen from the students', the TAs' and my viewpoints. Success was realized when seeing pride on the students' faces as they stood beside their end-product.

Monday, July 18, 2011
Canadian Botanical Association
Canadian Society of Plant Physiologists
Session 2: ***Teaching Symposium Continues***
Evaluating student learning – How can we tell if our Assignments are making a difference?

Oral Presentations
Time: 1300-1500h
Room: 260 Sobey Building

Chair: John Markham
University of Manitoba

1300 Invited speakers:
John Markham
University of Manitoba
Open discussion teaching panel on "Teaching and evaluating scientific writing" Led by John Markham, University of Manitoba. John Markham will start discussion by presenting results of nationwide survey: "Undergraduate scientific writing trends in biology Programs across Canada"

Panelists: Lyn Baldwin, Thompson River University
Christian Lacroix, University of Prince Edward Island
Jane Eddington, Dalhousie University
Norm Hüner, University of Western Ontario

General Session

Chair: Rodger Evans
Acadia University

1400 **Christina Lord**
Do mitochondria play a role in remodeling lace plant leaves during programmed cell death?

1415 **Gaolathe Rantong**
The role of ethylene, ethylene receptors and caspase-like genes in lace plant programmed cell death during leaf morphogenesis

1430 **Moira Galway**
Mutation-mediated disruption of cellulose synthesis in *Arabidopsis thaliana*

1445 **Lauren Remmler**
Quantifying spatial and temporal growth patterns of developing leaves in 3D

1400 **Do mitochondria play a role in remodeling lace plant leaves during programmed cell death?** Christina Lord[1*], Jaime Wertman[2], Stephanie Lane[3], Arunika Gunawardena[4]. Department of Biology, Dalhousie University, Halifax, NS, Canada, B3H 4J1[1,2,3,4] (e-mail: arunika.gunawardena@dal.ca)

The lace plant, *Aponogeton madagascariensis* is an aquatic monocot that forms perforations in its' leaves between longitudinal and transverse veins over its' entire leaf surface through developmentally regulated programmed cell death (PCD). Developmental PCD is a genetically encoded process employed throughout normal development in plant life cycles. The role of mitochondria during PCD has been recognized in animals; however, it has been less studied during PCD in plants, and a time line for organelle changes is still unclear. A single areole within a window stage leaf (where PCD is occurring) was divided into three areas based on the progression of PCD; cells that will not undergo PCD (NPCD), cells in early stages of PCD (EPCD), and cells in late stages of PCD (LPCD). Window stage leaves were stained with the mitochondrial dye MitoTracker Red CMXRos and examined. Mitochondrial dynamics were delineated into one of four categories (M1-M4) based on characteristics including distribution, motility, and membrane potential ($\Delta\Psi m$). A TUNEL assay portrayed fragmented nDNA in a gradient over these mitochondrial stages. Chloroplasts and transvacuolar strands were also examined using live cell imaging. The importance of the mitochondrial permeability transition pore (PTP) formation during PCD was examined via in vivo cyclosporine A (CsA) treatment. This treatment resulted in lace plant leaves with a significantly lower number of perforations compared to controls, and that displayed mitochondrial dynamics similar to that of NPCD cells. Results illustrate mitochondrial dynamics in vivo as PCD progresses within the lace plant, and highlight the correlation of the mitochondria with the nucleus, chloroplasts and transvacuolar strands during developmental PCD. Overall, our findings implicate the mitochondria as playing a critical and early role in developmentally regulated PCD in the lace plant.

1415 **The role of ethylene, ethylene receptors and caspase-like genes in lace plant programmed cell death during leaf morphogenesis.** Gaolathe Rantong[1], Arunika Gunawardena[2]. [1,2] Dalhousie University, 1355 Oxford Street, LSC, Halifax, NS. B3H 4J1

The lace plant, *Aponogeton madagascariensis*, is an aquatic monocot that forms perforations in its leaves as a part of its normal growth and development. This process of perforation formation is extremely regulated and has been shown to be orchestrated by developmentally regulated programmed cell death (PCD). Up to the present, the molecular and hormonal basis of PCD in lace plant is unknown. In this study, the role of ethylene during perforation formation in lace plant leaves was examined. The amount of ethylene emitted by leaves at different stages of development was measured and it varied. Window and senescence stage leaves (in which PCD is occurring) produced more ethylene than mature stage leaves (in which PCD is not taking place). Given that the amount of ethylene produced varied, a degenerate primers approach was used to isolate cDNA of lace plant ethylene receptors, which are negative regulators of the ethylene signal transduction pathway. Fragments of ETR1, ERS1 and ERS2 lace plant ethylene receptor cDNA were isolated. Transcript levels of the most abundant ethylene receptor (ETR1) were determined at different stages of lace plant leaf development. ETR1 usually makes up a large proportion of total ethylene receptors number (more than 50 %). QPCR and Semi-quantitative PCR experiments showed significantly higher ETR1 mRNA levels in window stage as compared

to pre-perforation (in which PCD has not started yet) and mature stage leaves. Pre-perforation and mature stage leaves appeared to display similar levels of ETR1 mRNA. Ethylene is thought to be a trigger signal for PCD. It was expected that window stage leaves will have less ethylene receptors compared to the other stages since the receptors are negative regulators of the ethylene signal transduction pathway. Based on the unexpected results, a new model for ETR1 expression during lace plant perforation formation was proposed. Due to preliminary evidence which suggested the involvement of caspase activity in perforation formation in lace plant, isolation of caspase-like enzymes in lace plant is underway.

1430 **Mutation-mediated disruption of cellulose synthesis in *Arabidopsis thaliana***. Sara A. MacLellan and Moira E. Galway.* Department of Biology, St. Francis Xavier University, Antigonish, Nova Scotia, Canada B2G 2W5 (email mgalway@stfx.ca)

Using atmospheric carbon dioxide, plants synthesize sugars which are incorporated into cell wall polysaccharides and other products. Cell wall strength depends on crystalline cellulose, perhaps the most abundant cell wall polymer. Cellulose is essential for the production of paper, textiles, building materials, and is often added to processed foods and pharmaceuticals. It can also be degraded to fermentable sugars for biofuel production. Biofuel production costs could be lowered by using plants that make less crystalline cellulose. Recently it was reported that the ixr1-2 allele of the cellulose synthase gene CESA3 can reduce the relative crystallinity of cell walls in the model plant Arabidopsis thaliana without adverse effects on plant growth. However, we have compared the growth of wild type plants, plants with mutations in cellulose synthase genes (including ixr1-2) and plants with mutations in the cellulose synthase-like gene CSLD3 (which is required for cell wall integrity in root hairs), and found that ixr1-2 significantly reduced root and shoot growth. Moreover, impaired regulation of cell expansion in stem inflorescences altered pith and vascular bundle cell organization, which could affect plant survival under field conditions. When ixr1-2 was combined with a partially-functional allele of CSLD3 (rhd7-4), stem anatomy was more normal, but on the other hand, seedling root growth rate was severely reduced. Root cell swelling and altered cellulose staining patterns were observed. This complex gene interaction suggests a role for CSLD3 in cellulose synthesis throughout this model plant. Attempts to manipulate plant cellulose content will benefit from a better understanding of the cellulose synthase-like genes and their functions.

1445 **Quantifying spatial and temporal growth patterns of developing leaves in 3D** L. Remmler*[1] and A.G. Rolland-Lagan[1]. [1] Department of Biology, University of Ottawa, Ottawa, Ontario, Canada K1N 6N5

How a developing organism organizes its tissues into specific patterns and functional shapes is an intriguing, yet largely unanswered question in the field of developmental biology. This may be attributed to the fact that shape and changes in shape are difficult to describe and measure. Tools that allow researchers to quantify the tightly controlled spatial and temporal patterns in the rates and directions of tissue expansion over the course of development could be extremely useful in studying the underlying mechanisms of morphogenesis. Tools to quantify these parameters in leaves, more specifically, would be of interest not only to developmental biologists, but also to researchers in the fields of evolutionary biology, agriculture, and biotechnology. Thus it is not surprising that some such tools do exist, but to date are only applicable to leaves in later stages of development, when most growth and shape changes have already occurred, and are limited to 2-dimensional surfaces and therefore not suitable for the study of more curved and complex leaves that are often seen in plants that have altered growth. We will present a novel technique and computational tools that overcome these limitations. The method employs topically applied microscopic fluorescent beads whose divergence on the leaf surface can be tracked over time, by

time-lapsed imaging with a fluorescent macroscope. The computational tools include image analysis and point tracking algorithms that semi-automate the processing of the images, allowing for a higher throughput of data, and software that allows us to extract the 3-dimensional surface of the leaf and compute a variety of spatial and temporal growth parameters from the 3D coordinates of the beads. This tool could be used to study the influences of different phytohormones, genes, and environmental conditions on growth, as well as in plant phenomics, and to obtain data for the development of computational models of plant growth.

Monday, July 18, 2011
Canadian Botanical Association
Session 3: ***Systematics and Evolution***

Oral Presentations
Time: 1530-1700h
Room: 260 Sobey Building

Chair: Hugo Cota-Sanchez
University of Saskatchewan

1530 **Carole Sinou**
Biogeographic and phylogenetic patterns in the pantropical genus *Bauhinia* s.l. (Leguminosae)

1545 **Claire Gilmour**
Phylogenetic relationships within the hyper-diverse Cariceae/Scirpeae s.s./Dulicheae clade (Cyperaceae) with emphasis on the circumscription of *Eriophorum* and *Scirpus* s.s**.**

1600 **Shaik Mahammad Khasim**
Genetic diversity in *Coelogyne nervosa* R. Rich., an endemic orchid from Southern India

1530 **Biogeographic and phylogenetic patterns in the pantropical genus *Bauhinia* s.l. (Leguminosae).** Ms. Carole Sinou[1*] and Bruneau, Anne[2], [1,2]IRBV, 4101 Sherbrooke est, Montréal, QC, H1X 2B2

Bilobed leaves are a key feature allowing the identification of *Bauhinia* L. species within the Leguminosae (Cercideae tribe). Traditionally recognized as a monophyletic genus, new molecular data have shed light on our misconception about the evolutionary history of this pantropical genus. In order to comprehensively reconstruct the evolutionary history of the genus, both plastid (trnL-trnF, matK) and nuclear (Leafy, LegCyc) regions have been sequenced for a representative sampling of the Cercideae. Indeed it appears that the genus *Bauhinia* sensu lato is paraphyletic (inclusion of the monospecific genus *Brenierea* Humbert) and that it is divided into two separate lineages. One of these (the *Phanera* clade) includes the segregate genera *Gigasiphon* Drake, *Barklya* F. Muell, *Tylosema* (Schweinf.) Torre & Hillc., *Phanera* Lour., *Lasiobema* (Korth.) Miq. and *Lysiphyllum* (Benth.) deWit, while the other (*Bauhinia* s.s. clade) includes the genus *Brenierea*, the segregate genus *Piliostigma* Hochst. and *Bauhinia* sensu stricto. Considering this dichotomous history of *Bauhinia* s.l. and recent studies of divergence times for the Leguminosae, biogeographic hypotheses of independent long distance dispersal must be addressed. In both *Bauhinia* ss and *Phanera* clades the first lineages to diversify are almost entirely composed of African species suggesting an African origin for the genus. Our analyses also suggest several independent long distance dispersals. In the *Bauhinia* ss clade, diversification of the lineages occurs in Madagascar, and in seasonally dry biomes of Asia and America. Similarly, in the *Phanera* clade, Australian dry habitat species and seasonally dry habitat species from Asia and America occur.

1545 **Phylogenetic relationships within the hyper-diverse Cariceae/Scirpeae s.s./Dulicheae clade (Cyperaceae) with emphasis on the circumscription of *Eriophorum* and *Scirpus* s.s..** Claire Gilmour[1*], Julian R. Starr[2], Robert F.C. Naczi[3.] Canadian Museum of Nature, Ottawa, ON, K1P 6P4,[1,2] The New York Botanical Garden, Bronx, NY, 10458-5126, U.S.A.[3]

The Scirpeae s.s./Dulicheae/Cariceae clade is a cosmopolitan group that represents more that 40% of the approximately 5,000 species that form the Cyperaceae or sedge family. Despite its global ecological significance and cultural importance to many communities, relationships within the clade are poorly known and the limits of many of its genera are not well defined. With emphasis on the circumscription of *Eriophorum* L. (c. 18 spp.) from *Scirpus* L. s.s. (c. 66 spp.), two closely related genera whose limits are blurred by several intermediate species in these and other genera, we examine the relationships within the clade using the chloroplast gene regions ndhF and matK. Results confirm that *Eriophorum* and *Scirpus* s.s. (Scirpeae s.s.) form a strongly supported clade (100% bootstrap) within a wider group (91% bootstrap) that includes tribe Cariceae and a monophyletic *Trichophorum* Pers. (100% bootstrap; Scirpeae s.s.). Current analyses suggest the Southeast Asian genus *Khaosokia* D.A.Simpson, Chayam. & J.Parn. is sister to the Scirpeae s.s./Cariceae clade and that tribe Dulicheae may form the basal elements of the entire Scirpeae s.s./Dulicheae/Cariceae clade. Although taxonomic sampling was restricted at this preliminary stage, our results currently suggest the possibility of a new genus of two species within the group, although further molecular support and taxonomic sampling will be needed to verify and support this hypothesis.

1600 **Genetic diversity in *Coelogyne nervosa* R. Rich., an endemic orchid from Southern India**. Shaik Mahammad Khasim[1] and Jujjuvarapu Ramudu[2], Acharya Nagajuna University, Nagarjunanagar 522 510, Guntur, Andhra Pradesh, India[1,2](e-mail: dr_smkhasim@yahoo.co.in)

Genetic diversity of *Coelogyne nervosa* A. Rich. was investigated by using SDS-PAGE, RAPD markers and morphological characters. *C. nervosa* is growing as epiphyte as well as lithophytes in Eastern and Western Ghats of India. The six populations collected from these two geographical regions exhibited significant variation in their morphological and molecular characters. The stomata are tetracytic and hypostomatic in distribution. The highest thickness of cuticle and midrib region in leaf and extensive lignification in exodermis and endodermis of root were recorded in populations located in Western Ghats as compared to those of Eastern Ghats. It is interpreted to be associated with the conservation of water. RAPD and protein profile data indicate the inter population diversity between these two sites. This can be attributed to the ecological and climatic conditions prevailing in the Eastern and Western Ghats of India.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Botanical Association **Time:** 0830-1000h
Session 4: ***Climate change: Canada's plants on the run!*** **Room**: 260 Sobey Building

Chairs: Liette Vasseur, Brock University; Art Fredeen, University of Northern British Columbia

0830 **David Clements**
Vulnerability of plant communities in coastal British Columbia to past and future environmental change

0900 **Andrew Trant**
Treeline ecology: fast changing, slow growing and a little disturbing

0930 **Liette Vasseur**
Assessing climate change impacts on traditional plants and species at risk in coastal regions

0830 **Vulnerability of plant communities in coastal British Columbia to past and future environmental change.** D.R. Clements, Biology and Environmental Studies, Trinity Western University, Langley, B.C., V2Y 1Y1 (e-mail: clements@twu.ca)

In the 200 years since Europeans began colonizing the region, coastal British Columbia has undergone environmental change on a massive scale. First Nations practices such as burning which kept many habitats relatively free of woody vegetation were curtailed, and the landscapes were fragmented by urban and agricultural development. Natural predators of deer such as wolves or cougars were also eliminated from many habitats in coastal British Columbia. Garry oak ecosystems are particularly vulnerable to these changes. These changes have had consequences seen in both declines of specialized native plants within Garry oak ecosystems and increasing abundances of invasive plants that have taken advantage of the altered disturbance regimes. Garry oak ecosystems were historically fostered by drier conditions in rain shadow areas along the east coast of southern Vancouver Island and the Gulf Islands to the lee of Vancouver Island mountain ranges. There has been some speculation that the warmer and drier conditions produced by global warming should promote Garry oak habitat. However, unless extensive restoration of existing pockets of Garry oak habitat is completed, the predicted change in climate will do little to reduce the extreme vulnerability of many rare plant populations. In British Columbia, red-listed species are indigenous species that are extirpated, endangered, or threatened while blue-listed species are indigenous species of special concern. As of 2010, there were 54 red-listed and 17 blue-listed plant species associated with Garry oak ecosystems in British Columbia. The historic and future challenges to such rare plants are very apparent when examining the specific issues faced by four of these 71 endangered species: *Lomatium dissectum* (fern-leaved desert-parsley), *Castilleja levisecta* (golden paintbrush), *Viola praemorsa ssp. raemorsa* (yellow montane violet) and *Silene scouleri* (coastal Scouler's catchfly). For example, a population of *V. praemorsa* ssp. *raemorsa* is being monitored and exclosures constructed on Mt. Tuam on Salt Spring Island to prevent grazing by sheep, but more information on how best to restore populations of *V. praemorsa* ssp. *raemorsa* is urgently needed.

0900 **Treeline ecology: fast changing, slow growing and a little disturbing.** Andrew Trant**,** PPS Arctic - Labrador Highlands Research Group, Department of Biology, Memorial University, St. John's, Newfoundland A1B 3X9, work: (709) 864-8258. E-mail: andrew.trant@gmail.com

With significant changes in climate being observed in sub-arctic and arctic regions, the general sentiment is that trees and shrubs are advancing poleward, replacing the tundra. In work focused in Labrador, complimented by circumpolar collaborations, questions of treeline expansion and persistence will be explored both mechanistically and anecdotally. Using tree rings, ecological stories will be told about past fire and insect disturbance, treeline expansion, carbon storage and climate-growth relationships. In addition, the use of tree rings and forest ecology in exploring issues of climate change in northern communities will be discussed.

0930 **Assessing climate change impacts on traditional plants and species at risk in coastal regions.**
Liette Vasseur, Department of Biological Sciences, Brock University, 500 Glenridge Avenue, St Catharines, Ontario L2S 3A1 E-mail: lvasseur@brocku.ca

In Atlantic Canada, most communities live within the coastal zone where climate change, mainly sea level rise and storm surges, will impact on their environment. For the First Nations, and especially the Mi'kmaq communities of the New Brunswick eastern coast like Elsipogtog, climate change is an issue that they already have to deal with. This is especially important for the sustainability of the traditions and the use of natural resources, mainly the traditional foods and medicines found in salt marshes. This research examined how climate change might affect some of the traditional species, such as sweetgrass (*Hieriochloe odorata*), a species that has been traditionally used by the Mi'kmaq, based on population surveys and using projection and digital elevation models. A total of 41 species were identified in these marshes. Of them, 3 were considered as species of concern (being rare either provincially or federally) and 2 species were known to be considered of high importance for traditional use by the First Nations. Six other species from these marshes were also used as traditional species. Under the scenario of the level of flooding for the 2000 storm of 2.05m, the results showed that the four traditional marsh zones surveyed would be flooded with the advanced scenarios showing levels of water reaching the forested area. This is mainly due to the low relief found in this region. Considering that only a few of their traditional plant species can support both flooding and higher than usual salinity levels, the Elsipogtog community is concerned about losing the traditional populations. The decline is exacerbated by the overharvesting of sweetgrass and current residential expansion of Richibucto along the coast, further reducing the size of these marshes.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Botanical Association **Time:** 1030-1200h
Session 5: ***Ecology and Phytogeography*** **Room**: 260 Sobey Building

Chair: Paul Catling
Agriculture and Agri-Food Canada

1030 **Laurie Consaul**
Traditional knowledge and botanical collections help to study climate change effects in the southern Arctic

1045 **Hazel Cameron-Inglis**
Timing it right: implications of climate variation on a mixed mating, early-flowering plant

1100 **Irene McKechnie**
Impacts of landscape disturbance on plant reproductive success: are there general trends and patterns?

1115 **Andrew Browne**
Rate and form of native and exotic plant recolonization after disturbance of forest communities in southern Ontario

1130 **Karen Harper**
Forest structure, understorey composition and bryophyte abundance across bog and lakeshore forest edges in southwest Nova Scotia

1145 **David Garbary**
Invasion of *Rosa rugosa* into coastal plant communities of Brier Island, Nova Scotia

1030 **Traditional Knowledge and botanical collections help to study climate change effects in the southern Arctic.** Laurie Consaul[1], Morgan Ip[2], Don Charette[3], Paul M. Catling[4], Emily Kattuk[5], Sarah Kudluarok Jr.[5], Christine Ekidlak[6], Megumu Tsujimoto[7], and Nancy Doubleday[8]. 1 Canadian Museum of Nature, P.O. Box 3443, Station D, Ottawa, ON, K1P 6P4 Canada; 2 Carleton University, 1125 Colonel By Drive, Ottawa, ON, K1S 5B6; 3 University of Ottawa, Ontario, K1N 6N5; 4 Agriculture and Agri-Food Canada, Ottawa, ON, K1A 0C6, Canada; 5 Sanikiluaq, Belcher Islands, NU, X0A 0W0; 6 Iqaluit, Baffin Island, NU, X0A 0H0; 7 The Graduate University for Advanced Studies, Tokyo, Japan; 8 McMaster University, Department of Philosophy, Faculty of Humanities, Hamilton, ON, L8S 4L8, Canada

The monitoring of changes in plant species in the arctic tundra is important with respect to climate change research and specifically to ground-truth and supplement satellite data. The inclusion of northern community members in the analysis of their surroundings means that local knowledge can be paired with scientific knowledge to create richer and more informative datasets. In the summer of 2010, we conducted a botanical survey on the Belcher Islands, Nunavut, one of the most southern Arctic regions in the world. We compared plant species found with those recorded in two previous surveys in 1960 and 1989. Local knowledge holders were interviewed about changes in the vegetation and the resultant effects of these changes on their lives. These local community scientists also participated in the plant inventory and learned fundamental monitoring procedures. Through the surveys and interviews over 200 vascular plant species records were obtained. At least 10 plant species were new records for the islands. Based on a phytogeographic analysis of the previously known flora, the proportion of southern species would have been lower than that found. Thus the changes are believed to be a result of climate change. *Platanthera aquilonis* and *Botrychium lunaria* are both now found more commonly than in 1960 reports; suggesting a shift in relative abundance of southern species. *Rumex occidentalis* and *Petasites frigidus* var. *palmatus*, also being considered as likely indicators of climate change, were collected on the islands for the first time in 2010. Also in 2010 we made the first reports of the common dandelion, *Taraxacum officinale,* on the Belcher Islands, suggesting an improving climate for invasive species in the north. We now have a list of ~230 species on the Belcher Islands to compare in future years for continued monitoring of vegetation changes on the islands. The success of this study in gathering extensive data indicates the value of historical botanical research along with present day monitoring with the assistance of the local community.

1045 **Timing it right: implications of climate variation on a mixed mating, early-flowering plant.** H. Cameron-Inglis, A. Simcox, A. Percell, and L. Baldwin. Department of Biological Sciences, Thompson Rivers University, 900 McGill Road, Kamloops, BC, V2C 5N3

Earlier flowering plants in moisture limited environments have shown advanced flowering concurrent with climate change, causing concern for potentially disrupted plant-pollinator interactions. Plants capable of mixed mating strategies, *like Ranunculus glaberrimus* Hooker (the sagebrush buttercup), may respond to variable environmental conditions with plastic shifts in phenology or variation in rates of reproduction. In this study, flowers limited to specific reproductive modes (e.g. selfing and outcrossing) were studied to determine how early-flowering plants could reproductively adapt to highly variable conditions. First flowering date and reproductive fitness (seed set and seed mass) were measured in the same population of primary (2008-2010) and secondary (2010) flowers in Kamloops, British Columbia. Three distinct patterns of primary flower onset were observed across years (early extended, early short and late

short). In the early extended year, occurring in a prolonged cold season, primary flowers produced, on average, only two seeds compared to eight or nine seeds per flower in the subsequent years. Seed set and total seed mass were positively associated with day of emergence for primary flowers in two out of three years and negatively associated with emergence day in secondary flowers. Flowers limited to a single mode of reproduction had significantly lower seed set and seed mass than natural flowers for all three years of study. However, in the warm, early flowering period of 2010, selfing contributed to a higher seed set and seed mass in primary flowers than outcrossing. Despite a lower investment in reproductive parts, secondary flowers produced more seeds through outcrossing than primary flowers. Assuming seeds produced via selfing are less viable due to inbreeding depression, ample seed production from primary flowers was only observed in the warm, late spring of 2009. Advanced flowering associated with climate change may produce more selfed seeds, making secondary flowers more important for short-term fitness.

1100 **Impacts of Landscape Disturbance on Plant Reproductive Success: Are There General Trends and Patterns?** Irene McKechnie[1], Risa Sargent[2]. University of Ottawa, Department of Biology, 30 Marie Curie, Ottawa, ON, K1N 6N5. (e-mail: imcke019@uottawa.ca)

Landscape disturbance has been shown to negatively impact the overall abundance and richness of unmanaged bee species; however the impacts of similar disturbances on plant reproductive success have not been quantitatively synthesized. To address this question we carried out a meta-analysis of published studies of animal-pollinated plants with measures of female reproductive success. Effect size was calculated as Hedges' unbiased standardized mean difference (Hedges'd) and analyzed using random-effects models grouped by disturbance type, biome, crop type, and growth form. Publication bias was assessed using visual inspection of funnel plots, Spearman's rank correlation testing, and Rosenberg's fail-safe number estimates. Overall disturbance showed no negative impact on plant reproductive success. However, when we looked at the data by categories, we found that plants classified as non-woody or non-crop species, plants found in tropical locations, and plants being disturbed by footpaths or livestock do demonstrate a negative relationship between disturbance and reproductive success. Conversely, plants classified as woody or crop species, plants found in temperate locations, and plants being disturbed by surface digging, deforestation, burning, and agriculture show no negative relationship between disturbance and reproductive success. These results lead us to conclude that disturbance type is an important factor in determining the outcome for plant reproductive success.

1115 **Rate and form of native and exotic plant recolonization after disturbance of forest communities in southern Ontario.** Andrew Brown[1], Liette Vasseur[2]. [1,2] Department of Biological Sciences, Brock University, 500 Glenridge Ave, St Catharines, ON, L2S 3A1, CAN

Increasing human activity, habitat loss, and disturbance of natural habitats has led to changes in the rate of re-establishment and higher rates of species invasion in the biologically diverse forest communities of southern Ontario. Exotic species threaten the native flora as many exhibit high competitive ability and invasibility in disturbed landscapes. Rates and mechanisms of recolonization after disturbance have yet to be understood and compared between exotic and native species. The aim of our study was to examine the responses, mainly the short term recolonization rate, of understory plant communities from three different ecosystems (5 open fields, 5 dense young forests, and 5 open mature forests) to three levels of disturbance (no disturbance: control; medium: scarification; and high: soil screening). Ground vegetation was surveyed during the summer of 2010, once before the disturbance event and three times after disturbance in five quadrats of 1m2 per treatment for each site. Repeated analyses of variance showed that there were significant changes in species composition in the quadrats during the

summer and there was a significant treatment effect showing that recolonization was slower in highly disturbed quadrats. However, there was no significant difference among the types of ecosystems, suggesting a similar pattern of recolonization regardless of the ecosystem. While the patterns were similar among ecosystems, richness remained significantly different over the season between ecosystems. Exotic and native species did not react differently, but species with higher invasibility status had higher rates of recolonization across all sites. This suggests that invasive species (regardless of whether they are exotic or native) will dominate recolonization of sites, confirming the issue of slowdown of the rate of natural regeneration of biodiversity in forest ecosystem after disturbance.

1130 **Forest structure, understorey composition and bryophyte abundance across bog and lakeshore forest edges in southwest Nova Scotia**. K. A. Harper[1*], W. B. Wilson[2], and K. O'Handley[3]. [1]School for Resource and Environmental Studies, Dalhousie University, Canada, e-mail: Karen.Harper@Dal.ca; [2] Environmental Science, Dalhousie University, Canada; [3]Environmental Studies, Saint Mary's University, Canada

Transitions between plant communities on the landscape have become a focus of research due to their relatively high diversity and sensitivity to climate change. However, little is known about how vegetation changes across natural landscape boundaries such as the forested edges of wetlands. We investigated forest structure, understorey composition and bryophytes at bog and lakeshore forest edges. Our objectives were to estimate distance of edge influence, to compare patterns across the transition and to determine if diversity is greatest at the edge. Transects were set up across 4 bog and 4 lakeshore edges in spruce forests in southwest Nova Scotia with sampling points at 5, 15, 25, 40, 60, 100, 140 and 180 m from either side of the edge where we sampled forest structure and collected moss samples. Contiguous 1m x 1m quadrats -60 to +60 m and across 5 m spans at 100, 140, and 180m were used to estimate cover of understorey and bryophtye species. We used randomization tests to compare data at each edge distance with the reference data (100, 140 and 180m) to determine distance of edge influence. There was little difference in the structure or composition of the edge compared to interior forest at either bog or lakeshore edges. Distance of edge influence was 40 m into the bog for increased tree density, greater canopy cover and greater abundance of some species compared to further into the bog; and 5 m into the forest for Sphagnum. Both transitions exhibited some different habitat features compared to the adjacent communities such as greater canopy cover and tree density at bog edges and lower total moss cover at both edge types. Bryophyte species richness was higher at both edge types and tree structural diversity was either higher or lower at bog edges. Shrub species richness decreased from the bog to the forest as herb richness increased. Higher diversity and different characteristics of the edge zone indicate that its unique habitat on the landscape could be important for conservation.

1145 **Invasion of *Rosa rugosa* into coastal plant communities of Brier Island, Nova Scotia**. Dr. David Garbary[1], Dr. Nicholas Hill[2], Anthony, Miller[3]. Department of Biology, St Francis Xavier University[1,3], Fernhill Institute of Plant Conservation, Berwick, Nova Scotia[2]

During August and September 2010 we surveyed the entire 20.4 km perimeter of Brier Island for the invasive shrub, *Rosa rugosa*. This island in the outer reaches of the Bay of Fundy of Nova Scotia is geographically isolated and relatively undeveloped. Our objective was to determine the extent of the invasion of *R. rugosa* into different coastal habitats and its apparent impact on native plant communities in a landscape similar to that of its native range in Asia. Over 300 colonies of *R. rugosa* with mean height over 1 m occupied over 2089 m of the island perimeter (10% of 20.4 km) within 10 m of the shore. The mean distance between colonies was 61 m. At least 33 colonies formed almost impenetrable walls, each over 10 m in length, and two colonies occupied

about 500 m2 where there was continuous cover. Colony length (parallel to the shore) varied from 2.8 ± 1.1 m to 10.7 ± 17.3 m (mean ± s.d.) in different shore segments. *R. rugosa* had greatest density of colonies in a sand-gravel barrier beach in which 88 colonies occupied 22% of the area and 37.5% of beach margin. Exponential growth of the population of this invasive rose (inferred from aerial photographs of 1970, 1988 and 2000) may be due to the varied system of seed dispersal agents that includes natural primary dispersers (mink and red squirrel) and short distance (unidentified rodent) and longer distance (Off Road Vehicles) secondary dispersers. We conclude that *R. rugosa* is having a significant impact on marine coastal plant communities, and has the potential to dominate windswept, shrub habitats on coastlines of much of Nova Scotia.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Botanical Association **Time:** 1400-1530h
Session 6: ***Symposium& General*** **Room**: 260 Sobey Building

Symposium: Effect of environmental change on fungal diversity

Chair: Michele Piercey-Normore
University of Manitoba

1400 **Stephen Clayden**
Lichens and allied fungi of old wet cedar (*Thuja occidentalis*) forests in Northeastern North America: Indicators of environmental change

1415 **Melissa Day**
Decomposition of moss by filamentous fungi and its potential role in arctic/alpine pedogenesis

1430 **Georg Hausner**
The blue-stain fungi of Manitoba and NW Ontario

1445 **Troy McMullin**
Monitoring ecological integrity and air quality with lichens at Kejimkujik national park and national historic site

1500 **Brinda Timsina and Michele Piercey-Normore**
Effects of environmental change on lichen fungi

General Session

1515 **David Richardson**
The distribution, structure and ecophysiology of *Peltigera hydrothyria*, 'The Water Fan', a rare and endangered macrolichen that grows under water

1400 **Lichens and allied fungi of old wet cedar (*Thuja occidentalis*) forests in Northeastern North America: indicators of environmental change.** Stephen R. Clayden[1], Kendra E. Driscoll[1], Steven B. Selva[2], Dwayne L. Sabine[1] . [1]Botany and Mycology Section, New Brunswick Museum, 277 Douglas Avenue, Saint John, NB, E2K 1E5, Canada; [2] Department of Natural and Behavioral Sciences, University of Maine at Fort Kent, 23 University Drive, Fort Kent, ME 04743, U.S.A.

Recent surveys of remnant old wet cedar (*Thuja occidentalis*) forests in eastern Canada and Maine indicate that these communities have the highest diversity of lichens and allied fungi known in any forest type in northeastern North America. Of the nearly 350 species detected to date, many were previously unknown in this region. Climatically-determined gradients of species composition are present across the region, with differing assemblages occurring in southern-coastal, central-interior, and northern areas. The coastal forests have a reduced representation of cyanolichens, possibly due to acid precipitation. Overall, the cedar community and its lichens and allied fungi could be a benchmark system for monitoring the effects of expected increases in precipitation and temperature.

1415 **Decomposition of moss by filamentous fungi and its potential role in arctic/alpine pedogenesis.** M. Day*. CW 405 Biological Sciences Building, University of Alberta, Edmonton, Alberta, T6G 2E9, Canada

Arctic and alpine areas are expected to be some of the hardest hit by climate change. Due to increased temperatures, glacial retreat in these areas is expected to increase, leaving larger areas of bare ground and the process of primary plant succession. Primary colonisers in these forefields are lichens and mosses, mainly because they can survive in the glacial till that forms the developing soil. Mosses in the Saskatchewan Glacier forefield form an organic grout between the larger rocks that acts as a catchment basin for water- and airborne organic material (e.g. pollen, chytrids). Stands of these mosses typically stratified with an upper, green, photosynthesising layer and a lower, brown, decomposing layer. The grout is also heavily colonised by fungal hyphae. As the arctic and alpine areas experience greater change due to climate fluctuations, there is an increased need to understand the process of pedogenesis after glacial retreat. Three filamentous fungal species (*Curvularia inaequalis*, *Ulocladium atrum*, and *Chalastospora gossypii*) were isolated from mosses and vascular plants in the Saskatchewan Glacier forefield. Fungi were inoculated onto sterile *Hylocomium splendens* gametophytes to determine if they were capable of breaking down their glacial hosts. All three species were able to remove the cellulose rich outer layer of the moss cell wall, but not the inner, polyphenol rich layer. After decomposition, the moss fragments are fragile and break apart easily, with the fragments becoming part of the detritus bound up in the moss grout and contributes to the organic fraction of the developing soil.

1430 **The Blue-stain fungi of Manitoba and NW Ontario.** G. Hausner, University of Manitoba, Department of Microbiology, Winnipeg, MB, R3T 2N2, hausnerg@cc.umanitoba.ca

Species of *Ophiostoma* and its mitotic counterparts (asexual species of *Leptographium, Pesotum, Hyalorhinocladiella* etc.) are of interest as these fungi include many insect-vectored forest pathogens (Dutch Elm disease) and so-called blue-stain fungi. These fungi cause economic losses by staining lumber and therefore making it less desirable for high-end usage and export, and

Canada could even facing trade embargoes for stained wood products/lumber. In recent years several reports have been published suggesting that blue-stain fungi are being introduced into Canada by importing products shipped in or on wooden grates or palettes. Also, potentially due to climate change insects that vector these fungi appear to be spreading northward bringing along their fungal associates (eg. Mountain Pine beetle). This also introduces new fungal species into Canada potentially threatening some of our tree species and adding more blue-stain fungi to our forests that can stain lumber. In the past we have periodically surveyed Manitoba and NW Ontario for blue-stain fungi looking for evidence that new species (exotics) have been introduced into Canada. Species identification is a challenge due to the presence of cryptic species and the observation that many morphological traits among these fungi are subject to convergent evolution as they have adapted to similar life styles. However, these fungi are also of interest from a biotechnological point of view as their mitochondrial genomes are rich in mobile elements such as group I and II introns (ribozymes) and homing endonucleases.

1445 **Monitoring ecological integrity and air quality with lichens at Kejimkujik National Park and National Historic Site.** R. Troy McMullin, Biodiversity Institute of Ontario Herbarium, Department of Integrative Biology, University of Guelph, Guelph, Ontario, N1G 2W1, Work: 519-824-4120 ext. 53594. Email: rmcmulli@uoguelph.ca

Lichens are well-established bioindicators and have been used globally for many years to monitor air pollution. They are particularly sensitive to changes in their environment due to the lack of a cuticle, uptake of nutrients from the atmosphere and slow rate of growth and development. Since 2006, a protocol for using arboreal lichens as bioindicators has been under development for Kejimkujik National Park and National Historic Site in Nova Scotia. Lichens are monitored as one component of integrated forest plots at Kejimkujik, which are designed to assess and monitor the state of forest ecosystems and their changes over time. The measures for monitoring the status and trends in lichens at Kejimkujik include: (i) lichen species richness (of 50 field identifiable lichen species); and (ii) an Index of Air Purity (IAP)(based on a suite of pollution-intolerant lichen species). The species used to monitor lichen richness were selected from onsite assessments and published records from the region. The IAP is based on the sum of the frequency of occurrences of pollution intolerant lichen species in a plot. Pre-established pollution-intolerant lichens are used to calculate the IAPs. Baseline data has been gathered, but trends cannot be observed until the next year of data collection (2011), which will be on-going every five years.

1500 **Effects of Environmental change on species of the lichen-forming fungal genus *Ramalina*.** B. Timsina[1], P. Francisco[2], J. Sorensen[3], and M. D. Piercey-Normore[1]. [1]Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada, R3T 2N2 (umtimsib@cc.umanitoba.ca); [2]Center for Molecular Biology and Genetic Engineering (CBMEG), State University of Campinas, Campinas, Brazil; [3]Department of Chemistry, University of Manitoba, Winnipeg, Manitoba, Canada, R3T 2N2

Fungal plasticity allows for adaptation to changing environments, which can be measured by changes in phenotype including production of secondary compounds (polyketides) in lichen fungi. One hypothesis suggests that polyketide-rich species are more recently derived than polyketide-poor species for Eurasian and Australian species of the genus *Ramalina*. This hypothesis raises questions as to why more polyketides are produced in more recent than ancestral species and what effect the environment has on the production of these compounds. The goal of this study was to examine the effects of changing environmental conditions on species of *Ramalina* by first testing the same hypothesis on North American *Ramalina* species. The objectives are to examine 1) changes in the algal partner in nature, 2) changes in fungal morphology, and 3) production of secondary metabolites (polyketides) in culture. Nucleotide

sequences of two domains in the polyketide synthase (PKS) gene, mitochondrial small subunit ribosomal DNA (mtSSU rDNA) and the internal transcribed spacer (ITS) of rDNA were used to estimate a phylogenetic history among species of *Ramalina*. ITS rDNA sequences were compared between fungal and algal partners of *R. sinensis*. Different growth media were prepared to measure fungal morphology in spore isolates of *R. dilacerata* and polyketide production by HPLC. The proposed hypothesis was supported by North American species of *Ramalina*. For objective 1, variation in ITS sequences suggest that one predominant algal species associates with two clades of *R. sinensis* and *R. americana*. For objectives 2 and 3, preliminary results from experimental manipulation of lichen fungi in culture show different morphological features in *R. dilacerata* cultures. Environmental factors, temperature, pH, and light, have also been reported to affect the regulation of PKS gene expression, but this study is still in progress. Knowledge of gene expression may help us to understand the function of PKS paralogs and further expand our understanding of the genes that are available to produce polyketides. Understanding the effects of environmental conditions on polyketide production may lead to increasing the pool of polyketides that are of interest to the pharmaceutical industries and those that play a role in lichen adaptation to environmental changes.

1515 **The distribution, structure and ecophysiology of *Peltigera hydrothyria*, 'The Water Fan', a rare and endangered macrolichen that grows under water.** D.H.S. Richardson[1], F. Anderson[2], and R.P. Cameron[3], Saint Mary's University, Halifax, (david.richardson@smu.ca)[1], Nova Scotia Museum, Halifax[2], Protected Areas Branch, Nova Scotia Environment, Halifax[3]

Many lichens occur on the banks of streams or on the seashore in habitats that are periodically covered by water. There are a few lichens that grow under water on the beds of fast flowing streams and shallow rivers but most are small dark coloured crustose species. An important exception is Peltigera hydrothyria, a lichen endemic to North America, which has dark green or brownish lobes that are up to 1 cm wide and which looks much like a small seaweed. It is found in upland streams in both eastern and western North America. The species is both rare and endangered in much of its range. An assessment report is being prepared for the Committee on the Status of Endangered Wildlife in Canada. This presentation will outline what is currently known about this interesting and unusual lichen.

Thursday, July 21, 2011
Canadian Botanical Association
Session 7: ***Ecology***

Oral Presentations
Time: 0845-1000h
Room: 260 Sobey Building

Chair: Hugues Massicotte
University of Northern British Columbia

0845 **Michael Shane**
Plant resurrection on the rocks: drought tolerance strategies in granite outcrop species of southwest Western Australia

0900 **Cindy Ross Friedman**
Are endophytic fungi hosted by the lodgepole pine dwarf mistletoe (*Arceuthobium americanum*)?

0915 **André Arsenault**
Distribution of arboreal lichens in a dry Douglas-fir forest of southern British Columbia

0930 **John Markham**
Boreal forest moss-associated nitrogen fixation in a changing climate

0945 **Jeremy Lundholm**
Sensitivity of green roof functioning to plant type and diversity

0845 **Plant resurrection on the rocks: drought tolerance strategies in granite outcrop species of southwest Western Australia.** M.W. Shane[1*], M.E. McCully[2], J.S. Pate JS[1], C. Miller[2]. [1]School of Plant Biology, M084, The University of Western Australia, 35 Stirling Highway, Crawley, WA, Australia, 6009. [2]Plant Industry, CSIRO, Canberra, ACT, Australia, 2601. Corresponding author email: michael.shane@uwa.edu.au

Members of our study species *Borya sphaerocephala* R.Br. are mainly denizens of shallow moss aprons on exposed surfaces of granite outcrops where they are often accompanied by drought tolerant species of non-resurrection character. These include drought avoiding winter annuals, micro stilt plants and a range of geophytes aestivating by means of root or stem tubers. Applied to organisms generally, the term resurrection denotes the ability of a species to become extremely desiccated on drying of its habitat, remain alive but quiescent under such conditions and then, on rewetting of its surroundings quickly rehydrate to recover full vital activities. We examined these peculiar resurrection plants which survive even after leaf water and root water contents have decreased to 2-8% during harsh summer droughts in the western Australian environment. For the first time we show how roots and leaves maintain vitality during dehydration (metabolite accumulation, root dormancy, etc.) and follow resuscitation in inherently dehydrated organs by cryo-scanning electron microscopy, showing what anatomical features really look like when roots and leaves dehydrate and rehydrate. Previous examinations have been done almost entirely on leaves and relied upon vapour fixation and dehydration which can introduce artefacts. We report on anatomical features of leaves and roots but especially introduce the species development of highly unusual 'bubble-like' diminutive rootlets on finest, high-order roots and demonstrate root dormancy phenomena as part of a broader programme autecological studies on rooting characteristics of native south west Western Australian species of arid, nutrient poor habitats and severe Mediterranean type climates. Our talk will compare selected examples of each category of resurrection and geophytic species under the same habitat conditions in terms of there alternative biological and phenological strategies and adaptive qualities of shoots and roots in structure and functioning.

0900 **Are endophytic fungi hosted by the lodgepole pine dwarf mistletoe (*Arceuthobium americanum*)?** Cindy Ross-Friedman[1*], Lyssa Martin[2], Arvin Dwarka[3], Lori A. Phillips[4]. Department of Biological Sciences, Thompson Rivers University, Box 3010, 900 McGill Road, Kamloops BC, V2C 5N3[1,2,3]; Department of Primary Industries-Vic AgBiosciences Centre, 1 Park Drive, Bundoora, VIC 3083, Australia[4]

Arceuthobium americanum, a flowering plant and obligate parasite of two pine species, *Pinus contorta* var. *latifolia* and *P. banksiana*, poses a serious threat to the Canadian forest industry through wood destruction and increased tree mortality. The development of control mechanisms is difficult, as *A. americanum* and its host have a shared physiology. Fungal endophytes exist in obligate symbiotic relationships with their plant host: they are known to induce host disease resistance pathways, provide certain nutrients, and secrete targeted antimicrobial compounds. Interrupting an endophyte-host relationship could leave a host plant susceptible to nutrient starvation or pathogen attack, a tactic that could be employed in dwarf mistletoe control. The objective of this work was to determine if *A. americanum* hosts endophytic fungi. In this study, healthy *A. americanum* aerial tissue was collected at Stake Lake, British Columbia in June 2009. To detect fungi, *A. americanum* was examined with fluorescence microscopy. Calcofluor White, a fluorescent stain for cellulose (plant cell walls) and chitin (fungal cell walls), and fluorescein

isothiocyanate-labelled wheat germ agglutinin, a fluorescent stain specific to chitin, were used in combination to visualize fungal structures and differentiate them from plant tissue within *A. americanum*. Fungal haustoria, hyphae and vesicles were found within stem tissue; haustoria and hyphae were found within fruit tissue. These results are highly indicative of a healthy symbiosis *between A. americanum* and fungi. Identification of the fungal species via PCR amplification of the fungal nuclear rDNA internal transcribed spacer (ITS) region in conjunction with 454 sequencing is ongoing.

0915 **Distribution of arboreal lichens in a dry Douglas-Fir forest of southern British Columbia.** A. Arsenault[1*], C. Björk[2], and T. Goward[3] [1]Atlantic Forestry Centre, Canadian Forest Service, Natural Resources Canada, P.O. Box 960, Corner Brook Newfoundland and Labrador, Canada, A2H 6J3, [2]Stillinger Herbarium, University of Idaho, Moscow Idaho, 83843, U.S.A.[3]Herbarium, Department of Botany, University of British Columbia, Vancouver, British Columbia V6T 2B1 Canada

The Opax Mountain Silviculture Systems Project is located in the Interior Douglas-Fir biogeoclimatic zone, approximately 30 km north of Kamloops, BC. It is divided into six treatment units replicated twice at 2 different elevations. The units represent varying amounts and patterns of tree harvesting, including uncut controls, 20% removal of merchantable volume using individual tree selection (ITS), 50% ITS, 50% ITS with uncut reserves, 20% removal using a mixture of patch cuts of 0.1, 0.4 and 1.6 hectares, and 50% removal with patch cuts of a similar nature as the 20% removal. Logging took place in the winter of 1993-1994. Patch cuts were subsequently planted with saplings of Douglas fir, lodgepole pine and ponderosa pine. The distribution of the arboreal lichen flora was examined in each experimental unit in the fall of 2007. The flora is surprisingly rich with over 300 species within a 400 hectare area. The crust lichens constitute 58% of the species, while 30% are macrolichens, and 11% are calicioids. Species diversity did not seem to be closely associated with treatment type. However trees in the unlogged perimeter of the patch-cuts had much greater richness, 196 species, compared to 57 and 18 for epiphytes growing on advanced regeneration and planted trees inside patch-cuts. Mean species richness followed the same pattern for macrolichens and crusts increasing with increasing substrate age. Calicioid lichens were only found in unlogged perimeters of patch-cuts. This study reveals for the first time that Interior Douglas–fir forests have a highly rich and diverse arboreal lichen flora. These findings have important implications for retention of key lichen habitats in managed landscapes and should help foresters and planners minimize impact on biodiversity resulting from harvesting, silviculture, biofuel and ecosystem restoration activities.

0930 **Boreal forest moss-associated nitrogen fixation in a changing climate.** Dr. John Markham, University of Manitoba, Department of Biological Sciences, Winnipeg, MB Canada R3T 2N2

Productivity in boreal forests is generally thought to be nitrogen limited, due to low rates of decomposition, which is limited primarily by temperature and secondarily by litter quality. Inputs of fixed nitrogen have also been thought to be low due the rarity of nitrogen fixing plants. Over the last decade these assumptions have been questioned. It is becoming clear that boreal forest plants access organic nitrogen, although the contribution this makes to ecosystem productivity is not well understood. There is also a renewed interest in nitrogen fixation that is not associated with plant symbioses. Mosses can have substantial populations of cyanobacteria and contribute significant inputs of fixed nitrogen to boreal ecosystems. I examined moss-associated nitrogen fixation in upland and lowland forest stands in southeastern Manitoba. The rate of nitrogen fixation associated with *Sphagnum* (mainly *S. capillifolium* (Ehrh.) Hedw.) was 20 times higher than with *Pleurozium schreberi* (Brid.) Mitt., contributing 2 kg N per hectare per year. This was the result of both higher nitrogen fixing activity and total ground cover. While stand level

contributions of *P. schreberi* were low, this moss can have a substantial localized effect on nitrogen cycling. Light availability and nutrients had little effect on rates of fixation but should not be ruled out as controlling factors. Rates of nitrogen fixing activity were inversely related to moisture content in *P. schreberi*, but not in *Sphagnum*. In both species, temperature was positively correlated nitrogen fixation. Based on annual rates of fixation, a 3˚C increase in temperature is predicted to increase fixation by 40 % in *Sphagnum* dominated forests. This could potentially increase rates of organic matter decomposition and the release of carbon from these forests.

0945 **Sensitivity of green roof functioning to plant type and diversity.** Jeremy Lundholm, Saint Mary's University, 923 Robie St. Halifax NS B3H 3C3

Extensive green roofs provide many environmental and economic benefits. It is well known that the engineered components of green roofs can strongly influence the degree to which thermal and stormwater benefits are realized, as well as building variables such as roof:wall ratio and roof slope. Less well known is the role of the "soft" components of the system in influencing green roof function. Here I examine the sensitivity of key green roof performance indicators, such as roof temperature, albedo, evapotranspiration and stormwater retention to plant type and functional group diversity. We have tested about 20 plant species, and over 40 combinations of two or more species in a replicated modular extensive green roof system. Our research shows that the vegetation cooling the roof most in summer resulted in soil temperatures 4.5ºC lower than the worst, which were comparable to soil-only controls. The best species can reflect 40% more light than the least reflective. Evapotranspiration varied by 36% between vegetation types, with the best monocultures losing 20% more water than the worst, and the best mixtures losing 7.4% more than the best monocultures. Stormwater capture was 34% higher in the best vegetation types compared with the worst. Species that provided the highest level of these benefits, differed depending on which benefit was examined. This work shows that ecological or biological properties of the green roof system can influence performance of desired functions as much as the built or engineered components of the system. Plant species mixtures deserve further testing if the goal of extensive green roof construction is to maximize benefits while minimizing weight and cost.

Thursday, July 21, 2011 **Oral Presentations**
Canadian Botanical Association **Time:** 1030-1200h
Session 8: ***Mycology*** **Room**: 260 Sobey Building

Chair: Hugues Massicotte
University of Northern British Columbia

1030 Felix Baerlocher
Weresub Memorial Lecture: "Research on aquatic hyphomycetes in a changing world"

Aquatic hyphomycetes are a polyphyletic group of stream fungi. They enrich autumn-shed leaves with proteins, lipids and modify them with exoenzymes. This conditions the leaves for consumption by stream invertebrates. Much of the early research has been process-oriented, partly due to the difficulty of identifying fungal mycelia in the opaque leaf matrix. Molecular techniques (PCR) have greatly expanded the range of accessible information, and have consistently revealed the presence of other fungal groups (Zygomycetes, zoosporic fungi). Global change is predicted to increase CO_2 levels, the average temperature and its variability. These changes will have direct and indirect (via plants, consumers) effects on diversity and functions of stream fungi.

Monday, July 18, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 1030-1200h
Session 1: ***Plant Responses to Climate Change*** **Room**: 201 Sobey Building

Chair: Peter Pauls
University of Guelph

1030 **Jonathan Newman**
Mission accomplished or mission impossible: Predicting biological impacts of climate change

1115 **Sally Aitken**
Adapting forest genetic resource management to climate change

1030 **Mission accomplished or mission impossible? Predicting the biological impacts of climate change**. Jonathan Newman, School of Envrionmental Biology, University of Guelph, Guelph, Ontario.

Society expects that biologists can and will provide accurate predictions about the likely biological consequences of climatic change. In principle, biologists are up to this task. In practice, biologists face a number of daunting methodological and philosophical challenges to providing such predictions. These challenges include, but are not limited to: time, cost, geographical extent, statistical, and uncertainty about exactly what the future climate will look like. In this presentation I will spell out these challenges in detail. I will suggest that we need to move beyond simplistic climate change 'scenarios' in our models and experiments, and embrace the challenge of predicting the consequences of more realistic climatic changes, but herein lies the difficulty. Biologists are not capable of considering such realistic changes, at least not experimentally, and we have often failed to do so in our modelling efforts. I will end with some reflections on what I think is needed to advance the research agenda in this field, and to achieve so-called 'robust predictions'.

1115 **Adapting forest genetic resource management to climate change**. Sally N. Aitken, Centre for Forest Conservation Genetics, Department of Forest Sciences, University of British Columbia

Climate change is already changing the face of Canadian forests, and reforestation decisions made today will impact the health of our forests over the next century. Population selection for future climates has been greatly informed by long-term provenance trials that generate population response functions to climate, but comprehensive experiments are lacking for many species, and there is a pressing need for relevant information in the shorter term. Population genomic approaches to identifying genes involved in adaptation to climate combined with high-throughput phenotyping in growth chamber experiments and spatial climatic models have the potential to fill this gap.

Monday, July 18, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 1300-1500
Session 2: ***Plant crop and Eco-physiology*** **Room**: 201 Sobey Building

Chair: Doug Campbell
Mount Allison University

1300 **Art Fredeen**
Importance of residual vegetation to net carbon uptake in pine stands following mountain pine beetle attack in central British Columbia, Canada

1315 **Line LaPointe**
Effect of water stress and temperature on growth of wild leek

1330 **Allison Hayward**
Mechanisms involved in the multi-metal tolerance of *Deschampsia cespitosa*: The role of metal chelators

1345 **Lee Kalcsits**
Using nitrogen isotopes at natural abundance to measure genetic variation in nitrogen-use traits and source preference in *Populus balsamifera* L

1400 **Harold Weger**
Ferric reductase activity of iron-limited cells is both promoted and inhibited by ferric chelators,

1415 **Guy Samson**
Characterization and physiological importance of complex oscillations of photosynthesis induced by changing light

1430 **Eric Lyons**
Down regulation of Glutamine synthetase is correlated to ammonium accumulation and chlorosis in "SR7200" velvet bentgrass (*Agrostis canina* L.)

1445 **Zhen Guo Ma**
The glycolytic and antioxidant H_2O_2 scavenging capacity of germinating barley seeds with different levels of dormancy

1300 **Importance of residual vegetation to net carbon uptake in pine stands following mountain pine beetle attack in central British Columbia, Canada.** R. Bowler1, A.L. Fredeen[1,2]*, M. Brown[3], T.A. Black[3]. Ecosystem Science and Management Program[1], Natural Resources and Environmental Studies Institute[2], University of Northern British Columbia, Prince George, British Columbia, Canada V2N 4Z9; and [3]Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada V6T 1Z4

An unprecedented epidemic of mountain pine beetle (MPB: *Dendroctonus ponderosae*) has resulted in extensive mortality of lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia* ex. Engelm.) across British Columbia. The goal of this study was to quantify the contribution of residual live vegetation to forest-level daytime gross ecosystem productivity (GEP) as measured by eddy covariance flux-towers in two lodgepole pine-dominated forests during and/or after MPB-attack, 70km (MPB-03: first attacked in 2003), and 170 km (MPB-06: first attacked in 2006) north of Prince George in central British Columbia, respectively. Diurnal foliar net photosynthesis (pn) of residual live herb, shrub and tree foliage was measured periodically at both sites throughout the growing seasons of 2007, 2008 and 2009. Yearly averages of all component pn combined were very comparable to average growing-season GEP. A bottom-up up model of ecosystem-scale carbon uptake was undertaken. Net photosynthesis was modeled with non-rectangular hyperbolic functions between instantaneous measures of pn and photosynthetically active radiation (Q). These functions were used to scale up to stand level temporally by using continuous diurnal measures of Q, and spatially using measures of leaf area of vegetation components to provide estimates of ecosystem-scale net photosynthesis (PN). PN of all plant components (PN ECOSYSTEM) was similar to GEP at MPB-06 and MPB-03. Of note, broadleaf species were responsible for the majority (65- 68%) of PN ECOSYSTEM at MPB-03, and about one-third (33-35%) of PN ECOSYSTEM at MPB-06. Thus, residual vegetation and particularly broadleaf species, is very important to growing-season CO2-uptake in MPB-attacked pine stands in central British Columbia and cannot be neglected in larger scale modeling estimates of forest carbon dynamics in these locations when determining the impact of MPB attack.

1315 **Effect of water stress and temperature on growth of wild leek.** A. Bernatchez and L. Lapointe* Département de biologie and Centre d'étude de la forêt, Université Laval, Québec, Canada G1V 0A4 (line.lapointe@bio.ulaval.ca)

Wild leek (*Allium tricoccum* Ait.) is a common spring ephemeral of hardwood deciduous forest of North Eastern America. It takes advantage of the short period of high light conditions between snowmelt and canopy closure to complete its vegetative life cycle and accumulate carbohydrate reserves for the following year. Previous studies on another spring ephemeral have shown that these species exhibit better growth when grown at low temperature typical of very early spring. Water stress, more frequent as temperature increases , could exacerbate the negative impact of higher temperature on these species. We thus quantified the impact of an episode of water stress on the growth of wild leek under control conditions along with the impact of three growth temperatures: 18/14°C, 12/8°C, 8/6°C (day/night) previously tested on *Erythronium americanum*, another spring ephemeral. These temperatures represent the actual late spring, early spring, and a lower temperature regime, respectively. Gas exchange and chlorophyll a fluorescence were measured repeatedly during the growth season along with bulb biomass accumulation. One episode of water stress had negative impact on wild leek growth. Bulbs at final harvest were twice as heavy in control plants despite longer leaf life duration in water stressed plants. Pn, g_s, Ci, electron flux through PSII (ΦPSII) and the fraction of the energy dedicated to photochemistry

(qP) decreased rapidly over time during the water stress. Once plants were re-watered, at first signs of leaf wilting, gas exchange and fluorescence values exhibited only partial recovery. Highest growth was recorded at 12/8°C, in accord with higher Pn at this temperature regime throughout the season. Pn was similar at 18/14°C and 8/6°C but leaves lasted longer at 8/6°C leading to final larger biomass at 8/6°C than at 18/14°C. This study confirmed that wild leek is sensitive to water stress. Wild leek was not as efficient as *Erythronium americanum* at low temperatures, which could explain its more southern limit of distribution than *E. americanum*. Both species performed less efficiently at 18/14°C than at 12/8°C, confirming the sensitivity of spring ephemerals to warmer temperature and the potential negative impact global warming could have on such species.

1330 **Mechanisms involved in the multi-metal tolerance of *Deschampsia cespitosa*: The role of metal chelators.** AR. Hayward*[1]; TC. Hutchinson[2]; RJN. Emery[3]. [1]Environmental and Life Sciences Program, Trent University, 1600 West Bank Drive, Peterborough, Ontario K9J 7B8; [2] Environmental and Resource Studies Department, 1600 West Bank Drive, Trent University, Peterborough, Ontario K9J 7B8; and [3] Biology Department, Trent University, 1600 West Bank Drive, Peterborough, Ontario K9J 7B8

Certain species or ecotypes of plants have developed the ability to tolerate and even thrive in heavily metal contaminated environments. The physiological mechanisms allowing for these elevated levels of tolerance to a range of metals have yet to be fully understood. One such mechanism is the production of metal chelators that bind to the toxic metal ions. The productions of these various chelators are thought to be metal specific, resulting in the potential for the involvement of a number of chelators in multi-metal tolerance. This study quantified the occurrence of a number of metal chelators, including amino acids and phytochelatins (PCs), in two ecotypes of *Deschampsia cespitosa* with multi-metal tolerant. These ecotypes types of *D. cespitosa* have displayed hyper-tolerances to a numbers of metal including Ni, Cu, and Zn. Plants were collected from contaminated mine sites in the Sudbury Ontario region and propagated in the lab in hydroponic culture. A highly sensitive method for PC2 PC3 and GSH detection was developed using a High Performance Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometer (LC-(ESI)MS/MS). Ecotypes responded to Cd additions with PC production, however, this response was not observed from Ni exposure. Though Ni did not induce PCs, other chelators were up regulated. One such chelator was histidine, an amino acid known to be involved in Ni transport in Ni hyperaccumulating plants. This, along with chelator profiles in response to other metals, will be discussed.

1345 **Using nitrogen isotopes at natural abundance to measure genetic variation in nitrogen-use traits and source preference in Populus balsamifera L**. L. Kalcsits*; R. Guy. Department of Forest Sciences, University of British Columbia, 2424 Main Mall, Forest Sciences Centre, Vancouver, BC, Canada, V6T 1Z4 (kalcsits@interchange.ubc.ca)

Nitrogen is one of the limiting nutrients in most natural ecosystems and nitrogen source availability varies with climate and edaphic conditions. For wide ranging boreal forest tree species such as Populus balsamifera L., the climatic range extends from prairie through to forest and tundra ecosystems. Nitrogen source availability varies from higher nitrate at the southern range of the species to higher ammonium at the northern limit and is a function of soil and climate. Intra-specific adaptation or variability in nitrogen utilization of P. balsamifera along this complex gradient is unknown. Using nitrogen isotopes at natural abundance as an integrated measure of nitrogen-use traits based on a predictive model of intra-plant variability in isotopic composition (δ15N), differences in use of either nitrate or ammonium can be determined. Five populations of P. balsamifera were grown in large volume, open-source hydroponics to ensure

minimal change in either source nitrogen concentration or δ15N, with either nitrate or ammonium as the sole nitrogen source. There was significant within population variability in nitrogen-use traits including biomass, net nitrogen influx, efflux:influx ratio across the root epidermis, and partitioning of nitrate assimilation. There was little between population variability in any measurements relative to within population variability. Nitrogen-use traits were independent of overall plant growth. Plants were larger when grown with nitrate compared to ammonium, and nitrogen content was greater in plants grown with nitrate. Although biomass was greater for nitrate-grown plants, net flux was greater with ammonium in at least some genotypes. The results demonstrate considerable intra-specific variability in nitrogen uptake, assimilation and allocation of nitrogen in P. balsamifera.

1400 **Ferric reductase activity of iron-limited cells is both promoted and inhibited by ferric chelators**. M. B. Sonier and H. G. Weger. Dept. of Biology, University of Regina, Regina, Saskatchewan, Canada S4S 0A2 (e-mail: harold.weger@uregina.ca)

Iron-limited cells of the green alga Chlorella kesslerii Fott et Nováková UTEX 263 use a reductive mechanism to access extracellular Fe(III). Plasma membrane ferric reductase reduces Fe(III)-chelates to Fe(II), which is subsequently taken up by the cell. Previous work with synthetic chelators has demonstrated that non-chelated Fe(III) is not a substrate for ferric reductase activity, and that synthetic chelators both support ferric reductase activity (when supplied as Fe(III)-chelates) and inhibit ferric reductase, and also inhibit Fe(II) uptake by competing with the plasma membrane Fe(II) transport system for Fe(III). Here, we extend these observations to naturally-occurring chelators and their analogues (e.g. desferrioxamine B mesylate, schizokinen, two forms of dihydroxybenzoic acid) and also two formulations of the commonly-used herbicide N-(phoshonomethyl)glycine (glyphosate). The ferric forms of the larger siderophores (desferrioxamine B mesylate, schizokinen) and Fe(III)-phosphonomethylglycine all supported rapid rates of ferric reductase activity, while the iron-free forms inhibited reductase activity. The smaller siderophores/siderophore precursors, 2,3- and 3,4-dihydroxybenzoic acids, did not support high rates of reductase in the ferric form but did inhibit reductase activity in the iron-free form. Bioassays supported the idea that ferric compounds that supported high rates of ferric reductase activity also supported a large stimulation in the growth of iron-limited cells, and that an excess of iron-free chelator decreased the growth rate. With respect to N-(phosphonomethyl)glycine, there were differences between the pure compound and the most common commercial formulation (which also contains isopropylamine) in terms of supporting and inhibiting ferric reductase activity and growth. These results suggest that photosynthetic organisms that use a reductive strategy for iron acquisition both require, and are potentially simultaneously inhibited by, ferric chelators. Furthermore, these results also may provide an explanation for the frequently contradictory results of N-(phosphonomethyl)glycine application to crops: low concentrations of this molecule likely solubilize Fe(III), making it available for plant growth, but higher sub-lethal concentrations appear to decrease iron acquisition.

1415 **Characterization and physiological importance of complex oscillations of photosynthesis induced by changing light**. G. Samson, L. Bonin, R. Carpentier, & E. Lévesque. Groupe de Recherche en Biologie Végétale, Université du Québec à Trois-Rivières, Trois-Rivières, Québec Canada, G9A 5H7 (email : guy.samson@uqtr.ca)

Models of photosynthesis rely mostly on steady-state reactions that do not integrate the rapid and large variations of light intensity occurring in natural environments. To better understand how the different regulation mechanisms interact to optimize the photosynthetic efficiency under these changing conditions, we aimed to 1) characterize the oscillations of photosynthesis induced by

sinusoidal lights of different amplitudes (200, 400 … 1000 μmoles photons m^{-2} s^{-1}) and periods (20, 40, 60, 90, 120 sec), and 2) compare the photosynthetic efficiency under different intensities of constant versus sinusoidal lights. Dwarf sunflower plants were grown indoor (350 μmoles photons m^{-2} s^{-1}, 14 hrs/day) and outdoor (natural sunlight). For the experiments, their leaves were exposed to blue LED lights and their photosynthetic efficiency was monitored by chlorophyll-*a* fluorescence (ChlF). We observed that sinusoidal lights induced various and complex oscillatory patterns of ChlF. Fourier analysis showed that these ChlF patterns are the sum of three main components (C1, C2, C3) with periods corresponding respectively to 1, ½, and ⅓ of the period of the sinusoidal incident light. Variations of C1, C2, and C3 amplitudes under our experimental conditions indicate that the ChlF oscillations were 50% larger in leaves of outdoor than indoor plants, and suggest that C1 corresponds to the closure of photosystem II reaction centers, C2 to the state transitions SI-SII, and C3 to the thermal dissipation of absorbed energy through zeaxanthin. Furthermore, in leaves from indoor plants, photosynthetic efficiency under constant light were always higher than those measured under sinusoidal lights of equivalent average intensities. In contrast, leaves from outdoor plants were able to maintain photosynthetic efficiencies under sinusoidal lights at similar and even superior levels to those measured under equivalent intensities of constant lights. Globally, our results suggest that 1) the oscillations of the photosynthesis under dynamic light are typical of complex systems regulated by different mechanisms and 2a) plant acclimate not only to light intensities but also to rapid light variations, 2b) the amplitudes of ChlF oscillations would determine the capacity of photosynthesis to adjust rapidly and maintain its efficiency under changing light.

1430 **Down regulation of Glutamine synthetase is correlated to ammonium accumulation and chlorosis in "SR7200" velvet bentgrass (Agrostis canina L.).** H. Xu; B. Micallef; K. Jordan; E. Lyons* Department of Plant Agriculture University of Guelph, Guelph ON. N1G 2W1. (email: elyons@uoguelph.ca)

Velvet bentgrass (*Agrostis canina* L.) varieties are reported to have high nitrogen use efficiency and increased disease resistance. Unfortunately, velvet bentgrass exhibits chlorosis or nitrogen toxicity symptoms at nitrogen rates typically associated with optimal growth of other bentgrass species. Previously presented research has shown that this is correlated to ammonium accumulation when fertilizers with a high ammonium content or urea are applied. We have examined enzymes involved in nitrogen assimilation pathway to determine why ammonium accumulation may be occurring. The cultivar 'SR7200' of velvet bentgrass was exposed to 4 different nitrogen forms including 5% ammonium, 45% ammonium, 95% ammonium, and urea in a hydroponic system. We then measured nitrate, nitrite and ammonium content in addition to nitrate reductase, nitrite reductase and glutamine synthetase (GS) glutamate synthase (GOGAT) at various time points after exposure to the different nitrogen forms. Nitrate reductase and nitrite reductase could not be correlated to the ammonium accumulation. Interestingly, GS activity in the leaves of SR7200' had a sudden decrease in the 95% ammonium- and urea-treated plants at the 24 hour time point. The accumulation of ammonium may be caused by the inability of GS to convert the pools of ammonium into amino acids, resulting in chlorosis of velvet bentgrass plants.

1445 **The glycolytic and antioxidant H2O2 scavenging capacity of germinating barley seeds with different levels of dormancy**. Z. G. Ma*, A. U. Igamberdiev and N. V. Bykova. Department of Biology, Memorial University of Newfoundland, St. John's, Newfoundland, Canada A1B 3X9

Several enzymes of the glycolytic and antioxidant metabolism were tested during germination of two cultivars of barley (*Hordeum vulgare* L.) with different levels of seed dormancy: Harrington (non-dormant, 95% seeds germinated in 24 hours) and Sundre (more dormant, slowly germinating, with only 40% seeds germinated after 48 hours from imbibition). The key enzymatic

activities were determined for alcohol dehydrogenase (ADH) to measure the capacity for the glycolytic fermentation, for pyruvate phosphate dikinase (PPDK) to estimate the capacity for pyrophosphate-dependent glycolysis, and for catalase (CAT) and ascorbate peroxidase (APX) to determine the capacity for H_2O_2 scavenging. All investigated enzymes revealed the highest activity in dry seeds which decreased by several times after radicle protrusion. The ADH showed 20% higher activity in Harrington, decreasing five times after 24 hours in germinating seeds of both cultivars and remaining at a higher level in dormant non-germinated seeds. PPDK activity in dry seeds was five times higher in more dormant variety and was also kept at a higher level in non-germinated seeds. The activities of two antioxidant enzymes (APX and CAT) scavenging H_2O_2 initially increased after 9 hours of imbibition in non-dormant Harrington seeds but further decreased dramatically upon radicle protrusion. The activities remained at approximately the same level in dormant imbibed seeds of cv. Sundre. It is concluded that the process of germination is characterized by drastic changes in the activities of glycolytic and antioxidant enzymes and that dormant barley seeds maintain higher capacity for H_2O_2 scavenging and high rates of pyrophosphate-dependent glycolysis.

Monday, July 18, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 1530-1700
Session 3: ***Plant Stress and Plant Development*** **Room**: 201 Sobey Building

Chair: Sophia Stone
Dalhousie University

1530 **Sarah Schoor**
Effect of abiotic stress on cytoskeleton and chloroplast arrangement

1545 **R. Brendan Porter**
Adaptation and acclimation of *Alnus rubra* in a changing climate

1600 **Karina Neimanis**
Alternative Oxidases of Non-angiosperm Plants

1615 **Guillaume Théroux Rancourt**
Changes in mesophyll conductance and plant hydraulic properties during a drought–rewatering cycle in hybrid poplars with contrasting water stress tolerance

1630 **Belay Ayele**
Gibberellin Metabolism and Transport during Germination and Young Seedling Growth of Pea (*Pisum sativum* L.)

1645 **Wendy Lyzenga**
Exploring two ethylene biosynthetic enzymes as potential targets of Arabidopsis RING E3 ligases, XBAT32, during lateral root production

1530 **Effect of abiotic stress on cytoskeleton and chloroplast arrangement. S.M. Schoor[1]*, A. Kondo[2], S. Chuong**[1]. [1]University of Waterloo, Waterloo, Ontario, Canada N2L 3G1 (email: sschoor@gmail.com); and [2]Faculty of Agriculture, Meijo University, Tempaku-ku, Nagoya 468-8502, Japan

Plants have evolved numerous strategies including changes to chloroplast arrangement and structure for adapting to their external environment. Plants from various photosynthetic backgrounds including C3 *Suaeda linifolia*, C4 *Portulaca oleracea,* single cell C4 species *Bienertia sinuspersici* and CAM *Kalanchoe blossfeldiana*, were studied in order to observe chloroplast response to abiotic stress treatments (eg. light, drought, cold). In addition to altered structure, stress treatments resulted in some form of chloroplast rearrangement in the plant species studied. The organization of the cytoskeleton was also examined in stress treated plants to investigate the mechanisms controlling the intracellular movement of chloroplasts. Immunofluorescent observations of the cytoskeleton in fixed protoplasts showed altered actin and microtubule arrangement correlating with the rearrangement of chloroplasts. Furthermore, drug treatments to depolymerize either actin or microtubules inhibited stress induced chloroplast re-localization. Thus, these results show that the stress-induced chloroplast rearrangement in the plants is dependent on the cytoskeleton.

1545 **Adaptation and acclimation of *Alnus rubra* in a changing climate**. R.B. Porter*, B.J. Hawkins. Centre for Forest Biology, University of Victoria, Victoria, BC, Canada, V8W 3N5 (brendanp@uvic.ca)

Red alder (*Alnus rubra* Bong.) is a rapidly-growing tree species of the northwest Pacific coast. Alder favours riparian or highly disturbed sites with exposed mineral soil. Through symbiosis with the actinomycete bacteria *Frankia* sp., *A. rubra* fixes atmospheric nitrogen, much of which is added to the soil via foliage drop at the end of the growing season. Previous studies (Ager *et al.* 1993, Xie *et al.* 2002, others) have found evidence for regional adaptation, however, little is known about the variation in physiological characteristics over the range of alder, or its ability to acclimate to contrasting environments. Similarly, genotypic variation in rates of nitrogen fixation has been little studied. The current study is an inventory of physiological variation in 50 wild-sourced adult alder half-sibling families grown for 15 years in two common gardens of contrasting climate. Measured physiological traits include height and diameter after 15 years' growth, rates of nitrogen fixation (both instantaneous and integrated over the growing season), frost and drought hardiness, timing of bud burst and leaf senescence. Early results show significant differences in frost hardiness among alder families, especially during the early autumn hardening phase. Timing of leaf senescence was also found to vary among families, while rates of nitrogen fixation and timing of bud burst exhibit less variation across families. Frost hardiness was found to vary between sites, however, no significant site x family interactions have been identified. In fact, to date, only spring bud flush has been found to exhibit a significant genotype x site interaction, though the magnitude of the difference between sites is not biologically significant. Results from this study will be correlated with climatic variables from the location of origin of alder families to explore patterns of adaptation. Results will also be integrated with climate models and silvicultural data to inform and guide selection of genetic material for reforestation.

1600 **Alternative oxidases of non-angiosperm plants** K. Neimanis* and A.E. McDonald, Department of Biology, Wilfrid Laurier University, Waterloo, Ontario, N2L 3C5, Canada

Alternative oxidase (AOX) is a mitochondrial inner membrane protein that introduces a branch point in the respiratory electron transport chain at ubiquinol. AOX bypasses two sites of proton translocation across the inner mitochondrial membrane resulting in a lower ATP yield per oxygen consumed. Despite the fact that AOX seems energetically wasteful, AOX transcripts, protein levels, and enzymatic activity increase during environmental stress. In Arabidopsis thaliana, tobacco, soybean, and rice, much is known about AOX multigene families, gene expression, and post-translational regulation of the enzyme. Given the data available for angiosperm AOXs, it is surprising that it has not been studied in non-angiosperm plants as a logical starting point for comparative studies. Our bioinformatics results show that AOX is present in a moss, liverwort, fern, lycopod, and several species of conifers. An analysis of these sequences indicates that conserved glutamate and histidine residues required for enzyme activity are conserved in non-angiosperm AOXs and that they are likely active quinol terminal oxidases. Our results also indicate that these proteins will exhibit a different mode of post-translational regulation compared to angiosperm AOX proteins. We are confirming the expression of AOX genes using reverse transcriptase PCR in several species, especially those for which molecular database information is currently unavailable.

1615 **Changes in mesophyll conductance and plant hydraulic properties during a drought–rewatering cycle in hybrid poplars with contrasting water stress tolerance**. G. Théroux Rancourt1*, G. Éthier1, S. Pepin2. 1Département de phytologie; and 2Département des sols et du génie agro-alimentaire, Université Laval, Québec, QC, Canada, G1V 0A6

Mesophyll or internal conductance (g_i) has been shown to impose a significant limitation to net CO_2 assimilation (A_n) in various species during water stress. Although the relationship between g_i and A_n has received much attention during the last decade, the links between g_i and plant hydraulics have not been investigated. This study examined the change in gas exchange and plant hydraulic properties of four hybrid poplar clones known for their contrasting sensitivity to drought stress and one balsam poplar (*Populus balsamifera* L.) subjected to two weeks of progressive soil drying followed by one week of rewatering. During the drought cycle, a decrease in A_n, stomatal conductance (g_s) and g_i was observed in all clones as soil water content declined. Drought-sensitive clones maintained greater A_n and g_s levels than less sensitive clones during soil drying, up to a threshold in leaf water potential (Ψ_l) of –1 MPa, after which both declined considerably. Changes in g_i during drought were related to plant hydraulic conductance (K_{plant}, estimated from transpiration and soil-leaf pressure gradient), soil water potential (Ψ_s) and percent loss of stem conductivity (PLC = stem hydraulic conductivity (K_s) / maximal stem conductivity). However, g_i responses to K_{plant}, Y_s and PLC varied among clones. Upon rewatering, A_n and g_i recovered fast and were closely related to soil moisture conditions (i.e. Ψ_s). Stomatal conductance usually reached its pre-stress level within a week, depending on the recovery of plant hydraulic properties, mainly Ψ_l and K_s. A fast recovery of g_i after a short water stress has previously been reported for several species. The present study shows that g_i is influenced by soil water and plant hydraulic properties during a progressive drought, and that the responses differ between sensitive and less sensitive clones. Moreover, g_i and g_s can vary independently during soil drying and rewatering. Further research is needed to determine the specific effects of K_s and leaf hydraulic conductance on g_i.

1630 **Gibberellin metabolism and transport during germination and young seedling growth of pea (Pisum sativum L.).** B.T. Ayele[1]*, J.A. Ozga[2], A.D. Wickramarathna[2], and D.M. Reinecke[2]. [1]Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2 (email: b_ayele@umanitoba.ca); and [2]Plant BioSystems, Department of Agricultural, Food and Nutritional Science, 4-10 Agriculture/Forestry Centre, University of Alberta, Edmonton, Alberta, Canada T6G 2P5

The role of gibberellins (GAs) during germination and early seedling growth is examined by following metabolism and transport of radiolabeled GAs in cotyledon, shoot and root tissues of pea using an aseptic culture system. Mature pea seeds have significant endogenous GA_{20} levels that fall during germination and early seedling growth, while the seedling develops the capacity to transport GA_{20} from the cotyledon to the shoot and root of the seedling. Even though cotyledons at 0 to 2 days after imbibition (DAI) have significant amounts of GA_{20} , the cotyledon retains the ability to metabolize labeled GA_{19} to GA_{20} and express significant levels of *PsGA20ox2* message (encodes for a GA biosynthesis enzyme, GA 20-oxidase). The pool of cotyledonary GA_{20} likely provides the GA requirement for the cotyledons during germination, as well as for shoots and roots during early seedling growth. Early in development the shoots and roots express GA metabolism genes (*PsGA3ox genes* encoding GA 3-oxidases for synthesis of bioactive $GA_{1,}$ and *PsGA2ox genes* encoding GA 2-oxidases for deactivation of GAs to GA_{29} and GA_8) and develop the capacity to metabolize GAs to regulate the levels of bioactive GA as part of growth and development leading to seedling establishment. Auxins also show an interesting pattern during early seedling growth with higher levels of 4-chloro-indole-3-acetic acid (4-Cl-IAA) in mature seeds and higher levels of indole-3-acetic acid (IAA) in young root and shoot tissues that suggest a changing role for auxins during early seedling development.

1645 **Exploring two ethylene biosynthetic enzymes as potential targets of Arabidopsis RING E3 ligases, XBAT32, during lateral root production**. W.J. Lyzenga*; and S.L. Stone. Department of Biology, Dalhousie University, Halifax, NS B3H 4J1 (email: W.Lyzenga@Dal.ca)

Ubiquitin-mediated proteolysis is a widespread mechanism used by plants to respond to environmental stimuli and to regulate hormone signals that influence development. Central to the ubiquitination pathway are E3 ligases which are the substrate recruiting component of this process. XBAT32 is a RING type E3 ligase and studies indicate that XBAT32 regulates the abundance of ethylene biosynthetic enzymes (1-aminocyclopropane-1-carboxylate synthase - 4 and ACS7). Loss of *XBAT32* results in ethylene overproduction and reduced lateral root production. Our current model suggests that overproduction of ethylene in the *xbat32* root, disrupts auxin transport and blocks essential auxin uploading into pericycle cells preventing specification of lateral root founder cells. We are currently investigating whether auxin transport is altered in the *xbat32* mutant and if loss of *acs4* and/or *acs7* can rescue the lateral root phenotype of *xbat32* mutants. ACS family members are regulated by ubiquitin-mediated proteolysis and ACS4 has been suggested to be regulated by a BTB E3 ligases. We demonstrate with a cell free degradation assay that recombinant ACS4 protein is stabilized in *xbat32* compared to wild type. This suggests that XBAT32 is another E3 ligases that contributes to proteasome dependent regulation of ACS4. The C-terminal extensions of ACS family proteins are thought to be points of proteasome-dependent regulation and they are required for degradation. However it was thought that ACS7, which has the shortest C-terminal extension, is not regulated by ubiquitin-mediated degradation. Using a cell free degradation assay and transgenic plants expressing HA-ACS7 we demonstrate that ACS7 is turned over in a proteasome dependent manner. In addition, we have shown *in planta* that HA-ACS7 is stable in *xbat32* mutant seedlings and treatment with proteasome inhibitors does not increase ACS7 protein levels in *xbat32*

seedlings. This suggests that XBAT32 is indeed responsible for ubiquitin-mediated degradation of ACS7. We are currently investigating if the single conserved lysine in the C-terminal extension of ACS7 plays a role in its turnover.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 0830 –1000h
Session 4: ***Plant Adaptations to Stress*** **Room**: 201 Sobey Building

Chair: Peter Constabel
University of Victoria

0830 **Wayne Snedden**
Plant adaptations to abiotic stress - Role of calcium in signaling plant stress response

0915 **Armand Seguin**
Forest pathology in the era of genomics

0830 **Role of calcium in signalling plant stress response**. W.A. Snedden, Department of Biology, Queen's University, Kingston, ON, Canda, K7L 3N6

My research program investigates the cellular mechanisms that plants use to interpret and communicate information about their external environment. Given their sessile nature, when faced with adverse conditions plants must mount an adaptive defence that excludes fleeing to "safer, greener pastures". Plants react to environmental stimuli through complex signal transduction pathways that coordinate timely and robust physiological responses. The generalized model of stress signalling involves: (i) detection of an environmental stimulus by a cellular receptor which triggers (ii) the production or release of second messengers that propagate and amplify the signal by (iii) activating downstream protein targets (eg. kinases, transcription factors, etc.). The collective action of these targets directs the cellular response that is needed. In stress response signalling, the second messenger Ca^{2+} is a ubiquitous early regulatory component. In resting cells, cytosolic Ca^{2+} levels are kept low through active transport but, in response to external stimuli, rise rapidly, often displaying an oscillating pattern of influx/efflux. The Ca^{2+} signature hypothesis posits that distinct spatio-temporal patterns of Ca^{2+} flux are evoked by different stimuli and thus "encode" information about the nature of the stimulus to help direct downstream responses. In this model, Ca^{2+}-binding proteins act as Ca^{2+} sensors to "decode" Ca^{2+} signals and activate various downstream protein targets. My lab is interested in understanding how plants use Ca^{2+} sensors to regulate signal transduction pathways. The most widespread Ca^{2+} sensor in eukaryotes is calmodulin (CaM), an evolutionarily conserved protein that regulates an array of proteins within cells. CaM has been shown to play important roles in many signalling pathways in plants. Interestingly, plants possess many CaM-related (CML) proteins not found in other eukaryotes. The Arabidopsis genome encodes ~50 CMLs but very few have been studied in detail. My lab has been using a combination of gene expression analyses, protein biochemistry, physiology, and reverse genetics to study Arabidopsis CMLs. I will present our findings to date on the roles of CMLs in stress response and development.

0915 **Forest pathology in the era of genomics**. Armand Séguin. Forest Genomics, Laurentian Forestry Centre, St. Foy, QC Email: armand.seguin@nrcan.gc.ca

With the recent sequencing of the *Populus trichocarpa* genome as well as several associated micro-organisms, poplar has the hallmark of a model woody system with great potential of obtaining breakthrough knowledge in the field of tree-microbe interactions. With their long life cycle, trees must have accurate mechanisms of sensing microbial invasion and elaborate signalling networks in order to activate the appropriate defense response. We pursued various approaches to identify poplar genes involved in the interaction with the biotrophic Melampsora rust pathogen. We will present what we have done with regards to the components involved in poplar defense response resulting from transcript profiling and data from genetic transformation experiments.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 1030-1200h
Session 5: ***The Norm Hüner Symposium*** **Room**: 201 Sobey Building

Chair: Carl Douglas
University of British Columbia

1030 **Norman Hüner**
CSPP Gold Medal Address- Shedding some light on plant adaptation and acclimation

1110 **Denis Maxwell**
From stress sensing to cell death in *Chlamydomonas*

1135 **Ingo Esminger**
How will climate change affect conifer forests?

1030 **Shedding some light on plant cold acclimation and adaptation**. Norman PA Hüner, Dept. of Biology and The Biotron Experimental Climate Change Research Centre, University of Western Ontario, London, Canada N6A 5B7

Photoautotrophy is crucial in linking all other organisms to the sun through their ability to absorb, trap, and transform light energy into useable forms of electrochemical potential energy to reduce CO_2 to complex carbohydrates. However, this transformation of light energy requires the integration of extremely fast, temperature-insensitive photophysical and photochemical processes with much slower, temperature-dependent biochemical processes whose rates differ by more than 10 orders of magnitude. This creates a potential for an imbalance in cellular energy budget, quantified as excitation pressure which is a reflection of the relative reduction state of the intersystem plastoqinone (PQ) pool. Consequently, acclimation to low temperature mimics photoacclimation due to comparable modulation of excitation pressure and energy imbalance. Photoautotrophs exhibit a dynamic capacity to remodel the structure of the photosynthetic apparatus in order to maintain an energy balance. Such a balanced state is called photostasis. This is attained through molecular and biochemical mechanisms that are temporally and spatially integrated at various levels of organization – genetic, biochemical, organellar, cellular and whole organism. Thus, the chloroplast is not only a primary cellular energy transformer, but this organelle also acts as global energy sensor whose impact extends to plant and cell form and function by governing plastid and nuclear gene expression through retrograde regulation. Acclimation and adaptation to low temperature and irradiance to attain photostasis will be discussed in terms of the remarkable phenotypic plasticity that cyanobacteria, green algae, crop plants and *Arabidopsis thaliana* exhibit in response to environmental change.

1110 **From stress sensing to cell death in *Chlamydomonas***. Denis P. Maxwell. Department of Biology and The Biotron, The University of Western Ontario, London, Ontario, Canada N6A 5B7

Recent research indicates that the mitochondrion may play an important role in intracellular stress sensing and signalling. As an energy-transducing organelle the mitochondrion is well suited as a depot within the eukaryotic cell where stress factors may become integrated with overall metabolism and responses from acclimation through cell death may be initiated. Using the model green alga *Chlamydomonas reinhardtii* my laboratory investigates this role for the mitochondrion by studying the alternative oxidase (AOX), responsible for alternative pathway respiration, which is induced by a range of environmental stresses. As a mitochondrial protein that is encoded by a nuclear gene (*AOX1*), AOX is a model for understanding the pathway of mitochondria-to-nucleus communication that may be critical to integrated stress responses. A unique aspect of AOX in *Chlamydomonas*, that is also being studied by my laboratory, is its potential involvement in nitrate assimilation. We use reporter gene analysis to investigate the regulation of *AOX1* transcription and mutagenesis to study mitochondria-to-nucleus signal transduction. As well, we are employing RNA interference to investigate the role of AOX in the maintenance of carbon/nitrogen balance and in oxidative stress defences. A second major avenue of research that will be discussed involves cell death in the Antarctic green algae *C. raudensis* (strain UWO241). This green alga has an optimum growth temperature of about 10°C yet dies above about 20°C. Using confocal laser scanning microscopy in combination with a range of molecular techniques we are investigating whether UWO241 exhibits hallmarks of programmed cell death, and what role mitochondrial dysfunction may play in the cell death response of this green alga. As well, we

beginning to use the technique of experimental evolution to investigate how readily UWO241 can increase its optimum growth temperature.

1135 **How will climate change affect conifer forests?** I. Ensminger. Department of Biology, University of Toronto at Mississauga, Mississauga, Ontario, Canada, L5L 1C6 (e-mail: ingo.ensminger@utoronto.ca)

Cold hardening in conifers includes growth cessation and long-term changes in metabolism. In conifers of the boreal forest, this process is induced by short days and potentiated by low temperature. Increased autumn and spring air temperature due to climate change is likely to affect the cold hardening process in autumn and the dehardening in spring. It is projected that the length of the growing season in boreal forests will increase by 20 to 30 d by 2080, and this will possibly improve the productivity of northern boreal forests. However, it has also been suggested that boreal conifers might fail to fully exploit an extended growing season because prolonged warmer temperatures during autumn may interfere with the physiological, molecular and metabolic reorganisation involved in the cold hardening process. To isolate the effect of temperature from the cellular to the ecosystem level, we studied the dynamics of photosynthesis under boreal climate conditions in the field as well as in controlled experiments in phytotrons. While photosynthesis of many species responds positively to temperature, recent findings in pine suggest that photoperiod control of autumn cold hardening appears to negate any potential for an increased carbon gain associated with higher temperatures during the autumn season. By contrast, the onset of CO2 assimilation in spring is clearly triggered by increasing air temperatures, however, low soil temperatures and intermittent frost can decrease the rate of the recovery of photosynthesis. We conclude that adaptation of photosynthesis to varying temperatures revolves around the trade-off between utilizing the full growing season and minimizing damage (frost, oxidative stress) through proper timing of hardening in autumn and dehardening in spring.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 1400-1530
Session 6: ***Gene Regulation & Molecular Biology*** **Room**: 201 Sobey Building

Chair: Tamara Western
McGill University

1400 **Carl Douglas**
Regulation of secondary cell wall biosynthesis in Arabidopsis by a KNAT7 transcription factor repression complex

1415 **K. Peter Pauls**
Characteristics of fibres from soybean stem residue: Gene identification and quantitative trait loci (QTL) mapping

1430 **Chad Stewart**
What causes the pointed first leaf phenotype in *Arabidopsis thaliana* ribosomal protein mutants?

1445 **Michael Prouse**
Characterization of a transcriptional circuit involving the transcription factor, AtMYB61

1500 **Denise Cooper**
Towards Identifying Candidates for a Major Resistance Gene to Common Bacterial Blight in OAC Rex (*Phaseolus vulgaris*)

1515 **Dimitre Ivanov**
Extracellular glycosidases of *Pythium irregular*

1400 **Regulation of secondary cell wall biosynthesis in Arabidopsis by a KNAT7 transcription factor repression complex**. C. J. Douglas*; Y. Liu; E. Li, and S. Wang. Department of Botany, University of British Columbia, Vancouver, BC CanadaV6T1Z4 (carl.douglas@ubc.ca)

The plant secondary cell wall is a composite network of complex polymers that provides protective and structural properties to the cell wall. The *Arabidopsis thaliana KNOX* TALE homeodomain gene *KNAT7* has been identified in transcriptional profiling and other experiments as a member of a transcriptional network regulating secondary wall formation during in xylem and fiber cell differentiation in *Arabidopsis* inflorescence stems. *knat7* mutants display an irregular xylem (*irx*) phenotype, as well as increased fiber wall thickness, suggesting that KNAT7 plays a key role in the regulation of secondary cell wall biosynthesis. Using a protoplast transfection assay, we found that KNAT7 is a potent transcriptional repressor. Consistent with this, sets of lignin and hemicellulose biosynthetic genes are upregulated in the *knat7* mutant, which also exhibit increased lignin content. This suggests that KNAT7 is involved in a negative feedback loop in the secondary wall regulatory network. To further investigate this hypothesis, we tested KNAT7 interaction Ovate Family Protein (OFP) transcription co-regulators. We confirmed the KNAT7-OFP1 and KNAT7-OFP4 interactions by yeast two hybrid (Y2H) analyses and by biomolecular fluorescence complementation (BiFC) analyses *in planta*, and showed that the interaction enhances KNAT7 transcriptional repression activity *in planta*. Furthermore, an *ofp4* mutant exhibits similar phenotypes as *knat7*, and the pleiotropic effects of *OFP1* and *OFP4* overexpression depend upon *KNAT7* function. Co-expression and Y2H analyses suggest that BELL-LIKE HOMEODOMAIN (BLH) transcription factors also interact with KNAT7. BiFC analyses showed specific interaction of KNAT7 with a BLH protein, which also functions as a potent transcriptional repressor. Taken together, these data support the hypothesis that KNAT7 is part of a KNOX-BELL-OVATE transcription factor repression complex that functions to negatively modulate secondary cell wall biosynthesis. The nature of the in *vivo* complex, its physiological role, and the existence of a similar complex in developing secondary xylem of poplar are under further investigation.

1415 **Characteristics of fibres from soybean stem residue: Gene identification and quantitative trait loci (QTL) mapping.** Y. Reinprecht[1], M. Arif1, V. W. Poysa[2], G. R. Ablett[3], I. Rajcan[1], and K. P. Pauls[1]*. [1]University of Guelph, Department of Plant Agriculture, Guelph, ON N1G 2W1, Canada (e-mail: ppauls@uoguelph.ca); [2]Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, ON N0R 1G0, Canada; and [3]University of Guelph, Ridgetown Campus, Ridgetown, ON N0P 2C0, Canada

The use of plant fibres in automotive parts is an attractive new market for agricultural biomass but is limited by their poor performance in composite materials. The principal aim for the current study was to analyze the structure and properties of soybean stem fibres with a view of assessing their potential as reinforcing additions for composite materials to be used in the automotive industry. Future selections of plant cultivars optimized for this use could be accelerated and simplified by the information about the structural and regulatory genes that control the physical properties of plant-derived fibres. The specific objectives of this research were to identify genes that contribute to soybean fibre performance in composites, map quantitative trait loci (QTL) for fibre traits and develop gene-specific markers related to those traits. Databases were searched for the genes involved in cell wall biosynthesis and modification. Gene-specific PCR primers were designed and screened with genomic DNA of parents (RG10 and OX948) of a recombinant

inbred line (RIL) mapping population. Fibre genes were isolated and gene-specific markers for key enzymes in lignin, hemicellulose, cellulose and pectin biosynthetic pathways were developed. A soybean oligo microarray was also hybridized with the genomic DNA of the parents or RILs and RNA from stem tissue to identify additional fibre genes and develop single feature polymorphism (SFP) markers. Mapping of fibre genes is underway. Fifty RILs (selected based on height/ lodging index) and parents were evaluated under controlled and field conditions in 2008 and 2009. Significant negative correlations were detected between lignin and cellulose and lignin and hemicellulose, while cellulose and hemicellulose were positively correlated. Some fibre performance QTL were associated with fibre genes. Initial thermogravimetric analysis (TGA) of ground stem tissues indicated that parental genotypes have degradation properties suitable for composite materials. Formulation and characterization of composites is underway. This work will allow identification of key factors in fibre quality and the development of quick, marker-based screening method(s) to facilitate rapid introgression of genes for good fibre quality into new soybean cultivars.

1430 **What causes the *pointed first leaf* phenotype in *Arabidopsis thaliana* ribosomal protein mutants?** C.S. Stewart[1*] and P. C. Bonham-Smith[1]. [1]Department of Biology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5E2

Originally believed to be housekeeping genes, ribosomal proteins (RPs) are now known to be involved in numerous cellular processes. My research follows the effects two *Arabidopsis thaliana* RP mutants; *pointed first leaf 1* (*pfl1*), T-DNA insertion in *RPS18A* and *pfl2*, Ds transposon insertion in *RPS13A*, have on plant development. *pfl1* and *pfl2* were crossed with a *RPL18B* overexpressor, with the resulting progeny of each showing unique phenotypes. While *rpl18B* plants exhibit wildtype (WT) characteristics, *pfl1* and *pfl2* demonstrate the classical *pointed first leaf* phenotype (associated with many RP mutants) that includes a reduction in the fresh weight of rosette leaves, growth delays of approximately ten days and retarded root development. However, *pfl1:rpl18B* heterozygous mutants show a delayed flowering phenotype of 20-30 days, a proliferation of rosette leaves (26-37 prior to bolting compared to 9-10 for WT) and thick primary bolts (2.6 fold larger in diameter then WT). In contrast, the *pfl2:rp18B* heterozygotes, restores the WT phenotype. To gain further insight, proteins from each member of the *RPS18*, *RPS13* and *RPL18* gene families were fused with Green Fluorescent Protein, expressed in a heterologous tobacco system and viewed with a Confocal Laser Scanning Microscope to document cellular localization. Each chimeric protein demonstrated varying degrees of nuclear/nucleolar/cytoplasmic localization common to many RPs. In an effort to determine the global effects these mutants have on cellular transcription status, RNA was extracted from 13-day-old seedlings and sequenced. Using an Illumina Genome Analyzer IIx, 36 base pair reads were generated and analyzed using NextGENe next generation sequence analysis software (Version 2.1). Preliminary results have revealed that 16 genes, common to both *pfl1 and -2* mutants are upregulated and 4 are downregulated. *pfl1* has 47 genes showing unique regulation (44 upregulated and 3 downregulated) and *pfl2* has 98 genes showing unique regulation (86 upregulated and 12 downregulated). These data suggest that the *pfl* phenotype may be attributed to abnormal ribosome biogenesis leading to reduced ribosome capability from the up or downregulation of one or more of the 20 genes that show aberrant transcription in both of the mutants.

1445 **Characterisation of a transcriptional circuit involving the transcription factor, *At*MYB61**. Michael Prouse*[1,2]; Julia Romano[1,2]; Christian Dubos[1]; and Malcolm M. Campbell[1,2]. [1]Department of Cell & Systems Biology, [2]Centre for the Analysis of Genome Evolution & Function, University of Toronto, ON M5S 3B2, CANADA

*At*MYB61, a member of the R2R3-MYB family of transcription factors in *Arabidopsis thaliana*, alters gene expression in response to sugars, resulting in pleiotropic modifications of carbon allocation throughout the plant body. *AtMYB61* transcript abundance increases in response to the major product of photosynthesis, sucrose, and is repressed in response to two major products of photorespiration, glutamate and glycine. Phylogenetic footprinting, bioinformatic, and biochemical analyses support the hypothesis that *AtMYB61* expression is de-repressed by soluble sugars in a mechanism involving intragenic sequences. Current experiments suggest the involvement of specific proteins in the regulation of *AtMYB61* expression by interaction with gene regulatory sequences embedded in an *AtMYB61* intron. The gene targets that reside downstream of *AtMYB61* have also been characterised. Putative downstream target genes of *At*MYB61 were predicted on the basis of comparative transcriptome analysis. *At*MYB61 targets include genes that encode the following proteins: a KNOTTED1-like transcription factor (KNAT7, At1g62990); a caffeoyl-CoA 3-O-methyltransferase (CCoAOMT7, At4g26220); and a pectin-methylesterase (PME, At2g45220). Statistically over-represented motifs were identified in the 5' non-coding regions of the putative target genes, and these correspond to previously characterized AC element motifs that function as R2R3-MYB targets. The consensus motif functions as a *bona fide* target for *At*MYB61 binding as determined by an electrophoretic mobility shift assay. Binding between the gene regulatory sequences of the putative target genes, which contain multiples of these motifs, was confirmed via electrophoretic mobility shift assays. Altogether these experiments provide assessment of the ability of *At*MYB61 to bind to gene regulatory sequences present in the 5' non-coding sequences of the three putative downstream targets: *KNAT7*, *CCoAOMT7* and a *PME*, substantiating its role as a potential regulator of the transcription of these genes. Together with the analysis of the regulation of *AtMYB61* expression, these studies provide insights into the entire transcriptional regulatory circuit centred around *AtMYB61*.

1500 **Towards identifying candidates for a major resistance gene to common bacterial blight in OAC Rex (*Phaseolus vulgaris*).** D. M. Cooper*, G. E. Perry, K. P. Pauls. Department of Plant Agriculture, University of Guelph, Guelph, Ontario N1G 2W1

Phaseolus vulgaris L.,is an important agricultural species that is cultivated across the globe. It is the primary host for the pathogen *Xanthomonas axonopodis* pv. *phaseoli* and *Xanthomonas axonopodis* pv. p*haseoli* var. *fuscans*, which causes the disease Common Bacterial Blight (CBB). The pathogen is soil and seed-born, and is endemic to all regions where dry beans are cultivated. OAC Rex is a registered variety of common bean resistant to CBB in Canada, selected from a cross between HR20-728 and MBE 7. Quantitative Trait Loci (QTL) analysis has determined the presence of one major CBB resistance QTL and at least two resistance QTL in the OAC Rex genome. The sequences of binary bacterial artificial chromosome (BiBAC) clones containing regions of the B4 linkage group associated with the major resistance QTL in OAC Rex were analyzed using the NCBI basic local alignment search tool (BLAST) to find regions coding for plant resistance proteins with nucleotide binding site and leucine rich repeat motifs. This analysis identified two potential gene locations in contig 1701 (1701-2 and 1701-3) that encode LRR proteins. The potential CBB resistance genes and hypothetical proteins they encoded are highly conserved which may be the result of a gene duplication event. Both potential genes will be cloned and transferred into the model plant *Arabidopsis thaliana*, which has been shown to be susceptible to infection by *X. axonopodis* pv. *phaseoli*. Transformed *A. thaliana* plants will be

inoculated by *X. axonopodis* pv. *phaseoli* to determine whether the genes 1701-2 and 1701-3 confer resistance to CBB. Isolation of the major OAC Rex CBB resistance gene will facilitate its integration into other *P. vulgaris* varieties and may lead to an understanding of the resistance mechanism.

1515 **Extracellular glycosidases of *Pythium irregulare***. D.A. Ivanov[1] *; M.A. Bernards[1].[1]Department of Biology, University of Western Ontario, London, ON, Canada, N6A 5B8 (e-mail: divanov2@uwo.ca)

The ginseng (*Panax quinqufolius* L.) pathogen *Pythium irregulare* 'Buis' is able to selectively metabolize the 20(*S*)-protopanaxadiol ginsenosides Rb1, Rb2, Rc, Rd, and gypenoside XVII *in vitro* via extracellular glycosidases, leading to the formation and partial assimilation of ginsenoside F2. To determine whether there is a correlation between the activity of ginsenoside metabolizing β-glucosidases and the pathogenicity of *P. irregulare* towards ginseng, the production of ginsenoside-specific glycosidases and pathogenicity of various isolates of *P. irregulare* were determined. For this, 10 isolates of *P. irregulare* were selected on the basis of their genetic variability and the host plant they were isolated from (including ginseng), and obtained from the Canadian Collection of Fungal Cultures. These isolates were cultured *in vitro*, in the presence of ginsenosides and the level of ginsenoside-specific glycosidase activity in their extracellular proteins was measured. Meanwhile ginseng seedlings were inoculated with the same suite of *P. irregulare* isolates and scored for disease symptoms to estimate the relative pathogenicity of each isolate towards ginseng plants. When combined this data shows evidence of a positive correlation between glycosidase activity in *P. irregulare* and the pathogenicity of this organism towards ginseng.

Thursday, July 21, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 830-1000h
Session 7: ***Biochemical Process and Biotechnology*** **Room**: 201 Sobey Building

Chair: Chris Todd
University of Saskatchewan

0830 **Hernan Del Vecchio**
Biochemical and molecular characterization three cell wall-localized purple acid phosphatase isozymes upregulated by phosphate-starved *Arabidopsis thaliana*

0845 **Whitney Robinson**
The secreted purple acid phosphatase isozymes AtPAP12 and AtPAP26 play a pivotal role in extracellular phosphate-scavenging *by Arabidopsis thaliana*

0900 **Brendan O'Leary**
Tissue-specific expression, phosphorylation, and monoubiquitination of phosphoenolpyruvate carboxylase isozymes of the castor oil plant, *Ricinus communis* L

0915 **Nat Kav**
Engineering Tolerance to Multiple Fungal Pathogens in *Brassica napus* canola

0930 **Vikramjit Bajwa**
Cytosolic NADPH-dependent glyoxylate reductase from Arabidopsis: crystal structure and kinetic characterization of active site mutants provide evidence for β-HAD family membership

0945 **Surinder Singh**
In Vitro Expression of Transposase Promotes Reactivation of Ds Transposons

0830 **Biochemical and molecular characterization three cell wall-localized purple acid phosphatase isozymes upregulated by phosphate-starved *Arabidopsis thaliana*.** H. A. Del Vecchio* and W. C. Plaxton. Department of Biology, Queen's University, Kingston, Ontario, Canada K7L 3N6

Upregulation of intracellular and secreted purple acid phosphatases (PAPs) is a universal response of orthophosphate-starved (-Pi) plants (Tran *et al.* 2010 Plant Science: PAP review). PAPs catalyze Pi hydrolysis from a broad spectrum of phosphomonoesters at an acidic pH. They belong to a relatively large multigene family whose specific functions in plant Pi metabolism are poorly understood. This study focuses on the identification and characterization of cell wall (CW) PAPs upregulated by -Pi Arabidopsis. Three glycosylated PAP isozymes secreted into the CW of -Pi Arabidopsis suspension cells were purified using FPLC and identified by peptide mass fingerprinting (MALDI-TOF MS) as AtPAP12 (At2g27190; subunit size 60-kDa), AtPAP25 (At4g36350; subunit size 55-kDa), and AtPAP26 (At5g34850; subunit size 55-kDa). Their deduced protein sequences were compared using multiple sequence alignment and phylogenetic analysis. Concanavalin-A chromatography resolved a pair of CW AtPAP26 glycoforms, one of which co-purified with curculin (At1g78860) a lectin hypothesized to participate in the control of AtPAP26 activity. AtPAP26 is dual targeted during Pi stress since it also the principal vacuolar PAP upregulated by –Pi Arabidopsis (Hurley *et al*. 2010 Plant Physiology). Differential glycosylation may control the subcellular targeting and activity of AtPAP26. Studies are in progress to determine: (i) the substrate selectivity of the three CW PAP isozymes of –Pi Arabidopsis, (ii) their tissue-specific distribution and relative abundance in CW of -Pi versus Pi-replete plants, and (iii) their role in recycling Pi from Pi-esters that may leak from the cytoplasm into the apoplast during Pi stress. This research is helping to shed light on the functional importance of specific PAP isozymes in facilitating plant acclimation to nutritional Pi deficiency. This is important because there is an urgent need to engineer Pi-efficient transgenic crops so as to minimize the huge input of expensive, non-renewable, and polluting Pi fertilizers in agriculture.

0845 **The secreted purple acid phosphatase isozymes AtPAP12 and AtPAP26 play a pivotal role in extracellular phosphate-scavenging by *Arabidopsis thaliana.*** W. D. Robinson*, H. T. Tran, and W. C. Plaxton. Department of Biology, Queen's University, Kingston, Ontario, Canada K7L 3N6

Phosphate (Pi) is an essential, but environmentally limiting macronutrient for plant metabolism and development. Extensive soil Pi reserves exist in the form of organic Pi-esters which are unavailable for root uptake until hydrolyzed by secreted purple acid phosphatases (PAPs). Plant PAPs belong to a relatively large multigene family whose specific functions are poorly understood. Two secreted PAP isozymes upregulated by Pi-deficient Arabidopsis cell cultures and seedlings were purified, characterized, and identified as AtPAP12 (At2g27190) and AtPAP26 (At5g34850) (Tran *et al.* 2010 Plant Cell Environ). Here, a functional genomic approach was undertaken to test the hypothesis that AtPAP12 and AtPAP26 scavenge Pi from soil-localized organophosphates. Initial studies established that exogenous Pi-esters such as glucose-6-P, glycerol-3-P, P-*enol*pyruvate, phenyl-P, ATP, or PPi (that are all effective *in vitro* substrates for purified AtPAP12 or AtPAP26), as well as nucleic acids (salmon sperm DNA) generally supported near optimal growth of wild-type Arabidopsis seedlings cultivated on Pi-free nutrient media. Homozygous *atpap12* or *atpap26* T-DNA insertional loss-of-function mutants lacked the corresponding transcripts and immunoreactive polypeptides, but displayed no obvious phenotype

when cultivated on these organic-P sources (suggesting that AtPAP12 could compensate for AtPAP26 and *vice versa*). However, when cultivated on exogenous Pi-esters or DNA as their sole source of P nutrition homozygous *atpap12/atpap26* double knockout mutant seedlings exhibited significantly impaired shoot and root development, correlated with 30 - 50% reductions in free Pi and esterified-Pi levels. By contrast, no obvious phenotype or deleterious effects were apparent when *atpap12/atpap26* plants were cultivated on Pi-replete media. These results: (i) prove that secreted AtPAP12 and AtPAP26 helps Arabidopsis to scavenge Pi from a broad spectrum of extracellular Pi-esters, (ii) are relevant to applied efforts to engineer Pi-efficient transgenic crops, needed to minimize the input of expensive, non-renewable, and polluting Pi fertilizers in agriculture.

0900 **Tissue-specific expression, phosphorylation, and monoubiquitination of phosphoenolpyruvate carboxylase isozymes of the castor oil plant, *Ricinus communis L.*** Brendan M. O'Leary*[1], Eric T. Fedosejevs[1], and William C. Plaxton[1,2]. Departments of [1]Biology and [2]Biochemistry, Queen's University, Kingston, Ontario, Canada K7L 3N6

Phosphoenolpyruvate carboxylase (PEPC) is a tightly controlled cytosolic enzyme situated at a pivotal branch point of plant carbohydrate metabolism. This study employs transcript profiling together with immunoblotting and co-immunopurification to assess the tissue-specific expression, protein:protein interactions, and post-translational modifications (PTMs) of plant- and bacterial-type PEPC isozymes (PTPC and BTPC, respectively) in the castor plant, *Ricinus communis*. Previous studies established that the Class-1 PEPC (PTPC homotetramer) of castor oil seeds (COS) is activated by phosphorylation at Ser^{11} during endosperm development and inhibited by monoubiquitination at Lys^{628} during endosperm germination. Elimination of photosynthate supply to developing COS by depodding caused the PTPC of the endosperm and cotyledon to be completely dephosphorylated, and then subsequently monoubiquitinated *in vivo*. PTPC monoubiquitination rather than phosphorylation is widespread throughout the castor plant and appears to be the predominant PTM of Class-1 PEPC that occurs *in planta*. The distinctive developmental pattern of PTPC phosphorylation *versus* monoubiquitination indicates that these two PTMs are mutually exclusive. By contrast, the BTPC: (i) is abundant in inner integument, cotyledon, and endosperm of developing COS, but occurs at low levels in roots and cotyledons of germinated COS, (ii) shows a unique developmental pattern in leaves such that it is present in leaf buds and young expanding leaves, but undetectable in fully expanded leaves, and (iii) tightly interacts with co-expressed PTPC to form the novel and allosterically-desensitized Class-2 PEPC heteromeric complex. BTPC and thus Class-2 PEPC upregulation appears to be a distinctive feature of rapidly growing and/or biosynthetically active tissues that require a large flux towards organic acids to replenish tricarboxylic acid cycle intermediates being withdrawn to support anabolism.

0915 **Engineering tolerance to multiple fungal pathogens in *Brassica napus* canola.** N. Kav[1*], S. S. Verma[1], M. H. Rahman[1], W. Yajima[2], A. Ekramouddoullah[3] and S. Shah[4]. [1]Department of Agricultural, Food and Nutritional science, University of Alberta, Edmonton, Alberta, Canada T6G 2P5(e-mail: Nat.Kav@ales.ulaberta.ca), [2]Department of Plant Pathology, North Dakota State University, Fargo, ND 58108, [3]Pacific Forestry Centre, Victoria, British Columbia V8Z 1M5; and [4]Alberta Innovates – Technology Futures, Vegreville, Alberta, Canada T9C 1T4

Different strategies have been used to engineer durable disease resistance in plants including genes encoding cysteine-rich peptides (CRP) among others. Here we report the introduction of one such small molecular weight (10-12 kDa) CRP into canola towards protecting this crop against multiple, fungal phytopathogens. Expression of this CRP sequence into canola was driven by the constitutive promoter *CaMV-35S*. The incorporation of the CRP cDNA into *Brassica*

napus L. genome and its expression was confirmed by PCR, qRT-PCR and Western blots. These transgenic canola lines were challenged with the various canola phytopathogens of economic importance (*Alternaria brassicae, Leptosphaeria maculans* and *Sclerotinia sclerotiorum*). Our results indicate that the transgenic *B. napus* plants expressing the CRP cDNA were significantly more tolerant to all three fungal pathogens. Our results are presented and discussed within the context of improving multiple-disease tolerance in canola for the benefit of the Canadian economy.

0930 **Cytosolic NADPH-dependent glyoxylate reductase from Arabidopsis: crystal structure and kinetic characterization of active site mutants provide evidence for β-HAD family membership.** V.S. Bajwa[1*], G.J. Hoover[1], R. Jørgensen[2], A. Rochon[1], A.R. Merrill[2], B.J. Shelp[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada (email: vbajwa@uoguelph.ca); and [2]Department of Molecular and Cellular Biology, University of Guelph, Guelph, ON N1G 2W1, Canada

Plants accumulate two highly reactive and toxic aldehyde intermediates namely glyoxylate and succinic semialdehyde during some stresses. In *Arabidopsis thaliana*, GLYR1 is an aldehyde reductase with a capacity to convert both these semialdehydes into their less toxic counterparts, glycolate and γ-hydroxybutyrate, respectively. Recently, a new small family of oxidoreductases known as β-hydroxyacid dehydrogenases (β-HAD), has emerged as a unique family. The four known members of β-HAD family include 3-hydroxyisobutyrate dehydrogenase, tartronate semialdehyde reductase, 6-phosphogluconate dehydrogenase, and 2-(hydroxymethyl)glutarate dehydrogenase. All members of β-HAD family share some common features including a highly similar 3-D structure, strictly conserved glycine residues dispersed throughout the primary sequence, and a highly conserved core consensus sequence for substrate binding and catalysis. Here, the crystal structure of *At*GLYR1 was solved to 2.1 A° resolution by molecular replacement and site-directed mutagenesis revealed that *At*GLYR1 shares common 3D architecture and functionally important residues with other β-HAD family members. Mutagenesis of the active-site residue, followed by kinetic characterization of the resultant mutant protein, revealed K170 of *At*GLYR1 as a critical residue required for the general acid/base catalysis. Site-directed mutagenesis of T95 and D239, which are putatively hydrogen bonded to a conserved active site water molecule, indicated its involvement in acid/base catalysis of *At*GLYR1. These findings suggest AtGLYR1 as the fifth structurally and functionally confirmed member of the β-HAD family and provide an initial understanding of the active site mechanism that will further define this family.

0945 **In vitro expression of transposase promotes reactivation of *Ds* transposons.** Surinder Singh*[1], Han Qi Tan[1], Manjit Singh[1] and Jaswinder Singh[1]. [1]Department of Plant Science, McGill University, 21111 Rue Lakeshore, Ste Anne De Bellevue, QC, Canada, H9X 3V9

The *Activator* (*Ac*) and *Dissociation* (*Ds*) transposons of maize are important tools for functional genomics in plants. Introduction of *Ac/Ds* transposable elements in heterologous species such as barley has unlocked new potential for characterization of genes affecting important traits in this *Triticeae* crop. However, it has been observed that the *Ac* transposase (*Ac*TPase) locus is prone to silencing in the T3 and subsequent generations, which drastically reduced the efficiency of this system. To enhance the utility of *Ac/Ds* transposon system in barley, we devised a novel approach for the reactivation of *Ds* transposon through extra-chromosomal transient expression of AcTPase. For this purpose, three lines containing a stable single *Ds* insertion (TNPs) with intact and damaged terminal inverted repeats (TIRs), TNP-29, TNP-79 and TNP-13 were selected. A construct containing *Ac*TPase and *GFP* was engineered in a Ti plasmid to detect transiently expressing transposase through *Agrobacterium* mediated transformation. Tissues

transiently expressing GFP were analyzed to monitor *Ac*Tpase expression. A reactivation frequency of 30.4%, 33.8% and 10.5% was observed in TNP-29, TNP-79 and TNP-13 respectively. This frequency is significantly higher than the conventional techniques of remobilizing *Ds* through crossing. More interestingly, 10.5 % reactivation observed in TNP 13, a line with damaged TIRs, which seldom happens with conventional methods. These results indicate that extra-chromosomal in-vitro expression of Transposase promotes reactivation of *Ds* transposons. This new technique for in-vitro reactivation of *Ds* transposons can overcome the problem of *Ac* silencing in subsequent generation would immensely facilitate generation of TNPs for functional genomics.

Thursday, July 21, 2011 **Oral Presentations**
Canadian Society of Plant Physiologists **Time:** 1030-1200h
Session 8: ***Breeding and Production*** **Room**: 201 Sobey Building

Chair: Gale Bozzo
University of Guelph

1030 **Gregory Perry**
Sequencing the bean genome: the applied bean genomics and bioproducts project

1045 **Anthony Anyia**
Quantitative trait loci for water-use efficiency in barley (*Hordeum vulgare* L.) under rain-fed conditions on the Canadian Prairies

1100 **Jocelyn Ozga**
Identification and quantification of anthocyanins and flavonols in saskatoon fruits (*Amelanchier alnifolia* Nutt.) during development and at maturity

1115 **Chris Trobacher**
Is glutamate decarboxylase-derived γ-aminobutyrate involved in physiological disorders of apples during controlled atmosphere storage?

1130 **Jessica Turnbull**
SPAD chlorophyll meter as a decision-making tool to optimize recoverable white sugar in sugarbeet production

1030 **Sequencing the bean genome: the applied bean genomics and bioproducts project.** GE Perry[1*]; W Crosby[2]; K Yu[3]; C Shi[3]; K Power[3]; F Marsolais[4]; W Xie[1]; A Weersink[1]; R Cao[3]; D Cooper[1] and KP Pauls[1]. [1] University of Guelph; [2] Windsor University; [3] Agriculture and Agri-Food Canada; [4] University of Western Ontario

Phaseolus vulgaris (common bean) is an important crop for Canadian farmers and consumers for both its economic and health benefits. As a food source, it is high in dietary fibre, protein and folates, while being low in fat and simple carbohydrates. Although beans are a staple food source in many countries, there is little sequence information available compared to other crops such as *Zea maize* or *Glycine max*. The Applied Bean Genomics and Bioproducts project aims to sequence and annotate the genome of OAC-Rex, a registered variety of white bean, which is also resistant to common bacterial blight because it was developed from an interspecific cross between *P. vulgaris* and *Phaseolus acutifolius*, a South American tepary bean. Nuclear DNA was extracted from the mature leaves of OAC-Rex and will be forwarded for sequenced using the Roche 454 platform using a combination of shotgun and paired-end 2 and 8Kb library reads. In order to aid in the sequence assembly, a partial skeleton BAC was designed by identifying clones from BAC libraries of HR67, another CBB-resistance white bean line. The clones were selected by hybridization with 110 markers from across the bean genome (11 markers per chromosome). These clones will be sequenced, and as their positions in the bean genome have been previously identified, they will serve as guides for the shotgun sequence data. The results of this study will serve to identify genes involved in disease resistance, the phenylproponoid pathway and seed storage protein, and to provide a wealth of genetic information for use in breeding new bean varieties with enhanced yield and stress tolerance.

1045 **Quantitative trait loci for water-use efficiency in barley (*Hordeum vulgare L.*) under rain-fed conditions on the Canadian Prairies.** J. Chen[1], S.X. Chang[1] and A.O. Anyia[1,2*]. [1]Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada T6G 2E3; and [2]Alberta Innovates - Technology Futures, Vegreville, Alberta, Canada T9C 1T4 (Anthony.Anyia@albertainnovates.ca)

Barley (*Hordeum vulgare* L.) yield is commonly limited by low rainfall and high temperature during the growing season on the Canadian Prairies. Empirical knowledge suggests that carbon isotope discrimination ($\Delta^{13}C$), through its negative relationship with water-use efficiency (WUE), is a good index for selecting stable yielding varieties in some rain-fed environments. Identification of quantitative trait loci (QTL) and linked markers for leaf $\Delta^{13}C$ will enhance its use efficiency in breeding programs. In the present study, two mapping populations of barley (W89001002003 × I60049 or W× I, six-row type, and Merit × H93174006 or M × H, two-row type), containing 200 and 127 recombinant inbred lines (RILs) of $F_{5:6}$ generation advanced by the single seed descent (SSD) approach, were phenotyped for leaf $\Delta^{13}C$, biomass, grain yield and harvest index under rain-fed environments in Alberta, Canada. The W× I population was additionally phenotyped for leaf area index (LAI), plant height and days to maturity. All measured traits varied significantly between the parents and RILs of both populations in all locations. A transgressive segregation pattern for leaf $\Delta^{13}C$ was observed among RILs. The broad-sense heritability (H^2) of leaf $\Delta^{13}C$ was 0.8 while H^2 for grain yield was 0.74, and there was no significant interaction between genotype and environment for both traits in the W × I population. Leaf $\Delta^{13}C$ of RILs was significantly correlated between the different environments suggesting a high stability of this trait. A total of 12 QTLs in the W × I population and 5 QTLs in

the M × H population were detected for leaf $\Delta^{13}C$ using the composite interval mapping (CIM) method across tested field locations. For the W × I population, a major QTL located on chromosome 3H near marker Bmag606 (9.3, 9.4 and 10.7 cM interval) was identified. This major QTL overlapped with several agronomic traits, with W89001002003 alleles favoring lower leaf $\Delta^{13}C$, increased plant height, and reduced LAI, grain yield, HI and days to maturity at this locus or loci. This marker when validated may be useful in breeding programs for improving WUE and yield stability of barley on the Canadian Prairies.

1100 **Identification and quantification of anthocyanins and flavonols in saskatoon fruits (*Amelanchier alnifolia* Nutt.) during development and at maturity.** A. Jin; J.A. Ozga*; and D.M. Reinecke. Plant BioSystems Group, Dept of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5

Saskatoon fruit (an emerging North American fruit crop) contain anthocyanins (which are chiefly responsible for the red, blue and purple pigments located throughout the skin and the flesh of the fruit) and other flavonoids such as flavonols, that have attracted much interest due to their antioxidant properties and perceived health benefits. Quantitative analysis of the anthocyanins and flavonols from the fruits of pigmented-fruit cultivars, and a non-pigmented fruit cultivar 'Altaglo' (white-coloured fruit at maturity), was carried out over fruit development using a reverse-phase HPLC-DAD method. Anthocyanin and flavonol identification was confirmed by LC-MS. The anthocyanin species detected throughout fruit development were cyanidin mono-glycosides and the flavonol species were quercetin mono-, di-, and tri- glycosides. The concentration of anthocyanins in the pigmented-fruit cultivars dramatically increased from mid-development to maturity. Minimal to no anthocyanins were detected in 'Altaglo' throughout development. In general, the maximum total flavonol concentration occurred during early to mid-fruit development, followed by a decline in flavonol concentration as the fruit entered into the fruit ripening stage in all cultivars. A subsequent increase in total flavonol concentration occurred in some pigmented-fruit cultivars at fruit maturity. Using histochemical methods, flavonols were detected in the epidermis, mesocarp, placenta, and seed tissues of the fruit. In summary, biosynthesis of anthocyanins and flavonols is regulated temporally and spatially over saskatoon fruit development, leading to maximal levels of anthocyanins and moderate levels of flavonols in the mature fruit.

1115 **Is glutamate decarboxylase-derived γ-aminobutyrate involved in physiological disorders of apples during controlled atmosphere storage?** C.P. Trobacher[1*], A. Zarei[1], J. Liu[1], G.G. Bozzo[1], J.R. DeEll[2], B.J. Shelp[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1(e-mail: gbozzo@uoguelph.ca); and [2]Ontario Ministry of Agriculture, Food and Rural Affairs, P.O. Box 587, 1283 Blueline Rd & Hwy #3 Simcoe, ON N3Y 4N5

In controlled atmosphere (CA) storage, the metabolic activity of apple fruit is decreased by controlling the O_2 and CO_2 partial pressures in combination with a reduction in temperature. CA-storage can induce physiological disorders, and optimal conditions are a balance between prolonged storage and minimizing these disorders. Both low temperature and elevated CO_2 induce the accumulation of the stress metabolite, γ-aminobutyrate (GABA), in photosynthetic tissues. GABA production typically involves Ca^{2+}/calmodulin (CaM) activation or low-pH stimulation of glutamate decarboxylase (GAD) activity. However, the role of GABA and potential mechanisms associated with its accumulation in bulky fruits are largely unexplored. Here, we tested the impact of elevated CO_2 (5% versus 0.03%) and/or low temperature (3°C versus 0°C) in the presence of 2.5% O_2 on the incidence of disorders in 'Empire' apples. The high

CO_2 level resulted in a higher incidence of external disorders, whereas chilling had no effect. A two-fold increase in relative GABA concentration was apparent after two weeks of CA storage at both CO_2 levels. The GABA level was maintained in high CO_2-stored fruit during prolonged storage, whereas that in low CO_2-stored fruit GABA levels declined and then returned to the level of high CO_2-stored fruit after 16 weeks of storage. The expression of two 'Empire' GAD genes, *MdGAD1* and *2*, in CA-stored fruit was differentially stimulated by chilling, elevated CO_2, and storage time, and the *MdGAD1* transcript was typically more abundant than that of *MdGAD2*. GAD activity in cell-free extracts from 'Empire' fruit was regulated by pH and stimulated by Ca^{2+}/CaM. Two 'Empire' fruit GAD genes were cloned, and recombinant *Md*GAD1 displayed maximal activity at pH 5.5, but no stimulation by Ca^{2+}/CaM. Biochemical characterization of recombinant *Md*GAD2 is currently underway.

1130 **SPAD® chlorophyll meter as a decision-making tool to optimize recoverable white sugar in sugarbeet production**. J. J. Turnbull[1*] and L. L. Van Eerd[1]. [1]School of Environmental Sciences, University of Guelph, Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0 (e-mail: lvaneerd@ridgetownc.uoguelph.ca)

For sugarbeet production maximizing root yield and recoverable white sugar (RWS) is key to optimizing profitability. Critical to maximizing RWS ha-1 is managing nitrogen fertilizer because N fertility is positively correlated to sugarbeet root yield but inversely related to RWS per tonne of sugarbeets. Thus, it would be advantageous for sugarbeet farmers to have diagnostic tools to predict N fertilizer requirements that optimize RWS ha-1. In 2006-2008 at a commercial field, an N fertilizer rate-sugarbeet response experiment with five N rates (0-225 kg N ha-1) showed significant correlations between the Minolta SPAD®-502 chlorophyll meter readings and N fertilizer applied, sugarbeet yield, and RWS ($p<0.05$). In 2010, a trial was conducted to determine if SPAD® meter and presidedress soil nitrogen test (PSNT) can be developed as tools to predict in-season N fertilizer needs and/or sugarbeet root yield and RWS ha-1. Trials at seven commercial field sites had a randomized complete block design with four replications and three N fertilizer rates of zero N, starter only, and growers' rate, where the mean N fertilizer applied was 5.6, 40, and 106 kg N ha-1, respectively, and calcium ammonium nitrate was the N source at most sites. Soil mineral N to 30cm depth and SPAD® readings were taken simultaneously three times during the growing season and at harvest. Preliminary results show that the zero N control treatment, compared to the grower N rate, had 0.97% higher sugar content but 12.1 t ha-1 lower root yield and 1.2 t lower RWS ha -1. Yield of the starter-only treatment was 9.8 t RWS ha-1, which was not statistically different than the grower rate. At the time of split-N fertilizer application and at harvest, the zero N control had significant correlations between SPAD® readings and yield (r=0.462, 0.661, respectively), %sugar (r=-0.712, -0.756, respectively), RWS t-1 (r=-0.708, -0.758, respectively) and RWS ha-1 (r=-0.314, -0.671, respectively). Preliminary results suggests that the SPAD® meter may be a useful predictive tool for sugarbeet growers at the time of split-N fertilizer application in mid-May to early June and at harvest in October.

Monday, July 18, 2011 **Oral Presentations**
Canadian Phytopathological Society **Time:** 1030-1200h
Session 1: ***Climate Change and Plant Pathogens*** **Room:** 255 Sobey Building

Chair: Jeannie Gilbert
Agriculture and Agri-Food Canada

1030 **G.R. Dixon**
Impact of global climate change on plant diseases and world food production

1115 **Stella Coakley**
Projected effects of climate change on plant disease and how plant pathologists can prepare to meet the challenge

1030 **Impact of global climate change on plant diseases and world food production.** G. R. Dixon*, Centre for Horticulture, University of Reading and GreenGene International, Hill Rising, Horsecastles Lane, Sherborne, Dorset DT9 6BH United Kingdom. (e-mail: geoffrdixon@btinternet.com / Geoffrey.dixon62@imperial.ac.uk)

Worldwide climates are changing at rates not previously experienced in geological time, this is having substantial effects on the natural world and crop production. This presentation charts the evidence for climate change, impacts on crop growth and yields, affects on plant diseases and resultant changes in food supplies worldwide. Irrespective of the causes of climate change, it is crucial that scientists develop understandings of its implications and impacts on natural biodiversity, artificial landscapes and production agriculture. Currently, worldwide 20 to 25% of harvested crops are lost due to diseases. Climate change appears to be characterised by increased variability in temperature, rainfall and wind velocity. As the world's environments alter so the activities and vigour of aerial and edaphic microbes appears to change, some are becoming considerably more active and damaging. Pathogen vigour and dispersal appear to be changing. There are pressing needs for an understanding of how plant pathogenic microbes respond to climatic changes and how the scale of losses caused by soil-borne and air-borne microbes is set to increase. These effects will be examined using examples drawn from crops and diseases of worldwide significance indicating how lost production will damage international food and commodity supplies. Reductions in food and commodity supplies comes at a time when the world's population is increasing, its demands on all natural resources are outstripping supplies and biodiversity in Nature is being damaged frequently beyond repair. Plant pathologists in their attempts at combating escalating losses caused by plant diseases will need to take into account the economic, medical, social and political issues which will be central for survival and the continuing quality of life as the 21st century progresses. In the past visionary plant pathologists have contributed hugely in solving humanity's problems. Our profession's capacity for working with "one foot in the furrow (and) one hand on the bench" has increasing relevance.

1115 **Projected effects of climate change on plant disease and how plant pathologists can prepare to meet the challenge.** S. Melugin Coakley, Botany and Plant Pathology, College of Agricultural Sciences, Oregon State University, Corvallis OR 97331 USA (stella.coakley@oregonstate.edu)

Global climate change may seriously limit our ability to provide adequate food and fiber production for the rapidly growing world population. In addition to the evidence of an increased severity of soil borne pathogens, there are numerous observations of changing patterns of plant disease in managed and native plant systems. A recent volume of *Plant Pathology (*2011*) 60,* provides a comprehensive overview of the many facets of climate change and its potential impact on plant diseases. This volume contains twelve papers that are a valuable resource for identifying the current status of the field; these papers and the hundreds referenced within them, provide a unique opportunity to evaluate progress to date, identify gaps in our current understanding, and identify research that might help manage disease under the unpredictable nature of global warming and associated changes in precipitation. Plant disease epidemics develop as a convergence of abundant susceptible hosts, pathogens, any vectors required, and a sustained favorable environment. The best way for plant pathologists to meet the challenge of a changing, and predominately warming climate, is to ensure that we have a sufficient number of broadly based scientists prepared to respond both in diagnosing the pathogens and utilizing all available tools to manage them. There are numerous economic factors which will affect what crops are grown, the balance of annual versus perennial, and the management strategies available. For

example, more frequent application of fungicides can result in fungicide resistant pathogens and a more durable alternative may be multi-gene resistance. Because pathogens can evolve more rapidly than their hosts, they hold an advantage under favorable conditions when there is an abundance of susceptible hosts. One expects that in the long term, some diseases will increase and that others will decrease but the speed of climate change and the expected increase in local climate variability may result in significant and difficult to manage losses in some crops before adjustments can be made. This presentation will provide an overview of changes observed and what management options may be available.

Monday, July 18, 2011 **Oral Presentations**
Canadian Phytopathological Society **Time:** 1300-1500h
Session 2: ***Molecular and Physiological Plant Pathology*** **Room:** 255 Sobey Building

(Graduate Student Competition)

Chair: Deena Errampalli
Agriculture and Agri-Food Canada, Vineland, Ontario

1300 **Erin Morrison**
Investigating the impact of fungal produced cytokinins on fungal development and disease progression in the *Ustilago maydis-Zea mays* pathosystem

1315 **Kitty Cheung**
The effect of *Upe* expression on *Ustilago maydis* pathogenic development

1330 **Rony Chamoun**
SmkA MAP kinase is involved in the mycoparasitism of the plant fungal pathogen *Rhizoctonia solani*

1345 **Vincent Huang**
18S rDNA Phylogenies:All that glitters may not be gold

1400 **Sean Walkowiak**
Characterization of a virulence gene responsive to nitrogen stress in *Fusarium graminearum*

1415 **Brady Nash**
Chelated copper induces disease resistance in *Agrostis stolonifera L*

1430 **Raphaël Sansregret**
Extreme resistance induced against tomato bush stunt virus requires an active RNA silencing pathway

1445 **Linda Jewell**
Infection biology of *Microdochium nivale*

1300 **Investigating the impact of fungal produced cytokinins on fungal development and disease progression in the *Ustilago maydis* – *Zea mays* pathosystem.** E.N. Morrison[1*], K.M. Marsh [3], R.J.N. Emery[1,2] and B.J. Saville[1,3] . [1]Environmental & Life Sciences Graduate Program, Trent University, DNA Building, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada; [2] Biology Dept, Trent University, DNA Building, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada, [3]Forensic Science Program, DNA Building, Trent University, 2140 East Bank Dr. Peterborough, ON K9J 7B8, Canada. (e-mail: barrysaville@trentu.ca)

The involvement of fungal produced cytokinins in plant disease development has not been thoroughly examined. Cytokinins are a group of phytohormones that are often associated with actively dividing tissues. Infection of corn by the smut fungus *Ustilago maydis* D.C. Corda stimulates uncoordinated cellular division, resulting in the formation of tumors on all aerial organs of the plant. Early studies identified altered cytokinin [CK]-like activity associated with these tumors. The first and rate-limiting step in cytokinin biosynthesis in plants is catalyzed by isopentenyltransferases (IPTs). In fungi, related IPTs are usually tRNA-isopentenyltransferases (tRNA-IPTs). *U. maydis* is amenable to molecular manipulation and biochemical characterization. This allowed us to create solopathogenic strains (SG200) of *U. maydis* in which the sole tRNA-isopentenyltransferase (tRNA-IPT gene) was deleted. We determined, by liquid-chromatography-electrospray ionization-tandem mass spectrometry, LC- (ESI) MS/MS, that none of the major CKs produced in wild type cultures are detectable in the *tRNA-IPT* deletion mutant strains. These strains have different disease development profiles, when compared to wild type strains, during seedling and cob pathogenesis assays in corn. The role of CK production by *U. maydis* in disease development was further investigated through the over expression of the *tRNA-IPT* gene in solopathogens and compatible haploids. A comparison of CK production, growth and pathogenic development by these strains will be presented. Further, we are beginning to investigate the control of cytokinin production by *U. maydis* and will present preliminary data on the detection and characterization of a putative natural antisense transcript to the *U. maydis* tRNA-IPT mRNA.

1315 **The effect of *Upe* expression on *Ustilago maydis* pathogenic development.** H.Y. K. Cheung[1*] and B. J. Saville[1,2]. [1]Environmental & Life Sciences Graduate Program, Trent University, DNA Building, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada; [2]Forensic Science Program, DNA Building, Trent University, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada

Ustilago maydis D.C. Corda is the causal agent of common smut of corn. Since this biotrophic fungus requires *in planta* growth to become meiotically competent, we hypothesize that *U. maydis* meiosis is triggered by signals received from the host plant. Annotation of the *U. maydis* genome identified *Um01961* as an ortholog of the transcription regulator *Ume6*, and it was hypothesized that it plays a role in *U. maydis* meiosis. However, deletion of *Um01961* had no discernable effect on completion of meiosis, or haploid cell growth. The ability of haploid *Um01961* deletion strains to mate was also indistinguishable from that of wild type haploids as determined by a plate mating assay. In contrast, infection with the deletion strains displayed an altered pathogenesis profile relative to wild type, suggesting a role for this gene in pathogenic development. As a result, *Um01961* was named *Upe* for unregulated pathogenesis gene expression. We now hypothesize that *Upe* is either a repressor of pathogenesis genes or an activator of genes that suppress the host plant response. The solopathogenic *U. maydis* strain SG200 was altered to increase the level of transcription of *Upe* above that normally found in these cells. These altered SG200 strains were found to be deficient in filamentous growth and had

altered pathogenesis profiles, supporting the hypothesis that *Upe* is involved in pathogenic development. The creation of compatible haploid cell lines with elevated *Upe* transcript levels showed an alteration in mating efficiency and the influence on pathogenesis will be presented. Progress on determining variation in gene expression of the *Upe* mutant strains will also be discussed.

1330 **SmkA MAP kinase is involved in the mycoparasitism of the plant fungal pathogen *Rhizoctonia solani*.** R. Chamoun[1*] and S. Jabaji[1]. [1] Plant Science Department, McGill University, Ste Anne de Bellevue, Quebec, Canada H9X 3V9 (email: rony.chamoun@mail.mcgill.ca; e-mail: suha.jabaji@mcgill.ca)

Mycoparasitism comprises the interaction between two fungi involving an elaborate cross-talk of the host and the pathogen. Several studies on the signalling pathways participating in this interaction revealed high conservation of the mitogen-activated protein kinases (MAP kinases). MAPK phosphorylation cascade transduces a variety of signals in eukaryotes which affects gene expression. Three MAPK pathways exist: Erk1/2, JNK/SAPK, p38/HOG. The latter two modules are activated by abiotic stress such osmotic/oxidative shock. Erk1/2 has been implicated in fungal parasitism as well as in the production of asexual spores. We isolated a MAPK homolog belonging to the YERK1 class, *smkA*, from the biocontrol fungus *Stachybotrys elegans* a mycoparasite of the plant pathogenic fungus *Rhizoctonia solani.* We have cloned the gene and shown via alignment of similar and related fungal MAP kinases, that *smkA* encode the Erk1/2 MAP kinase. Southern blot analysis confirmed the existence of a single copy gene of *smkA*. Similar to the mycoparasite *Trichoderma virens*, we believe that SmkA might be involved in activation of transcription factors for genes encoding one or more enzymes responsible for the degradation of the host. To confirm the role of SmkA in mycoparasitism of *R. solani* and to rule out that it does not respond to abiotic stress, *S. elegans* was subjected to the following types of stress: 1) biotic stress involving confrontation assays leading to mycoparasitism of *R. solani*; and 2- abiotic stress involving the application of osmotic (0.8 M NaCl/0.8 KCl) and oxidative (10 mM H_2O_2) stresses for 20, 40 and 60 min). Immunoblot analyses using monoclonal antibodies against the active forms of the target proteins (Erk1/2 and p38) were used. Western blot analyses revealed that SmkA was highly expressed in *S. elegans* during mycoparasitism, and was not expressed when the mycoparasite was exposed to osmotic/oxidative stress. On the other hand, p38 was highly expressed in *S. elegance* under oxidative stress. A solid understanding of transduction pathways following perception of signals and the identification of key components of signal transduction pathways is essential in the attempt to recognize the essential key factors that play roles in the mycoparasitism process of *R. solani.*

1345 **18S rDNA Phylogenies: All that glitters may not be gold**. V. C. H. Huang*, and T. Hsiang. School of Environmental Sciences, University of Guelph, Guelph, ON, Canada N1G 2W1

Ribosomal DNA (rDNA) codes for rRNA, which is part of the DNA translation machinery found in all living organisms. Regions within rDNA such as the internal transcribed spacer (ITS) and the small ribosomal subunit (18S) have been used for species identification and phylogenetics. Trees constructed from 18S are commonly used as the “gold standard” as 18S is considered to be representative of the true species phylogeny. However, it is not known whether a plurality of genes in a genome will give the same topology as 18S, nor if combined gene datasets (superalignments) will yield trees that also agree with 18S. Recent developments in genome sequencing technologies have generated copious amounts of "glittering" data that may be used to resolve true species relationships and assess whether 18S data is representative. Using BLAST,

the genome of *Neurospora crassa* Shear & Dodge was compared against 47 other filamentous ascomycete genomes to calculate the mean identity of all 10,000+ genes. Because identity values retrieved from BLAST may not accurately represent the match between the query and target sequence, a BioPerl module was used to stitch matching segments together and recalculate the identity. Genes were then placed into 10 ten-percentile bins based on mean identity, and up to 20 genes per bin were systematically selected for individual multiple sequence alignment and neighbor-joining (NJ) tree construction. Genes from the highest and lowest identity bins were, respectively, too conserved or too divergent to separate or group taxa. Out of the 191 NJ trees, the largest concordant group contained 67 genes, mostly from the 30% to 80% bins, and was found to have the same topology as 18S in distinguishing the 48 taxa. Furthermore, 50 maximum likelihood (ML) trees were constructed based on superalignments of 5, 10, 15, 20 and 25 genes, and from those, 40 trees yielded the same topology as 18S. These results reconfirm and reinforce the usefulness of 18S in phylogenetic studies.

1400 **Characterization of a virulence gene responsive to nitrogen stress in *Fusarium graminearum*.** S. Walkowiak[1,2 *], W. Leung[1], A. Johnston[1], L. Harris[1], C. Rampitsch[1], and G. Subramaniam[1,2] . [1] Agriculture and Agri-Food Canada, 960 Carling Ave. Ottawa, Ontario, Canada; and [2] Carleton University, 1125 Colonel-By Dr, Ottawa, Ontario, Canada

Fusarium graminearum [Schwabe] is a broad range phytopathogen that infects a variety of economically important cereal crops in Canada. The fungus produces a mycotoxin, deoxynivalenol, a secondary metabolite that contributes to the spread of the fungus during infection and therefore acts as a virulence factor. The toxin accumulates in infected plants and appears in grain products after downstream processing; consumption of contaminated products causes vomiting and reduced appetite. Recent studies indicate that nitrogen availability and other environmental cues are important triggers for secondary metabolism and virulence, which is also true for deoxynivalenol biosynthesis. This study focuses on a regulatory gene *Fg03881* which responds to nitrogen availability and is involved in virulence. Disruption of *Fg03881* causes increased virulence of the pathogen in a susceptible variety of wheat 'Roblin'. A high throughput assay was developed to assess various environmental cues that are required to activate *Fg03881* expression. A transcription fusion of the promoter of *Fg03881* and GFP was transformed into *F. graminearum* and was used in a 96 well plate reader system to identify compounds that modulate the promoter activity of *Fg03881*. Overall, results indicated that both preferred and complex sources of nitrogen strongly repressed the promoter activity, while non-preferred sources and reduced nitrogen had the opposite effect. Finally, comparative proteomics and gene expression profiling performed in the *Fg03881* mutant identified genes involved in virulence.

1415 **Chelated copper induces disease resistance in *Agrostis stolonifera* L.** B. Nash[1]*, T. Hsiang[1] and P.H. Goodwin[1]. [1]School of Environmental Sciences, University of Guelph, Guelph, ON, Canada N1G 2W1

In 2007, Petro-Canada developed Harmonizer™, a copper-containing pigment dispersion. Field work showed that it could decrease the severity of several turfgrass diseases. Lab tests showed it to have a slight direct inhibitory effect on fungal growth in agar tests. However, when applied to the roots of *Agrostis stolonifera* L., there was increased resistance to foliar infection by the fungal pathogen *Sclerotinia homoeocarpa* F. T. Bennett, hence appearing to systemically activate resistance. Initial gene expression analyses using relative reverse-transcriptase (RT) PCR found no change in expression of several genes thought to be related to induced systemic resistance (ISR). To identify genes in *A. stolonifera* which might be affected by pigment treatment, RNA-seq based on the Illumina/Solexa Next Generation Sequencing platform was used to sequence cDNA derived from pigment-treated or water-treated *A. stolonifera* leaf tissues. The sequence

reads were then assembled, and reads were compared to the assembled contigs to derive gene expression profiles of the treatments. Over 3,300 contigs were found with greater than two-fold increase in read count between pigment-treated versus water-treated samples. Comparisons of these 3,300 contigs against the GenBank NR database provided annotations for 75% of these contigs. Among these, 20 contigs were identified as putative disease resistance-related genes, and relative RT-PCR of several of these genes confirmed the increased expression results obtained from the RNA-seq analysis. These results demonstrate that the pigment dispersion is able to activate systemic resistance in leaves when applied to roots, and to affect expression of many plant genes, including some putative defense-related genes.

1430 **Extreme resistance induced against *tomato bushy stunt virus* requires an active RNA silencing pathway**. R. Sansregret[1], V. Dufour[1], K. Bouarab[1]. [1]Centre en amélioration végétale, Département de Biologie, Université de Sherbrooke, QC, J1K 2R1, Canada (email: Kamal.bouarab@usherbrooke.ca)

Plants deploy an immune system that recognizes and responds to different sorts of molecules produced by microbes. Some of those molecules induce the apparition of a hypersensitive response which is a type of programmed cell death that is thought to confine the pathogen at the entry point and signal its presence to the neighbouring cells. In some cases, the defense response is fast and efficient enough that no cell death is required to prevent the infection. This response is called extreme resistance. Here we show that the suppressor of RNA silencing P19 produced by tombusviruses acts as an elicitor of plant immunity and its recognition confers an extreme resistance against tomato bushy stunt virus (TBSV). We also show that P19-induced immunity requires its dimerisation and its capacity to bind small RNAs generated by RNA silencing pathways. Interestingly, suppressor of RNA silencing breaks the extreme resistance mediated by P19 against TBSV. These data highlight the extraordinary adaptation of some plants to the RNA silencing suppression machinery restored by the virus.

1445 **Infection biology of *Microdochium nivale*.** L.E. Jewell* and T. Hsiang. School of Environmental Sciences, University of Guelph, Guelph, ON N1G 2W1, Canada

Microdochium nivale (Wollenw.) Samuels & Hallett is a common pathogen of turfgrasses and cereal crops in Europe and North America. Traditionally it has been divided into two subspecies, vars. *majus* and *nivale* based on morphological and host-specific differences, and a recent study elevated the subspecies to *M. nivale* and *M. majus* (Wollenw.) Glynn & Edwards based on differences in the elongation factor-1 alpha gene. Several aspects of the infection biology of these fungi are unclear, including the relative importance of conidia in causing new infections and whether there are differences between the infection processes of the two varieties on various host plants. The infection process of three var. *majus* and eight var. *nivale* isolates from a variety of host plants and geographic origins was investigated on detached leaves of *Triticum aestivum* L. (wheat) or *Poa pratensis* L. (Kentucky bluegrass) using either hyphal plugs or conidial suspensions as sources of inoculum. Conidia were not observed to germinate nor cause infection within the one week experiments. Unexpectedly, isolates of var. *majus* generally caused infection on both wheat and Kentucky bluegrass more rapidly than isolates of var. *nivale* despite the common field observation that var. *majus* is generally isolated only from wheat while var. *nivale* is readily found on either host. Despite these field host preferences, hyphal plug inoculation allowed each isolate to quickly colonize plant surfaces, and to penetrate the leaves by direct growth into stoma within three days of inoculation on both host plants. Among var. *nivale* isolates, penetration occurred most rapidly on the host species from which the isolate originated. This information may be useful in the development of cultural protocols to mitigate the damage caused by these pathogens.

Monday, July 18, 2011
Canadian Phytopathological Society
Session 3: ***Ecology, Epidemiology and Management***
(Student General Session continued)
Pathogen detection, identification and taxonomy
(General Session)

Oral Presentations
Time: 1530-1700h
Room: 255 Sobey Building

Chair: Rick Peters
Agriculture and Agre-Food Canada, Charlottetown

Student Session

1530 **Subrata Mowlick**
Biological soil disinfestations: Analyzing the process and its bacterial community structure

1545 **Hema Kasinathan**
Efficacy of Serenade and Prestop against clubroot is affected by soil type

General Session

1600 **Danielle Morissette**
Molecular aerobiology: the contribution of new spore quantification methods

1615 **Upeksha Nanayakkara**
Genetic diversity of potato virus Y (PVY) in seed-lot potatoes in New Brunswick

1630 **James Tambong**
Specificity and sensitivity of a TaqMan real-time PCR assay for detection of several pathovars of Pseudomonas syringae

1530 **Biological soil disinfestations: Analyzing the process and its bacterial community structure.** S. Mowlick[1*], K. Hirota[2], T. Takehara[3], N. Kaku[1], and A. Ueki[1]. [1]Faculty of Agriculture, Yamagata University,Yamagata, Japan (mowlick07@yahoo.com); [2]Tokushima Agricultural Research Institute, Tokushima, Japan and [3] National Agricultural Research Center for Western Region, Hiroshima, Japan

Biological soil disinfestation (BSD) is a good alternative to chemical and other physical fumigation methods for controlling soil borne plant pathogens. Some anaerobic bacteria grown in the soil are known to produce toxic substances during BSD that may kill many soil borne pathogens. In this study, bacterial communities were analyzed during model experiments of BSD using mainly molecular methods. *Brassica*-, wheat bran-, and *Avena*-treated (BSD samples) and control (no plant materials) soils were collected from the treated pot experiment. The earlier dropping of soil redox potential indicated the rapid development of an anaerobic condition in BSD soil. The population of pathogenic *Fusarium oxysporum* Schlecht. in the pot soil was significantly decreased during BSD. Acetate and especially butyrate were the major volatile fatty acids (VFA) from the wheat bran-treated soil detected during BSD. The PCR-DGGE results revealed significant changes of bacterial community profiles due to biomass incorporation and variation in moisture content or temperature. Based on the clone library analysis, the original field soil showed diverse bacterial clones without any dominant bacterial groups that were similar to other control soils. The clone libraries from BSD samples showed members of the *Firmicutes* phylum, especially of the class *Clostridia* were exclusively dominant. *Brassica*-treatment at high (30^{o}C) and wheat bran-treatment at lower temperature (25^{o}C) of incubation were effective to increase clostridial ratios in the bacterial community during BSD. Most of the closely related clostridial species of the clones from *Brassica*- and *Avena*-treated soil were acetate-producers and those of wheat bran were acetate- and butyrate-producers. The development of clostridial communities was poor in the treated soil without plant biomass. The strictly anaerobic clostridial groups might be involved in killing soil borne pathogens by their fermentation products during BSD.

1545 **Efficacy of serenade and prestop against clubroot is affected by soil type.** H. Kasinathan[1*], B.D. Gossen[2], G. Peng[2] and M.R. McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1 (e-mail: mrmcdona@uoguelph.ca) and [2]Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada S7N 0X2

Clubroot of canola (*Brassica napus* L.) and other brassica crops is caused by *Plasmodiophora brassicae* (Woronin). A study was conducted to determine if soil type: muck soil, mineral soil, non-calcareous sand and soil-less mix, influences the efficacy of the biofungicides Serenade (*Bacillus subtilis*) and Prestop (*Gliocladium catenulatum*) against *P. brassicae* in canola under controlled environmental conditions (25°/20° C day/night). The trial was arranged in a factorial randomized complete block design with three factors (soil type, biofungicides, and pathotypes 3 and 6), four replicates, and 12 plants per experimental unit. Canola (cv: 46A76) was sown directly into muck soil and soil-less mix and transplanted into sand and mineral soil. Serenade (5% v/v) and Prestop (7.5 g L^{-1} of water) were applied at 50 mL solution per plant, 5 days after seed germination. Three days later, each seedling was inoculated with 5 mL of a resting spore suspension of *P. brassicae* containing 1 x 10^5 spores mL^{-1}. Clubroot severity was assessed at 6 weeks after inoculation using a 0–3 scale, and a disease severity index (DSI, range 0–100) was calculated. Pathotype 3 resulted in slightly more clubroot (74% incidence, DSI = 52) than

pathotype 6 (65% incidence, DSI = 43). The most important interaction was biofungicide x growing media. Incidence was low in plants treated with Prestop when grown on mineral soil (53% incidence) and soil-less mix (32% incidence), and severity was lower on mineral soil (DSI = 33) and muck soil (DSI = 43) than the check (81% incidence, mean DSI = 58). Serenade was effective only in sand (55% incidence, DSI = 33). These results indicate that growing medium is an important factor in evaluation of biofungicides in controlled environments and that soil type will likely influence the efficacy of these biofungicides in field trials.

1600 **Molecular aerobiology: the contribution of new spore quantification methods**. D. C. Morissette[1]*, M. Tremblay[2], L. Brodeur[1], H. van der Heyden[1], and O. Carisse[2]. [1]Phytodata Inc., Sherrington, Quebec, Canada J0L 2N0 (e-mail: danielle.morissette@phytodata.qc.ca); and [2]Horticulture Research and Development centre, Saint-Jean-sur-Richelieu, Quebec, Canada J3B 3E6

For several foliar diseases such as Botrytis leaf blight of onion (*Botrytis squamosa* J.C. Walker) and grey mould of tomato (*Botrytis cinerea* Pers. ex Fr.), airborne inoculum is a key factor influencing disease progress and hence monitoring airborne inoculum is essential to disease management. Since more than a century, several spore samplers were developed. For most spore samplers, spore counts are made by microscopic observations which are time consuming and not always reliable as specific spores are often difficult to identify or to distinguish from similar spores from different fungal species. In addition, in several situations, several spore samplers may be needed which would considerably increase the delay between sampling and information delivery. Molecular techniques such as quantitative PCR (qPCR) circumvent this problem. On average using microscopic observations may require 15 to 30 min to count the spores on one sample, up to 40 samples can be processed by qPCR in less than 2.5 h. This molecular technique allows processing a huge number of samples and hence to deliver information on abundance of inoculum in a timely manner and to identify best time to apply a control measure. From a research stand point, the ability to process large number of samplers make possible studies on the spatio-temporal dynamics of airborne inoculum. The benefits of monitoring airborne inoculum of *B. squamosa* and *B. cinerea* with qPCR will be used as an example.

1615 **Genetic diversity of potato Virus Y (PVY) in seed-lot potatoes in New Brunswick.** U. N. Nanayakkara[1*], X. Nie[1], M. Singh[2], Y. Pelletier[1]. [1]Potato Research Centre, AAFC, 850 Lincoln Rd, Fredericton, New Brunswick, Canada E3B 9H8; and [2]Agricultural Certification Services, 1030 Lincoln Rd, Fredericton, New Brunswick, Canada E3B 8B7

Recently *Potato virus Y* (PVY) has reemerged as a major problem in seed potato production in North America including New Brunswick (NB), Canada. It is widely believed that a change in the genetic composition of PVY strains has resulted in high PVY incidences. This study investigated genetic diversity of PVY in 20 seed-lots in NB growing 11 different cultivars in 2009. Multiplex RT-PCR, serological and biological assays were used to reveal and characterize the strain identity. PVY^{O} strain is the predominant strain in NB seed-lots. However, recombinant strains, $PVY^{N:O}$ and European (Eu) PVY^{NTN} are widespread and becoming prevalent in NB. $PVY^{N:O}$ was identified in 19 of the 20 seed-lots and accounted for ~13% of the isolates. Eu-PVY^{NTN} was identified in 13 of the 20 seed-lots and accounted for ~ 5% of the isolates. When these tubers were planted in the field, progeny tubers did not develop tuber necrosis at the time of harvest or after 5 months in storage. North American (NA) $PVY^{N/NTN}$ strains were conspicuously absent in these seed-lots. Mixed infections with PVY strains, mainly PVY^{O} and $PVY^{N:O}$ or PVY^{NTN} were found in 18 of the 20 seed-lots and accounted for ~10% of the isolates (total 728). A coat protein gene based RT-PCR assay differentiated the dominant PVY^{O} strain into three groups: PVY^{O}-Oz/-FL type, PVY^{O}-139/-RB type, and an uncharacterized PVY^{O} type. The PVY^{O}-Oz/-FL type is the

predominant followed by the uncharacterized PVY^O type. Incidences of PVY^O-139/-RB are either low or completely absent. PVY^O-Oz/-FL type generally produced severe symptoms in all 11 cultivars compared to other PVY^O types and PVY strains. Biological assays on tobacco and 'Yukon Gold' confirmed the findings from RT-PCR assays and serological assays. Results from this study clearly demonstrate the diverse nature of PVY in NB, Canada.

1630 **Specificity and sensitivity of a TaqMan real-time PCR assay for detection of several pathovars of *Pseudomonas syringae*.** J. T. Tambong* and R. Xu. Agriculture and Agri-Food Canada, Ottawa, ON, Canada K1A 0C6. (email: james.tambong@agr.gc.ca)

The identification and detection of eight pathovars of *Pseudomonas syringae*, bacterial pathogens of several important agricultural plants, was achieved by TaqMan real-time polymerase chain reaction of a specific DNA fragment of cytochrome o ubiquinol oxidase gene. Under optimal conditions, the selected primers and probe were specific for the detection of pathovars *syringae, tomato, maculicola, tabaci, atropurpurea, phaseolicola, pisi* and *glycinea* by real-time PCR. Two pathovars (*coriandricola* and *morsprunorum*) tested could be differentiated from the other eight due to a single nucleotide mismatch. Thirty other *Pseudomonas* and 20 non-*Pseudomonas* strains were negative. The real-time PCR assay detected 100 fg of DNA and 4.5×10^3 *P. syringae* colony forming units per millitre (4 cells per reaction). In growth chamber experiments, tomato plants were inoculated using strain DC3000 and assayed by TaqMan real-time PCR. Serial dilution of leaf extracts spiked with lambda DNA and processed by real-time PCR indicated the presence of inhibitors. A 1:10 dilution of the crude extract reduced threshold cycles to those of milliQ water spiked with the same amount of lambda DNA. The TaqMan real-time assay consistently detected the pathogen in inoculated tomato leaves after a 1:10 dilution of crude extracts. TaqMan real-time results were validated by dilution plating of leaf extracts and conventional PCR using the same primer set. This assay offers real-time monitoring of the targeted amplicon with high specificity and sensitivity, with no post-amplification analysis needed. This reduces opportunity for contamination of the reaction mixtures with target DNA, making this assay suitable for routine diagnosis.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Phytopathological Society **Time:** 0830-1000h
Session 4: ***Mycotoxins in Grain: An Accumulating Problem*** **Room:** 255 Sobey Building

Chair: James Menzies
Agriculture and Agre-Food Canada, Winnipeg

0830 **Sheryl Tittlemier**
An overview of ochratoxin A in Canadian grains

0900 **Barbara Blackwell**
Trichothecenes and other secondary metabolites from Fusarium graminearum – is it just about DON?

0830 **An overview of ochratoxin A in Canadian grains.** S.A. Tittlemier, M. Roscoe, R. Blagden, C. Kobialka, T. Nowicki. Grain Research Laboratory, Canadian Grain Commission, 1404-303 Main St, Winnipeg, MB, R3C 3G8

Ochratoxin A (OTA) is a fungal secondary metabolite. In areas with temperate climates (including Canada) OTA is produced in grain by *Penicillium verrucosum*. OTA is produced during storage, as opposed to in the field, as is the case with fusarium trichothecene mycotoxins such as deoxynivalenol. OTA shares a structural similarity to the essential amino acid phenylalanine, and affects the enzymes involved in the metabolism of phenylalanine. OTA is a relatively stable molecule and can accumulate in kidney, liver, muscle, and body fat. Health Canada has recently proposed maximum limits of 3 to 5 □g/kg for OTA in a number of cereal grains for human consumption. The Canadian Food Inspection Agency has recommended tolerance levels of 200 to 2000 □g/kg for swine and poultry diets. The analysis of OTA in grains is particularly challenging. There are no visible signs when grain is infected with *P. verrucosum*, nor when OTA is produced. OTA is generally present in grain at very low concentrations – in the low □g/kg range. It is also heterogeneously distributed, from one individual kernel or seed to the next as well as throughout a bulk sample of whole grain. The Canadian Grain Commission has been monitoring grain for OTA since the mid 1990s. Ongoing monitoring activities include the sampling of vessel loadings bound for export, as well as loadings from shipments across the Great Lakes. Much work has also been performed on developing adequate sampling protocols in order to minimize the effect of OTA's heterogeneity in whole grain on the variance of analytical results. Data generated by the Canadian Grain Commission's monitoring programs demonstrate that OTA is only infrequently detected in bulk lots of Canadian grain. OTA has been found more frequently in cereals than oilseeds or pulses, but the concentrations of OTA measured in cereals were not different than those observed in oilseeds and pulses. OTA has also been detected in western and eastern varieties of Canadian wheat, suggesting a widespread geographical occurrence of *P. verrucosum* and production of OTA. Overall, the majority of OTA quantified in samples have been below the maximum limits of OTA recently proposed by Health Canada.

0900 **Trichothecenes and other secondary metabolites from *Fusarium graminearum* – is it just about DON?** B.A. Blackwell[1*], C. Seguin[1], and D. Overy[2]. [1] Eastern Cereal and Oilseed Research Centre, Agriculture and Agrifood Canada, 950 Carling Ave., Ottawa, ON K2J 2R2 Canada and [2] Department of Chemistry, University of Prince Edward Island, Charlottetown, PEI, Canada

Fusarium graminearum (*Gibberella zeae* Schwabe) and closely related *Fusarium* species cause fusarium head blight (FHB) in wheat and barley and ear rot in maize. The disease results in reduced yield and quality as well as kernel contamination with the mycotoxin deoxynivalenol (DON). DON has been shown to be phytotoxic, thus acting as a virulence factor in the spread of the disease on the plant as well as potent non-specific inhibitor of eukaryotic protein synthesis. Within the *F. graminearum* species complex found in North America, there are three chemotypes, those producing 15-acetyl-DON and those producing 3-ADON as precursors to DON, and to a minor extent those producing nivalenol. In the past, the *F. graminearum* isolates with the 15-ADON chemotype were the primary cause of FHB in western Canadian grain. *F. graminearum* DAOM 233423 (a 15-ADON chemotype) is a particularly virulent strain that is a good producer of 15-ADON in the laboratory. In addition, it is genetically well characterized and has been the

source for gene knockouts in biosynthetic and virulence factor studies. In the course of isolating quantities of 15-ADON from large scale liquid cultures of this strain for use as analytical standards and in toxicological testing, other secondary metabolites were isolated and characterized. The crude fungal extract from a ten liter culture was fractionated by preparative HPLC into the pre-15-ADON (more polar components), 15-ADON itself (the primary metabolite) and the post-15-ADON (less polar components). The pre- and post- were further fractionated into 20 fractions which were combined based on their HPLC/UV profile. These fractions were characterized by UPLC/MS. The more polar metabolite fraction was dominated by a compound that is virtually indistinguishable from DON by HPLC. This compound was determined to be 3-deacetyl- 7,8 dihydroxy-calonectrin, a plausible oxidative precursor to 15-ADON. Other metabolites in this fraction included cyclonerodiol, butenolide and sambucinol. Metabolites identified in the less polar included culmorin, culmorone and sambucoin and 15-acetyl-4,7-dideoxynivalenol was found in the semi-pure 15-ADON fraction. While the role of these metabolites and whether they occur *in planta* is unknown, both analytical and genetic methods are under development to detect these metabolites in the field.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Phytopathological Society **Time:** 1030-1200h
Session 5: ***Ecology, Epidemiology and Management*** **Room:** 255 Sobey Building

Chair: Tom Hsiang
University of Guelph

1030 **Jeannie Gilbert**
Ratio of 3-ADON and 15-ADON isolates of *Fusarium graminearum* recovered from wheat plants inoculated and incubated at various temperatures.

1045 **Aijamada Kushalappa**
Metabolic profiles of barley genotypes inoculated with trichothecene producing and nonproducing isolates of *Fusarium graminearum*

1100 **Deena Errampalli**
Effect of methyl jasmonate for suppression of postharvest Botrytis in different grape cultivars

1115 **Elisa Becker**
Trichoderma spp.: antagonistic effects to *Phytophthora ramorum* growth and spore germination *in vitro*

1130 **Xiuling Tian**
Species susceptibility and biocontrol of Fusarium wilt of *Hiemalis begonias* in Canada

1145 **Michael Harding**
An innovative, high throughput screening technology for identification and optimization of effective anti-biofilm fungicides

1030 **Ratio of 3-ADON and 15-ADON isolates of *Fusarium graminearum* recovered from wheat plants inoculated and incubated at various temperatures.** J. Gilbert[1*], R. Clear[2], S. Patrick[2], K. Slusarenko[1], and C. Wolfe[1]. [1]Agriculture and Agri-Food Canada, Cereal Research Centre, 195 Dafoe Road, Winnipeg, MB R3T 2M9 (e-mail: jeannie.gilbert@agr.gc.ca); and [2] Canadian Grain Commission, Grain Research Laboratory, Winnipeg, MB R3C 3G8

Fusarium head blight (FHB) of wheat, caused principally by *Fusarium graminearum sensu stricto* in North America, can reduce crop value due to accumulation of mycotoxins in the grain. The fungus produces predominantly deoxynivalenol (DON) and its acetylated forms 3-ADON or 15-ADON. Recent analyses of *F. graminearum* isolates collected between 1998 and 2004 identified higher numbers having the 3-ADON chemotype, whereas prior to 1998 the 15-ADON chemotype was considered the only significant cause of FHB in North America. To monitor the ratio of 3-ADON to 15-ADON chemotypes, strains of *F. graminearum* were isolated from harvested samples of six check varieties in FHB disease nurseries in 2008 and 2009. In 2008, the ratio of 3-ADON to 15-ADON was 79:21%. However, the following year the ratio changed dramatically to 55:45%. The 2009 summer was characterized by lower temperatures with mean daytime highs of 22.4° C compared to 25.5° C in 2008. To determine the effects of temperature on recovery of 3-ADON and 15-ADON chemotypes, plants of the six check varieties were grown under controlled conditions. After heading, plants were maintained at 20, 24 or 28° C. At anthesis, plants were inoculated with a 1:1 ratio of *F. graminearum* isolates of 3- and 15-ADON chemotype. At maturity, 100 kernels were plated on potato dextrose agar and as *Fusarium* developed, up to 40 isolates were taken for which monospore cultures were established. DNA was extracted from these cultures and isolates identified to chemotype using PCR. At 20° C the ratio of 3-ADON to 15-ADON isolates was 30:70%; at 24° C this was 53:47%, while at 28° C the pattern was reversed to 69:31%. These preliminary data indicate that in Manitoba, 15-ADON isolates may be favoured in cooler seasons and 3-ADON chemotypes in warmer ones.

1045 **Metabolic profiles of barley genotypes inoculated with trichothecene producing and nonproducing isolates of *Fusarium graminearum*.** G. K. Kumaraswamy[1], A. C. Kushalappa[1*], T. M. Choo[2], Y. Dion[3], and S. Rioux[4]. [1]Plant Science Department, McGill University, Ste. Anne de Bellevue, QC, Canada H9X3V9 (e-mail: ajjamada.kushalappa@mcgill.ca); [2]Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON, Canada K1A 0C6; [3]Centre de recherche sur les grains inc. (CEROM), 740 chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, Canada J3G 4S5; [4]CEROM, 2700 rue Einstein, Ste. Foy, QC, Canada G1P 3W8

Resistance in barley to fusarium head blight (FHB), caused by *Fusarium graminearum* Schwabe (teleomorph: *Gibberella zeae* Schwein (Petch)), is quantitatively inherited. Four recombinant inbred lines, resistant and susceptible, black and yellow barley (derived from a cross between AC Legend/CH9403-2), were used in this study. Metabolic profiles were used to discover novel mechanisms of resistance. The spikelets were inoculated with a trichothecene-producing isolate, trichothecene-nonproducing isolate (*tri5*$^-$ mutant) or mock solution. Spikelets were sampled, metabolites extracted in aqueous methanol, and analyzed using a LC-hybrid-MS (LC-ESI-LTQ-Orbitrap). A pair wise comparison between the resistant and susceptible genotypes, and pathogen and mock-inoculations, was separately made for the black and yellow colored genotypes. Student's *t*-test was used to select treatment significant peaks, which were further used to identify resistance related constitutive (RRC), resistance related induced (RRI), and resistance indicator (RI) metabolites. The RRC, RRI and RI metabolites were putatively identified. A signal

molecule, jasmonic acid, was induced in barley only following inoculation of the trichothecene-producing isolate. Phenylpropanoids: cinnamic acid, sinapoyl alcohol, coniferin, catechin and naringin were identified as RRI metabolites, only against *tri5*$^{-}$ mutant. *p*-Coumaric acid, coniferaldehyde and sinapaldehyde were induced in greater abundances against *tri5*$^{-}$ mutant. Deoxynivalenol production and its degradation to DON-3-*O*-glucoside, designated as resistance indicator (RI) metabolites, also varied among genotypes. The roles of these RRC, RRI and RI metabolites in plant defense, and their further use as potential FHB resistance biomarkers will be discussed.

1100 **Effect of methyl jasmonate for suppression of postharvest Botrytis in different grape cultivars.** D. Errampalli[1*], M. A. MacDonald[1], A. Sharon[2] and P. H. Goodwin[3]. [1]Agriculture and Agri-Food Canada, 4902 Victoria Ave N., Vineland Station, Ontario L0R 2E0, Canada. (e-mail: Deena.Errampalli@agr.gc.ca). [2]Department of Molecular Biology and ecology of Plants, Tel Aviv University, Tel Aviv 69978. [3]School of Environmental Sciences, University of Guelph, Guelph, Ontario, Canada N1G 2W1 Canada

Botrytis bunch rot, caused by the fungus *Botrytis cinerea* Pers.: Fr., is a common problem wherever grapes (*Vitis vinefera* L.) are grown. The disease can cause serious losses in both yield and quality. Methyl jasmonate (MeJA) occurs naturally in plant tissues and has a signalling role in eliciting induced systemic resistance against disease. The present study investigates the effect of exogenous MeJA, on suppression of postharvest Botrytis bunch rot in four, 'Flame', 'Niagara', 'Sugar One', and 'Thompson' cultivars of grapes. A strain of *B. cinerea* collected from Israel (BC-I) was used in all the experiments. The surface sterilized grape bunches (15 grapes/bunch) were spray-treated with 1mM of MeJA, air dried for 3 hours and kept in the growth chamber at 12C. Four days after the MeJA treatment, each of the grape berry in the bunch was wounded with a needle and inoculated with 1 x 10^4 spores of *B. cinerea* (BC-I) and incubated in the dark at 12 C and 85% RH. Control treatment did not receive MeJA. There were three replicate bunches per treatment. Experiments were repeated at least once for each of the cultivars. The lesion diameter was recorded at 7, 14 and 21 days after inoculation. MeJA significantly suppressed the disease caused by *Botrytis* in three green grape cultivars, 'Niagara' 'Sugar One', and 'Thompson', and in the red grape cultivar, 'Flame'. Within the green grape cultivars, significant disease suppression was observed for up to 14 days in 'Sugar One' and 'Thompson' and for up to 7 days in 'Niagara' grapes. There was no significant disease suppression in any of the grape cultivars after 21 days of treatment. In conclusion, 1mM concentration of MeJA treatments have been shown to suppress disease caused by *B. cinerea* (BC-I). Pretreatment with MeJA could be an alternative to traditional fungicides in the management of post-harvest diseases of grapes.

1115 ***Trichoderma* spp.: antagonistic effects to *Phytophthora ramorum* growth and spore germination *in vitro*.** E.M. Becker*, N. Rajakulendran, and S.F. Shamoun. Canadian Forest Service, Pacific Forestry Centre, Victoria, BC, Canada V8Z 1M5 (e-mail: elisa.becker@NRCan-RNCan.gc.ca)

The pathogen *Phytophthora ramorum* (Werres, De Cock & *Man* in't Veld), is responsible for Sudden Oak Death in California and Oregon and Sudden Larch Death in the UK, and causes foliar blight symptoms in many host plant species. In British Columbia, several nurseries have reported *P. ramorum*-infected plants, and eradication measures have been taken to prevent the spread of the pathogen beyond these points of entry and limit this potential pathway for escape into forested or wild areas. We are investigating the potential use of *Trichoderma* spp. to limit infection of plants and reduce the spread of *P. ramorum*. About 50 isolates of *Trichoderma* of eight species were assayed. Direct contact antagonism of *P. ramorum* was evaluated using a dual-

culture assay in Petri plates, which measured the ability of *Trichoderma* isolates to overgrow and kill cultures of *P. ramorum*. In dual culture, the species with the fastest rates of overgrowth were *T. atroviride, T. koningii* and *T. virens* (9.0, 7.8, and 6.9mm/day), which also had the fastest rates of lethal effect on *P. ramorum* (9.0, 6.1, and 5.5mm/day). A high rate of overgrowth did not always translate to a lethal effect on *P. ramorum*. These results suggest that certain species of *Trichoderma* have the ability to kill *P. ramorum* after it has established. The effects of *Trichoderma* metabolites on *P. ramorum* (antibiosis) were investigated using a microplate assay. Zoospores of *P. ramorum* were added to media containing cell-free *Trichoderma* culture extracts, and germination and growth were evaluated over several days. The species that produced the most inhibitory extracts in microplate assays were *T. polysporum, T. pseudokonigii, and T. harzianum* (99, 73 and 68% inhibition). *Trichoderma* isolates were also tested for their ability to tolerate chemical controls that are registered for use in Canada by measuring their growth on media containing either fosetyl-Al (Aliette™) or metalaxyl (Subdue Maxx™). All isolates were inhibited by Aliette, but many isolates were tolerant of Subdue Maxx. This allows for the possibility of combining or alternating promising *Trichoderma* isolates with Subdue Maxx in an integrated pest management approach.

1130 **Species susceptibility and biocontrol of Fusarium wilt of *Hiemalis begonias* in Canada.** X. Tian* and Y. Zheng, School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada (email: xitian@uoguelph.ca)

In 2010 a hitherto unknown disease caused major economic losses in *Hiemalis begonias* (*Begonia* × *Hiemalis* Fotsch) in commercial greenhouses in southern Ontario, Canada. The foliage of affected plants first appeared dull green and subsequently wilted. Lower portions of the stems became water soaked and the vascular tissues turned brown. It was identified that sporodochia of *Fusarium foetans* Schroers developed on affected portions of the stems. The pathogen was shown to be the causal agent in inoculation tests and the disease is referred to as Fusarium wilt. The resistance tests were conducted in the greenhouse of different begonia species and cultivars to Fusarium wilt, drenched inoculation plants with 50 ml conidia suspension at 10^6 conidia ml^{-1}. Begonias showed different symptoms post inoculation time, and different species and cultivars showed different resistance to this pathogen. Disease symptoms were severe on *Hiemalis begonia* 'Golden Edith' even at low concentrations of 100 conidia/ml; and cultivar 'Camilla' was ranked as moderately resistant. For biological control with five microorganisms and five substrates in the greenhouse, vermicompost tea treatment delayed the symptoms three weeks. And vermicompost and yard waste substrates significantly suppressed Fusarium wilt on *Hiemalis begonias*.

1145 **An innovative, high throughput screening technology for identification and optimization of effective anti-biofilm fungicides.** M.W. Harding[1*], R.J. Howard[2], N.D. Allan[3], and M.E. Olson[3]. [1]Innovotech, Inc., 301 Horticultural Station Rd. E., Brooks, Alberta, Canada T1R 1E6 (e-mail: michael.harding@innovotech.ca); [2] Crop Diversification Centre South, Alberta Agriculture and Rural Development, 301 Horticultural Station Rd. E., Brooks, Alberta, Canada T1R 1E6; and [3]Innovotech, Inc. Suite 101, 2011 – 94 Street, Edmonton, Alberta, Canada T6N 1H1

A fundamental challenge in the development of crop protection fungicides is the gap between *in vitro* laboratory efficacy results compared with performance in field tests. For example, a compound may prove to be highly effective at low doses in laboratory tests, but fail to provide significant disease control when applied as an in-crop fungicide. Why do compounds demonstrate *in vitro* antimicrobial activity, but then fail to provide disease control when taken to clinical or field tests? In some cases, this phenomenon can be linked to differences in pathogen biology between microbial cells in laboratory cultures and those found in natural settings. In natural (and agricultural) environments, microorganisms grow as biofilms – layered communities of cells

encased in a slimy extracellular matrix. However, most laboratory testing is done using cultures of solitary, free-floating cells in nutrient rich broths or semi-solid agar gels. It is well documented that cells within biofilms commonly display heightened tolerance to antimicrobial treatments compared to those of planktonic cells, and are commonly linked to failures in clinical settings. Traditionally, *in vitro* culturing of biofilms has been cumbersome and tedious, especially for replicated experiments. Recently, the development of multi-well plate technologies for high throughput biofilm culturing and testing have provided methods for rapid screening of anti-biofilm compounds, and for optimization of treatment performance. The purpose of this study was to determine whether fungicide testing versus microbial biofilms would provide a more accurate estimation of treatment rates necessary for field efficacy versus foliar fungal pathogens. The results are presented within the context of accelerating fungicide product discovery and development.

Wednesday, July 20, 2011 **Oral Presentations**
Canadian Phytopathological Society **Time:** 1400-1530h
Session 6: ***Molecular and Physiological Plant Pathology*** **Room:** 255 Sobey Building

Chair: Solke De Boer
Canadian Food Inspection Agency, Charlottetown

1400 **Kalpana Sharma**
Effect of temperature on cortical infection and disease severity by *Plasmodiophora brassicae* on Shanghai pak choy

1415 **Abhinandan Deora**
Effect of host resistance on infection by *Plasmodiophora brassicae* in canola

1430 **Rick Peters**
Susceptibility of potato and other hosts to late blight caused by Canadian genotypes of *Phytophthora infestans*

1445 **Barry Saville**
A new class of gene expression control molecules in *Ustilago maydis*

1500 **Tom Hsiang**
Sequencing and assembly of a fungal genome

1400 **Effect of temperature on cortical infection and disease severity by *Plasmodiophora brassicae* on Shanghai pak choy.** K. Sharma[1*], B. D. Gossen[2], M. R. McDonald[3] [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1 Canada; [2]Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK S7N 0X2 Canada; and [3]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1 Canada (email: mrmcdona@uoguelph.ca)

Clubroot, caused by *Plasmodiophora brassicae* Woron, is an important worldwide root disease of Brassica crops. The life cycle of *P. brassicae* consists of two phases, a primary phase (infection and development in root hairs) and a secondary phase (cortical infection and gall development). Studies were conducted to assess the effect of temperature on development of *P. brassicae* in roots of Shanghai pak choy (*Brassica rapa* subsp. *Chinensis*) and on clubroot severity. Three-day-old seedlings were transplanted into root-trainers containing soil-less growing media, kept at 20º C for 1 wk, and inoculated by pipetting 800 µL of resting spore suspension (10^8 spores of *P. brassicae* /mL) onto the base of each seedling. Control plants were inoculated with sterile water. After inoculation, the seedlings were transferred to growth cabinets at 10º, 15º, 20º, 25º and 30º C (14-h photoperiod, 65% RH). The roots of four plants per treatment were collected, washed, and assessed for cortical infection, stage of development of secondary infection, and clubroot severity at 4-day intervals from 10 to 42 days after inoculation (DAI). Cortical infection, visual symptoms, and clubroot severity were highest and initiated earliest at 25° C, intermediate at 20° C and 30° C, and lowest and latest at 15° C. No cortical infection or symptoms were observed at 42 DAI in plants grown at 10° C. Regression analysis indicated that the effect of temperature on cortical infection was quadratic, with an optimum temperature near 25° C ($R^2 = 0.88$; $P < 0.001$). Cortical infection was positively correlated with disease severity index ($r = 0.95$; $P < 0.01$). These results demonstrate that temperature affects secondary infection by *P. brassicae*, and that under ideal moisture and pH conditions, secondary infection is highly correlated with subsequent symptom development and severity.

1415 **Effect of host resistance on infection by *Plasmodiophora brassicae* in canola**. A. Deora[1,2*], B.D. Gossen[1], and M.R. McDonald[2]. [1]Agriculture and Agri Food Canada, 107 Science Place, Saskatoon, Saskatchewan, Canada S7N 0X2 (bruce.gossen@agr.gc.ca); and [2]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1

Several commercial cultivars of canola (*Brassica napus* L.) with resistance to clubroot caused by *Plasmodiophora brassicae* Woronin have been developed recently, but how and when this resistance is expressed is not known. Assessments of root hair infection (RHI) (% roots infected) and cortical infection (CI) (% cortical area infected) were made over time in four commercial cultivars that differed in reaction to two pathotypes (P3 and P6) of *P. brassicae*: '45H29' (resistant), '46A76' (susceptible), 'Invigor 5030' (intermediate) and '45H21' (susceptible to P3, resistant to P6). The trial was arranged in a factorial RCBD with four replications and three plants per experimental unit. The plants were grown individually in sand at 25/20 °C (day/night) and inoculated with 10^6 resting spores/ml 7 days after seeding. Samples were taken at 4, 8 and 12 days after inoculation (DAI) for RHI assessment and 16, 22 and 28 DAI for CI assessment. RHI occurred quickly in susceptible cultivar x pathotype combinations and slowly in resistant combinations. However, the maximum RHI was similar across reaction types. For example, RHI at 12 DAI in '45H29' (resistant) and '46A76' (susceptible) was about 70% for both pathotypes. At 28 DAI, there was no CI in '45H29' for both pathotypes, CI was high in '46A76' for P3 (45%)

and P6 (35%), and moderate for P3 (23%) and P6 (16%) in 'Invigor 5030'. There was no CI in '45H21'inoculated with P6, but CI was high (35%) in this cultivar inoculated with P3. The extent of cortical infection by P3 was consistently higher than by P6. Results of this trial indicated that resistance affected both RHI and CI, but that the differences in CI were larger and more distinct than for RHI. The observation that the pattern of response in CI was substantially different in 'Invigor 5030' (intermediate) than the other cultivars indicates that there may be differences in the mechanism(s) of resistance among various sources of genetic resistance.

1430 **Susceptibility of potato and other hosts to late blight caused by Canadian genotypes of *Phytophthora infestans*.** R.D. Peters*, H.W. Platt, B.W. Beaton, C. Banks, and I.K. Macdonald. Agriculture and Agri-Food Canada, Charlottetown, PE C1A 4N6, Canada; (B.W.B., C.B.) PEI Dept. of Agriculture, Charlottetown, PE C1A 4N6, Canada

Late blight, caused by *Phytophthora infestans* (Mont.) de Bary, has caused significant yield losses in both potato and tomato crops in Canada in recent years. In some cases, the initiation of disease epidemics has been traced to diseased tomato plantlets for sale at local retail outlets. To better understand the host range of Canadian genotypes of the pathogen, a greenhouse trial was conducted in 2010. Various cultivated varieties of potato, tomato, pepper and petunia were grown in the greenhouse and then inoculated with either the US-8 (A2 mating type; resistant to metalaxyl-m; common in eastern Canada) or US-11 (A1 mating type; resistant to metalaxyl-m; common in western Canada) genotypes of *P. infestans*. Plants were spray-inoculated with *P. infestans* sporangia and then maintained in a humid environment (mist chamber) to facilitate infection and subsequent disease development. Plants were rated for percent foliar necrosis three times per week and the experiment was ended prior to secondary spore development and dispersal within the foliage. Disease severity varied among potato cultivars with 'Dorita' showing the least susceptibility to symptom development. Similarly, tomato varieties differed in disease response, with 'Mountain Magic' displaying the most resistance to disease. No disease symptoms were found on the pepper varieties inoculated in the trial, however, necrotic lesions were found in petunia. In general, plants responded similarly to both genotypes of the pathogen. These results confirm the susceptibility of a range of horticultural crops to late blight and underscore the need for vigilant monitoring of plantlets distributed widely to the general public. As well, options exist for organic growers and home gardeners to choose varieties that resist disease development, thereby reducing potential sources of initial inoculum.

1445 **A new class of gene expression control molecules in *Ustilago maydis*.** M.E. Donaldson[1], S.C. Lambie[2], and B.J. Saville[1,3*]. [1]Environmental & Life Sciences Graduate Program, Trent University, Peterborough, ON, Canada K9J 7B8; [2]Department of Biology Trent University, Peterborough, ON, Canada K9J 7B8; and [3]Forensic Science Program, Trent University, Peterborough, ON, Canada K9J 7B8 (e-mail: barrysaville@trentu.ca)

Ustilago maydis D.C. corda is the model basidiomycete for investigating biotrophic plant pathogens. cDNA libraries from different cell-types and nutritional conditions were created to facilitate annotation of the *U. maydis* genome. Natural antisense transcripts (NATs) complementary to *U. maydis* open reading frames were identified and classified during analysis of the resulting expressed sequence tag (EST) libraries. NATs have been discovered in a broad range of plants, animals, and fungi; although studies have only identified a handful of functions for specific antisense transcripts. The RNA interference (RNAi) pathway is a broadly conserved mechanism whereby short antisense transcripts mediate the degradation of complementary sense mRNAs. Phylogenetic and functional analyses have revealed that select yeast species and *U. maydis* do not contain functional RNAi machinery. The lack of an RNAi pathway allows the study of NAT function without the complication of interacting with the RNAi machinery. Using

strand-specific RT-PCR, it was determined that some NATs are expressed in a cell-type specific manner in *U. maydis*, notably in the dormant teliospore. Teliospore specific NATs were conserved between *U. maydis* and *U .hordei* (which unlike *U. maydis*, contains functional RNAi-machinery), supporting a functional role for antisense transcripts in these two species. *U. maydis* teliospore specific NATs were characterized using RNA ligase mediated rapid amplification of cDNA ends (RLM-RACE). Haploid cells normally lacking these specific NATs were transformed to artificially express select antisense transcripts. These transformants were used to determine how sense-antisense pairs interact. Quantitative-PCR revealed increased levels of sense transcripts in the antisense over-expression mutants, suggesting that specific *U. maydis* antisense transcripts have the ability to stabilize complementary sense mRNA. Furthermore, double stranded (ds) RNA was detected by S1 nuclease protection assays, suggesting that dsRNA formation facilitates this stabilization. These experiments indicate that the presence of antisense transcripts in the dormant teliospore may be linked to stabilizing mRNA during teliospore dormancy.

1500 **Sequencing and assembly of a fungal genome**. T. Hsiang, School of Environmental Sciences, University of Guelph, Guelph, Ontario, Canada N1G 2W1 (email: thsiang@uoguelph.ca)

With the Next Generation Sequencing technologies, it is now feasible, within a small research program, to attempt de novo sequencing and assembly of small eukaryotic genomes (<100 Mb in size). In late 2009, we decided to attempt sequencing of the genome of the fungus *Colletotrichum cereale* Manns. Since this species had been split from *C. graminicola* (Ces.) Wils. in 2006, and a draft genome assembly of *C. graminicola* became available in 2008, we thought that the two species would be similar enough for *C. graminicola* to act as the reference genome for sequencing of *C. cereale*. We prepared genomic DNA of an isolate of *C. cereale* using standard methods, and sent in 10 µg as requested. The sequencing center then took two weeks for DNA library construction, and another two weeks to run out on a Illumina GAIIx sequencer. They generated ~25-fold coverage in 35 bp paired-end reads of this 60 Mb genome (1.5 Gb worth of sequence data plus 4 Tb worth of image files and other data associated with sequencing). They attempted assembly of the 35 bp reads, based first on the *C. graminicola* genome and then other fungal genomes, and then provided the results. We then also attempted assembly of this data with a variety of programs and a multitude of program settings. With genomes of species that have already been sequenced, data from new sequencing technologies may be sufficient for assembly of an isolate of the same species; but for species lacking a reference genome, the technology in terms of assembly software and sequencing equipment may have limitations.

Monday, July 18, 2011
Canadian Weed Science Society
Session 1: ***New Weeds in Canada***

Oral Presentations
Time: 1030-1200h
Room: 296 Loyola Conference Hall

Chair: Scott White
University of Guelph

1030 **Marian Munro**
New weeds in Maritime Canada

1100 **Mirwais Qaderi**
Weed responses to climate change

1130 **David Clements**
Predicting weed invasion of Canada under climate change: measuring evolutionary potential

1030 **New weeds in Maritime Canada.** M. Munro, Nova Scotia Museum of Natural History, 1747 Summer Street, Halifax, NS, Canada B3H 3A6

In the last 30 years, eastern Canada has experienced the rapid spread of many new weedy or invasive plant species. From 1600-1800s plants arrived on Maritime shores with the colonists and settlers from Europe. Many were intentionally brought over for food, fibre and landscaping (carrots, wheat and roses). Others arrived inadvertently in ballast. Ships whose owners hoped to backhaul timber and other natural resources, used ballast in empty holds. This material was often gathered from the shore near the departure points. European species such as Ragweed and Coltsfoot rapidly spread in such fashion. With the advent of the National Railway across Canada, plant species spread eastward from the west as the east made more use of western produce. The much-touted and equally reviled lupine originally arrived from the montane west by rail. As personal automobile usage exploded from 1960 onward, so too did recreational travel and the need for travel corridors. These linear paths have allowed plants to migrate as efficiently as people. Plant species such as Sweet Whitlow grass and Garlic Mustard have reach NB and NS in such fashion. The search for new and unique plant materials for gardens has kept up with travel. Travellers buy or collect seeds from distant places and once established many may become problematic in native plant communities. Giant Hogweed and Purple Loosestrife have been present for decades but only recently have spread from their original site of introduction. This presentation will introduce some of the past weedy species, some of the present problem plants and those that concerned researchers expect in the future.

1100 **Weed responses to climate change.** M. M. Qaderi, Department of Biology, Mount Saint Vincent University, 166 Bedford Highway, Halifax, Nova Scotia, Canada B3M 2J6

In natural habitats, multiple co-occurring environmental factors affect plants. Few studies have considered the combined effects of multiple climate change components on plants, especially weeds. It is, therefore, important to examine weed responses to multiple components of climate change. Overall, higher temperature, water stress and enhanced ultraviolet-B radiation, as components of climate change, negatively affect plants, whereas elevated atmospheric carbon dioxide concentration ameliorates some of the adverse effects of these factors. Although, as a single factor, each of the higher temperature, water stress or enhanced UVB adversely affects some weeds, the interactive effects of these factors on plants are different from those of a single factor. For instance, the combined effects of higher temperature and enhanced UVB radiation or the interactive effects of enhanced UVB and water stress on weeds, such as stinkweed (*Thlaspi arvense* L.), are less than the effects of each of these individual factors. Also, some weeds, such as night-flowering catchfly (*Silene noctiflora* L.), can tolerate two-fold increase of UVB radiation. Velvetleaf (*Abutilon theophrastus* Medic.), for example, can grow well under conditions of higher temperatures (6^{o}C higher) than under the normal temperatures found in their natural growing habitats. In conclusion, further field and controlled-environment experiments, with multiple environmental factors, should be conducted on a wide range of important weeds from agricultural and natural ecosystems in order to understand better weed responses to the factors contributing to global climate change.

1130 **Predicting weed invasion of Canada under climate change: measuring evolutionary potential,** D. R. Clements[1*], and A. DiTommaso[2]. [1]Biology and Environmental Studies, Trinity Western University, Langley, B.C., V2Y 1Y1 and [2] Department of Crop and Soil Sciences, Cornell University, Ithaca, N.Y. 14853

Many weed species have already advanced northward from the U.S. into Canada and their number threatens to increase with climate change. For many weed species, this range expansion can be attributed to evolutionary adaptation to cooler climates among the northern populations. Invasive species predictive schemes often fail to account for this evolutionary potential, and thus range expansion by some weeds could be much greater than expected. In this paper we will attempt to synthesize available information on developing metrics to evaluate evolutionary potential for different weed species, so that the extent of weed invasion can be better predicted and understood. Ten character traits of interest for evaluating evolutionary potential are: (1) high growth rate, (2) wide climatic or environmental tolerance, (3) short generation time, (4) prolific or consistent reproduction, (5) small seed size, (6) good dispersal, (7) uniparental reproduction capacity, (8) no specialized germination requirements, (9) high competitive ability and (10) effective defenses versus natural enemies. If any one of these traits is selected for in an invasive species, it would give the species potential to invade further than anticipated by a model assuming a static genotype. Four weed species of interest for their potential northward dispersal within North America will be evaluated as to whether these ten traits could be quantified for modeling purposes: Himalayan balsam (*Impatiens glandilifera*), velvetleaf (*Abutilon theophrasti*), Japanese knotweed (*Polygonum cuspidatum*), and johnsongrass (*Sorghum halapense*). In some cases, the required information is already available in the literature, whereas further information is required for some parameters, and may be difficult to accurately assess in some instances. The population genetics of invasive plants are difficult to model, as is climate change itself, but taking into account weed evolution in some way should enable a measure of improved predictive power.

Monday, July 18, 2011
Canadian Weed Science Society
Session 2: ***General Session***

Oral Presentations
Time: 13:00-15:00h
Room: 296 - Loyola Conference Hall

Chair: Marie- Josée Simard
Agriculture and Agri-Food Canada

1300 **R. E. Blackshaw**
Potential oilseed crops for biodiesel feedstock on the Canadian prairies

1315 **Amanda Green**
Determining the mechanism of resistance to glyphosate in giant ragweed *(Ambrosia trifida L.)* in Ontario

1330 **Melody De Jong**
Environmental conditions, growth stages and fungicides affect herbicide tolerance of winter wheat

1345 **Darren Robinson**
Cumulative stress occurs between hail damage and in-crop herbicide applications in tomato and sweet corn

1400 **R. E. Blackshaw**
A historical perspective on overcoming weed concerns in conservation tillage systems on the Canadian prairies

1430 **Brian Wallace**
The decline of diffuse knapweed in British Columbia

1445 **Darren Robinson**
Rolling fall rye for weed suppression in cucumber and squash

1300 **Potential oilseed crops for biodiesel feedstock on the Canadian prairies.** R. E. Blackshaw*, Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada T1J 4B1

A multi-site field study was conducted in 2008 and 2009 to determine the oil yield potential of various oilseed crops relative to that of napus canola (*Brassica napus* L.) for biodiesel feedstock on the Canadian prairies. Oilseed crops evaluated were rapa canola (*Brassica rapa* L.), juncea canola (*Brassica juncea* L.), Ethiopian mustard (*Brassica carinata* L.), oriental mustard (*Brassica juncea* L.), yellow mustard (*Sinapis alba* L.), camelina (*Camelina sativa* L.), flax (*Linum usitatissimum* L.), and soybean [*Glycine max* (L.) Max.]. Crop emergence and growth was generally good for all crops but soybean did not fully mature at some locations. The number of site-years (out of a total of 9) that crops attained similar or greater yields compared to napus canola were camelina (6), oriental mustard (5), juncea canola (3), flax (3), soybean (3), rapa canola (2), yellow mustard (2), and Ethiopian mustard (1). The ranking of seed oil concentration was napus canola = rapa canola = juncea canola = flax > camelina = oriental mustard > Ethiopian mustard > yellow mustard > soybean. Considering yield and oil concentration, the alternative oilseed crops exhibiting the most potential for biodiesel feedstock were camelina, flax, rapa canola, and oriental mustard. Oils of all crops were easily converted to biodiesel and biodiesel quality analyses indicated that all crops would be suitable for biodiesel feedstock with the addition of antioxidants that are routinely used in biodiesel fuels. Information will be provided to growers and the agricultural industry to facilitate successful expansion of the biofuel industry in Canada.

1315 **Determining the mechanism of resistance to glyphosate in giant ragweed (*Ambrosia trifida* L.) in Ontario.** A.C. Green [1*], F.J. Tardif[1], P.H. Sikkema[2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1 and [2]Department of Plant Agriculture, University of Guelph, Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0

Glyphosate resistance populations have been found in Ontario since 2008. The mechanism of glyphosate resistance in giant ragweed has yet to be determined. Resistant plants exhibit two different phenotypes after treatment of glyphosate. One phenotype exhibits an unusual symptomology; their mature leaves develop very rapid necrosis while the growing points escape injury. The other phenotype exhibits similar sympotomology to a susceptible plant but after 10 days there is recovery followed by regrowth. The objectives of the experiments are to determine the level of resistance, and to investigat possible mechanisms of resistance. A dose response experiment comparing two resistant populations to two susceptible populations revealed the two resistant populations with different phenotypes to have similar levels of reistance. Target-site sensitivity was determined through a shikimate assay. Shikimate is the dephosphorylated substrate of the enzyme EPSPS (5-enolpyruvylshikimate-3-phosphate synthase) which is involved in the synthesis of aromatic amino acids and also the target site of glyphosate. Leaf discs collected from young and mature tissue were placed in 3 assay solutions of glyphosate at 0, 250 and 500μM in microtiter plates, incubated under light for 23 hours, frozen, shikimate extracted and quantified using a mass spectrophotometer. There was a significant difference in shikimate accumulation at 250 and 500 μM between the susceptible and resistant populations but not between the two resistant populations. In the mature tissue there was a significant difference between the one resistant population exhibiting the rapid necrosis phenotype and the other resistant and susceptible populations at 250 and 500 μM.

1330 **Environmental conditions, growth stages and fungicides affect herbicide tolerance of winter wheat.** M. De Jong[1]*, F.J. Tardif[1], P.H. Sikkema[2], and M. Cowbrough[3]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1; [2]Department of Plant Agriculture, Ridgetown College, University of Guelph, Ridgetown, Ontario, Canada N0P 2C0; [3]Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, Ontario, Canada N1G 4Y2

Profitable winter wheat (*Triticum aestivum* L.) production in Ontario is largely dependent on grain yield and as such, yield losses due to weeds and diseases will have a greater impact when crop prices are high. It is common for producers to tank-mix herbicides and fungicides to reduce application costs and save time. These applications are often made early in the season when temperatures approach freezing. In the spring of 2008, a number of producers experienced significant crop injury when they applied herbicide-fungicide tank-mixes to winter wheat. Field studies were conducted at four Ontario locations to determine the extent of crop injury and associated yield loss, and to explore whether it was due to the environmental conditions at application, the crop stage at application, or the specific combination of herbicide and fungicide. Estaprop (dichlorprop/2,4-D), Buctril M (MCPA/bromoxynil), and Infinity (pyrasulfatole/bromoxynil) herbicides were applied singly and in combination with four fungicides and applications were made following a frost (night-time forecast of 0ºC) and at a late growth stage (Zadoks 37-39). Visual injury ratings indicated herbicide-fungicide tank-mixtures of Estaprop+Folicur (tebuconazole), Buctril M+Folicur, and Buctril M+Quilt (azoxystrobin/propiconizole) consistently caused injury at frost (2-15%) and 'late' (8-30%) application timings. Despite the level of injury, wheat plants recovered and, in the majority of cases, yields were unaffected. These results suggest that tank-mixtures containing the fungicide Folicur consistently injure winter wheat plants. In addition, herbicide-fungicide tank-mixes are more likely to injure winter wheat when applied at a late crop stage. These results contribute to profitable winter wheat production by identifying herbicide and herbicide-fungicide combinations that minimize crop injury and yield loss.

1345 **Cumulative stress occurs between hail damage and in-crop herbicide applications in tomato and sweet corn.** D. E. Robinson[1]* and R. E. Nurse[2], [1]University of Guelph, Ridgetown Campus, Department of Plant Agriculture, Ridgetown, Ontario, Canada N0P 2C0 and [2]Agriculture and Agri-Food Canada, Harrow, Ontario, Canada N0R 1G0

Trials were established in 2009 and 2010 at two locations each year to determine tolerance of transplanted tomato or sweet corn to combinations of simulated hail damage and three registered postemergence herbicides. For comparison, additional treatments of hail alone, as well as each herbicide on their own, were also applied. In tomato, these herbicides were thifensulfuron – 6 g ai ha^{-1}, rimsulfuron – 15 g ai ha^{-1}, and metribuzin – 200 g ai ha^{-1}. In sweet corn, herbicides were mesotrione – 100 g ai ha^{-1}, nicosulfuron – 25 g ai ha^{-1} and bromoxynil – 280 g ai ha^{-1}. In tomato, the combination of hail damage with either thifensulfuron or rimsulfuron did not increase crop injury, or reduce plant dry weight or yield more than hail damage alone. However, cumulative stress of the combination of hail damage plus metribuzin caused more crop injury than hail alone. Dry weight was 34, 64 and 73 g $plant^{-1}$ in the hail plus metribuzin, hail alone, and untreated treatments, respectively. Yield was 79, 108, and 111 T ha^{-1} in the hail plus metribuzin, hail alone, and untreated treatments, respectively. The combination of hail damage plus metribuzin caused more injury, and reduced dry weight and yields more than hail alone in tomato. In sweet corn, crop injury, dry weight reductions and yield reductions caused by simulated hail treatments were not increased by the addition of a herbicide application. This study provided evidence for a cumulative effect of simulated hail and herbicide injury, though this effect varied depending on the herbicide applied and crop species.

1400 **A historical perspective on overcoming weed concerns in conservation tillage systems on the Canadian prairies.** R. E. Blackshaw*, Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada T1J 4B1

One of the primary reasons for tillage throughout history has been weed control. Tillage usually provides good control of annual weeds but tillage can also stimulate a subsequent flush of weeds. Control of most perennial weeds with tillage is only partially effective as multiple passes are required to reduce energy reserves in the rhizome or root system. Despite the somewhat mixed success of using tillage to manage weeds, there was widespread concern about increasing weed populations and 'out-of-control' weeds if tillage was reduced or eliminated. A second major concern revolved around the perceived need to increase herbicide use in conservation tillage systems. Farmers were worried about increased herbicide costs and environmentalists were concerned about greater potential environmental impacts. Many researchers worked over several decades to address these issues. One of the first tasks was developing and implementing conservation tillage weed control practices on 14 million ha of fallow; one of the first success stories in terms of reducing wind erosion in this region. Subsequently, long-term multi-site research studies were conducted to determine which weed species became more prevalent with conservation tillage and then to identify herbicides and crop management methods specifically tailored for their control. This work resulted in the first farmer adoption of integrated weed management programs in western Canada. Farmers adopted these programs because only integrated methods provided adequate control of weeds such as foxtail barley (*Hordeum jubatum* L.) and Canada thistle [*Cirsium arvense* (L.) Scop.]. Ongoing research has facilitated farmers utilizing higher crop seeding rates, competitive cultivars, subsurface banded fertilizer, and more diverse crop rotations to effectively manage weeds in conservation tillage productions systems without increasing herbicide use beyond levels previously used in conventional systems. New and effective weed management systems have contributed to conservation tillage being practiced on 75% of the cropland on the Canadian prairies.

1430 **The decline of diffuse knapweed in British Columbia.** B. Wallace*[1], R. Newman[2], S. Turner[2] and S. Cesselli[2], [1]Organic Agriculture Centre of Canada, Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3 and [2]British Columbia Ministry of Forests, Lands and Natural Resource Operations, Victoria, BC, Canada V8W 9E2

Diffuse knapweed (*Centaurea diffusa* Lam.) is an invasive weed that was introduced to North America in the early 1900s, and has since spread to over a million hectares of rangeland in western Canada and the United States. Diffuse knapweed easily establishes on disturbed sites and forms large stands that displace native vegetation. In British Columbia (BC), ten biological control agents have been introduced to control this invasive weed since the early 1970s with varying levels of establishment and success. Five previously monitored diffuse knapweed-invaded sites were sampled for plant species cover and biological control insect abundance. Diffuse knapweed populations and soil seed reserves were shown to decline by an average of 74% and 78% respectively at five sites in BC from the 1990's to 2009. Three factors were discussed as possible causes for the decline of diffuse knapweed at the five sites. Climate warming/drying was shown to have occurred over the same period as the reported decline in diffuse knapweed at three sites and is a possible contributing factor. Increased plant competition due to improved range management may also be a contributing factor. The ubiquitous nature of biological control agents at five sites, combined with their known abilities to damage knapweed, also places biological control as a possible contributing factor for the decline of diffuse knapweed. It is also possible that two or more of the three factors are acting in concert to reduce

diffuse knapweed. The demonstrated decrease in diffuse knapweed at the five sampled sites provides baseline data that may contribute to a better understanding of how biological control agents, climate warming/drying, and improved grazing management may be interacting on weed-invaded sites in BC.

1445 **Rolling fall rye for weed suppression in cucumber and squash.** D. E. Robinson[1*] and S. Vink[1]. [1]University of Guelph, Ridgetown Campus, Department of Plant Agriculture, Ridgetown, Ontario, Canada N0P 2C0

The objective of this research was to determine the effect of time of cover crop rolling on weed suppression, soil moisture and fertility in cucumber and squash. In the fall prior to growing each vegetable crop, fall rye was planted at 100 or 150 kg ha^{-1}. The following spring, the fall rye was rolled prior to flowering, and at 25%, 50%, 75% and 100% flowering, at each of the two fall rye seeding rates and planted with either cucumber or squash. Additional treatments included mowing or disking-under the fall rye prior to planting. Available moisture, nitrogen, weed biomass at 56 days after emergence and marketable yield were determined. Soil moisture did not differ among any of the cover crop rolling treatments. Where fall rye was rolled at 50%, 75% or 100% flowering, soil nitrate levels increased, whereas, when fall rye was disked, soil nitrate levels decreased. Weed biomass was greatest in those treatments where the fall rye was disked, mowed, rolled prior to, or at 25% bloom, and squash and cucumber yield were less in these treatments, than when fall rye was rolled at 50% bloom or later. Squash yields ranged from 17 to 20 t ha^{-1}, while cucumber yields ranged from 7 to 10 t ha^{-1} in those treatments where fall rye was rolled at 50% bloom or later. The integration of cover crop rolling with other techniques such as organic herbicides and/or compost or mulches may provide the basis for a reduced tillage weed management system in organic vegetable production.

Wednesday, July 20, 2011
Canadian Weed Society
Session 4: ***New Crops as New Weeds in Canada Mitigating Threats Posed by New Weeds In Canada***

Oral Presentations
Time: 0830-1000h
Room: 296 Loyola Conference Hall

Chairs: Robert Blackshaw (0830-0915h), Agriculture and Agri-Food Canada
David Clements (0915-1000h), Trinity Western University

8:30 **Linda Hall**
New crops and crops with new traits: are they weedy or invasive?

8:50 **Rene Van Acker**
The role and impact of volunteer and feral crop plants in the era of novel traits

9:15 **Claire Wilson O'Driscoll**
Preventing new introductions: A federal response to emerging weed and invasive plant threats in Canada

9:35 **Marie-Josée Simard**
History of the detection of a new weed in Canada: The wooly cupgrass (*Eriochloa villosa)* case

0830 **New crops with new traits: are they weedy or invasive?** L. M. Hall[1]*, Hugh J. Beckie[2], Marie-Josée Simard[3], Robert E. Nurse[4] and David Clements[5]. [1]Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, T6G 2P5, [2]Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan S7N 0X2, [3]Agriculture and Agri-Food Canada, Quebec, Quebec G1V 2J3, [4]Agriculture and Agri-Food Canada, Harrow, Ontario, N0R 1G0 and [5]Biology Department, Trinity Western University, BC V2Y 1Y1

New oilseed crops are being field tested in Canada including: camelina (*Camelina sativa L*), carinata (*Brassica carinata* L.), hybrids of cuphea (*Cuphea lanceolata* Ait.*)*, while field pennycress (*Thlaspi arvense* L.) and prairie carnation (*Saponaria vaccaria* L.) have been recently sidelined. Traditional cereal and oilseed crops modified to express abiotic stress resistance and nitrogen efficiency are being tested in field trials, many with multi-trait stacks. While these plants may have many benefits to Canada, it is not established if they are also invasive species. Presently, the Canadian Food Inspection Agency conducts an initial screen of potential introductions using the plant's invasive history, climate matching and the presence of weedy traits. For crops with new traits, for which data is limited, or where species have both weedy and domestic traits, the introduction of new crops can be stalled. To address the gap between literature-based assessments and broad scale release, we are recommending field-based testing in key agro-ecological regions across Canada. Demographic analysis can provide comparative data on the ability of crop populations to survive and perpetuate. Crops and traits can be compared and recommendations for mitigation based on key interventions points in the life cycle validated. Other factors to consider in field trials of new crops are density effects and the influence of site disturbance. Intermittently disturbed ruderal areas often serve as bridges or corridors for expansion of invasive species. Field-testing could reduce the risk of release of new crops. Once invasive species are established, they are difficult and costly to eradicate.

0850 **The role and impact of agricultural metapopulations in the era of novel Traits**. R. C. Van Acker*.Ontario Agricultural College, University of Guelph, Guelph, Ontario, Canada, N1G 2W1

Genetic Engineering (GE) technologies allow for truly novel traits in plants. In some cases these traits pose risks to human health, the environment or markets. Risks associated with the production of plants with novel traits are often linked to escape and movement of the novel trait either into wild type populations or into areas of the agricultural supply chain where the trait is unintended and perhaps unexpected. In cases where it causes a problem, novel trait movement is unique in that containment is very challenging and given that the trait agents are self-replicating, self-disseminating and can persist in the environment, trait escape can be permanent. The intraspecific movement of novel traits in agriculture involves both the metapopulation and the latent population for a given species. For crop species, a metapopulation includes cropped, volunteer and feral subpopulations while a latent population includes any viable seed for that species anywhere within the agricultural supply chain. Latent populations can be considered a subset of metapopulations. In the case of metapopulations, an assessment or a model of novel trait movement relies on a good understanding of volunteer and feral populations, unfortunately our understanding of these populations is often superficial as was the case with both canola (*Brassica napus* L.), where GE varieties have been commercially grown in Canada for more than a decade, and alfalfa (*Medicago sativa* L.), where a GE synthetic has been deregulated in Canada but not commercially grown. Research in the past 5 years has shown that both alfalfa and canola form effective feral populations that can or are capable of acting as sources and sinks for novel traits.

In the case of latent populations, an assessment or model of novel trait movement relies on a deep understanding of supply chain operations, processes, protocols and equipment. The complexity of supply chains, and managing trait segregation within complex supply chains is often underestimated and this has been shown to lead to problems. Studying both metapopulations and latent populations can provide insights into and useful data for modeling novel trait containment and reducing risks associated with novel trait introduction.

0915 **Preventing new introductions: A federal response to emerging weed and invasive plant threats in Canada.** Claire Wilson O'Driscoll*[1], Ken Allison[2], Karen Castro[2], Sarah Davis[2], Amy Kehoe[2] and Andrea Sissons[2]. [1]Canadian Food Inspection Agency, Darmouth, Nova Scotia, Canada B3B 1Y9, [2]Plant and Biotechnology Risk Assessment Unit, Plant Health Science Division, Canadian Food Inspection Agency, Ottawa, Ontario, K1A 0Y9, Canada

The Canadian Food Inspection Agency (CFIA) is the federal agency responsible for plant protection in Canada. The primary focus of its plant protection program is preventing the introduction of new plant pests, including weeds and invasive plants. Since the release of "An Invasive Alien Species Strategy for Canada" in September 2004, the CFIA has been working with a variety of partners to develop a coordinated invasive plant program for Canada. This paper will introduce the new federal program, including a draft Invasive Plants Policy and a "Least Wanted Invasive Plants" pilot project that proposes the regulation of 25 new plant species as quarantine pests for Canada. The remainder of the paper will focus on some of the risk assessment tools used for predicting and preventing new weed introductions, including results of a Canadian test of the Australia weed risk assessment system which indicate that it does not perform as well in Canada as it has in other countries around the world. Other approaches to weed risk assessment are currently being explored, and include elements of pest distribution modeling under current and future climates.

0935 **History of the detection of a new weed in Canada: The Wooly Cupgrass (*Eriochloa villosa*) case.** M.-J. Simard[1]*, S.J. Darbyshire[2], and R.E. Nurse[3]. [1]Agriculture and Agri-Food Canada, Soils and Crops Research and Development Centre, Québec, Québec, Canada G1V 2J3, [2]Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, Ottawa, Ontario, Canada K1A 0C6 and [3] Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, Ontario, Canada N0R 1G0

Eriochloa villosa (Thunb.) Kunth is an annual grass of east Asian origin that is now present in much of the U.S. Corn Belt. The species was discovered in Canada for the first time in 2001 in Saint-Hyacinthe, QC. In 2002, an eradication program was initiated at the Saint-Hyacinthe site by the provincial ministry of agriculture (MAPAQ) and the Canadian Food Inspection Agency (CFIA). In 2005, the species was added to the Canadian Weed Seeds Order. Since then, at least five new seemingly independent locations have been discovered. Once all points of introduction are located, local spread has to be prevented. Farmers often rent/purchase land and equipment/services from others, so that weed seeds can spread locally through a shifting network of pathways. Growers already try to manage their weeds so that a profitable crop yield is maintained. Managing for eradication is more challenging. Ten years after its first detection, what lessons have we learned from the *Eriochloa villosa* case?

Thursday, July 21, 2011 **Oral Presentations**
Canadian Institute of Food Science and Technology **Time:** 0830-1000h
Session 7: *Frui* ts: *Bioactives and Health Benefits* **Room:** 415 Sobey Building

Chair: Vasantha Rupasinghe
Nova Scotia Agricultural College

0830 **Wilhelmina Kalt**
Blueberries and human health

0855 **Nileeka Balasuriya**
Antihypertensive properties of selected fruit bioactives

0915 **Surangi H. Thilakarathna**
Inhibition of LDL oxidation *in vitro* and regulation of cholesterol metabolism in hamsters by apple skin boactives

0935 **Amy B. Howell**
Latest research on health benefits of cranberry

0830 **Blueberries and human health.** Wilhelmina Kalt, Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, NS

Research on the positive effects of fruit and vegetable phytochemicals on the health of living systems has led to a novel integration among the fields of plant science, food science and biomedicine to more fully capitalize on opportunities to improve health through dietary means. Flavonoid phytochemicals, which are ubiquitous in plant foods andparticularly abundant in berry crops, are being studied in relation to health maintenance, disease risk reduction and especially in models of chronic and acute physiological stress. Studies in biomedicine are being complemented by chemistry research in order to associate specific phytochemicals moieties with bioactivity, since this knowledge will give rise to a continuum of opportunities in food and health product development. Compared to other crops blueberries and their flavonoids have been well studied, particularly in the fields of neuroscience and cardiovascular research and more recently diabetes. An overview ofblueberry health research will be presented.

0855 **Antihypertensive properties of selected fruit bioactives.** Nileeka Balasuriya, H.P.Vasantha Rupasinghe. Nova Scotia Agricultural College, Department of Environmental Sciences, Truro, NS

Consumption of fruits is associated with numerous health benefits. Recent research findings prove that the bioactive compounds present in fruits are playing a major role in beneficial health properties. In the current study, fruit flavonoids were investigated on their angiotensin converting enzyme (ACE) inhibitory property where ACE is a key enzyme responsible in increasing blood pressure. A fluorescence based enzyme inhibition assay was used to assess the % enzyme inhibition. Flavonoids were found to be effective as ACE inhibitors. Concentration at 100 ppm of most flavonoids tested exhibited 40 to 60% enzyme inhibition ($p<0.05$). When five concentrations were tested to assess the concentration dependent enzyme inhibition, most flavonoids showed a concentration dependent enzyme inhibition. For all flavonoids tested, IC_{50} values varied within the range of 70-200 μM. Quercetin-3-O-glucoside, epicatechin and naringenin showed the lowest IC_{50} values among the tested flavonoids. The results demonstrated that flavonoids can inhibit ACE in vitro and the inhibitory property varies depending on the flavonoid structure. There is a high potential to use fruit flavonoids as moderate ACE inhibitors in prevention and treatment of mild to moderate hypertension.

0915 **Inhibition of LDL oxidation *in vitro* and regulation of cholesterol metabolism in hamsters by apple skin bioactives.** Surangi H. Thilakarathna[1], H.P. Vasantha Rupasinghe[1], and Yanwen Wang[2], [1]Nova Scotia Agricultural College, Truro, NS, [2]National Research Council - Institute for Nutrisciences and Health, Charlottetown, PE

Elevated blood cholesterol, especially low-density lipoprotein (LDL) level has long been considered as a primary risk factor for cardiovascular disease. Although drugs are available, consumers are nowadays actively seeking natural health products to maintain or control their blood cholesterol levels. The present study was carried out to investigate the effects of two apple skin extracts, on *in vitro* LDL oxidation and *in vivo* cholesterol metabolism. For the animal study, 60 male Golden Syrian hamsters were housed individually in cages. After 2 weeks of adaptation with free access to regular rodent chow and water, they were divided into four groups and fed an

AIN-93G purified diet as a normal control (NC), the normal diet with addition of 0.15% cholesterol as an atherogenic control (AC), the atherogenic diet supplemented with 50 mg/kg body weight/day of quercetin-rich apple extract (QAE), and triterpene-rich apple extract (TAE), respectively for 5 weeks. The results showed that both QAE and TAE effectively inhibited *in vitro* Cu^{2+}- and peroxyl-radical induced LDL oxidation at concentrations of 0.5 to 5 mg L^{-1} and 50 to 200 mg L^{-1}, respectively. The QAE diet lowered ($p<0.05$) serum total cholesterol and non-high density lipoprotein cholesterol levels by 12.6% and 30.7% respectively compared to AC. In contrast, the TAE diet increased ($p<0.05$) serum total cholesterol level relative to AC diet. The two apple skin extracts did not affect serum triglycerides and high-density lipoprotein levels, as well as *in vivo* oxidative stress biomarkers such as serum thiobarbituric acid reactive substances (TBARS) and ferric reducing antioxidant power. In conclusion, QAE is able to lower blood cholesterol, in addition to its anti-oxidant property. Further studies are required to understand the mode of action of TAE on the regulation of cholesterol metabolism.

0935 **Latest research on health benefits of cranberry.** Amy B. Howell**,** Marucci Center for Blueberry Cranberry Research, Chatsworth, NJ

Research on the health benefits of cranberry has expanded beyond prevention of urinary tract infections. Specific compounds in cranberry called proanthocyanidins (PACs) have been widely studied and are thought to be responsible for inducing a bacterial anti-adhesion effect, preventing bacterial colonization and subsequent infection not only the urinary tract, but also in the stomach, gut and oral cavity. The cranberry PAC structures contain A-type, double interflavanoid linkages, as opposed to the all B-type linkages found in PACs from other foods, such as grape and cocoa. The A-type linkages may be important in eliciting anti-adhesion bioactivity. The role of cranberry in preventing bacterial adhesion will be reviewed, as well as the emerging research into the fruit's impact on markers for heart disease and cancer. Issues concerning cranberry dosage, processing, and different forms of cranberry (juice and dried powder) will be discussed in relation to efficacy, PAC molecular structure, quantification and standardization.

Posters

Canadian Society of Agronomy

Student Posters

CSA-S1 **Compost tea for the management of dollar spot (*Sclerotinia homoeocarpa*) on creeping bentgrass (*Agrostis stolonifera*).**S.W. Kelloway[1*], K.J. Sibley[1], J. Norrie[2], B. Prithiviraj[1], [1]Department of Environmental Sciences, Nova Scotia Agricultural College, PO Box 550, Truro, NS, B2N 5E3 [2]Acadian Seaplants Limited, 30 Brown, Dartmouth, NS, Canada B3B 1X8

Turfgrasses are unique in their capability of tolerating foot traffic and physical wear, while still remaining functional and aesthetically pleasing. Fungal disease represents one of the most common limiting factors in managing turf for economical purposes. Dollar spot (*Sclerotinia homoeocarpa* F.T. Bennett) represent one of the most common and persistent fungal diseases of turf grasses here in the Maritime Provinces. We studied the effect of compost tea on turfgrass in terms of disease resistance as well as quality of the turf post infection. We also investigated the effect of compost tea on root growth as influenced by the fungal toxin. The results demonstrated the potential of compost tea to negate the harmful effects of the fungal toxic metabolite produced during a dollar spot infection.

CSA-S2 **Hup statuse of pulse nodules and growth promotion of barley by soil adjacent to pulse nodules.** X. Yang*[1], Y. Gan[2], and Z. Dong[1]. [1]Saint Mary's University, Halifax, Nova Scotia, Canada B3H 3C3; and [2]Semiarid Prairie Agricultural Research Centre of Agriculture and Agri-Food Canada, Swift Current, Saskatchewan, Canada S9H 3X2

H_2 released from N-fixation process in legume nodules has been recognized to play an important role in crop rotation. As members of legume family, pulse plants are important crops in western Canada. To understand the effect of pulse plant on the soil microbial community and their rotation benefit, lentils, peas, chickpeas, dry beans, and faba beans were used to study their effect on growth of barley in greenhouse conditions. Eight different pulse varieties have been tested. All the pulse nodules collected lack uptake hydrogenase (HUP-), and release H_2 into surrounding soil. Soil samples around nodules showed higher H_2 uptake rate than rhizosphere soil of the control plants. Inoculation of barley seeds with soil collected around nodules at the rate of one ml soil per seed increased both barley shoot and root dry mass dramatically after 8 weeks growth with half strength Hoagland solution relative to the controls. The inoculation also promoted barley tiller numbers. The preliminary results of this study suggest that H_2 evolved from pulse nodules has positive effects on the growth of succeeding crops.

CSA-S3 **Plant-microbe interaction and rotation benefit.** Yinan Zou, Zhongmin Dong, Saint Mary's University, Halifax, Nova Scotia

H_2 serves as by-product of N_2 fixation process in legume root nodules and released to rhizosphere due to the lack of uptake hydrogenase activity in some symbiosis (HUP-). A taxonomical diverse group of H_2 oxidizing bacteria living in soil adjacent to root nodules is responsible for H_2 uptake in soil. Soil H_2 oxidation is connected with O_2 uptake, CO_2

fixation, NO_2 production and plant growth promotion. Soil microbial community structural changes induced by soil H_2 oxidization have been investigated. However, biological and biochemical mechanism on plant growth promotion stimulated by H_2 treatment still remain unclear. Among thousands of species of bacteria living in soil, over 90% of them have not been studied and are regarded as "unculturable". Although the taxonomy knowledge gained from molecular fingerprint analysis and 16s rRNA gene sequence is very useful in ecological studies, it provides limited information on mechanisms of H_2 fertilization. To fully understand the process responsible for microbial activity changes induced by H_2, prokaryotic whole-transcriptome analysis will be applied to study the gene expression. Key genes activated by H_2 for plant growth promotion will also be identified and sequenced. Results of this study will shed lights on bonds among H_2 treatment, plant growth promotion and NO_2 production.

CSA-S4 **A farm survey of phosphorus in bulk and rhizosphere soil of organically managed soybean plots across Prince Edward Island, Canada.** T.D. Fraser[1], D.H. Lynch[2], K.E. Dunfield[1], [1]School on Environmental Science, University of Guelph, Ontario, Canada N1H 2W1 (e-mail: tandra@uoguelph.ca),[2]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Widespread phosphorus shortages have been reported in organically managed soils across Canada. As certified organic acreage continues to increase, optimising soil P fertility becomes increasingly important. Since plant available orthophosphate fertilizer is not approved in organic production, a detailed understanding of P cycling is essential. Soybeans fields under organic management were sampled at twelve locations throughout Prince Edward Island, Canada during the 2010 growing season. At soybean pod initiation, composite soil samples were collected (n=20) and nine soybean plants taken from each plot with the roots and shoots separated. The rhizosphere soil, defined as soil adhering to roots after shaking, was collected for soil test P (Mehlich 3 extraction) and acid phosphatase analysis. Preliminary results indicate higher STP and phosphatase activity in the rhizosphere compared to the bulk soil. Results from plant P uptake and total organic and inorganic P will also be discussed. Sampling will be continued in 2011 combined with greenhouse studies to intensively study changes in P forms over the life cycle of the plant. Relative abundance and diversity of active bacterial communities as related to changes in P will be investigated using 16S rRNA DGGE and real-time PCR.

CSA-S5 **Post-harvest organic carbon amendments to minimize mineral nitrogen losses in cole crop production: *in vitro*.** K.A. Congreves[1], R.P. Voroney[2], I.P. O'Halloran[1], L.L. VanEerd[1], [1,2] School of Environmental Sciences, University of Guelph, [1]Ridgetown Campus, Ridgetown Ontario, N0P 2C0 and [2]Guelph, Ontario, Canada N1G 2W1 (Email lvaneerd@ridgetownc.uoguelph.ca)

Cole crop residues are rich in nitrogen and large amounts of mineral N (NH_4^+-N and NO_3^--N) can be released through rapid decomposition in autumn, posing high risk of N losses during the post-harvest period. A management practice of amending soil with readily decomposable organic carbon has the potential to immobilize N in agricultural systems, however, it has not been studied in cole crop production. A randomized complete block laboratory study, with four replications was conducted to determine the effects of organic carbon amendments with broccoli residue on soil mineral N. Mineral N concentrations and CO_2 mineralization rates were assessed throughout a 56 day incubation in microcosms containing 60 g loam soil (from 0-15 cm depth, collected after broccoli

harvest) amended with 268 mg dry broccoli residue and 207 mg/moisture factor organic carbon. Treatments included three organic carbon amendments: (i) crop residue + wheat straw, (ii) crop residue + yard waste, and (iii) crop residue + used cooking oil, a control (crop residue), a blank (no amendments), and three organic carbon + 34 mg ammonium-nitrate controls. By d 56, broccoli residue resulted in the mineralization of 67 mg total mineral N kg^{-1} soil, relative to blank soil. Wheat straw, yard waste, and used cooking oil lowered the total mineral N content by 16.9, 12.3, and 86.0 mg N kg^{-1} soil by d 56, respectively. Carbon mineralization rates were greatest in crop residue + used cooking oil, with peak C mineralization of 23.8 mg C kg^{-1} soil d^{-1} by d 4. Rates of CO_2 evolution returned to baseline levels by the end of the incubation study. Thus, the application of organic carbon to soil with broccoli residue appears to stimulate mineral N immobilization, which in turn may reduce the risk of N loss during the post-harvest period. Applying wheat straw, yard waste, and used cooking oil should be evaluated on a field scale to assess this strategy as a best management practice minimizing N loss after cole crop harvest.

CSA-S6 **Rotational effects of cool season pulses on barley and canola yields in central Alberta.** C.M. Williams[1*], J.R. King[1], S.M. Ross[1], M.A. Olson[2], C.F. Hoy[2], K.J. Lopetinsky[3]. Department of Agricultural, Food and Nutritional Science, University of Alberta, 4-10 Agriculture-Forestry Centre, Edmonton, AB T6G 2P5; [2]Alberta Agriculture and Rural Development; [3]Pulse Research Consultant

Inclusion of pulses in crop rotations will affect the nitrogen (N) balance of the agricultural system and impact subsequent crop yield. To address the need for more information on the effects of adding pulse crops to current rotations, a two year rotational study was initiated in 2008. The effects of 'Snowbird' tannin-free faba bean (*Vicia faba* L.), 'Arabella' narrow-leafed lupin (*Lupinus angustifolius* L.), and 'Canstar' field pea (*Pisum sativum* L.) on subsequent barley and canola crop yields were investigated at two sites in central Alberta – Barrhead and St. Albert. In the first year of rotation (YR1), barley (with and without N fertilizer), canola (with and without N fertilizer), faba bean, lupin and pea were grown. In the following year (YR2), barley and canola was grown across all YR1 treatments. In YR1, N fixation was determined for each pulse crop and N removal and N return for all seven treatments. N fixation (kg N ha^{-1}) averaged 55, 58, and 51 at Barrhead and 201, 41, and 123 at St. Albert for faba bean, lupin and pea, respectively. N removed from the system in harvested seed ranged from 61 to 252 kg N ha^{-1} with faba bean and canola crops removing the most N and barley crops the least. Only 15-35% of total N found in above ground biomass was returned to the soil with straw and pods/chaff. YR2 barley yields (Mg ha^{-1}) averaged 2.60 at Barrhead and 4.50 at St. Albert. The highest yielding YR2 barley crop was produced on faba bean or pea stubble or with the addition of N fertilizer. YR2 canola yields averaged 1.97 at Barrhead and 2.95 at St. Albert. There were no significant differences in canola yield at Barrhead between YR1 treatments. At St. Albert, canola yields were greatest when grown on faba bean, pea or barley (with N fertilizer) stubble and lowest when grown on canola stubble. Results from this study indicate that the inclusion of faba bean or pea crops in rotations can maintain barley and canola yields without the addition of N fertilizer.

CSA-S7 **Quantification of bacterial rubisco genes and their expression in soils adjacent to hydrogen releasing legume nodules by *cbbL* targeted real-time PCR.** B. C. Flynn[1*], M. Schloter[2], A. Hartmann[3], F. Haesler[2], Z. Dong[1]. [1]Saint Mary's University, Biology Department, 923 Robie St., Halifax, NS, B3H 3C3, Canada; [2]Helmholtz Zentrum München, Department of Terrestrial Ecogenetics, Ingolstädter Landstraße 1, D-

85764 Neuherberg, Germany; and [3]Helmholtz Zentrum München, Department of Microbe-Plant Interactions, Ingolstädter Landstraße 1, D-85764 Neuherberg, Germany

Bacterial nitrogen fixation that takes place in the nodules of legume plants is responsible for many of the positive effects of legume plants on the soil environment. Hydrogen gas (H_2) is an obligatory by-product of the nitrogen fixation pathway. The release of H_2 into soil from legumes nodules has many positive effects on soil health including, among other benefits, an increase in soil microbial CO_2 fixation. RubisCO plays a major role in bacterial CO_2 fixation and is coded in part by the large subunit gene, *cbbL*. Soil was treated using a controlled source of H_2 gas and through H_2 released from legume root nodules in order to study *cbbL* gene activity in soil in response to H_2 exposure. RubisCO large subunit genes, red-like and green-like *cbbL*, have been found in all soil treatments. Real time quantitative PCR was used to quantify the gene copy numbers (DNA) and gene expression (mRNA) of the *cbbL* genes. Hydrogen treated soils measured up to 55.7 times more *cbbL* DNA copies per g soil than air treated soil. Rhizosphere soils did not show significant differences based on inoculants used but did show up to 49.1 times more copies than air treated soil. Expression levels for H_2 treated soils were up to 16.2 times higher than that of air treated soil. There was no significant difference in expression levels for rhizosphere samples but nodulated soils had up to 7.6 times more expression than air treated soil. This study shows that H_2 induces an increase in both gene copy number and gene expression of bacterial *cbbL* in soil.

CSA-S8 **Integrated nutrient management on NB and PEI dairy farms.** J. Nimmo[1]*, D. Lynch[1], M. Main[1], J. Owen[2]. [1]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3 (e-mail:nimmoj@nsac.ca); [2]Agriculture and Agri-Food Canada, Bouctouche, NB, Canada, E4S 2J2

Whole farm nutrient budgets (WFNB) enable producers to link productivity and efficiency in the barn with more traditional field nutrient management plans. The budgets monitor nitrogen, phosphorous, and potassium (N, P, and K) being imported onto the farm and nutrients leaving as managed outputs such as milk or animals. Findings from a two year project recording WFNBs on ten dairy farms in NB and PEI indicate that the dairy farms operate with surpluses of N, P, and K. A detailed study of one farm from each province has provided greater insight into the movement and nutrient use efficiency (NUE) among farm animal and field components. The two year average whole farm NUEs (farm outputs as a percent of inputs) were 26% (N) were, 23% (P), and 18% (K) and 22% (N), 15% (P), and 19% (K) on the detailed sites in NB and PEI, respectively. The contribution of biological nitrogen fixation (BNF) to nitrogen inputs was assessed on the sites using the ^{15}N natural abundance technique. Models based on forage legume dry matter yields were evaluated using the ^{15}N natural abundance data and re-calibrated to provide estimates for legume BNF in the Atlantic Canada region. BNF tended to be the second largest input of N to the dairy farms after N in purchased feeds.

CSA-S9 **Assessment of genetic diversity in *Pisum sativum* through transposon and microsatellite markers.** S. Ahmad[1*], M. Singh[1], M. lefsrud[2], J. Singh[1]. [1] Department of Plant Science, McGill University, Ste Anne de Bellevue, Quebec, Canada H9X 3V9; and [2] Department of Bioresource Engineering, McGill University, Ste Anne de Bellevue, Quebec, Canada H9X 3V9

Genetic diversity is key component for creation of novel and desirable germplasm including the development of future breeding lines. With the advent of molecular marker

technologies, several DNA markers including RFLPS, RAPDs, AFLPs, SSRs, ISSRs, SCARS/CAPS, SRAPs, SNPs, and etc., have opened the possibility of assessing allelic diversity and fingerprinting in genome. Among various molecular markers developed, microsatellites or SSR markers have recently gained much importance due to their accuracy, reliability, co-dominancy, reproducibility and high polymorphism. Another useful and fast approach is transposon based fingerprinting as transposons are widely distributed in genome. Transposons are playing an important role in evolution and genetic diversity through duplication, insertion and excision. The objective of the present study is to assess genetic diversity in the pea germplasm through microsatellites and transposons based molecular markers. For this purpose, 35diverse *Pisum* accessions were collected to investigate genetic diversity. Primers from several polymorphic SSR markers and five major transposon species such as *Ty3-gypsy, Ac/Ds* and *MITES* were generated. As expected SSR markers were found highly polymorphic. Using maize *Ac/Ds* primers, amplified products from pea were cloned and sequenced. The preliminary results indicate that both SSRs and transposon markers can play an important role to fingerprint pea germplasm.

CSA-S10 **Tolerance of transgenic canola expressing pea *PR 10* to the flea beetles, *Phyllotreta cruciferae* (Goeze) and *P. striolata* (Fabricius).** A. Sultani*, N. Kav and L. Dosdall. Department of Agricultural, Food and Nutritional science, University of Alberta, Edmonton, Alberta, Canada T6G 2P5 (e-mail: sultani@ulaberta.ca)

Adult flea beetles [*Phyllotreta cruciferae* (Goeze) and *Phyllotreta striolata* (Fabricius)] (Coleoptera: Chrysomelidae) emerging from overwintering pose significant threats to early canola seedling establishment throughout North America. Laboratory flea beetle trials from 2009-2010, May-September, were used to test antixenosis potential of transgenic *Brassica napus* expressing cDNA encoding pea PR 10.1 and 10.4 in Westar and DH19 backgrounds, respectively. In addition, the effects of treatments with different concentrations of the cytokinin 6-benzylaminopurine (BAP) and with Helix® (thiamethoxam insecticide) on tolerance to insect attack were investigated. These studies were undertaken to investigate the potential role for cytokinins in PR10-mediated antixenosis effects as well as to compare the degree of tolerance exhibited by the transgenic lines with insecticide treatments. Our results demonstrate that transgenic lines expressing *PR 10.4* suffered the least damage from *P. cruciferae* when compared with Helix®-treated doubled haploid or Westar genotypes. Cytokinin treatments resulted in some tolerance to flea beetle attack with maximum protective effects observed at 25 µM. Results for *P. striolata* were different with the insecticide treatments being most effective in reducing damage brought about by this species. In conclusion, our results indicate that *PR 10.4*-transgenic *B. napus* canola is significantly more tolerant to *P. cruciferae* and may be part of an integrated approach towards preventing damage from this species of flea beetle prevalent in Alberta. Such integrated approaches may have utility in reducing chemical insecticide use in canola. Future studies are aimed at characterizing the mechanism underlying PR 10-mediated insect tolerance and enhancing the efficacy of this PR 10 protein to broaden its effectiveness against *P. striolata* as well as other insects.

CSA –S11 **Growth and stress response of *Medicago sativa* L. (alfalfa) grown in mine tailings under greenhouse conditions.** C. Naguit[1]*, S. Renault[1], J. Markham[1], and I. Young[1]. [1]Duff Roblin Trailer, The University of Manitoba, Winnipeg, MB R3T 2N2

Plant growth is often limited on mine tailings (waste from the mining industry) due to their physicochemical properties. Revegetation methods involve ameliorating tailings

with organics to improve tailings physicochemical structure and vegetation cover. Although current methods have proven to be successful in establishing vegetation, the effects of amendments on the physiology of plants growing on amended tailings is unknown. We determined plant growth, stress responses, and tailings structure in a greenhouse experiment on four amended, acid-generating tailings: Central Manitoba Tailings (CMT), Lynn Lake, Thompson and Creighton. The CMT were amended with humic substances applied at rates up to 4 g kg^{-1} through roto-tilling and seeded with a grass-legume mix in 2003. The Thompson tailings were capped with clay and sewage sludge and seeded with graminoids in 2003. The Creighton tailings were capped with slag (125 cm), clay (10 cm), and straw matting and seeded with grasses in 2004. The Lynn Lake tailings were capped with gravel and seed bank-containing peat (20 cm) for re-colonization in 2007. Unamended and amended tailings were collected from each site. Potting media served as a control. The pots were seeded with alfalfa and grown under controlled, greenhouse conditions. Humic substances, straw matting, and sewage sludge improved tailings structure by increasing pH and available PO_4^{-3}. Peat did not increase pH (3.50) and PO_4^{-3} (< 0.65 mg kg^{-1}). Dry biomass yield was the highest for potting media (159 ± 33 mg), Creighton unamended (425 ± 34 mg) and amended tailings (567 ± 50 mg), and Thompson amended tailings (246 ± 43 mg) plants due to near neutral pH (6.76-7.15) and adequate available PO_4^{-3} (> 1.5 mg kg^{-1}). Transpiration was reduced in all treatments relative to the control. Proline content increased in all treatments relative to the control. Photosynthesis, pigments, anti-oxidants, total protein, and tailings organic carbon and inorganic nitrogen will be discussed. Our results indicate that amendments with pH-buffering capacity and adequate nutrients best promote growth and alleviate stress responses. Amendment selection is key in revegetation since mine tailings vary in pH and elemental composition and there is no cure-all for promoting plant growth.

CSA-S12 **New Hairy Canola line and its potential for resistance to Crucifer insects.** U. I. Alahakoon[1,2*], P. C. Bonham-Smith[1] & M. Y. Gruber[2], [1]Department of Biology, University of Saskatchewan, Saskatoon, SK, [2]Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK

Different crucifer plant species possess different physical and chemical characteristics commonly thought to provide resistance to herbivores. The surface of many plant species are covered with protective trichomes which are specialized unicellular or multicellular structures derived from the epidermal cell layer. These structures can negatively impact wandering herbivores by physically obstructing the animal's movement or releasing protective chemicals. Therefore, understanding the molecular biology behind trichome development in essentially glabrous oil seed crop species *Brassica napus* is important to be able to improve trichome density and provide the crop with stable resistance to insect pests. More than 50 genes controlling various aspects of trichome initiation, spacing, size and morphology in Arabidopsis have been cloned. *Brassica* EST libraries were searched for the presence and number of orthologous genes of *Arabidopsis GL1*, *GL2*, *GL3* and *TTG1* (positive regulators) and *TRY* (negative regulator). *TTG1* plays an important role in the early stages of the trichome development pathway. To study its function, over-expression and knocked-down *TTG1* constructs driven by CaMV 35S promoter have been introduced in to *B. napus* cv Westar and 35S:*GL3* transgenic *B. napus* backgrounds using *Agrobacterium*-mediated gene transformation. Our experiment to knock-down *TTG1* in the *B. napus GL3+* hairy background has produced two lines with greater coverage of trichomes on the first 12 true leaves and lower stems, as well as greater seedling vigor, and normal growth compared to the hairy canola background. Relative transcription of key trichome regulatory genes Bn:*TTG1*, Bn:*GL1*, Bn:*GL2*, Bn:*GL3*,

At:*GL3*, Bn:*TRY* and Bn:*CPC* was analyzed to understand the molecular mechanism underlying this increased trichome phenotype. We are also testing these two very hairy lines in insect feeding trials.

CSA-S13 **A study of N_2 fixation ability of different common bean genotypes in Ontario.** M. Farid[1]*, K. P. Pauls[1], and A. Navabi[2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1 (mfarid@uoguelph.ca); and [2]Agriculture and Agri-Food Canada, c/o Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1

The Common bean (*Phaseolous vulgaris* L.) is one of the most important pulses, comprising approximately 50% of the grain legumes that are consumed worldwide and a valuable part of the Ontario agri-food industry. Common beans are inherently capable of establishing a symbiotic relationship with N_2-fixing soil bacteria, with beneficial effects to cropping systems. Despite this inherent ability, symbiotic N_2 fixation potential in common bean is relatively low compared to other legumes and even lower than average in Ontario. Although common beans are overall poor in terms of atmospheric N_2 fixing ability, noticeable diversity has been reported among different common bean genotypes. The objective of this research is to examine the N_2 fixation ability of some Ontario-adapted bean genotypes as the basis for subsequent efforts to improve N_2 fixation in common bean. Twelve genotypes of different market classes from the two gene pools of common bean were planted under controlled environment in an N-free medium with and without common bean-specific rhizobia (*Rhizobium leguminosarum* bv. *Phaseoli*). Total N content of different plant organs, leaf chlorophyll content, number, dry weight and color of nodules, and total biomass were measured to study the N_2 fixation ability of each genotype. The variation among genotypes will be presented and the association of morpho-physiological traits with N_2 fixation will be discussed.

CSA-S14 **Effects of intraspecific variation in determining the genome origin and duplication dynamic of tetraploid *Elymus* StY species.** Chi Yan* and Genlou Sun. Biology Department, Saint Mary's University, 923 Robie Street, Halifax, Nova Scotia, B3H 3C3, Canada (e-mail: yanchi2008@yahoo.cn)

Recent analysis of *Elymus* species and extensive samples of *Pseudoroegneria spicata* (Pursh) À. Löve using random amplified polymorphic DNA (RAPD) suggested that one accession of *P. spicata*, which is from the **St** genome, may be the most likely donor of the **Y** genome. Our study tests this theory and estimate whether intraspecific variation during the sampling would affect the result on the origin of the **Y** genome in allotetraploid **StY** species, as well as explore the evolutionary dynamics of these species. Two single copy nuclear genes including the translation elongation factor G (*EF-G*) and the second largest subunit of RNA polymerase II (*RPB2*) were sequenced from 58 accessions of *Pseudoroegneria*, *Elymus* and other diploid species in Triticeae. Phylogenetic relationships were estimated using MP, ML and Bayesian analyses. Sequence comparisons revealed extensive sequence variations between the sequences from the **St** and **Y** genomes. Phylogenetic analyses confirmed that the **Y** genome evolved in an independent diploid species and has a different origin from the **St** genome. Our results demonstrated that intraspecific variation does not affect the identification of genome

origin in polyploids. Moreover, sequence data showed evidences to support the suggestion of the genome convergent evolution in allopolyploid **StY** genome species.

CSA-S15 **Comparative mapping of QTL's affecting oil content in Oats.** B.T.Hizbai[1*] (biniam.hizbai@agr.gc.ca), K. Gardner[1], C. P. Wight[1], R. K. Dhanda[3], S. J. Molnar[1], D. A. Johnson[2], J. Frégeau-Reid[1], W. Yan[1], B. Rossnagel[3], V. Burrows[1], A. Deiderichsen[4], N. A. Tinker[1], [1]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Avenue, Central Experimental Farm, Ottawa, OntarioK1A 0C6 Canada; [2]Department of Biology, University of Ottawa, 30 Marie Curie, Ottawa ON Canada K1N 6N5; [3]Crop Development Centre, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8; and [4]AAFC, Saskatoon Research Centre, 107 Science Place, Saskatoon, Saskatchewan, S7N 0X2

Groat oil content is one of the major quality traits in oats (*Avena sativa L*). We investigated this trait in a population of 146 recombinant inbred lines (RIL) from the cross between Dal (high oil) and Exeter (low oil). Using these progenies, we constructed a linkage map consisting of 525 DArT markers in 38 linkage groups. We measured groat oil content and composition in grain samples grown at Aberdeen, Idaho, in 1997, which had been kept at minus 20°C since harvest. Total lipids were extracted using an Accelerated Solvent Extractor (ASE-200). In addition, multiple agronomic traits were analyzed on all 146 lines of the mapping population planted in two environments, hill plots and field plots, in Ottawa, 2010. Interval mapping was used for QTL analysis. Some linkage groups were associated with multiple traits. Linkage groups DE2, DE3, DE6 and DE10 contained QTL for oil: one locus each in groups DE2 and DE3, two loci in group DE6 and three loci in group DE10. Group DE7 was associated with multiple traits including plant height, lodging and heading date.

CSA-S16 **Isolation and characterization of *Bradyrhizobium* associated with genetically modified soybean root nodulation in dykeland**. P. Katulanda[1*], H. Li[1] and S. Asiedu[1]. [1]Department of Plant & Animal Sciences, Nova Scotia Agricultural College, and P.O Box 550, Truro, NS, B2N 5E3 (e-mail: katulandap@nsac.ca)

Dykeland, a unique agricultural resource found in Atlantic Canada, where soybean is cultivating as the main field crop. *Bradyhizobium* strains are known to determine the efficiency of soybean root nodulation and symbiotic nitrogen fixation, hence they are introduce to the cropping system with seeds to enhance the soybean productivity and seed quality. However, it is unknown the implication of existing *rhizobia* present in the dykeland soil in soybean root nodulation and symbiotic nitrogen fixation. The objective of this study was to isolate and characterize the *Bradyrhizobium* associated with soybean root nodulation in Habitant and Wellington dykelands. A capture experiment was conducted in a growth chamber under the temperatures of 25/20 ^{o}C (day/night) and relative humidity of 80%. Sterilized soybean seeds were sown in sterilized Pro-mix media. Seedlings were inoculated at 0, 1, 2 and 3 ml of soil suspension (1:10, soil/water) two weeks after sowing in a completely randomized design with 3 replicates. The plants were uprooted 35 days after inoculation for *rhizobium* isolation and the number of nodules was recorded. The nodule numbers were 0, 9, 14 and 20 per plant at the soil suspension levels of 0, 1, 2 and 3 ml respectively. The selected active (red pigment leghaemoglobin) nodules were streaked on yeast manitol agar (YMA) containing congo red and typical *rhizobium* colonies were selected based on the colony morphology (round shape, smooth margins, white to opaque in colour and gummy). Isolates were verified as

gram negative bacteria by observing the viscosity under 3 % potassium hydroxide solutions. Seven fast growing strains were observed based on the colour change on YMA medium containing bromothymol blue. The authenticity of these isolates will be confirmed by conducting a nodulation test under controlled environment.

CSA-S17 **An assessment of wood ash application on perennial forage stands**. D. MacEachern[1]*, N. McLean[1]. [1]Department of Plant & Animal Sciences, Nova Scotia Agricultural College, PO Box 550, Truro, NS, B2N 5E3

Soils in Nova Scotia are naturally acidic due to a number of factors including; high precipitation and acidic parent material. For these reasons, agricultural soils must be limed in order to raise soil pH, and insure maximum availability of soil nutrients. Wood ash is the byproduct produced from the burning of wood/wood based fuels, and it is has been promoted in Nova Scotia as a substitute for agricultural lime. An independent study is being undertaken to assess the quality of wood ash available to Nova Scotia producers and determine if the ash is actually a safe, effective alternative to agricultural lime. Preliminary results have shown that the wood ash produced in south eastern Nova Scotia, can significantly increase soil pH.

CSA-S18 **Agro-morphological and molecular characterization of barley (*Hordeum vulgare* L.).** D. R. Ray[1]; J. C. Goyali[2*]; S. K. Nag[1] and A. K. Chowdhury[3], [1] 218 Beaudoin Rue, Montreal, Quebec, Canada H4C 2Y2, [2]Department of Biology, Memorial University of Newfoundland, St. John's, Newfoundland and Labrador, Canada A1B 3X9 (e-mail: juran_goyali@yahoo.co.in), [3] Department of Genetics and Plant Breeding, Patuakhali Science and Technology University, Dumki, Patuakhali, Bangladesh

Genetic diversity among twenty eight elite barley genotypes (*Hordeum vulgare* L.) grown in Bangladesh Agricultural Research Institute (BARI), Joydevpur, Bangladesh was assessed using agro-morphological characters and randomly amplified polymorphic DNA (RAPD) markers. Significant variation was observed among all the genotypes for the characters viz. days to heading (DH), days to maturity (DM), plant height (PH), number of tillers per plant (NTP), length of seed (LSD), breadth of seed (BSD), length of spike (LSP), number of grains per spike (NGS), 1000-seed weight (TSW), yield per plant (YPL), yield per plot (YPT) and yield per ha (YH) studied. High genotypic co-efficient of variation (GCV) was observed for NTP followed by NGS, YPL and YH. High heritability with medium genetic advance in percent of mean was observed for PH, LSD, BSD, LSP and YPL. Path co-efficient analysis showed that YPT, DH and YPL had more contribution on YH in positive direction as compare to other characters. The genotypes were grouped into six clusters using Mahalanobis's distance (D^2) analysis. The inter cluster distances were larger than intra cluster distances. The intra cluster value was maximum in cluster III and minimum in cluster VI. The principal characters responsible for genetic divergence were DM and NTP. RAPD markers were used to assess the genetic diversity in barley genotypes. Twenty seven of thirty nine reproducible scorable DNA bands were polymorphic when genotypes were assessed using RAPD markers. The greater divergence in the genotypes due to agro-morphological characters and RAPD markers would offer a good scope in barley breeding.

CSA-S19 **Availability of Cu and Pb from compost amended soils to corn and Swiss chard**. A. Cooper[1]*, B. Rathgeber[2], and V.D. Zheljazkov[3]. [1]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3; [2]Atlantic Food & Horticulture Research Centre, Agriculture & Agri-Food Canada, Kentville, Nova Scotia, Canada B4N 1J5; [3]Sheridan Research and Extension Center, University of Wyoming, Sheridan, Wyoming, USA 82801-9619

Compost application to agricultural soils has many benefits associated with improved soil physical, chemical, and biological properties that result in greater crop productivity. A concern with the application of industrial compost such as Municipal Solid Waste (MSW) compost or Source Separated Sewage Sludge (SS) compost has been potentially high concentrations of heavy metals and trace elements. The objectives of this study were: (1) Evaluate the effect of compost application on Cu and Pb accumulation in soil and corn under field conditions, and (2) assess the bioavailability of Cu and Pb from compost-amended soils to Swiss chard in controlled environment conditions. Field and container studies were conducted to meet the objectives. In the field experiment, fertility treatments included MSW, SS compost, and chemical fertilizers in two application rates, unfertilized control, all in combination with three rates of lime application. In year 1, treatments differed for soil Cu, while in year 2, treatments affected both soil Cu and Pb, and plant tissue Pb. Overall, corn yields in both years were higher for the MSW-high rate treatment. The field experiment showed that successive applications of MSW and SS compost to meet N requirement for corn under no-till cropping systems on NS dykeland did not result in excessive accumulation of Cu or Pb in corn tissue. In the greenhouse experiment, Swiss chard grown in soil amended with high-Cu compost did not result in significant accumulation of Cu or Pb in plant tissue. MSW or SS compost that meet Canadian guidelines for compost quality may be safely used as a nutrient source for crops.

CSA-S20 **Sward complexity and grass species composition affects the performance of grass-white clover pasture mixtures.** Y.A. Papadopoulos[1], M.S. McElroy[2*], J.P. Winter[2], S.A.E. Filmore[3], K.B. McRae[3], A.H. Fredeen[2] and J. L. Duyinsveld[4], [1]Agriculture & Agri-Food Canada, Nova Scotia Agricultural College, PO Box 550, Truro, NS, Canada B2N 5E3; [2]Nova Scotia Agricultural College, PO Box 550, Truro, NS, Canada B2N 5E3; [3]Agriculture & Agrifood Canada, Atlantic Food and Horticulture Research Centre, Main St., Kentville, NS, Canada B4N 1J5. [4]Agriculture and Agri-food Canada, Atlantic Food and Horticulture Research Centre, Nappan, NS, Canada B0L 1C0

Productivity of managed permanent pastures is associated closely with the species composition of seeded mixtures. Ecological theory suggests that increasing plant species diversity will result in higher productivity, resilience, and resistance to invasive species. To better understand the relationship between sward species composition and pasture productivity, mixtures of four common pasture grass species, timothy (*Phleum pratense*), Canada bluegrass (*Poa compressa*), reed canarygrass (*Phalaris arundinacea*) and meadow fescue (*Festuca pratensis*) were seeded in 2004 with white clover (*Trifolium repens*). Binary (two grass), tertiary (three grass), and quaternary (four grass) combinations were compared. Plots were rotationally grazed for five years, with measurements of yield taken in the first post-establishment year (2005) and in three subsequent production years (2007, 2008, and 2009). Mean Dry Matter Yield (DMY) increased appreciably from post-establishment (3801 kg ha^{-1}) to the production years (6613 kg ha^{-1}). Contrasts revealed significantly higher DMY production in quaternary mixtures versus less complex plots in production years. Repeated measures analysis

found significantly different quadratic trends in DMY for plots containing bluegrass and timothy, showing different patterns of growth between the respective mixtures. Principal Components Analysis (PCA) of averaged yields over the production years revealed a strong association between seeded grass growth and DMY. This relationship between DMY and seeded grass growth was strongest in swards containing a combination of timothy and bluegrass. In general, the growth of weedy grasses and forbs were higher in mixtures with large proportions of timothy and reed canarygrass. In spite of the fact that mixtures containing timothy and bluegrass were shown to produce high DMY, it appears the aggressiveness of bluegrass was suppressing the yield potential of timothy. White clover yields and unseeded grasses/forbs were both significantly lower in mixtures containing bluegrass. Also, the PCA revealed a favorable compatibility between meadow fescue and white clover growth while bluegrass appears to suppress meadow fescue growth. Results demonstrate that complex sward mixtures were more productive over the long term, and that the presence of particular two grass species (timothy and bluegrass) had considerable influence on DMY production.

Canadian Society of Horticultural Science

Student Posters

CSHS-S1 **Phenolic contents and antioxidant properties of blueberry tea and fruit**. N. Chandrasekara[1], J. C. Goyali1,[2]*, P. Vyas[1,2], J. K. Shah[1], A. U. Igamberdiev[1] and S. C. Debnath[2]. [1]Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL, Canada A1B 3X9, [2]Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, P.O. Box 39088, 308 Brookfield Road, St. John's, NL, Canada A1E 5Y7

The herbal teas are being used frequently in the treatment of chronic diseases such as cancer, gastrointestinal diseases and type 2-diabetes. Blueberries (*Vaccinium angustifolium* Ait.) are known to possess great potential health benefits, mostly attributable to their high content of phenolic compounds. The objective of this study was to determine the phenolic contents and their antioxidant properties of berries and teas obtained from market available and/or Newfoundland-grown blueberries, using different extraction methods. Tea was brewed with boiling and cold water along with 5% lime juice and without lime juice for 5 and 10 minutes. Blueberry fruits were extracted with two alcohol and acetone solvents. Total phenolic (TPC), anthocyanin (AC), proanthocyanidin (PC) and flavonoid (FC) contents were determined. Antioxidant activities were measured using the 1,1-dipheny-2-picrylhydrazyl (DPPH) radical scavenging capacity and reducing power assays. Brewing with boiling water for 5 min extracted higher TPC, AC, PC and FC as compare with other brewing methods and they were 48.67±0.60 mg of gallic acid eq. (GAE) per 2 g tea bag, 68.98±2.64 mg cyanidin-3-glucoside eq. (Cy3GE) per bag, 222.45±14.59 mg catechin eq. (CE) per bag and 358±3.25 mg CE per bag, respectively. DPPH radical scavenging activity (495 mg GAE per tea bag) and reducing power (259.12±5.12 mg of ascorbic acid eq. per tea bag) were also higher when tea was brewed with hot water for 5 min. Adding of lime juice increased the TPC and antioxidant activities when it was brewed with cold water whereas it had no significant effect in brewing with hot water. In case of blueberry fruit, the acidified acetone was found to be better solvent for extracting TPC (4.64±1.05 mg GAE per g fruit), AC (11.5 ±1.29 mg Cy3GE per g fruit), PC (27.76±2.39 mg CE per g fruit) and FC (10.94±.67 mg CE per g fruit). Antioxidant activity was also higher when extracted with acidified acetone. Different brewing methods and solvents used for the extraction had a significant effect on the phenolic contents and antioxidant activities of blueberry tea and fruit.

CSHS-S2 **Impact of 1-Methylcyclopropene (1-MCP) on quality of apple juice.** Bizuayehu Mengstie Muche[1, 2*], H. P. Vasantha Rupasinghe[1], R. Alex Speers[2], Charles F. Forney[3] and Tess Astatkie[1]. [1]Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Dalhousie University, [3]Agriculture and Agri-Food, Canada

1-Methylcyclopropene (1-MCP), an inhibitor of ethylene production and action, is widely used as a pre-storage treatment to extend the storage life of apples. However, the impact of 1-MCP on the taste of apple juice has not been extensively investigated. This work determined the effect of 1-MCP (1-MCP treated, and control), storage atmosphere

(controlled atmosphere [CA], and regular air [RA]) and harvest date (early and late) on the content of fructose, sucrose, glucose and acidity (TA) of clear, cloudy, and fresh juices prepared from 'Honeycrisp' (HC) and 'McIntosh' (MC) apples stored for 4-months. Ethylene production and fruit firmness were also measured. The experimental design was a split-plot factorial with three blocks. In MC apples, ethylene production was significantly inhibited under 1-MCP + CA/RA (0.009 - 0.064 $\mu Lg^{-1}h^{-1}$) as compared to control + CA/RA (0.098 - 0.11 $\mu Lg^{-1}h^{-1}$) condition. In HC apples, lower ethylene production was observed only in CA + 1-MCP/control (0.003 - 0.017 $\mu Lg^{-1}h^{-1}$) but not in RA storage. While, HC apples maintained their firmness irrespective of any storage condition, 1-MCP treated MC apples were significantly firmer (by 7 N) than the control. In both cultivars, acidity level was not affected by juice type and harvest date. In MC apples, significantly higher TA (malic acid in g/L) was found under 1-MCP + CA/RA (4.70/4.40) and control + CA (4.40) as compared to control + RA treatments. Higher acidity was also observed in HC apples stored under 1-MCP + CA/RA condition as compared to the control + CA/RA. In both cultivars, fructose was the dominant sugar (70.2 (HC), 77.4 (MC) g/L) followed by sucrose (20.7 (HC), 11.1 (MC) g/L), and glucose (17.9 (HC), 16.8 (MC) g/L). Irrespective of apple cultivar, cloudy juice and late harvest apples yielded significantly higher fructose and glucose content. MC apples stored under 1-MCP + CA had reduced sucrose level (by 3 g/L) as compared to 1-MCP + RA condition. Generally, the results indicated that the taste of apple juice could be influenced by the storage atmosphere, 1-MCP treatment as well as by juice processing steps.

CSHS-S3 **Anti-hypertensive properties of fruit vinegars.** H. M. A. R. Nandasiri* and H. P. V. Rupasinghe. PO Box 550, Department of Environmental Science, Nova Scotia Agricultural College, Truro, NS, Canada B2N 5E3

Cardiovascular disease (CVD) is becoming the primary cause of mortality worldwide. In Canada, about 1.3 million people have been reported to suffering from heart diseases in 2007. Nine out of ten Canadians have at least one risk factor for heart disease or stroke. Hypertension is one of the common progressive disorders which often lead to coronary heart disease, stroke, renal diseases and heart failure. Canadian health measures survey indicates that 20% of Canadian adults are in the pre-hypertension stage. Dietary intervention of fruit vinegars (FV) has been reported in preventing chronic diseases such as CVD and diabetes. The bioactive compounds presence in fruit sources are suggested as potential inhibitors of angiotensin converting enzyme (ACE) and rennin which are involved in regulating the blood pressure. This study was conducted too investigate *in vitro* anti-hypertensive properties of fruit vinegar prepared from grape and apple with compared to commercial red wine vinegar product. Also, acetic acid, the major organic acid presence in vinegar, was also assessed. A concentration dependant inhibition of ACE was observed for the three vinegar products when 1.25%, 2.5%, 5%, 7.5% and 10% of vinegar was tested. The highest inhibition (97.8%) of ACE was observed for 7.5% apple vinegar followed by 10% commercial red wine vinegar (89.9%), 10% grape vinegar (62.5%) and 6% acetic acid (47.8%). Antioxidant capacity determined by ferric reducing ability of plasma (FRAP) assay has also indicated that apple vinegar has the highest value (27.9 TE µg Trolox equivalents (TE)/g of vinegar) followed by commercial wine vinegar (27.7 TE µg TE/g of vinegar) and grape vinegar (16.0 µg TE/g of vinegar). The results solidify that fruit vinegars have high anti-oxidant capacity as well as ability to inhibit ACE *in vitro*; therefore, further investigation of dietary effect of fruit vinegar for prevention of hypertension is important.

CSHS-S4 **Antioxidant protection of human LDL oxidation in vitro by ginger extracts**. K. D. P. P. Gunathilake* and H. P.Vasantha Rupasinghe. Department of Environmental Sciences, Nova Scotia Agricultural College, P.O.Box 550, Truro, NS, Canada B2N 5E3

Ginger (*Zingiber officinale*) is a medicinal herb that has been widely used in Ayurvedic, Chinese and Unani herbal medicines all over the world. Currently, there is a renewed inertest in ginger because of its pharmacological activities such as anti-inflammatory, antioxidant and cardio-protective properties. In this study, antioxidant protection of human low density lipoprotein (LDL) *in vitro* by ginger extract was examined. The ultrasonication-assisted extraction process was optimized for developing a bioactive rich ginger extract using a factorial experiment (4x3x3) design of solvent (0, 50, 70, and 95% ethanol), extraction temperature (30, 40 and 60 °C) and extraction time (20, 40 and 60 min). Total phenols of the extract were determined by using the Folin-Ciocalteau method. Results showed that phenolic content in water extract was low compared with ethanol extract in all experimental conditions. The optimum extraction conditions for water were as follows: extraction temperature, 40 °C; extraction time, 40 min; for ethanol: ethanol concentration, 50%; extraction temperature, 40 °C. A spectrophotometric method based on copper induced LDL oxidation was used for the determination of percent inhibition of LDL oxidation by ginger extract. The inhibition of LDL oxidation by ethanoilc extract of ginger (2.11 mg GAE/mL) was from 34-39% and inhibition by water extract (0.83 mg GAE/mL) was 16-24%. This study revealed that ginger extract exhibits ability to inhibit copper catalyzed LDL oxidation.

CSHS-S5 **Hydrogen peroxide treatment of fresh-cut spinach: potential for enhancement of shelf-life and microbiological safety.** M. L. A. Fisher[1,2]*, D. M. Hodges[2], G. S. Bezanson[2] and D. N. Kristie[1]. [1]Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6, [2]Atlantic Food and Horticulture Research Center, Agriculture and Agri-Food Canada, Kentville, Nova Scotia, Canada B4N 1J5

Production and processing can negatively impact the appearance, nutritional quality, and microbiological safety of fresh-cut produce. Chamber-grown spinach (*Spinacia oleracea* L. 'Unipak 12') was exposed to hydrogen peroxide (H2O2) in order to assess its efficacy at preserving and/or enhancing visual quality, leaf firmness, and microbiological quality during storage at 10 °C. Preliminary trials examining leaf quality, firmness and indigenous epiphytic (spoilage) bacteria (IEB) determined that 1.0 % weight/volume H2O2 (ambient temperature) for a 2.5 minute exposure time without a subsequent water rinse, was optimal. Under those conditions, leaves maintained a visual quality of above 9 (scored from 1-10) for 21 days compared to 14 days for the water-only control. Leaf firmness was also improved. A firmness score of above 4 (scored from 1-5) was retained for 28 days compared to only 21 days for the water control. In addition, the abundance of IEB was reduced by 3.41 to 3.89 logs following H2O2 treatment. To test for pathogen control, leaves were immersed in a solution containing 2x107 colony forming units per millilitre (CFU/mL) of *Escherichia coli* (*E. coli*) O157:H7 ATTC 700728 (verotoxin negative). Their subsequent exposure to the optimal H2O2 treatment reduced *E. coli* numbers by 2.62 logs as compared to 1.91 logs for the water control. Throughout the storage period, the concentrations of *E. coli* recovered from H2 O2 treated leaves increased; whereas water treated leaves displayed a decrease in *E. coli* numbers up to day 21. The greatest difference between H2O2 and water treated leaves was observed on day 21 (2.13 logs). Further experiments will involve replication trials with *E. coli*, the use of field-grown leaves, and an examination of the effect of H2O2 treatments on the nutritional/bioactive components of fresh-cut spinach.

CSHS-S6 **Antimicrobial activity of encapsulated allyl isothiocyanate when applied *in vitro* and to packaged, fresh-cut onions.** M. Piercey[1], S.M. Budge[1], G. Mazzanti[1], P. Delaquis[2], A.T. Paulson[1] and L. Truelstrup Hansen[1]. [1]Department of Process Engineering and Applied Science, Dalhousie University, NS, Canada; [2]Agriculture and Agri-Food Canada, Summerland, BC, Canada

The aim of this work was to determine the antimicrobial effect of allyl isothiocyanate (AIT) entrapped in alpha and beta cyclodextrin inclusion complexes (ICs) on *Penicillium expansum*, *Escherichia coli*, *Listeria monocytogenes* and packaged fresh-cut onions. AIT and its ICs were applied to filter paper placed inside sealed Petri dishes, where the agar substrate had been surface inoculated with the target organisms, to determine antimicrobial effects of AIT vapour. Solid phase microextraction (SPME) coupled with gas chromatography was used to determine relative static headspace concentrations of AIT formulations. The antimicrobial effect of beta IC was determined during storage of packaged fresh-cut onions at 5°C for 20 days. AIT vapour released from beta IC showed a significantly (p<0.05) better antimicrobial effect compared to unentrapped AIT. AIT vapour concentrations in the static system were highest for unentrapped AIT followed by beta IC and alpha IC. Application of beta IC (200 µl/l) to fresh-cut packaged onions effectively inhibited or killed inoculated *L. monocytogenes*, which was also found to be incapable of growth on the untreated cut onion. After 10 days, aerobic counts were 10^4 CFU/g lower on cut onions treated with beta IC (100 and 200 µl/l) compared to untreated controls. This work demonstrates the utility of beta IC as an antimicrobial treatment with potential applications in packaged fresh-cut vegetable products.

CSHS-S7 **Concentration-dependent effect of selected apple flavonoids on PUFA oxidation.** S. N. Warnakulasuriya*, P. Kathirvel and H. P. V. Rupasinghe. Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Polyunsaturated fatty acids (PUFA) are highly susceptible to oxidation due to the presence of double bonds. Natural antioxidants such as flavonoids can protect PUFA from oxidizing by many mechanisms: scavenging the free radicals, chelating the metals, etc. Due to the possible deleterious effects of synthetic antioxidants present in food, currently there is a growing demand for identifying naturally-sourced compounds as food antioxidants. Apple flavonoids have been reported as a promising source of dietary as well as food antioxidants. The objective of this study was to determine the concentration dependent effect of five major flavonoids present in apples viz., quercetin-3-*O*-galactoside, chlorogenic acid, epicatechin, cyanidin-3-*O*-galactoside and phloridzin on percentage inhibition of lipid oxidation in a bulk fish oil model system. Effect of selected flavonoids on inhibition of primary oxidation was evaluated based on the peroxide values of heat-induced (40 ^{o}C) oxidation in bulk fish oil system. The secondary lipid oxidation products of fish oil containing various concentrations of flavonoids (0.05, 1, 5 and 10 mM) were determined by using the Thiobarbituric Acid Reactive Substance (TBARS) assay. Under the experimental conditions, the greatest inhibition in primary oxidation was observed with chlorogenic acid and phloridzin. The percent inhibition of secondary lipid oxidation increased with increasing flavonoid concentrations. Higher concentrations (5 mM and 10 mM) of cyanidin-3-*O*-galactoside, phloridzin and chlorogenic acid exhibited over 50% inhibition of secondary lipid oxidation products in fish oil.

CSHS-S8 **Evaluating VIS/NIR spectra for in situ foliar nitrogen determination in wild blueberry.** R. Maqbool[1], D. C. Percival[2], M. S. Adl[1], Q. U. Zaman[3] and D. Buszard[4]. [1]Department of Biology, Dalhousie University, 1355 Oxford St., Halifax, NS, Canada B3H 4J1, [2]Department of Environmental Sciences, Nova Scotia Agricultural College, P.O. Box 550, Truro, NS, Canada B2N 5E3, [3]Engineering Department, Nova Scotia Agricultural College, P.O. Box 550, Truro, NS, Canada B2N 5E3, [4]College of Sustainability, Dalhousie University, 1459 LeMarchant St., Halifax, NS, Canada B3H 4R2

This study evaluated the remotely sensed visible-near infrared spectra (350-2500 nm) for nitrogen determination in wild blueberry production system. Four sampling missions were accomplished in 2006 encompassing entire sprout season. The canopy reflectance measurements were taken from two nutrient management experimental sites located in Nova Scotia and New Brunswick. Partial least square regression (PLS) predicted the nitrogen concentration with R^2 values ranging from 0.71 to 0.88 and root mean square error of cross validation (RMSECV) from 0.23 (± 11.92 % of mean) to 0.14 (± 7.25 % of mean) using different spectral ranges. These results are also comparable or even better in terms of R^2 and RMSECV to similar field studies conducted in cultivated crops, woody species and grassland.

CSHS-S9 **Inhibition of fish oil oxidation by polyphenols fractionated from apple peel extract.** S. K. Sekhon*, P. Kathrivel and H. P. Vasantha Rupasinghe. Department of Environmental Sciences, Nova Scotia Agricultural College, P.O. Box 550, Truro, NS, Canada B2N 5E3

Polyphenols of apple peels were studied as a potential fish oil stablizer. Previous studies have reported that apple peels has 3- to 6-fold higher flavonoid content, such as quercetin glycosides than apple flesh. The objective of this study was to fractionate the polyphenolic compounds from apple peel extract and to investigate ability of the fractions to inhibit fish oil oxidation. Ultrasound-assisted ethanol extraction was used to prepare a crude polyphenolic extract which was subjected to fractionation by a reverse phase chromatography using gradient elutions of 20-100% aqueous ethanol. The collected ten fractions were analysed by high performance liquid chromatography coupled with mass spectrometry (HPLC/MS/MS). The HPLC/MS/MS analysis indicated the presence of specific phenolic profiles in different ethanol elutions. The antioxidant properties of each phenolic fractions were evaluated for inhibition of fish oil oxidation using the thiobarbituric acid reactive substances (TBARS) assay. Fish oil was subjected to oxidation by exposing to high temperature (80^{o}C) after incorporating with phenolic fractions (200 ppm). The results indicated that phenolic fractions from apple peels have higher antioxidant activity when compared with the same concentration of α-tocopherol and butylated hydroxytoluene. The fractions rich in flavonols exhibited the greatest inhibition of fish oil oxidation.

CSHS-S10 **Impact of variable rate fertilization on nutrient runoff losses in wild blueberry fields.** S. Saleem[1], Q. Zaman[1], A. Schumann[2], D. Percival[1], A. Madani[11], A. Farooque[1] and F. Khan[1]. [1]Departmant of engineering, Nova Scotia Agricultural College, Truro, Nova Scotia Canada B2N 5E3, [2]Citrus Research and Education Centre, University of Florida, USA

The majority of wild blueberry fields have gentle to severe topography. Currently, inorganic fertilizers are implemented uniformly with inadequate attention being given to

substantial variation in soil/plant characteristics, topographic features, and fruit yield which not only increase the cost of production but also is a serious threat to surface and subsurface water quality. These variations within wild blueberry fields emphasize the need for variable rate (VR) fertilization. The objective of this study is to quantify the nutrient losses in surface runoff for a wild blueberry field under uniform and VR fertilization. A wild blueberry field was selected and divided into two sections i.e. uniform and VR . The slope data was collected to develop management zones. Three fertilizer rates (100,150 and 200 kg ha^{-1}) were applied in low, medium and steep zones respectively for the VR section of the field. Bare spots were incorporated in the prescription map and zero fertilizer was allocated to them. The other half of the field received growers uniform fertilizer rate of 200 kg ha^{-1} for comparison. The runoff collectors were installed at 24 different locations in the experimental field. Surface runoff samples were collected after every significant rainfall and were analyzed for total phosphorus (TP), dissolved reactive phosphorus (DRP) and ammonium nitrogen (NH_4^+-N) concentrations. A grid pattern was established to collect leaf samples from both VR and uniform sections of the field to assess the nutrient uptake by plants under different fertilizer rates. A GIS modeling approach was utilized to calculate the total runoff collected at each runoff collector and multiplied with concentration to quantify the nutrient losses in surface runoff ($kgha^{-1}$). The nutrient losses in VR section were significantly lower than nutrient losses from the uniform fertilization section. Although, phosphorus and nitrogen in leaf nutrients were significantly influenced by the VR fertilization but most of other nutrients were within the recommended optimal ranges. The VR fertilization section received 42% less fertilizer as compared to uniform fertilization. The results of this study suggested that variable rate fertilization would be helpful in reducing the cost the production and environmental risks.

Canadian Botanical Association

Student Posters

CBA-S1 **Diversification of agricultural riparian buffers with indigenous shrubs species.** É. Larivière[1]*, M. Poulin[1] and A. Vanasse[1]. [1]Département de phytologie, Université Laval, Québec, Québec, Canada G1V 0A6 (e-mail: elise.lariviere.1@ulaval.ca)

Agricultural riparian buffers are key components for bank stabilization. These systems also enrich the diversity of the agricultural landscapes and can potentially have positive impacts on the local fauna, such as the pollinators, that are present in this environment. In the province of Québec, the riparian management initiatives are actually limited to the use of a low diversity of species that are well-known for their ability to stabilize the banks. However this homogeneous approach generates little biodiversity on a watershed scale. The objective of the present study was to compare the establishment potential of different indigenous shrub species that are rarely used in riparian plantations with that of frequently used species. Shrubs were planted on the terraces and slopes of streams crossing agricultural fields in three areas of Québec: Bas St-Laurent, Montérégie and Portneuf. The species planted on the terraces were: *Cornus stolonifera* Michx. (control), *Shepherdia canadensis* (L.) Nutt., *Rosa blanda* Ait., *Spiraea alba* DuRoi. and *Corylus cornuta* Marsh. On the slopes, *Salix petiolaris* J. E. Smith. (control), *Myrica gale* L., *Salix eriocephala* Michx., *Cornus rugosa* Lam. and *Cephalanthus occidentalis* L. were the species studied. After two growing seasons, *S. canadensis* and *M. gale* showed the lowest survival rates i.e. 88% and 77% for the terrace and the slope respectively. In all three areas, *S. canadensis* had lower performances than the control species with regards to growth and general health parameters. Moreover, in Portneuf, *C. cornuta* and *R. blanda* were given a lower score for the health parameter in comparison to the control. On the slopes, all the test species performed better than or as well as the control with regards to growth and general health parameters except for *M. gale* in Montérégie. Variations observed in the initial rooting quality of the plants as well as different levels of invasion by competing species do not seem to be related to the survival or the health of the planted shrubs.

CBA-S2 **Comparative gene expression patterns in aerial and aquatic forms of *Myriophyllum aquaticum*.** Md. Shafiullah* and Christian Lacroix, Dept. of Biology, University of Prince Edward Island, C1A 4P3, Canada

Myriophyllum aquaticum is a plant with highly dissected simple leaves consisting of several lobes. It can produce two morphologically different forms of leaves based on whether they are aerial or aquatic. We hypothesize that the early stages of development of both aerial and aquatic leaves of *Myriophyllum aquaticum* are similar, and that the visual and morphological differences appear during later stages of development. *KNOX1 (KNOTTED1-LIKE HOMEOBOX)* genes are believed to have played an important role in the evolution of leaf diversity. Downregulation of *KNOX1* in the shoot meristem during leaf primordium formation leads to simple leaf forms, whereas its upregulation triggers compound leaf forms. Upregulation and subsequently overexpression of *KNOX1* during leaf primordium initiation can also lead to leaf dissection in plants with simple leaves.

Our results revealed that the aerial meristem, and leaf primordia of *Myriophyllum aquaticum* inserted at levels 1 (youngest), 2, and 3 show gene expression throughout these structures. The level of expression of this *KNOX1* gene progressively decreases in older leaf primordia (levels 4 to 7), and no expression is detected in leaf primordia at level 8 and beyond. In aquatic forms of *M. aquaticum*, high levels of expression persist in primordia of level 4. The expression of *KNOX1* decreases in successive primordia and is absent in midrib and older lobes in leaf primordia of level 11. Our results show that leaf dissection is linked to the level of expression of *KNOX1,* and that the highly dissected leaf morphology in aquatic forms of the plant is the result of a longer period of expression.

CBA-S3 **Effects of intraspecific variation in determining the genome origin and duplication dynamic of tetraploid *Elymus* StY species.** Chi Yan* and Genlou Sun. Biology Department, Saint Mary's University, 923 Robie Street, Halifax, Nova Scotia, B3H 3C3, Canada (e-mail: yanchi2008@yahoo.cn)

Recent analysis of *Elymus* species and extensive samples of *Pseudoroegneria spicata* (Pursh) À. Löve using random amplified polymorphic DNA (RAPD) suggested that one accession of *P. spicata*, which is from the **St** genome, may be the most likely donor of the **Y** genome. Our study tests this theory and estimate whether intraspecific variation during the sampling would affect the result on the origin of the **Y** genome in allotetraploid **StY** species, as well as explore the evolutionary dynamics of these species. Two single copy nuclear genes including the translation elongation factor G (*EF-G*) and the second largest subunit of RNA polymerase II (*RPB2*) were sequenced from 58 accessions of *Pseudoroegneria*, *Elymus* and other diploid species in Triticeae. Phylogenetic relationships were estimated using MP, ML and Bayesian analyses. Sequence comparisons revealed extensive sequence variations between the sequences from the **St** and **Y** genomes. Phylogenetic analyses confirmed that the **Y** genome evolved in an independent diploid species and has a different origin from the **St** genome. Our results demonstrated that intraspecific variation does not affect the identification of genome origin in polyploids. Moreover, sequence data showed evidences to support the suggestion of the genome convergent evolution in allopolyploid **StY** genome species.

CBA-S4 **Use of ampelographic methods in the identification of Nova Scotian grape (*Vitis spp.)* cultivars.** L.A. Wiser* and D.N.Kristie. Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada, B4P 246

In recent years the evaluation of suitable grape (*Vitis spp*.) cultivars for the Nova Scotia grape growing and wine industries has become increasingly important. Despite this, little material exists documenting the morphological characteristics of grape cultivars grown in Nova Scotia. This lack of material could make identifying unknown cultivars in a vineyard problematic. The objectives of this study were to describe grape cultivars based on several ampelographic characteristics proposed by Pierre Galet (1979), and to evaluate these characteristics to determine their usefulness in identification. Twenty-nine cultivars that are currently grown in Nova Scotia were described based on morphological characteristics such as leaf colour, hair type, tendril placement and tooth size and shape. Leaf measurements, such as vein length ratios, leaf size and sinus depth, were also used to describe cultivars. Results demonstrated which characteristics were useful in identification and which were not. For instance, indument, or hairiness, was useful as it allowed all cultivars to be divided into numerous small groups, and in some cases narrowed down the identities of single cultivars, such as Einset and KW96-1. Other

characteristics, such as tendril placement, were less useful as all sampled cultivars showed an identical pattern. In many cases vein length ratio measurements were also of little use, as these measurements tended to differ little between cultivars. The results of this study provided a preliminary means of cultivar identification and an approach to identification that did not previously exist for Nova Scotian viticulture. However, future work is required to test this proposed method of identification. Additional cultivars and characteristics should also be included in future work.

CBA-S5 **E107 shoot-controlled low nodulating pea mutant: a tool to study the regulation of symbioses.** C. Huynh*[1], F. C. Guinel[1]. [1]Department of Biology, Faculty of Science, Wilfrid Laurier University, Waterloo, Ontario, Canada N2L 3C5 (huyn9220@mylaurier.ca)

Legumes form at least two types of symbioses, one with rhizobia, and the other with arbuscular mycorrhizal fungi. In the former, the bacteria colonize root nodules in which they fix atmospheric nitrogen into bio-available ammonium. In the latter relationship, the plant benefits from an increase in phosphorus and water. In return, both rhizobia and AM fungi profit from a photosynthate source. Uncontrolled rhizobial symbiosis can be detrimental. To prevent this from occurring, plants have evolved a negative feedback system, named autoregulation of nodulation (AON), which controls the temporal and spatial development of nodules. Though AON has recently been under scrutiny, much remains to be elucidated. AON involves long-distance signalling between roots and shoots, whereby early nodulation events lead to an ascending signal, which is decoded in the shoot to produce a descending signal inhibiting further nodulation. The regulation of mycorrhization is suggested to be similar to that of nodulation, and would involve long-distance systemic signalling, which may overlap that of nodulation. A mutant in our collection, E107 (*brz*), may be useful in the study of the AON shoot component. It is a monogenic recessive mutant of *Pisum sativum* and is unique among low nodulating mutants because both its symbioses phenotypes are shoot-controlled. Based on preliminary data we hypothesize that this mutant overproduces a shoot-derived compound inhibitory to both symbioses. To test this, shoot extracts of nodulated plants, which are likely synthesizing the shoot-derived inhibitor, will be applied to carrot root-organ cultures that have been inoculated with AM fungi. The extracts, obtained by macerating shoots in ethyl acetate, are introduced to the cultures by a disk diffusion method. Whereas the effect of extracts on spore germination is evaluated by measuring hyphal growth towards the root, that on hyphal propagation is assessed by determining appressoria and arbuscule density in cleared roots. Control extracts are those obtained from roots and from shoots of wild-type pea and of non-inoculated E107. We expect E107 shoot extracts to prevent mycorrhizae formation. These results would confirm that E107 is producing a shoot-derived inhibitory substance, making it a useful tool to study AON and the regulation of mycorrhization.

CBA-S6 **Evolution and gene expression of reindeer lichens.** S.N.P. Athukorala*, M.D. Piercey-Normore. Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, R3T 2N2, Canada

Reindeer lichens in the former genus *Cladina* are the main winter diet for caribou and reindeer and form the dominant vegetation cover in northern ecosystems. Evolutionary relationships among species in the genus have been largely based on morphological evidence. Those based on genetic evidence have been taxonomically patchy and have not considered influence from the algal partner. Early gene regulation of the interaction

between the algal and fungal symbionts initiates development of the lichen, which might produce morphological variation in different growing conditions. The objectives of this study were 1) to estimate a phylogenetic history within the genus, and 2) to examine the morphological development and gene expression during the early stages of resynthesis in three species. Internal transcribed spacers 1 and 2 of the nuclear ribosomal DNA and mitochondrial small subunit genes were amplified and sequenced with fungal specific primers from 21 *Cladina* species to create phylogenetic trees. Axenic cultures of the mycobiont and the photobiont of three lichen species; *C. rangiferina, C. arbuscula,* and *C. stellaris* were obtained from thallus fragments using standard procedures. Each mycobiont was co-inoculated with a compatible (*Asterochloris*), an incompatible (*Trebouxia*) alga, and also with a non-lichenized alga, (*Chlorella*). Light microscopic observations were made at each week starting from 24 hrs post-inoculation. After 24 hrs, no interaction was observed. By day 7, growth of the mycobiont and the photobiont was observed in all treatments. At each day of observation, RNA and protein were extracted and cDNA and 1-D protein profiles were synthesized. This study estimates the evolutionary relationships among *Cladina* species, provides insight into gene regulation underlying the interaction between the mycobiont and the photobiont species, and describes the early development of the lichen thallus.

CBA-S7 **Anatomy and morphology of the floral nectary in *Cuscuta* L. (Convolvulaceae).** M.A.R. Wright*, M. Welsh, and M. Costea. Wilfrid Laurier University, Department of Biology, 75 University Ave. West, Waterloo, ON, N2L 3C5 (email: michael.a.wright@gmail.com)

Nectar is often considered to be the most important floral reward offered by angiosperms to their animal visitors. As part of a larger study of the evolution of the gynoecium in *Cuscuta* L. (Convolvulaceae), a genus of ca. 200 species of parasitic vines, we investigated the presence, morphology , and vasculature of the floral nectary found at the base of the ovary in 142 taxa using dried herbarium specimens. Structure was further examined using sections of fixed materials from a subset of five species. We contend here that the nectary is present, at least structurally, in all *Cuscuta* species. The nectary is restricted to the basal portion of the ovary wall and consists of a nectariferous parenchyma overlain by a cuticularized epidermis with modified stomata in a distinct band. The number and arrangement of stomata varies greatly, with stomata occurring singly or in clusters of two or more, and total stomata number ranging from 7 to over 140. Abnormal stomata were witnessed with extra guard cells, or where two stomata abutted against one another along their longitudinal axes and appeared to share a common, larger opening. The nectary is vascularized by radial branches from the central vascular cylinder of the ovary, which pass through the subnectary parenchyma just axial to the nectariferous parenchyma. These branches are composed entirely of phloem, except in subgenus *Monogynella* where the branches representing the carpellar dorsals possess xylem. While this overall tissue organization is similar to that found in other Convolvulaceae, it is much reduced compared to the expanded nectary disks found in most genera. Interestingly, the basal lineages of *Humbertia* and *Ericybe* also have a nectary restricted to the ovary wall. As there is only weak correlations between nectary stomata number and perianth size (r^2=0.1907, p<0.0001), pollen count (r^2=0.0706, p=0.0041), and total pollen volume produced (r^2=0.1402, p=0.0001), it can be concluded that the observed variation is more strongly linked to selection caused by pollinator preferences for pollen rewards vs. nectar rewards, as opposed to the breeding system.

CBA-S8 **Meta-analysis on the response of plant biomass and nitrogen concentration to ascomycetous root endophytes**. M.S. Mayerhofer[1*], G.G. Kernaghan[1,2], Harper[3]. Department of Biology (e-mail: michael.mayerhofer@mail.mcgill.ca), Saint Mary's University, 923 Robie Street, Halifax, Nova Scotia, Canada B3H 3C3; [2]Department of Biology, Mount Saint Vincent, 166 Bedford Highway, Halifax, Nova Scotia, Canada B3M 2J6; and [3]School of Resource and Environmental Studies, Dalhousie University, 1459 Oxford Street, Halifax, Nova Scotia, Canada B3H 4R2

Root endophytes are ubiquitous plant associates that colonize plant tissue asymptomatically. However, the effects of endophytic colonization on host plant growth are not well understood. The range of the response of plant biomass to the inoculation of a fungal root endophyte ranges from negative to positive depending on the identity of the host or endophyte and the experimental conditions. Significant increases in biomass have been attributed in particular to the use of organic nitrogen or to the secretion of phytohormones by the endophyte. We used meta-analysis to quantitatively determine the direction and significance of this response based on existing studies as well as discerning experimental conditions that may affect the plant-endophyte relationship. The response of plant growth (root, shoot and total biomass) and nitrogen concentration was recorded and the analyses were done at three taxonomic levels: Ascomycetes, Helotiales and *Phialocephala fortinii* C.J.K. Wang & H.E. Wilcox. One hundred and thirty-three studies derived from 30 publications were used in the analyses. Overall, plant response to the inoculation of a root endophyte seems to be neutral to slightly positive, with a limited number of studies demonstrating very high growth responses. The identity of the plant host and endophyte species, the use of an endophyte isolated from the same plant species as the host and the use of carbon, organic nitrogen or peat moss were among the most important factors explaining the variability in plant response to endophyte inoculation. This meta-analysis highlights the importance of controlling experimental conditions to obtain truly comparable responses and shows that, with the exception of certain cases, the increases in plant biomass are generally small and relationships between fungal root endophytes and their host plants may not be strictly mutualistic.

CBA-S9 **Diversity and evolution of infrastaminal scales in *Cuscuta* L. (Convolvulaceae).** S. Riviere*, C. Clayson, K. Dockstader, M. Wright, and M. Costea. Department of Biology, Wilfrid Laurier University, Waterloo, Ontario, Canada N2L 3C5 (e-mail: rivi4120@mylaurier.ca)

Infrastaminal scales (IFS) are staminode-like structures that surround the ovary in the flowers of the parasitic genus *Cuscuta* L. Their diversity has historically provided some of the most useful taxonomic characters in the genus. We have performed a comparative study of the IFS in 145 taxa using light and scanning electron microscopy, and results were analyzed in relation to a phylogeny obtained from a combined analysis of rbcL and 26S rDNA gene sequences. With a few exceptions, the IFS exhibit numerous fimbriae that contain laticifer cells secreting a resin glycoside latex. We have observed several evolutionary trends within the three subgenera of *Cuscuta*. In the most ancestral lineage of *Cuscuta*, subgenus *Monogynella*, laticifers are entirely exposed and fimbriae are similar to uniseriate glandular hairs. In the subgenera *Grammica* and *Cuscuta*, laticifers are enclosed and protected by an epidermis. In these subgenera, however, the distal ends of the fimbriae remain "open", not covered by the epidermis, and the exposed ends of laticifer cells protrude from the fimbriae. The slightest mechanical contact with the exposed part of the laticifer cells (for example by an insect) causes them to burst open and release the latex. For this reason, we hypothesize that IFS are involved in the defense

of the ovary against insect herbivory. In three of the fifteen clades of subgenus *Grammica*, IFS have undergone a reduction trend, and in some species they are completely absent. In Clade O from the same subgenus, we observed papillae on the fimbriae, a feature that appears to be an apomorphy. Our study confirms the diversity of the IFS in *Cuscuta*, and strongly suggests that different structures have a functional and evolutionary significance. In addition, IFS characters are useful for the systematics and taxonomy of the genus.

CBA-S10 **Patterns of organic nitrogen utilization in fungal root endophytes** E.A Fraser[1]*; G. Kernaghan[1]. [1]Biology Department, Mount Saint Vincent University, Halifax NS, B3M 2J6

Fungal root endophytes colonize plant root tissue internally and asymptomatically. Although their ecological function remains unknown, fungal root endophytes can potentially mineralize organic nitrogen in the soil and make the resulting nitrogen more available to host plant roots. In order to elucidate patterns of organic nitrogen utilization in fungal root endophytes, seven root endophyte species (three isolates each, with the exception of one species) were grown on six types of liquid media, each containing a different organic nitrogen source (two proteins, three amino acids and urea), as well as ammonium sulphate as an inorganic control. Media were buffered against pH shifts during fungal growth. Endophytes were grown for 33 or 66 days (depending on growth rate), filtered, oven-dried and weighed. Protease production by two dark-septate endophyte species was quantified by culture in protein-rich liquid media and using the fluorescent signal produced by the enzymatic degradation of fluorescein-isothiocyanate-labelled casein. All species tested generally grew better on organic nitrogen than on inorganic nitrogen. The endophyte *Oideodendron maius* (G.L. Barron) showed consistently and significantly better growth on proteins than on ammonium sulphate, while only some isolates of the other six species grew significantly better on protein. *Phialocephala fortinii* (Wang & Wilcox) and *P. sphaeroides* (Wilson) had contrasting abilities to degrade protein, which was reflected in differences in protease production. Although the ability to utilize organic nitrogen varied dramatically among and within species, the fact that all fungal root endophytes tested were able to successfully utilize organic nitrogen, especially in complex forms such as proteins, provides evidence for their potential role in supplying their host plants with more accessible forms of soil nitrogen.

CBA-S11 **Effect of different environmental conditions on fecundity of three saxicolous lichens on the Precambrian Shield in Manitoba.** C. Deduke[1]* and M. D. Piercey-Normore[2]. [1]Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada, R3T 2N2 (email: umdeduke@cc.umanitoba.ca); and [2]Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada, R3T 2N2

Three saxicolous lichens, *Arctoparmelia centrifuga* (L.) Hale, *Xanthoparmelia viriduloumbrina* (Gyeln.) Lendemer and *Xanthoparmelia cumberlandia* (Gyeln.) Hale all contain usnic acid, which has previously been suggested to protect developing spores and algae from excess UV light. All three species are also important early colonizers of the exposed bedrock and may play a significant role in community structure of the Precambrian shield. Therefore an understanding of fecundity of these species would be valuable to predict success in light of changing environmental conditions. The objective was to determine whether geographic location would show differences in fecundity and secondary compound production. Twenty-nine transects among three locations produced

almost 300 samples of the three species. Apothecia were collected for each species, where present, and placed onto spore rain plates in the lab to measure spore dispersal and germination. These spore rains were monitored for twenty weeks and 310 apothecia were examined (*A. centrifuga* (73), *X. viriduloumbrina* (147) and *X. cumberlandia* (90)). Quantified thin layer chromatography (TLC) was used to determine the presence and quantity of secondary compounds. The weight of each thallus sample was standardized to 5.0 mg. *A. centrifuga* was present only in the northwestern site, while both *Xanthoparmelia* species were present in all three sites. Contamination did not become a problem until the spores were released from the apothecia, suggesting contaminants were present within apothecia. Rate of germination among the three species was similar and began 1-4 weeks after the cultures were initiated. Preliminary data suggests that the average number of apothecia per thallus was higher in the northern sites for *X. viriduloumbrina*. Spore rain data shows that *A. centrifuga* produced the largest number of spores. Data will be further explored for relationships between geographic location, fecundity, and secondary metabolite production.

CBA-S12 **Are synthetic substrates substitutable for coarse woody debris?** Sean R. Haughian*(email: sean.haughian@unb.ca), Katherine A. Frego (email: frego@unb.ca). University of New Brunswick, PO Box 5050, Saint John, NB, E2L-4L5

Observational research has repeatedly shown that epixylic (growing on wood) bryophyte growth and diversity positively associates with log size and decay stage in boreal and temperate forests, but manipulative experimentation has lagged behind, leaving much room for speculation as to the mechanisms behind this pattern. Microclimate regulation is one potential mechanism; because larger logs hold more water, and more decayed (and therefore more porous) logs likely lose water faster, logs that are both large and well-decayed should be much better at both supplying and maintaining surficial humidity than smaller ones. Our goal was to find experimental substrates that allow us to manipulate moisture levels while controlling for other potentially important mechanisms such as chemistry, biology, and/or shape, as a first step towards testing microclimate regulation as the primary mechanism of influence. Four synthetic substrates (floral foam, mattress foam, and two kinds of upholstery stuffing), and four natural substrates (fresh vs. well-decayed, and drying-oven sterilized vs. air-dried logs) were thoroughly soaked in distilled water, and set in a growth cart with constant temperature and light exposure. Substrates were left to dry at ambient conditions with temperature and RH sensors fixed to the surface for ten days, and compared for their moisture supplying and maintaining abilities. The substrates that supplied moisture most abundantly and consistently were then chosen to test bryophyte growth, after which they were all re-wetted and inoculated with vegetative propagules of a representative epixylic bryophyte in the genus *Dicranum*. Substrates were watered regularly over the next 6 weeks, and the resulting growth was measured as the average length of new shoots. Preliminary observations show that wet floral foam holds more water and retains it for longer than other synthetic substrates, but does not maintain surficial humidity at high levels. Results will be used to inform field-experiments examining ways to promote epixylic bryophyte diversity in managed forests.

CBA-S13 **In vivo evidence for mitochondrial involvement during developmentally regulated programmed cell death during lace plant leaf morphogenesis.** Ms. Jaime Wertman*, Christina Lord and Arunika Gunawardena, Dalhousie University, 1355 Oxford St. Room 6076, Halifax, NS, Canada

Developmentally regulated programmed cell death (PCD) is a form of cell suicide

involved in the normal development of animals and plants. Much is known about the catalytic role of the mitochondria in animal PCD, but less is known about its role in plant development. The aquatic lace plant, Aponogeton madagascariensis, provides an excellent species to study developmental PCD in vivo. The predictability and accessibility of perforation formation, in addition to the transparent nature of the leaf, facilitate live cell imaging. In between the transverse and longitudinal veins of immature leaves, there is a gradient of PCD that can be observed: cells in the centre of this area in are in the late stages of cell death (LPCD), cells outside of this area are in the early stages of death (EPCD), and the cells bordering the vascular tissue will not undergo PCD (NPCD). This gradient is used to characterize mitochondrial dynamics throughout the PCD process, via histological staining with the membrane permeability-dependent dye, CMXRos. Results depict four distinct stages of mitochondrial dynamics throughout the gradient of NPCD-LPCD (M1-M4). Control cells, or NPCD cells, contain M1 mitochondria that are singular. EPCD cells display mitochondrial aggregates, characteristic of the M2 stage. LPCD cells contain M3 and M4 mitochondria; M3 mitochondria have stopped moving, and M4 mitochondria have lost fluorescence, indicating they have undergone the mitochondrial permeability transition (MPT). The occurrence of reactive oxygen species (ROS) during PCD was investigated and demonstrates the presence of ROS during EPCD and LPCD stages. Future work involves the localization of ROS in relation to both chloroplasts and mitochondria, via fluorescent staining.

CBA-S14 **Ethylene: does it induce developmentally regulated PCD during lace plant leaf morphogenesis?** Adrian Dauphinee and Arunika Gunawardena, Dalhousie University, Halifax, NS Canada

The lace plant (*Aponogeton madagascariensis*) is a fully submerged monocot endemic to Madagascar. The lace plant is one of the only known species to produce a complex leaf morphology by deleting cells through developmentally regulated programmed cell death (PCD). PCD during lace plant leaf morphogenesis begins in the center of the areoles, which are the areas between longitudinal and transverse veins. PCD begins in the center of the areoles and expands outwards, stopping 4-5 cell layers before the veins. The result is a perforated mature leaf that has the appearance of lacework, hence the common name. The lace plant provides an excellent system for studying PCD, however the developmental signals responsible for the induction of cell death during leaf morphogenesis remain unknown. Ethylene is a crucial phytohormone that plays a significant role in growth and development in higher order plants. The objective of this study was to investigate the role of ethylene in the induction of developmentally regulated PCD in the lace plant. To achieve this goal, the effects on morphology and the ethylene production of lace plants were evaluated following treatment with either the ethylene biosynthesis inhibitor aminoethoxyvinylglycine (AVG), or the promoter 1-aminocyclopropane-1-carboxylic acid (ACC). Ethylene values for AVG treated plants were significantly lower than control plants, and ACC treated plants had significantly higher ethylene concentrations. The leaves produced following the application of AVG showed a significant reduction in perforations compared to controls, suggesting that ethylene may play a role in the induction of PCD during lace plant leaf morphogenesis. There was no significant change in the number of perforations formed in ACC treated plants. Current investigation is determining the effects of a combination of AVG and ACC on morphology and ethylene production. The link between ethylene and anthocyanins is also being investigated, to elucidate their interaction during lace plant PCD signalling.

CBA-S15 **Determination of rooting activity present in commercial seaweed extracts derived from *Ascophyllum nodosum, Macrocystis integrifolia* and *Ecklonia maxima***. E.J. Whitcomb[1], D. Kristie[1], C. Craft[2] and S. MacKinnon[2]. [1]Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6; and [2]National Research Council- Institute for Marine Biosciences, Halifax, Nova Scotia, Canada B3H 3Z1

Extracts derived from various species of brown algae are known to benefit crop performance. Despite numerous studies on the effects of these products, the bioactive compounds responsible remain largely unknown. Objectives of this study were to attempt to isolate the compounds responsible for the high levels of rooting activity present within three seaweed extracts (SWEs), Acadian Marine Plant Extract Fertilizer (ASL), Kelpgrow Liquid Seaweed Extract (Kelpgrow) and Kelpak Liquid Seaweed Bioregulator (Kelpak). We also examined whether laminarin, a storage polysaccharide found in brown algae, could induce rooting effects similar to that of the SWEs. Fractions of the SWEs less than and greater than 1,000 MW or 13,000 MW were obtained by dialysis and tested using the Mung Bean Adventitious Rooting Bioassay. All three SWEs were able to elicit a significant rooting response; Kelpak elicited a rooting response characteristic of auxins as the majority of its rooting activity is found in its LMW (<13,000 MW) fraction and the roots generated resemble those induced by auxins. The root initiating activity of both ASL and Kelpgrow appeared to be split between molecules greater than 13,000 MW and smaller than 1,000 MW; however, root morphology suggested that the LMW compounds are not auxins. Commercial laminarin elicited a rooting response at concentrations found in SWEs that was similar to the extracts in both numbers and morphology. This activity was eliminated by digestion with laminarinase. The rooting activity of partially purified laminarin extracted from the SWEs and the possible role of laminarin in rooting activity of SWEs will be discussed.

CBA-S16 **Determination of diurnal rhythms in stem and leaf elongation rate in barley, oats, and corn, using rotary motion sensors.** J. P. Ross[1]*, J.Kusakina[2] and D. N. Kristie[1] [1]Department of Biology, Acadia University, Wolfville, N.S., Canada, B4P 2R6; and [2]Department of Biology, University of York, York, YO10 5DD, UK

Diurnal rhythms in stem elongation rates (SER) have been studied extensively in many dicots, particularly in the floriculture literature (Neily *et al*., 2000, HortScience 35(1):39-42). In contrast, there have been few studies on the diurnal rhythms of SER and leaf elongation rate (LER) in monocots. In this project, the diurnal rhythms of SER and LER in barley (*Hordeum vulgare* L. cv.'Chapais', oats (*Avena sativa* L. cv.'Triple Crown'), and corn (*Zea mays* L. cv.'Miracle') were examined under greenhouse conditions during May to August 2010. All measurements were made using rotary motion sensors (RMSs) connected to a LabPro interface (www.vernier.com) and then downloaded to a computer using a TI 84 calculator. Corn LER showed a peak during mid-day, with a trough occurring primarily at night. Oat leaf extension, however, exhibited a broad peak in growth rate during the night. Interestingly, barley showed a peak in LER during the day for leaves 2, 3 and 4, but the peak gradually shifted towards the night for leaves 5, 6 and 7. The stem elongation rate for both barley and oats showed a peak in elongation during the night. Overall, it is apparent that patterns of LER vary among cereals, with some species exhibiting peak elongation during the day, some at night, and others seeming to exhibit a shift in the peak of LER during later stages of development. Further studies will examine factors influencing the phase and amplitude of these rhythms.

CBA-S17 **Assessment and propagation of *Lippia integrifolia* (Griseb.) Hieron. wild germplasm, a native species from Argentina**. P.C. Brunetti[1]*, L.E. Torres[1], M.S. Ojeda[1] and S.I. Cameron[2]. [1] Facultad de Ciencias Agropecuarias, Universidad Nacional de Córdoba, Av.Valparaíso s/n C.U.CP:5000, Argentina (Paula.Brunetti@NRCan-RNCan.gc.ca) and [2]Canadian Forest Service, 1350 Regent St., Fredericton, N.B.E3C 2G6, Canada

Lippia integrifolia (Verbenaceae) is an aromatic woody perennial shrub, popularly known as "incayuyo", that grows in northwest and central Argentina. It is a native species of major economic importance currently under intensive harvesting pressure in the wild, according to the National Institute of Agricultural Technology of Argentina, due to its highly value medicinal uses and aromatic properties. Chemically the essential oil is composed of the terpenes camphor, limonene, camphene, methyl-isoeugenol, and the sesquiterpenes lippifoliane, bicyclo germacrene and africanane. The latter compound is of particular interest because *L. integrifolia* is the only plant species in which this compound is found. Morphological diversity within the species is high and has been studied in 5 populations, recording morphometric characters as the length of the longest branch (LB), height of the plant (HP), longest and shortest plant canopy diameter, growth form and number of primary branches (PB). Principal Component Analysis showed that the first two components explained 100% of the variability among populations. The most significant component for axis one were LB and HP (related to soil and climatic conditions), and PB for axis 2 (related to pressure of the resource collection). The germination percentage obtained was only between 0-7% for 32 of 45 samples collected within populations, so the rate of natural regeneration is very low. Asexual propagation thus far has only been successfully demonstrated using apical cuttings. Given its low rate of sexual and asexual reproduction, development of high efficiency methods would be of considerable value. For the multiplication in vitro, we have found MSG medium supplemented with KT/BA 1/0.2 mg/L an effective combination of hormones to induce frequent organogenesis from leaf segments, and MSG without hormones can be used for rooting of the shoots obtained. High frequency propagation may allow commercial scale field cropping, thereby relieving some of the harvesting pressure on wild populations.

CBA-S18 **Phylogeography and colonization history of the invasive Mediterranean annual grass *Avena barbata* in California**. Kate Crosby and Robert G. Latta, Department of Biology Dalhousie University, Halifax, NS, Canada B3H 4J1 (crosbyk@dal.ca)

Biological invasions may be hastened by recombination or hybridization from lineages originating from different sources, and might help invasives adapt to new habitats. Avena barbata is a highly-selfing invasive annual grass thought to have been introduced to California, USA within the past 200 years from Mediterranean Europe. We screened 25 current Californian accessions along with 25 old-world accessions ranging from the Canary Islands to central Iran with six variable chloroplast DNA (cpDNA) markers to evaluate the potential number of introductions that have occurred in California and to assess patterns of seed dispersal. There was a surprisingly small amount of variable sites for these cpDNA markers within both A. barbata's home and introduced range implying very recent divergence. Our preliminary results indicate that Californian lineages root to at least two separate points in its home range suggesting that there have been multiple introductions to California. This result supports the possibility that recombination could have occurred between different genotypes in California; however, this has yet to be confirmed. Further work with amplified fragment length polymophism (AFLP) nuclear markers will help determine the amount of recombination that has occurred between individuals in California and abroad.

Canadian Society of Plant Physiologists

Student Posters

CSPP- S1 **The impact of artificial night lighting in an urban environment on plant photosynthesis and gene expression.** J. Skaf[†1*], E. T. Hamanishi[†2], K. Braeutigam[1], O. Wilkins[1], S. Raj[1], M. M. Campbell[1, 3]. [1]Department of Cell & Systems Biology, University of Toronto, Toronto, Ontario, Canada M5S 3B2 (e-mail: joseph.skaf@utoronto.ca); [2]Faculty of Forestry, University of Toronto, Toronto, Ontario, Canada M5S 3B2; and [3]Centre for the Analysis of Genome Evolution & Function, University of Toronto, Toronto, Ontario, Canada M5S 3B2. [†]Contributed equally

Urban regions of the planet have a great amount of illumination at night due to artificial nighttime lighting (ANL), yet little is known how this may impact plants. Despite its prevalence in urban environments, little is known about how plants respond to ANL. The experiments presented here aim to test the hypothesis that ANL affects plant photosynthesis and transcript abundance patterns. To this end, trees of two genotypes of *Populus balsamifera* were planted in a stereotypical urban setting, where one half of the plants were exposed to ANL and, as a control, the other half were not. Net leaf carbon assimilation rate (A_N) of the trees was examined at four hour intervals throughout a 40 h time period. During the day, trees exposed to ANL showed lower levels of A_N than the control trees (Wilcoxon rank sum test, $P < 0.05$). Conversely, trees exposed to ANL showed higher levels of A_N at night than the control trees (Wilcoxon rank sum test, $P < 0.05$). This may suggest ANL perturbs the A_N levels of plants during day and night. Current experiments aim to test the hypothesis that ANL also affects trends of transcript abundance for diel-regulated genes. These findings will provide insights into the impact of ANL on plants in an urban environment.

CSPP-S2 **An evaluation of photoacclimation in *Chlamydomonas reinhardtii* using metabolomics and targeted expression analysis.** M Davis[1*], O Fiehn[2] and DG Durnford[1]. [1]Biology Department, University of New Brunswick, P.O. Box 4400, Fredericton, N.B., Canada, E3B 5A3 (email:f7iek@unb.ca); and [2] Davis Genome Centre, University of California, Davis, CA 95616 USA

Light energy is essential for photosynthesis, however high-light (HL) intensity causes photo-oxidative damage in photosynthetic cells. Photosynthetic organisms have evolved several photo-protective responses to cope with changes in light intensity. Here, we examine the metabolic changes during photoacclimation in *Chlamydomonas* during light stress using nuclear magnetic resonance (NMR) and mass spectrometry (GC/MS). Metabolic profiles obtained were evaluated using unsupervised and supervised multivariate statistical techniques. Principal component analysis (PCA) performed on NMR profiles revealed a clear short and long-term response to HL exposure in the intra- and extracellular metabolome of *Chlamydomonas*. Using GC/MS profiles, a significant increase in the abundance of photo-protective metabolites, ascorbate and dehydroascorbate, was observed over long-term HL exposure ($\geq$ 8 h). Our results also indicate that the amino acids identified in the metabolic profiles contribute significantly to the differences in the metabolic status of *Chlamydomonas* during light stress. Since

changes in metabolite concentration or flux through pathways may initiate compensatory changes in gene expression, expression analysis of select nuclear encoded genes whose products are involved in photosynthesis and metabolism of photosynthates was performed using real time-PCR. We observed a classic photoacclimatory response for plastid-localized gene products involved in the light reactions (Lhcbm6, PsaE) plus the malate shuttle (MDH1); gene expression declines rapidly within 2 h following a shift into HL, followed by gradual recovery in gene expression with continued HL exposure. By contrast, genes involved in the glyoxylate cycle (GYD1 and MAS1) and targeted to mitochondria and glyoxysome, respectively, are both induced after 30 min of HL, and expression oscillates with continued HL exposure. GYD1 and MAS1 contribute to metabolite pools involved in nitrogen assimilation that leads to the production of reducing equivalents that may play a direct role in balancing the high energy requirement during HL-acclimation.

CSPP- S3 **Inorganic carbon uptake at acid pH by the alga *Chlorella kessleri*.** O. El-Ansari*, and B. Colman. Department of Biology, York University, Toronto, Ontario, Canada M3J 1P3

Green eukaryotic microalgae when grown at alkaline pH express a CO_2-concentrating mechanism (CCM) which consists of active CO_2 and/or active bicarbonate uptake creating a high internal concentration of inorganic carbon (C_i) at the site of the carboxylating enzyme Rubisco. The ability to accumulate inorganic carbon increases the rate of carbon fixation and suppresses photorespiration. Some green algae have a wide pH range of growth, and at acid pH where CO_2 is the only form of C_i available, they appear not to require a CCM. The ability of the freshwater alga, *Chlorella kessleri*, to maintain a carbon concentrating mechanism at low pH was investigated. The alga grows over the pH range 4.0 to 9.0 and was found to take up bicarbonate and CO_2 actively at pH 6.0. At acid pH (below 5.5), *C. kessleri* does not have active bicarbonate or CO_2 uptake, but relies solely on the diffusion of CO_2 for photosynthesis. Glycolate release was detected colorimetrically indicating that *C. kessleri* cells are susceptible to photorespiration at acid pH. *C. kessleri* has a low affinity for CO_2 due to its high $K_{1/2}(CO_2)$. Therefore, the alga does not have a carbon concentrating mechanism when grown at acid pH but maintains an adequate supply of CO_2 by diffusive uptake making the alga vulnerable to photorespiration.

CSPP-S4 ***Brachypodium distachyon*: a valuable model to understand cold tolerance in temperate cereals?** Jean-Benoit Charron and Katia Colton-Gagnon, McGill University, 21,111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC, H9X 3V9

Cold tolerance is a critical trait for temperate cereals and crop losses due to cold and freezing stresses are still very significant in Canada The exposure to low non-freezing temperatures, a process known as cold acclimation, can initiate vernalization and freezing tolerance in plants. To date, several vernalization and cold-regulated genes with a functional role in freezing tolerance have been identified. The capacities of the cereal crop model *Brachypodium distachyon* to cold acclimate and develop freezing tolerance are not known. The current study aims at finding if Brachypodium can cold acclimate and resist freezing temperatures similarly as economically important cereals. Since there is a potential link between vernalization and cold acclimation, we will use an integrated approach involving double ridge formation, final leaf number, and electrolyte leakage assays. The double ridge and final leaf number assays will allow us to discover the number of days of cold acclimation required to reach vernalization saturation in the winter accessions. With electrolyte leakage assays, we will be able to classify

Brachypodium accessions as sensitive or tolerant to freezing temperatures. Taken together, the knowledge developed by pursuing this study will validate *Brachypodium distachyon* as a valuable model to study cold tolerance in temperate cereals.

CSPP- S5 **Impact of dormancy genotypes on differential protein expression profiles and redox-sensitive landscape of the proteome in hybrid spring wheat lines.** J. Hu[1]*, B. Hoehn[2], C. Rampitsch[2], R. Knox[3] and N. V. Bykova[1]. [1]Department of Biology, Memorial University of Newfoundland, St. John's, NL, Canada A1B 3X9; [2]Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, MB, Canada R3T 2M9; [3]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada S9H 3X2

Seed survival in the soil and cycling through states of dormancy is a key component determining entry and persistence in ecosystems, and seed dormancy is a major trait altered during domestication of wild species. The potential for dormancy is overcome through the time- and environment-sensitive process of after-ripening that occurs in the dry seed. The dormant condition is not a quiescent state; it is in fact a dynamic state in which cell metabolism is active, but growth is repressed. Dormancy is thought to be under the control of two distinct processes, the accumulation of damaging reactive oxygen species (ROS), a critical level of which leads to dormancy alleviation and a hormonal balance which regulates dormancy directly and also likely interacts with ROS and/or antioxidative pathways. The precise mechanisms by which ROS affect seed dormancy status and germination potential remain to be elucidated. Thiol-disulfide proteins are particularly important for redox-dependent regulation of metabolic and developmental activities in cells as functional 'hotspots' in the proteome. Differential proteomic analysis of six hybrid lines of spring wheat (*Triticum aestivum* L.) doubled haploid population, derived from the cross 8021-V2 (high dormancy) X AC Karma (low dormancy) segregating transgressively for dormancy phenotype, and two parent genotypes, was used to gain further insight into biochemical mechanisms underlying dormancy controlling events. The thiol redox-sensitive and the total proteome were quantitatively monitored by 2D-gel electrophoresis combined with solubility-based protein fractionation, fluorescent thiol-specific labelling, and mass spectrometry analysis in conjunction with wheat EST sequence libraries. We show, for the first time, that in dormant seeds, there is a shift in the accumulation of proteins from those active in biosynthesis and metabolism to those with roles in storage and protection against biotic and abiotic stresses. The results give an insight into the dormancy-related alteration of thiol-redox profiles in seed proteins that function in a number of major processes in seed physiology. The proteomic data provide evidence for an increased capacity of potent antioxidant machinery in seeds of high non-deep physiological dormancy wheat genotypes, which could be coupled with their ability to regenerate antioxidant systems rapidly upon rehydration for dormancy maintenance.

CSPP-S6 **The effect of Gluconacetobacter diazotrophicus on growth parameters of sugar beet (Beta vulgaris L.) grown under greenhouse conditions.** J. Z. MacDougall*, H. Fei, and J. K. Vessey. Department of Biology, Saint Mary's University (e-mail: zachary.macdougall@SMU.CA)

The agricultural sector in Canada is responsible for approximately 10% of our total national greenhouse gas emissions. The production and use of synthetic fertilizers accounts for a large portion of these emissions. Nitrogen fertilizer has an especially large impact on emissions due to the energy intensive methods used in its production, and the

ability of soil microbes to denitrify N-fertilizer. Denitrification can result in the production of nitrous oxide, a greenhouse gas 310 times more effective at trapping heat then CO2. There has been great interest in recent years in reducing greenhouse gas emissions through the use of biofuels. However current feed stocks used in North America are not as efficient as those used elsewhere. For example, in Brazil a large percentage of cars run on ethanol produced from sugar cane. One of the reasons this is feasible is that much of the sugar cane grown in Brazil is gown under low nitrogen input systems, without significantly reducing harvests. Sugar beet (*Beta vulgaris* L.) is a sucrose rich crop grown in temperate regions used as a feedstock in the production of ethanol. One way to increase the efficiency of ethanol production from sugar beet would be to decrease the necessary inputs for its cultivation. Nitrogen fertilizer is one of the major inputs for sugar beet cultivation; representing almost half of the required energy inputs for this crop. *Gluconacetobacter diazotrophicus* is a bacterium which fixes nitrogen in sugar cane, and it has been shown that this bacterium is able to colonize sugar beet. Our work addresses the use of this nitrogen-fixing bacterium to reduce the N-fertilizer requirements of sugar beet. We will look at the effects of initial bacterial concentrations in the inoculant, different levels of nitrogen fertilization and the effect of plant cultivar on the growth, sucrose concentration and nitrogen status of inoculated and non-inoculated plants under green house conditions in field soil.

CSPP- S7 ***In vivo* multi-site regulatory phosphorylation of bacterial-type phosphoenolpyruvate carboxylase from developing castor oil seeds.** K. Dalziel*, B. O'Leary, and W. C. Plaxton. Department of Biology, Queen's University, Kingston, Ontario, Canada K7L 3N6

Phosphoenolpyruvate carboxylase (PEPC) is a tightly controlled anaplerotic enzyme situated at a pivotal branchpoint of plant C-metabolism. Plant genomes encode several closely related plant-type PEPC (PTPC) isozymes, and a distantly related bacterial-type PEPC (BTPC). Two physically and kinetically distinct oligomeric PEPC classes occur in the endosperm of developing castor oil seeds (COS). Class-1 PEPC is a typical homotetramer composed of 107-kDa PTPC subunits, whereas the novel 910-kDa Class-2 PEPC hetero-octameric complex arises from a tight interaction between Class-1 PEPC and 118-kDa bacterial-type PEPC (BTPC) subunits (Gennidakis *et al*. 2007 Plant J). BTPC functions as a catalytic and regulatory subunit of the allosterically-desensitized Class-2 PEPC (O'Leary *et al*. 2009 J Biol Chem), hypothesized to support massive PEP-flux to malate for leucoplast fatty acid synthesis. Uhrig *et al*. (2008 Plant Physiol) provided evidence that the BTPC subunits of COS Class-2 PEPC are phosphorylated at multiple sites *in vivo*. LC MS/MS and LTQ-FT MS confirmed that Thr^{4}, Ser^{425}, and Ser^{451} are novel *in vivo* phosphorylation sites of COS BTPC (corresponding to acidophilic, Pro-directed, and basophilic protein kinase consensus sequences, respectively). Phosphopeptide antibodies have been raised to assess site-specific changes in BTPC phosphorylation during COS development and environmental perturbations. Kinetic effects of each phosphorylation site were examined using phospho-mimetic mutants of heterologously expressed COS BTPC. Our recent study established that BTPC phosphorylation at Ser^{425} provides a new tier of enzyme control in developing COS (O'Leary *et al.* 2010 Biochem J). BTPC's phosphorylation at Ser^{451} also appears to be inhibitory, as reflected by significantly increased K_m(PEP) values, and reduced I_{50}(malate) and I_{50}(Asp) values. By contrast, kinetic characterization of a T4D phosphomimetic mutant indicated that Thr^{4} phosphorylation is not regulatory in nature. However, Thr^{4} exists in a conserved FHA (forkhead-associated) binding domain (pTXXD) that have received considerable prominence as pThr-dependent protein

interaction modules. The physiological and metabolic implications of multisite *in vivo* phosphorylation of COS BTPC will be discussed. (supported by NSERC)

CSPP-S8 **Molecular and biochemical characterization of SUS1: a cytosolic sucrose synthase from developing castor oilseeds**. E. T. Fedosejevs* and W. C. Plaxton. Department of Biology, Queen's University, Kingston, Ontario, Canada K7L 3N6

Seed development requires a large influx of carbon and energy in the form of sucrose, which must be cleaved enzymatically as an initial step in the biosynthesis of storage end products. Sucrose synthase (SUS) is a key player in this process, catalyzing the UDP-dependent cleavage of sucrose into UDP-glucose and fructose. SUS has not been well-studied in developing oilseeds, and its role in oilseed carbon partitioning remains largely unexplored. The castor plant (*Ricinus communis*) is an ideal system for studies of oilseed SUS, as it has a sequenced genome and a high yield of large oil-rich seeds (>60% oil by weight). Five *SUS* genes were identified in the castor genome and their deduced polypeptides were compared to characterized SUS orthologs using multiple sequence alignment and phylogenetic analysis. Based on semi-quantitative RT-PCR, *SUS1* was the most transcriptionally-abundant isozyme in developing castor oilseed (COS) endosperm and cotyledons. *SUS1* expression was maximal early during COS development, whereas SUS activity and 93-kDa immunoreactive polypeptides peaked during mid-development and declined thereafter. No *SUS1* transcripts, SUS activity or SUS polypeptides were detected in the endosperm of fully mature seeds. SUS1's cytosolic localization was demonstrated by transient expression of a SUS1-GFP fusion protein in tobacco BY2 cells followed by imaging via epifluorescence microscopy. A SUS homotetramer composed of 93-kDa subunits was purified 170-fold to homogeneity (Sp. Act. = 3.5 units mg^{-1}) from developing COS using FPLC and identified as SUS1 by LC MS/MS sequencing of its tryptic peptides. Immunoblots probed with phosphorylation site-specific antibodies demonstrated that the purified SUS1 was phosphorylated at Ser^{11}. Work is in progress to characterize the: (i) pattern of *in vivo* SUS1 phosphorylation throughout COS development, (ii) influence of SUS1 phosphorylation on the enzyme's substrate saturation kinetics, and response to assay pH and allosteric effectors, and (iii) Ca^{2+}-dependent protein kinase that *in vivo* phosphorylates SUS1 in developing COS.

CSPP- S9 **Identification and biochemical characterization of apple glyoxylate reductase isoforms** C. Brikis[1]*; C.P.Trobacher; G.G. Bozzo[1]; J. DeEll[2]; B. J. Shelp[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1 (e-mail: cbrikis@uoguelph.ca); [2]Ontario Ministry of Agriculture Food and Rural Affairs, Simcoe, Ontario, Canada N3Y 4N5

Complementation of a succinic semialdehyde dehydrogenase-deficient yeast mutant with an *Arabidopsis* cDNA library enabled the identification of a novel cDNA (encoding cytosolic glyoxylate reductase1/succinic semialdehyde reductase or GLYR1), which when reinserted into the yeast mutant enables growth on GABA as the sole N source and results in the accumulation of γ–hydroxybutyrate. Subsequent research identified a plastidial GLYR isoform (GLYR2) in *Arabidopsis* (57% amino acid identity to GLYR1), demonstrated that GHB accumulation is a general response in plant leaves to abiotic stress, and established that recombinant proteins of both GLYR1 and 2 can reduce both SSA and glyoxylate to their corresponding alcohols. Here, we cloned two putative 'Empire' apple GLYR isoforms that possess 55% amino acid identity to each other and 54-79% identity to the *Arabidopsis* isoforms. The cDNAs for the apple GLYRs were expressed in *Escherichia coli* and the recombinant proteins purified for biochemical

characterization. To date, NADPH-based assays indicated that at an optimum pH of 7.3, GLYR2 has a K_m for SSA of about 5 mM, K_m for glyoxylate of about 18 µM, and a K_m for NADPH of 2-5 µM. Currently, the substrate specificity of GLYR1 is under investigation. This study will contribute to our understanding of aldehyde detoxification in plants and to future research on the comparative physiological role(s) of the GLYR isoforms in leaf and fruit tissues during exposure to abiotic stress.

CSPP-S10 **Biomechanics of stems and hypocotyls in *Arabidopsis thaliana* (L.) Heynh.** N. Hristozov[1*], T. R. Faisal[2], D. Pasini[2], and T. L. Western[1]. [1]Department of Biology, McGill University, Montreal, Quebec, Canada H3A 1B1 (e-mail: nicolay.hristozov@mail.mcgill.ca); [2]Department of Mechanical Engineering, McGill University, Montreal, Quebec, Canada H3A 2K6

While biomechanical factors significantly influence growth, morphogenesis and mechanical stress response in plants, the mechanical properties of plant structures remain largely unexplored. *Arabidopsis thaliana* (L.) Heynh, being amenable to subtle structural modification and well-controlled experimentation, will be used as a model system to elucidate these properties in stems. Stems are understood to be complex hierarchical systems displaying four to seven integrated levels of structural organization, each of which contributes to the mechanical properties of the whole organ. Firstly, to better understand the mechanical significance of these structural features, mechanical tests will be performed on segments of primary inflorescence stem from a set of candidate mutant lines. Ten mutants displaying tissue-level structural defects will be tested, as well as seven mutants displaying altered cell wall chemistry. Samples will be tested in tension, torsion and three-point bending. Additionally, wild type stem segments will be tested from different stages and portions of the stem, representing different degrees of tissue development. Secondly, to better understand the role of cell wall structure and anisotropy in plant cell growth, tests will be performed on etiolated hypocotyls from the aforementioned set of cell wall mutants. Samples will be tested in tension and subjected to creep testing, which simulates turgor-driven elongation. Thirdly, the role of cellulose microfibril angle (MFA) in cell wall anisotropy will be examined using confocal microscopy and pontamine fast scarlet dye. This angle will be measured across the cell wall layers in hypocotyls before and after creep testing. Mutants with altered cell wall anisotropy may display differences in MFA, and may also display difference in MFA reorientation during growth. The data collected from these experiments will serve to develop and validate a multiscale mechanics model of plant stems that integrates the entire hierarchy of structural organization. The integrated model will be used in the development of novel biomimetic materials and structures.

CSPP- S11 **PpASCL, a moss ortholog of anther-specific chalcone synthase-like enzymes, is a hydroxyalkylpyrone synthase involved in an evolutionarily conserved sporopollenin biosynthesis pathway.** C. C. Colpitts[1], R. Daku[1*], S. S. Kim[2], S. E. Posehn[1], C. Jepson[1], S. Y. Kim[1], A. G. H. Wee[1], C. J. Douglas[2], and Dae-Yeon Suh[1]. [1]Department of Chemistry and Biochemistry, University of Regina, Regina, SK S4S 0A2 (e-mail: suhdaey@uregina.ca); and [2]Department of Botany, University of British Columbia, Vancouver, BC V6T 1Z4

Sporopollenin is the main constituent of the exine layer of spore and pollen walls. Recently, several *Arabidopsis* genes including *PKSA*, which encodes an anther-specific chalcone synthase-like enzyme (ASCL), have been shown to be involved in sporopollenin biosynthesis. The genome of the moss *Physcomitrella* contains putative

orthologs of the *Arabidopsis* sporopollenin biosynthesis genes. We analyzed available *Physcomitrella* EST data for putative moss orthologs to the *Arabidopsis* genes of sporopollenin biosynthesis and studied enzymatic properties and reaction mechanism of recombinant PpASCL, the *Physcomitrella* ortholog of *Arabidopsis* PKSA. We also generated structure models of PpASCL and *Arabidopsis* PKSA to study their substrate specificity. *Physcomitrella* orthologs of most *Arabidopsis* genes of sporopollenin biosynthesis were found to be expressed in the sporophyte generation. Similarly to *Arabidopsis* PKSA, PpASCL condenses hydroxyfatty acyl-CoA esters with malonyl-CoA and produces, via *O*-acylation, hydroxyalkyl α-pyrones that probably serve as building blocks of sporopollenin. The ASCL-specific set of Gly-Gly-Ala residues modeled to be at the floor of putative active site is proposed to serve as the opening of an acyl-binding tunnel of ASCL. These results suggest that ASCL functions together with other sporophyte-specific enzymes to provide polyhydroxylated precursors of sporopollenin in a pathway common to land plants. In progress are site-directed mutagenesis to probe the predicted substrate-binding tunnel and gene knockout experiments to further study in planta functions of PpASCL.

CSPP-S12 **Analysis of exogenous protein expression in Flax (*Linum usitatissimum*).** B. Forward[1], M. Jordan[2], T. L. Western[1]. [1]Biology Department, McGill University, Montreal, Quebec, Canada H3A 1B1 (email: bronwen.forward@mail.mcgill.ca); and [2]Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9

The seeds of linseed flax (*Linum usitatissimum* (L.)) are harvested mainly for the oil derived from the embryo. More recently, flax seeds have emerged as a health food product, mainly due to their high levels of lignans, which have been implicated in the reduction of heart disease, prostate, and breast cancers. In addition, the seed coat of flax secretes a thick, pectinaceous mucilage that can be used as a soluble fibre, emulsifier, and a substitute for animal products in food. The mucilage secretory cells (MSCs) of *Arabidopsis thaliana* (L.) Heynh (Arabidopsis) have been well characterized and many genes involved in the synthesis and secretion of mucilage have been determined. This process remains poorly understood in flax, thus a study of MSC differentiation in flax has been initiated. Further, we are investigating a number of potential *RHAMNOSE SYNTHASE* (*RHM*) genes to gain a better understanding of the genes involved in pectin synthesis in flax. In addition to studying the mechanism of pectin secretion and synthesis, we are also interested in harnessing seed coat specific promoters in order to optimize the expression of exogenous proteins as means of producing value-added oilseed crops. Thus far, candidate seed coat promoters for protein expression include *GLABRA2* (*GL2*) from Arabidopsis, *PINORESINOL LARICIRESINOL REDUCTASE*, and the recently identified flax *RHM* gene promoters. Preliminary work with the Arabidopsis *GL2* promoter shows not only strong seed coat expression in flax, but that it targets protein secretion in the mucilage. Through developing a system whereby exogenous proteins can be expressed and secreted to the mucilage of flax seed coats, it could provide a means to easily isolate co-products, which would be removed before the embryos are crushed for oil extraction. Further tests with other candidate promoters will determine the most appropriate system for the expression of exogenous proteins in mucilage produced by flax seed coats.

CSPP-S13 **Regulation of secondary cell wall deposition: Not the usual suspects.** Heather L. Wheeler[1*], Michael E. Stokes[1], Malcolm M. Campbell[2,3] [1]Department of Cell & Systems Biology, University of Toronto, Toronto, Ontario, Canada, M5S 3B2, [2]Department of Cell & Systems Biology, University of Toronto at Scarborough, Toronto, Ontario,

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The secondary cell wall that surrounds xylem and fibre cells of vascular plants is primarily composed of cellulose, hemicellulose, and lignin. It is of high importance biologically and economically, and has therefore been intensely studied. Nevertheless, some aspects of secondary cell wall formation remain poorly understood. To identify new genes that may been involved in secondary cell wall formation, genes that are transcriptionally co-regulated with those encoding the enzymes of the lignin biosynthetic pathway were identified using the Bio-Array Resource (BAR) Expression Angler tool. *Arabidopsis thaliana* mutants with T-DNA insertions within the selected genes were then examined to test the hypothesis that such genes are involved in secondary cell wall formation. Inflorescence stems were sectioned, stained with toluidine blue and phloroglucinol, and examined using microscopy to identify xylem or interfascicular fibre cell wall phenotypes. Mutants were identified that had altered xylem or interfascicular fibre cells with respect to wild type. Mutant phenotypes are being characterised at the cellular, subcellular, molecular and chemical levels, and the genes underpinning the mutant phenotypes examined to better understand their precise contribution to the mutant phenotype.

CSPP-S14 **Fatty acid ω-hydroxylases in soybean.** J. Koteles* and M. A. Bernards. Department of Biology and the Biotron, University of Western Ontario, London, ON, Canada

Soybean (Glycine max) is one of the most widely cultivated crops in the world. A substantial cause of soybean yield loss worldwide is root rot, caused by the pathogen Phytophthora sojae and significant effort has been expended at improving soybean resistance to this devastating pathogen. It has been established that there is a strong correlation between preformed soybean root suberin (especially the poly[aliphatic] component) and high levels of innate resistance to the pathogen P. sojae. Enzymes that have been shown to be of critical importance to suberin biosynthesis and in particular the poly(aliphatic) domain are ω-hydroxylases. These specific enzymes catalyze the terminal carbon hydroxylation of fatty acids that introduces a second functional group into the main monomers allowing them to be cross-linked into a polymeric matrix. Therefore to better understand the relationship between innate resistance to P. sojae and preformed soybean root suberin, the expression, regulation and enzyme function of ω-hydroxylases in soybean must be elucidated. To initiate this research a comparative sequence-based in silico approach, using characterized ω-hydroxylases from Arabidopsis thaliana and *Solanum tuberosum*, was used to identify six putative ω-hydroxylase genes in soybean. We have designed gene specific primers for all six genes and are presently delineating their relative expression in a wide variety of tissues.

CSPP- S15 **Molecular analysis of freezing tolerance in *Brachypodium distachyon*.** J. Demone, McGill University, 21111 Rue Lakeshore, R2-003, Ste-Anne-de-Bellevue, QC, H9X 3V9

To survive freezing temperatures various cereal crop species will acclimate themselves during periods of low, non-freezing temperatures. The acclimation process requires the induction of cold-regulation (COR) gene expression. This set of genes encodes a wide array of structural components and regulatory factors that allow plants to avoid the deleterious effects of freezing damage. Our goal is to see if the induction of regulatory mechanisms of freezing tolerance prevails in *Brachypodium distachyon,* an emerging model plant for cereal crop research. Our initial efforts have consisted of the analysis of

the CBF (C-repeat binding factor) family of genes in *Brachypodium*. CBF genes are key regulators of the freezing tolerance mechanism and encode transcription factors that bind to the promoters of COR genes in response to low temperatures. We have currently identified and classified CBF family genes in *Brachypodium* through bioinformatic analysis and performed real-time PCR analysis to measure CBF gene expression in cold-treated *Brachypodium* plants. By elucidating the function of CBF family genes and other COR gene regulators in *Brachypodium* we hope to further clarify the mechanism of cold tolerance in cereal crops.

CSPP-S16 **Flavonol catabolism: A role for flavonol-3-O-glucosyl hydrolase in *Arabidopsis thaliana.*** J. Roepke[1]*, D. Brewer[2], G. G. Bozzo[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1 (email: jroepke@uoguelph.ca); and [2]Biological Mass Spectrometry Facility University of Guelph, Guelph, Ontario, Canada N1G 2W1

Quercetin (Que) and kaempferol (Kae) 3-*O*-glucoside-7-*O*-rhamnoside conjugates are flavonol diglycosides known to accumulate in *Arabidopsis* during abiotic stress (e.g. nitrogen deficiency, and chilling). However, flavonol diglycoside content and transcripts of flavonol biosynthesis enzymes of *Arabidopsis* seedlings are significantly reduced within 2 d of abiotic stress recovery. Although the enzymatic steps governing flavonol biosynthesis are well known for plants, flavonol catabolism is scantly described. To date, evidence for flavonol catabolism in senescing plant tissues and fungi coincides with the induction of flavonol-3-*O*-glucosyl hydrolase (F3GH) activity. Here, we tested the effect of N-repletion (with 10 mM nitrate) to N-deficient *Arabidopsis* on flavonol glycoside content and F3GH activity. Using reverse phase-HPLC coupled with photodiode array detection, analyses of N-replete *Arabidopsis* plants found no evidence for the accumulation of catabolic products: flavonol monoglycosides and their aglycones. Preliminary evidence indicates that F3GH activity of cell-free extracts (in the presence of quercetin-3-*O*-glucoside) increased by approximately 130% within 3 d of N-repletion to N-deficient *Arabidopsis*. F3GH activity of cell-free *Arabidopsis* extracts incubated with a methanolic extract of N-deficient plants containing a mixture of six flavonol diglycosides, yielded a single product, Kae-7-*O*-rhamnoside, as identified by QTOF-mass spectrometry. Together, these findings point to F3GH activity as an initial enzymatic step in catabolism of flavonol-3-*O*-glucoside-7-*O*-rhamnosides in *Arabidopsis* seedlings during abiotic stress recovery. We are currently investigating the biochemical properties of recombinant *Arabidopsis* glycosyl hydrolases, in order to identify the gene(s) encoding for F3GH.

CSPP- S17 **Regulation of resistant starch biosynthesis in barley.** Zaheer Ahmed*[1], Ian J. Tetlow[1], Duane J. Falk[2] and Michael J. Emes[1]. [1]Department of Molecular and Cellular Biology, University of Guelph, [2]Plant Agriculture, University of Guelph

Starch is an important part of the human diet and is widely used in processed foods in different forms. Some forms are referred to as Resistant Starches (RS) and are nutritionally very important because of their low digestibility in the small intestine and subsequent fermentation in the large colon, reducing glycemic load and improving colon health. However, production of RS is often associated with a reduction in yield in different crops. The present study was conducted to understand the regulation of starch biosynthesis and the relationship between genotype and phenotype of starch in barley. The grains of 33 genotypes of barley were analysed and considerable differences in their content of total and resistant starch observed. In some cereals including barley, starch is

found as two different types of granules, large A and smaller B granules. All the genotypes were analyzed for their A and B granule content, morphology and size. Smaller B-type granules were positively correlated with the amount of RS, while large A granules were negatively correlated with RS. Study of granule surface morphology and size by scanning electron microscopy revealed that all genotypes with a high RS content exhibited altered granule morphology and size. In high RS genotype, the size range of large A granules decreased as compared to reference genotype from 10-45µm to 10-30µm, while the size range of smaller B granules increased from 1.5-10 µm to 3.5-10µm. Several of the enzymes of starch biosynthesis which could give rise to variation in starch structure are known to be entrapped within starch granules, the proteome of which was analyzed. These proteins were identified by immunoblot analysis using antibodies specific to starch synthases (SSI, SSII, SSIII and SSIV), starch branching enzymes (SBEI, SBEIIa and SBEIIb), starch phosphorylase (SP), granule bound starch synthases (GBSS) and debranching enzymes (DBE). An analysis of total granule bound protein and individual granule SS and SBE isoforms found no relationship between the amount of individual granular enzymes and RS content. Further studies involving molecular biology and biochemistry are aimed at understanding the factors which give rise to variation in starch structure in developing barley grain.

CSPP-S18 **Differential signal requirement for Nuclear/Nucleolar localization of Arabidopsis ribosomal proteins RPL23a, RPL15 and RPS8a.** Raghavendra P. Savada & Peta C. Bonham-Smith. Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada, S7N 5E2

Ribosomes, the two-subunit enzymatic complexes comprised of rRNAs and ribosomal proteins (RPs), are responsible for protein synthesis in all organisms. Ribosomal subunit assembly in the nucleolus, is dependent on efficient targeting of RPs from the cytoplasm into the nucleus and nucleolus. Nuclear localization of a protein is generally mediated by one or more specific stretches of basic amino acids, in the form of Nuclear Localization Signals (NLSs). Similarly, nucleolar localization of a protein is thought to be mediated by one or more specific, Nucleolar Localization Signals (NoLSs). In this study, we show that nucleolar localization of Arabidopsis RPL23aA is mediated by a specific number of basic motifs, rather than any single or specific combination of motifs. RPL23aA has eight putative NLSs. Site-directed mutagenesis of any one pNLS had no effect on nuclear or nucleolar localization. Mutation of all pNLSs (50% reduction of total basic charge of the protein) had no effect on nuclear localization, but completely disrupted nucleolar localization, confirming that these pNLSs are not required for nuclear localization, but are required for nucleolar localization (putative NoLSs). Subsequent combinatorial mutations showed that simultaneous mutation of any four pNoLSs (25 % reduction in basic charge) did not affect nucleolar localization. However, serial mutations (in any order) of the remaining pNoLSs disrupted nucleolar localization to varying degrees, with mutation of all eight NoLSs resulting in 100% disruption, confirming that it does not matter which pNoLSs are present for nucleolar localization of RPL23aA, what matters is how many pNoLSs are present - total basic charge. By contrast, in RPS8A and RPL15A (each containing 10 pNLSs), mutation of just two and three N-terminal pNLSs, respectively, disrupted both nuclear and nucleolar localization. The differential signal requirements for nuclear and nucleolar localization, as demonstrated for RPL23aA, RPS8A and RPL15A suggest that different transport mechanisms probably govern the localization of these three RPs.

CSPP- S19 **Photoperiodic injury in tomato (*Solanum lycopersicum* L.) is linked to nitrate uptake and accumulation of nitrite.** M. E. Orozco-Gaeta*, B.J. Micallef. Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1

Photoperiodic injury (PI) is displayed by many plants when placed under long photoperiods, or when light /dark cycles are different than 24 h; PI is characterized by wilting, chlorosis, and necrosis of leaves. Tomato is particularly susceptible to PI. We have previously shown a correlation between PI, accumulation of toxic nitrite, and loss of circadian activities of nitrate reductase (NR) and nitrite reductase (NiR) in a tomato cultivar susceptible to PI under a 24 h photoperiod. The present study examined diel nitrate uptake patterns and physiological responses to different nitrate media concentrations under a 24 h photoperiod using cultivars either tolerant (Micro Tom, MT) or susceptible (Basket Vee, BV) to PI. Nitrite accumulation under a range of photoperiods was also examined. Interestingly, both 'MT' and 'BV' showed a semidian pattern of nitrate uptake even in 24 h light, although 'MT' showed the highest rate of nitrate uptake. The maintenance of semidian nitrate uptake patterns in 24 h light coupled with a loss of circadian coordination between NR and NiR can predispose 'BV' to PI. A reduction in the media nitrate concentration did reduce PI and nitrite accumulation in 'BV'. In 'BV', the severity of PI increased as the photoperiod increased. For 'BV', chlorophyll levels increased, nitrate levels remained stable and nitrite levels decreased over time up to a 16 h photoperiod. In contrast, 'BV' plants subjected to a 20 or 24 h photoperiod showed a reduction in chlorophyll levels after 7 d, the nitrate levels decreased, and the nitrite levels increased significantly. Thus, a correlation was found between severity of PI and nitrite accumulation under different photoperiods. In summary, the data provide evidence that PI in tomato is linked to nitrate uptake and accumulation of toxic levels of nitrite, the first intermediary compound in nitrate assimilation.

CSPP-S20 **Future carbon dioxide levels differentially alter the responses of *Thalassiosira pseudonana* and *Emiliania huxleyi* to light.** A. McCarthy*, S. Rogers, S. J. Duffy and D. A. Campbell. Department of Chemistry & Biochemistry, Mount Allison University, Sackville, Canada, E4L 1G7

The coccolithophore *Emiliania huxleyi* and centric diatom strains *Thalassiosira pseudonana* CCMP 1014 (offshore) and *Thalassiosira pseudonana* CCMP 1335 (coastal) were grown in low-density turbidostat photobioreactors bubbled with air containing 390 ppmv and 750 ppmv CO_2, to evaluate the effects of increased pCO_2 on these species. These partial pressure of CO_2 (pCO_2) levels reproduce the changes predicted to occur to ocean seawater chemistry between now (390 ppmv) and the year 2100 (750 ppmv), including increased concentrations of dissolved carbon dioxide and bicarbonate and decreased pH. The concomitant effects on phytoplankton are now a focus of concern with regard to potential shifts in community structure and primary productivity. Increased pCO_2 has a fertilization effect on growth rates. Furthermore, protein levels of Ribulose-1,5-bisphosphate carboxylase oxygenase (RubisCO) increased in the coastal strains of both *Thalassiosira pseudonana* and *Emiliania huxleyi* at 750 ppmv CO_2, suggesting a higher capacity for CO_2 assimilation. At increased pCO_2, *Thalassiosira pseudonana* suffers an increased susceptibility to Photosystem II (PSII) photoinactivation, resulting in a higher metabolic cost of maintaining PSII function. In contrast, in *Emiliania huxleyi*, pCO_2 did not affect susceptibility to PSII photoinactivation. Surprisingly, the protein content of the photosynthetic electron transport intermediary cytochrome b6f complex

(Cytb6f) increased 2-4 fold in *Thalassiosira pseudonana* under elevated pCO_2, suggesting changes in electron transport function. Electron transport rates estimated from the rate of electron generation from PSII light capture revealed that under increased pCO_2, *Thalassiosira pseudonana* achieves a higher growth rate by increasing the rate of PSII photochemical charge separation events per cell. In contrast, under increased pCO_2 *Emiliania huxleyi* does not change PSII electron generation per cell, yet achieves a higher growth rate. These results may be limited to low light, nutrient replete conditions, since other work shows interactive photophysiological responses to N-limitation.

CSPP- S21 **Determination of rooting activity present in commercial seaweed extracts derived from *Ascophyllum nodosum, Macrocystis integrifolia* and *Ecklonia maxima*.** E.J.Whitcomb[1], D. Kristie[1], C. Craft[2] and S. MacKinnon[2]. [1]Acadia University, Wolfville, Nova Scotia, Canada B4P 2R6; and [2]National Research Council- Institute for Marine Biosciences, Halifax, Nova Scotia, Canada B3H 3Z1

Extracts derived from various species of brown algae are known to benefit crop performance. Despite numerous studies on the effects of these products, the bioactive compounds responsible remain largely unknown. Objectives of this study were to attempt to isolate the compounds responsible for the high levels of rooting activity present within three seaweed extracts (SWEs), Acadian Marine Plant Extract Fertilizer (ASL), Kelpgrow Liquid Seaweed Extract (Kelpgrow) and Kelpak Liquid Seaweed Bioregulator (Kelpak). We also examined whether laminarin, a storage polysaccharide found in brown algae, could induce rooting effects similar to that of the SWEs. Fractions of the SWEs less than and greater than 1,000 MW or 13,000 MW were obtained by dialysis and tested using the Mung Bean Adventitious Rooting Bioassay. All three SWEs were able to elicit a significant rooting response; Kelpak elicited a rooting response characteristic of auxins as the majority of its rooting activity is found in its LMW (<13,000 MW) fraction and the roots generated resemble those induced by auxins. The root initiating activity of both ASL and Kelpgrow appeared to be split between molecules greater than 13,000 MW and smaller than 1,000 MW; however, root morphology suggested that the LMW compounds are not auxins. Commercial laminarin elicited a rooting response at concentrations found in SWEs that was similar to the extracts in both numbers and morphology. This activity was eliminated by digestion with laminarinase. The rooting activity of partially purified laminarin extracted from the SWEs and the possible role of laminarin in rooting activity of SWEs will be discussed.

CSPP-S22 **Determination of diurnal rhythms in stem and leaf elongation rate in barley, oats, and corn, using rotary motion sensors.** J. P. Ross[1]*, J.Kusakina[2] and D. N. Kristie[1] [1]Department of Biology, Acadia University, Wolfville, N.S., Canada, B4P 2R6; and [2]Department of Biology, University of York, York, YO10 5DD, UK

Diurnal rhythms in stem elongation rates (SER) have been studied extensively in many dicots, particularly in the floriculture literature (Neily *et al*., 2000, HortScience 35(1):39-42). In contrast, there have been few studies on the diurnal rhythms of SER and leaf elongation rate (LER) in monocots. In this project, the diurnal rhythms of SER and LER in barley (*Hordeum vulgare* L. cv.'Chapais', oats (*Avena sativa* L. cv.'Triple Crown'), and corn (*Zea mays* L. cv.'Miracle') were examined under greenhouse conditions during May to August 2010. All measurements were made using rotary motion sensors (RMSs) connected to a LabPro interface (www.vernier.com) and then downloaded to a computer using a TI 84 calculator. Corn LER showed a peak during mid-day, with a trough occurring primarily at night. Oat leaf extension, however, exhibited a broad peak in

growth rate during the night. Interestingly, barley showed a peak in LER during the day for leaves 2, 3 and 4, but the peak gradually shifted towards the night for leaves 5, 6 and 7. The stem elongation rate for both barley and oats showed a peak in elongation during the night. Overall, it is apparent that patterns of LER vary among cereals, with some species exhibiting peak elongation during the day, some at night, and others seeming to exhibit a shift in the peak of LER during later stages of development. Further studies will examine factors influencing the phase and amplitude of these rhythms.

CSPP-S23 **Physiological analysis of Arabidopsis Calmodulin-like proteins.** K. W. Bender; B. Vanderbeld; and W. A. Snedden. Department of Biology, Queen's University, Kingston, Ontario, Canada, K7L3N6

In plants, diverse developmentally regulated and stress responsive signal transduction pathways are coordinated by intracellular changes in calcium ion concentration ($[Ca^{2+}]$). These intracellular 'Ca^{2+}-signals' are interpreted by a superfamily of Ca^{2+}-binding proteins known as Ca^{2+}-sensors. The importance of Ca^{2+}-signaling in plant development and stress response is underscored by the expansion of Ca^{2+}-sensor gene families within plant genomes. Work in our lab focuses on one such family – the calmodulin (CaM) and CaM-like (CML) proteins. The Arabidopsis genome encodes a family of 50 *CML* genes whose protein products share 16-75% primary sequence homology with conserved plant CaMs (e.g. Arabidopsis CaM2). Biophysical analysis of recombinant CMLs indicates that, like CaM, they undergo a conformational change upon binding Ca^{2+}, which we hypothesize allows them to interact with and regulate their downstream targets. We have adopted a multi-faceted approach utilizing primarily reverse genetics and protein-protein interaction analyses in order to better understand the physiological functions of a subfamily of Arabidopsis CMLs. Our analysis of transgenic *CML* knockouts has provided insight into their physiological roles and suggests that closely related CMLs have distinct physiological functions.

CSPP-S24 **The basis of ABA phenotypes in *Arabidopsis det1* mutants.** V.C.D. Fernando* and D.F. Schroeder. Department of Biological Sciences, University of Manitoba, Winnipeg, Canada R3T 2N2

Seed germination and seedling development in plants are regulated by both light and phytohormones. Recent studies indicate light and hormone signalling pathways are connected with each other at the molecular level by means of signalling integrators such as LONG HYPOCOTYL 5 (HY5) in *Arabidopsis thaliana*. The phytohormone abscisic acid (ABA), plays an essential role in plant growth, development and as an endogenous messenger in stress signal transduction pathways. Thus, understanding ABA signalling is essential in improving plant performance. Genetic studies of ABA regulation of gene expression and seed germination have identified a number of *Arabidopsis* mutants with altered ABA sensitivities. Preliminary studies reveal that the light signalling mutant *de-etiolated 1 (det1)* shows altered sensitivity to ABA. Several genes including *HY5, ABSCISIC ACID INSENSITIVE 5* (*ABI5*)*, ABI3, DWD HYPERSENSITIVE TO ABA1* (*DWA1*) and *DWA2* potentially interact with both *DET1* and ABA and we are currently investigating which of these intermediates are essential for the *det1* ABA response. The findings of this research will allow us to investigate a novel phenotype involved in ABA signalling in *Arabidopsis* which will ultimately pave the way to improving abiotic stress performance of crop plants.

CSPP- S25 **Restructuring of the photosynthetic machinery of eukaryotes during plastid evolution.** JAD Neilson*, DG Durnford. Department of Biology, University of New Brunswick, Fredericton, NB

Three major lineages of photosynthetic eukaryotes—glaucophytes, red algae, and green plants—evolved from a single endosymbiotic event between a cyanobacterium and a eukaryotic host. Oxygenic photosynthesis then spread laterally through secondary endosymbiosis between a photosynthetic eukaryote and a non-photosynthetic eukaryotic host, giving rise to the great diversity of photosynthetic eukaryotes observed today. While the core of the photosynthetic machinery has remained fairly intact throughout the evolution of these different lineages, there has been extensive modification of the peripheral photosystem proteins and the light-harvesting antenna systems. The functional significance of these changes to the photosynthetic apparatus, especially in secondary endosymbionts, is poorly understood. The purpose of this study is to examine how the composition, organization, and functionality of the photosynthetic machinery has changed during plastid evolution. We began by searching a *Cyanophora paradoxa* (glaucophyte) genome database for peripheral photosystem proteins and light-harvesting antenna to construct a model predicting the composition and organization of the photosystems. Through comparisons to data obtained from cyanobacteria and other photosynthetic eukaryotes, we traced the structural changes in the photosynthetic machinery from each of the three major lineages of primary endosymbionts. To examine how the structure of the photosynthetic machinery changes during secondary endosymbiosis we performed a similar analysis using data mined from the recently completed *Bigelowiella natans* and *Guillardia theta* nuclear genome databases, which are organisms having plastids derived from a green and red alga respectively. Using these models we then made predictions on how the functionality of the photosynthetic machinery has evolved in the three major lineages of primary endosymbionts, and how this functionality has changed during the origin of plastids via secondary endosymbiosis.

CSPP-S26 **The living dead: thyonic reproduction in *Lobelia inflata*.** P.W.D. Hughes[1*] and A.M. Simons[1]. [1]Department of Biology, Carleton University, Ottawa, Canada K1S 5B6 (email: whughes@connect.carleton.ca)

The cause of secondary (i.e. post-senescent) reproductive behaviour in semelparous organisms remains an unsolved problem in life-history evolution. Our research examines 'thyonic' secondary reproduction in the monocarpic biennial *Lobelia inflata* (Campanulaceae), where we evaluate the influence of flowering phenology using an experimental manipulation of 231 plants bolted in four batches from June to September 2008. Previous studies of other semelparous systems explain secondary reproductive behaviour as an adaptation to specific adverse conditions, such as when primary reproductive effort is reduced by external forces (i.e. environmental disturbance, predation etc…). This adaptively plastic life-history is termed 'facultative iteroparity'. We test this hypothesis in a model species whose close evolutionary relationship to iteroparous congenerics suggests an alternative hypothesis: that secondary reproduction can be a vestigial feature of an iteroparous evolutionary history. We found that for *L. inflata*, secondary reproduction occurs in 68.2% of June-bolted plants (representing a mean value of 23.1% of total reproductive output per individual) but wanes significantly across the growing season, down to a low of only 12.1% of plants bolted in September (representing a mean value of 4.8% of total reproductive output per individual). We measured and germinated seeds sampled from primary and secondary reproductive episode fruits on the same stalk, and found that they did not significantly differ in linear

dimension, seed viability or in mean days to germination. We also found that there is no detectible difference between early- and late-bolted plants in terms of key resource indicators (i.e. rosette size at bolting, stem height, etc…) that varies consistently with secondary reproduction. We conclude that it is likely that *L. inflata* is not facultatively iteroparous, and that its thyonic reproduction is an indirect consequence of selection for semelparous reproductive behavior in late-season bolters.

CSPP-S27 **Antioxidant properties of *in vitro* and *ex vitro* propagated lingonberry cultivars**
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Lingonberry (*Vaccinium vitis-idaea* L. ssp *vitis-idaea* Britton) cultivars Regal, Splendor, and Erntedank were obtained by conventional softwood cuttings and by shoot regeneration from excised leaves of micropropagated shoots. Fruits and leaves of these cultivars were monitored for total antioxidant levels in terms of total scavenging activity, activities of antioxidant enzymes and metabolites, mainly phenolics. The activities of enzymes catalase, ascorbate peroxidase, glutathione reductase, dehydroascorbate reductase and monodehydroascorbate reductase were monitored in leaves. Berries of the investigated cultivars were quantified for total soluble phenolics, total flavonoids, for total anthocyanin and tannin contents. Total radical scavenging capacity was monitored in both leaves and berries of these differentially propagated cultivars. It was observed that leaves of plants obtained from the *in vitro* condition showed significantly higher antioxidant enzyme activities except for dehydroascorbate reductase which was approximately at the similar level in plants obtained by both propagation methods. Total soluble phenolics, tannins and flavonoids and total radical scavenging capacity were also found to be enhanced by the *in vitro* propagation method whereas higher anthocyanin content was observed in plants derived from softwood cutting. From this study, it is suggested that the active morphogenetic process is characterized by intensive formation and scavenging of reactive oxygen species which is reflected in the activities of antioxidant enzymes and metabolites as well as in total scavenging capacity. Possible correlations between the growth and morphological characteristics of the studied cultivars and their antioxidant properties are discussed.

CSPP-S28 **Growth of green *Arabidopsis thaliana* cell suspension cultures is dependent on a carbon source but not photosynthesis.**
M. Chung*, M. Krol, A.G. Ivanov, A. Naeem, N.P.A. Huner. The Department of Biology and The Biotrton Experimental Climate Change Research Centre, University of Western Ontario, London, Ontario, N6A 5B7

Plant cell cultures are typically grown in media supplemented with 3% (w/v) sucrose. Addition of an exogenous carbon source, such as sucrose, represses photosynthetic gene expression and chloroplast development resulting in a pale, non-green phenotype. The notion that sucrose represses photosynthetic gene expression remains an important characteristic of our understanding of sucrose sensing/signalling. Although one would expect cell cultures grown in the presence of sucrose to exhibit a non-green phenotype, here we show that *Arabidopsis thaliana* cell cultures remain distinctly green even at concentrations of sucrose as high as 15% (w/v) when grown in the light. However, when no exogenous carbon source was supplemented in the medium, growth was inhibited. Growth of these cell cultures, whether measured as changes in total chlorophyll content,

fresh weight or optical density, was substantial even in the dark when provided with sucrose. Light response curves for CO_2-dependent, O_2 evolution indicated that light-saturated rates of photosynthesis never exceeded the rates of respiration. Thus, these green cells grow below their light compensation points. However, increasing sucrose concentration from 3 to 15% decreased both the apparent quantum yield for O_2 evolution as well as the light saturated rates of photosynthesis. Immunoblots indicated that the major components of the photosynthetic apparatus (Rubisco, PsbA, PsaA, and Lhcb2) are present in these green cells when grown in the light and in the presence of sucrose. Furthermore, these green cells exhibit reversible photoacclimation in response to changes in their light environment. Energy partitioning measured by chlorophyll *a* fluorescence indicate that, in the light, the green cells are in fact dissipating a large portion of the light energy absorbed by both antennae and constitutive quenching mechanisms.

CSPP-S29 **Sub-cellular distribution of cadmium in lettuce (*Lactuca sativa*) and barley (*Hordeum vulgare*) roots using SEM-WDS.** M.F. Akhter[1*], S. M. Macfie[1], and D. Moser[2]. [1]Department of Biology (e-mail: makhter@uwo.ca); and [2] Department of Earth Sciences, University of Western Ontario, London, ON Canada N6A 5B7.

Cadmium (Cd) is a non-essential trace element and its environmental concentrations are approaching toxic levels, especially in some agricultural soils. Understanding how and where Cd is stored in plants is important for ensuring food safety. Previous experiments have determined that lettuce (*Lactuca sativa*) and barley (*Hordeum vulgare*) seedlings can grow in hydroponic nutrient solution containing 1.0 µM Cd without showing toxicity symptoms and, at this concentration, approximately 80% of the total Cd is translocated to leaves of lettuce, whereas only 20% of the total Cd is translocated to barley leaves. Preferential retention of Cd in the cell walls of barley roots would explain this difference. Histological examination of cross sections of roots stained with diathizone (a Cd-specific dye) confirmed the presence of Cd in the cell walls of both species. We tried to quantify cell wall (apoplast) and intracellular (symplast) Cd by desorption of apoplastic Cd using $CaCl_2$; however, the concentrations of Cd found in the plants were below the limits of detection. In the present study we used a Scanning and Electron Probe Microscope (SEM) in combination with a Wavelength Dispersive X-ray Spectrometer (WDS) to semi-quantitatively measure Cd at the sub-cellular level. Plants were grown in nutrient solution containing 0 or 1.0 µM $CdCl_2$ for 28 days. Root samples from control and Cd-treated plants were prepared as for conventional SEM, whereby tissue sections were fixed, dehydrated, and embedded in a resin; thin slices were then cut for electron probe microscopy. The results are expected to be useful in uncovering the mechanisms of Cd-tolerance and sequestration in lettuce and barley.

CSPP-S30 **The use of confocal microscopy to image and quantify bacteria-root associations.** M.P. Columbus[1]*, S.M. Macfie[1], G. Southam[2]. [1]Department of Biology and [2]Department of Earth Sciences, University of Western Ontario, London, ON, Canada N6A 5B7

Many of the mechanistic hypotheses for how plant growth-promoting bacteria (PGPB) are able to maintain plant growth under stress conditions depend on a direct association between the plant root and bacteria. For example, the ability of the bacterial enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase to outcompete the plant enzyme ACC oxidase for the ethylene precursor ACC requires a close association between bacteria and plant tissue. Additionally, the ability of the plant root to take up bacterially produced molecules may be enhanced if the bacteria are present on or near the root tip. It has also been suggested that the production of a bacterial biofilm on the root surface may

help to exclude stressors from the plant. It is therefore important to confirm location, physical proximity and quantity of bacteria on plant roots when studying PGPB. This study will analyze the association between one of two bacterial types (the ACC deaminase producing bacterium UW4, and an ACC deaminase minus mutant) on *Arabidposis thaliana* roots grown hydroponically, with or without cadmium. The fluorescence-based assay *Bac*Light™ in combination with confocal microscopy will be used to determine the amount and location of live and dead bacteria on the root surfaces of 7 and 14 day old plants. Images will be converted to grayscale and analyzed using the computer software AxioVision to determine the root surface area covered by live versus dead bacteria as well as the location of the bacteria on the plant root. It is predicted that more live bacteria will be located at the root tips, but that older root areas will be covered by a biofilm. The fixation of these specimens in plastic and imaging using SEM and TEM will reveal small scale differences in root morphology caused by the presence of the PGPB as well as the location of cadmium within the resulting bacterial biofilm or plant tissue.

CSPP-S31 **Allantoate amidohydrolase regulation in soybean.** M. J. Munson[1*] and C. D. Todd[1]. [1]Department of Biology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5E2

Soybean is an agriculturally important legume that can form symbiotic relationships with soil bacteria to fix atmospheric N_2. This fixed nitrogen is then converted into ureides through *de novo* purine synthesis in the uninfected cells of nodules. Ureides, primarily allantoin and allantoate, are then transported through the xylem sap to provide nitrogen to the rest of the plant. The first nitrogen releasing step in the ureide catabolic pathway is performed by allantoate amidohydrolase (AAH). Regulation of AAH in different tissues may affect nitrogen fixation, since the accumulation of ureides has been associated in the inhibition of nitrogen fixation during water limitation. To better understand regulation of AAH, enzyme activity was determined in seedlings, as well as in different tissues of N_2-fixing and non-fixing 35 day old soybean plants. High Performance Liquid Chromatography (HPLC) was used to quantify the ureides to determine if there is any correlation between ureide levels and enzyme activity. A water limitation experiment on 35 day old plants was set up to identify changes in AAH activity in water-limited plants and to correlate any changes in AAH activity with changes in ureide concentrations. Future work will investigate *AAH* transcript abundance in the different tissues or developmental stages to determine if changes in gene expression contribute to the regulation of AAH.

CSPP-S32 **Accumulation of ureides in soybean plants undergoing abiotic stresses.** J. R. Souter* & C. D. Todd. Department of Biology, 112 Science Place, University of Saskatchewan. Saskatoon, SK. S7N 5E2

In soybean (*Glcine max* [L.] Merr) and closely related legumes nitrogen is transported from the nodule to leaves as ureides, primarily allantoin and allantoate. In these species, ureides can accumulate in the leaf tissue when the plants experience water limitation. This accumulation is often associated with a decrease in nitrogen fixation and therefore significant effort has been spent trying to connect ureide accumulation with nitrogen export from the nodules. Recent evidence suggests ureide accumulation following water limitation is due to *de novo* ureide synthesis in the leaves. Ureide accumulation during oxidative stress has also been reported. My study examines the accumulation of ureides and their precursors in non-fixing soybean plants following water limitation or oxidative

stress. Metabolite accumulation was determined by High Performance Liquid Chromatography. Despite not fixing N_2, preliminary results show an increase in ureides in leaves and stems as soil water content is reduced. Additionally, the accumulation of ureides does not only occur following water limitation, but also occurs in plants undergoing other abiotic stresses. Soybean leaves were treated with methyl viologen (MV) to induce generation of reactive oxygen species. Treated plants also show an increase in ureide content shortly after application of MV. Moving forward, we plan to determine enzyme activity and gene expression of the enzymes responsible for ureide synthesis and catabolism to address the mechanism causing ureide accumulation and to help understand the biological role of these compounds during abiotic stress.

CSPP-S33 **Characterization of a novel GDP-O-FucosylTransferase in *B.napus* Microspore Embryogenesis**. Jerlene Nessia[*1], K. Peter Pauls[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON

Microspore embryogenesis (ME) is a developmental phenomenon in which microspores divert from their gametophytic pathway towards embryonic development when stressed or cultured. It is an effective breeding tool to generate doubled haploids for efficient cultivar development. Canola (*Brassica napus*) is one of the most economically significant crops in Canada. In the form of seed, oil and livestock feed this commodity contributes $14 billion to the economy and its value is projected to increase over the coming years. Therefore, continued development of cultivars with improved traits will be required to keep up with the pace of the rising demand for this crop. Although highly efficient, there are only a few genotypes that are highly responsive to ME induction and the mechanisms for this developmental switch are not fully understood. Thus, it is important to elucidate the genetic control of the embryogenic response in responsive cultivars and identify the factors limiting regeneration frequencies in recalcitrant lines. Our previous microarray analysis enabled us to identify genes that were significantly overexpressed in embryogenic cells. Of special interest is the Arabidopsis gene, AT2G44500 in which a Brassica transcript hybridized to and was consistently upregulated in embryogenic cells compared to pollen-like or non-responsive cells. Our bioinformatic analysis suggests that AT2G44500 has a conserved GDP-O-Fucosyltransferase (O-FucT) domain in Arabidopsis as well as in the two *B.napus* homologs that we have cloned and sequenced. We have also identified conserved amino acid residues that may play a role in the catalytic activity of this putative fucosyltransferse. We are currently characterizing Arabidopsis mutants to elucidate the function of this novel family of plant fucosyltransferases. Once characterized, this gene and its paralogs can potentially be used as genetic markers to identify cultivars that produce highly embryogenic microspore cultures. This will also allow us to understand the molecular mechanisms underlying the early stages of embryogenesis in plants, which is the basis of seed development and is fundamental to crop productivity.

CSPP-S34 **Novel microbial biodetoxification of type-A and type-B trichothecene mycotoxins.** R. Islam[1,2*], T. Zhou[1], J.C. Young[1] and K.P. Pauls[2]. [1]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada N1G5C9 (e-mail: mislam@uoguelph.ca). [2]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada, N1G2W1

Cereals are frequently contaminated with multiple type-A and/or type-B trichothecene mycotoxins, that are produced by the toxigenic *Fusarium* species during host plant infection. Interactions between the co-occurring mycotoxins have synergistic effects on

toxicity and result in serious adverse effects on animal and human health. Hence contamination of grains with several mycotoxins is increasingly of concern in terms of food safety, quality and trade. Currently, there is no method to remove trichothecene mycotoxins safely and completely from agricultural commodities. To address this problem, we isolated a novel bacterial strain ADS47 from agricultural soil capable of de-epoxydizing (i.e. detoxifying) ten different type-A and type-B trichothecene mycotoxins that had been detected in cereal foods and feeds. Microbial biotranformation of mycotoxins was examined by culturing the strain ADS47 in four broth media (namely nutrient broth, mineral salts broth, luria bertani and brain heart infusion) supplemented with 100 ppm of various toxins. After five days of incubation under aerobic conditions and moderate temperatures, biotransformation of the mycotoxins was determined by liquid chromatography-ultraviolet-mass spectrometry. Strain ADS47 completely bio-transformed all five type-A mycotoxins, namely HT-2 toxin, T-2 toxin, T2-triol, diacetoxyscirpenol and neosolaniol to de-epoxy and/or deacetyl metabolities. The tested five type-B trichothecene mycotoxins, namely nivalenol, verrucarol, FusarenonX, 3-acetyl-deoxynivalenol and 15-acetyl-deoxynivalenol were also completely biotransformed to de-epoxy and/or unknown products. Media compositions had considerable effects on microbial de-epoxydation of the evaluated mycotoxins. This is the first report of microbial de-epoxydation of multiple type-A and type-B trichothecene mycotoxins under aerobic conditions and moderate temperatures. We speculate that strain ADS47 can be used to detoxify animal feeds contaminated with different trichothecene mycotoxins. We are working on isolating the novel trichothecene de-epoxydation bacterial gene(s)/enzyme(s). The gene(s)/enzymes may have potential applications for biological detoxification of cereal grains contaminated with trichothecene mycotoxins. Thus, the study may contribute to improve the quality, safety and trade of grain-derived foods and feeds.

Canadian Institute of Food Science and Technology **Poster Presentation**
Session 1 **Room**: 290 Loyola Conference Hall

CIFST-1 **Bioconversion of apple processing by-products: Optimization of acid-catalyzed hydrothermal pretreatment and use of laccase for removal of polyphenols.**
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Biotechnological conversion of apple processing by-products (APP) into bio-ethanol and other high-value products entails hydrolysis of the polysaccharide into simple sugars. Hydrolysis of polysaccharide can be carried out with enzymes or mineral acids/ bases. In addition to sugars, APP also contain significant amount of polyphenols, which could be potential inhibitors to cellulose converting enzymes and fermentation using micro-organisms. The efficiency of the bioconversion process is based on removal of inhibitors from hydrolysates prior to fermentation. A pretreatment based on dilute sulfuric acid hydrolysis of APP was optimized for yield of glucose in relation to three independent variables: acid concentration (0.5-2% w/v), operating time (5-30 minutes) and temperature (80-100^{o}C) using response surface method. A 2^3 central composite design (CCD) was used to code the three variables at five levels. The optimal acid hydrolysis conditions obtained through canonical analysis of response surface method were: acid concentration - 1.86%; time - 14.35 minutes; and operating temperature - 97.44^{o}C.

Additionally, the effect of lacasse, a polyphenol oxidase, at three levels (10, 20 and 30 mg/25g fresh weight biomass) on polyphenol oxidation of acid hydrolyzed APP will be presented.

CSPP - General Posters

CSPP-1 **Influence of evaporative demand on aquaporin expression and root hydraulics in hybrid poplar.** A. Almeida-Rodriguez*, U. Hacke, and J. Laur. Department of Renewable Resources, University of Alberta. Edmonton, AB. Canada, T6G 2E3. e-mail: adriana@ualberta.ca

Uptake and transport of water through roots pose a constraint on water use. The control of water loss through stomata is influenced by many environmental and plant-specific factors, and there is accumulating evidence for an equally complex regulation of aquaporin (AQP) activity in roots. While environmental factors such as soil drought usually develop gradually, changes in irradiance can trigger rapid changes in transpiration demand. When light levels and evaporative demand increase, dynamic physiological changes in roots may be required to restore the water balance at the whole plant level. We hypothesized that a dynamic increase in root hydraulic conductance (L_P) and AQP expression could moderate the transpiration-induced drop in leaf water potential, allowing continued gas exchange in hybrid poplar (*Populus trichocarpa* x *deltoides*) saplings. 56 *AQP*s have been identified in poplar, but little information about their expression patterns in roots is available, especially from a whole-plant water relations perspective. We measured *AQP* expression and L_P in plants growing under shade that experienced a sudden increase in light level and evaporative demand. Light-exposed saplings exhibited a three-fold higher L_P than plants remaining in shade. This dynamic increase in L_P corresponded with increased transcript abundance of 15 *AQP*s out of a total of 33 genes simultaneously assessed by quantitative RT-PCR. The tissue-level localization of transcripts of four *AQP*s was studied with *in situ* hybridization. Comprehensive expression profiling in conjunction with physiological and morphological measurements is a valuable reference for future studies on AQP function in poplar.

CSPP-2 **Influence of endogenous and exogenous 5-aminolevulinic acid on etiolated cucumber (*Cucumis sativus*) seedlings grown under salinity.** N. Averina[1]*, I. Vershilovskaya[1], T., Samovich[1], L. Obukhovskaya[2], S. Chiruk[3], E. Yaronskaya[1]. [1]Institute of Biophysics and Cell Engineering and [2]Institute of Experimental Botany of National Academy of Sciences of Belarus, Akademicheskaya str. 27, Minsk 220072, Belarus; [3]Grodno State University, Ozheshko str. 22, Grodno 230023, Belarus

Soil salinity is an increasing threat for agriculture and is a major factor in reducing plant development and productivity. Application of plant growth regulators (PGR) helps to overcome harmful salt effect. 5-aminolevulinic acid (ALA) – chlorophyll and heme precursor, in low concentrations acts as PGR and improves plant salt tolerance. We have studied influence of 125 mM NaCl on rate of endogenous ALA formation, contents of heme and ATP, activity of cytochrome *c* oxidase and respiration rate in cotyledons of etiolated 7-days-old cucumber seedlings grown with or without of exogenous ALA. NaCl greatly decreased length and biomass of roots (by 60% and 30%) and hypocotyls (by 70% and 70%), biomass of seedlings by 50%, but slightly diminished biomass of cotyledons by 14%. In parallel salt significantly increased rate of endogenous ALA synthesis in cotyledons, amount of heme, preserved rate of respiration and content of ATP practically on a level of the control plants and decreased activity of cytochrome *c*

oxidase by 20%. We suggest that activated synthesis of endogenous ALA results in increasing heme biosynthesis and supporting the respiration process as energetic source to promote cotyledon salt tolerance. Activating endogenous ALA synthesis in cotyledons did not protect other organs from the salt inhibition. Only supplementation of NaCl with 1, 10 and 60 mg/l of exogenous ALA resulted in partial recovery of hypocotyl length and biomass as well as seedling biomass up to 125%, 150% and 130% accordingly as compared with the plants grown on NaCl solution alone. Exogenous ALA did not increase heme content and rate of respiration, slightly enhanced ATP amount and cytochrome *c* oxidase activity. We suggest that exogenous ALA shows mainly a property of PGR to improve salt tolerance of the etiolated cucumber seedlings.

CSPP-3 **Detoxification of succinate semialdehyde in *Arabidopsis* glyoxylate reductase and NAD kinase mutants subjected to submergence stress.** W.L. Allan[1], K.E. Breitkreuz[2], J.C. Waller[3], J.P. Simpson[1], G.J. Hoover[1], A.Rochon[1], D. J. Wolyn[1], D. Rentsch[2], W.A. Snedden, B.J. Shelp[1*]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada (email: bshelp@uoguelph.ca); [2]Institute of Plant Sciences, University of Bern, 3013 Bern, Switzerland; and [3]Department of Biology, Queen's University, Kingston, ON K7L 3N6, Canada

Succinate semialdehyde (SSA) is a mitochondrially-generated intermediate in the metabolism of γ-aminobutyrate (GABA), which accumulates in response to a variety of biotic and abiotic stresses. SSA can be reduced to γ-hydroxybutyrate (GHB) in plants exposed to various abiotic stress conditions. Recent evidence indicates that distinct cytosolic and plastidial glyoxylate reductase isoforms from *Arabidopsis thaliana* (L.) Heynh (GLYR1 and GLYR2, respectively) catalyze the *in vitro* conversion of SSA to GHB, as well as glyoxylate to glycolate, via NADPH-dependent reactions. In the present study, recombinant *Arabidopsis* GLYR1 was demonstrated to catalyze the NADPH-dependent reduction of both glyoxylate and SSA simultaneously to glycolate and GHB, respectively. Six-hour time-course experiments with intact vegetative wild-type *Arabidopisis* subjected to submergence demonstrated that GHB accumulates in rosette leaves and this is accompanied by increasing levels of GABA and alanine, NADH/NAD^+ and NADPH/$NADP^+$ ratios, and *GLYR1* and *GLYR2* transcript abundance. The use of *GLYR* (*glyr1* or *glyr2* knockout) and *NAD kinase1* (*nadk1* knockout, *NADK1* overexpression) mutants demonstrated that under submergence the production of GHB is mediated via both GLYR isoforms, the loss of either GLYR1 or GLYR2 activity influences redox status and the levels of GABA and alanine, and the manipulation of NADP(H) availability specifically in the cytosol influences the production of GHB. These results are interpreted as further evidence for the involvement of both biochemical and transcriptional mechanisms in the regulation of SSA detoxification in plants during the onset of submergence-induced oxygen deficiency.

CSPP-4 **Inorganic carbon acquisition in the acid-tolerant alga *Stichococcus bacillaris*.** C. Powe, and B. Colman*. Department of Biology, York University, Toronto, Ontario, Canada M3J 1P3

The processes of CO_2 acquisition were characterized for the acid-tolerant, free-living chlorophyte alga Stichococcus bacillaris, CPCC 177. The alga grows over a wide pH range of pH 3.0 to 9.0 and maintains an internal pH of 6.5 to 7.5 over this range. External carbonic anhydrase (CA) was detected in cells grown above pH 5.0, with the activity increasing markedly from pH 6.0 to 9.0. The capacity for HCO_3^- uptake of cells treated with the membrane-impermeable CA inhibitor, acetazolamide (AZA), was investigated

by comparing the calculated rate of uncatalyzed CO_2 formation with the rate of photosynthesis. Active bicarbonate transport was found in cells grown in media above pH 7.0. Monitoring CO_2 uptake and O_2 evolution by membrane-inlet mass spectrometry demonstrated that air-grown, AZA-treated cells caused a rapid drop in extra-cellular CO_2 concentration to a CO_2 compensation concentration of 18-19 μM at pH 8.0; this CO_2 concentration is above the equilibrium CO_2 concentration at this pH, indicating that the cells do not exhibit active uptake of CO_2. O_2 evolution continued when cells reached CO_2compensation point, confirming the capacity of these cells for active bicarbonate uptake. These results indicate that Stichococcus bacillaris, when grown at alkaline pH, possesses a CO_2-concentrating mechanism dependent on active HCO_3^- transport but rely on diffusive uptake of CO_2 when grown at acid pH.

CSPP-5 **Hormonal regulation of plant physiological and biochemical stress responses for salt, water and flooding stress.** T. G. Ross[1], J. Mehroke[1], and S. Singh[1*]. [1]Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4 (email: santokh.singh@botany.ubc.ca)

This study focuses on the effects of plant hormones and certain external environmental stresses, such as water and salt stress, using corn (*Zea mays* L.), and flooding stress, using green bean (*Phaseolus vulgaris* L.) plants. Salt and water stress tolerance was monitored by analyzing physiological responses such as transpiration and photosynthesis rates, and water potential. In addition, the levels of dehydrins, known stress induced proteins were analyzed by Western Blotting. All environmental stress treatments showed drastic decreases in the above-mentioned physiological responses. Exogenous application of the phytohormone, abscisic acid (ABA), a known stress signal, was shown to enhance salt and water stress tolerance, while inhibition of ABA synthesis with fluridone decreased stress tolerance as well as dehydrin levels. Ethylene, another phytohormone, has been shown in the literature to be involved in flooding-induced anoxic stress signaling. Morphological changes, such as epinasty were observed in both ethylene and flooding treatments. Flooding was shown to be more effective than the ethylene treatments in regulating the levels of alcohol dehydrogenase (ADH), a key enzyme produced during anoxia. Triggers of ADH remain unclear but a likely candidate is a build-up of cystolic Ca^{2+} which is the current direction of our research. The results of this investigation indicate that different environmental stresses exhibit their unique physiological and biochemical responses in plants. The results of this investigation help to further our understanding of hormonally-controlled stress-induced responses which will be crucial to improving crop yields in globally changing climates.

CSPP-6 ***Vitis* CBF1 and *Vitis* CBF4 have different effects on *Arabidopsis* abiotic stress tolerance, development and gene expression.** M. Siddiqua[1*] and A. Nassuth[2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1; and [2]Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada N1G 2W1 (email: anassuth@uoguelph.ca)

Plants growing in temperate regions encode several CBF/DREB1 proteins, which might have different functions in the acquisition of stress tolerance. In this study, *Arabidopsis* transformed with grape *CBF1* (*VrCBF1*) or grape *CBF4* (*VrCBF4*) were characterized. Electrolyte leakage assays showed that the freezing tolerance of transgenic lines was correlated with the level of *VrCBF* expression irrespective of the type of *CBF*, while drought tolerance was most increased by *VrCBF1*. *VrCBF* overexpression coincided with an increase in the expression of the cold-regulated genes genes *AtCOR15a*, *AtRD29A*,

AtCOR6.6 and *AtCOR47*. In addition, the development of grape *CBF* overexpressing plants was seen to be altered and result in dwarf plants, which flowered later and had thicker rosette leaves with a higher stomatal density. Analysis of gene expression showed that the morphological changes might be due to an increase in the expression of *AtRGL3* in *VrCBF4* lines or *AtGA2ox7* in VrCBF1 lines, and *AtFLC* in both. In addition, the results show for the first time that CBFs can positively affect the expression of *AtICE1/SCREAM1*, the gene that is known to induce *AtCBF3* expression. The difference in gene induction by *VrCBF1* compared to *VrCBF4* suggests that these CBFs have different regulons.

CSPP-7 **Senesced/stressed cells share common features with dedifferentiating cells.** G. Gideon[1], [2]M. Damri, [3]V. Fraifeld, [3]M. Wolfson, [4]Vered Chalifa-Caspi, [2]S. Barak, [2]V. Ransbotyn[1]Ben-Gurion University of the Negev, Institutes for Desert Research, Midreshet, Ben Gurion, 84990, Israel; [2]French Associates Institute for Agriculture and Biotechnology of Drylands, Ben-Gurion University of the Negev; [3]The Faculty of Health Sciences, Ben-Gurion University of the Negev; [4]The National Institute for Biotechnology, Ben-Gurion University of the Negev

Dedifferentiation signifies the capacity of somatic cells to acquire stem cell-like properties and in plants it characterizes the transition from leaf cells to protoplasts. Transcriptome profiling of dedifferentiating protoplast cells revealed striking similarities with senescing cells raising the hypothesis that senescing cells have acquired stem cell-like state. To test this hypothesis, tobacco plants were induced to senesce prematurely by prolong exposure to dark and tested for stem cell features. Indeed, dark-induced senescing cells display features of dedifferentiating cells including extensive widespread chromatin decondensation, disruption of the nucleolus, and condensation of rRNA genes. Considering that premature senescence can be induced by various stress conditions we suggest that a common response of cells to certain biotic and abiotic stresses converges on cellular dedifferentiation whereby cells first acquire a stem cell-like state before assuming a new fate. Indeed, Hierarchical clustering analysis reveals similarity in expression of transcription factor-encoding genes between dedifferentiation, senescence and various abiotic and biotic stresses including oxidative stress, UV-B irradiation, salt, drought and pathogen infection.

CSPP-8 **Identifying algal enzymes producing the climate-altering agent dimethylsulfoniopropionate by exploiting comparative genomics tools.** J. Waller, Mount Allison University, Biochemistry and Chemistry Dept., Barclay Building, 63C York Street, Sackville, NB, E4L 1G8

Dimethylsulfoniopropionate (DMSP) is an important algal metabolite enzymatically synthesized from methionine by a four-step pathway unique to algae. DMSP may then be degraded by algae or marine bacteria to the volatile compound dimethylsulfide (DMS). DMS is responsible for approximately half of the global atmospheric sulfur budget and is believed to play a role in the regulation of global climate. Given that algal DMSP is the source of DMS, it is surprising that little research has been done on DMSP biosynthesis and not a single biosynthetic enzyme has been identified at the molecular level. What are the molecular identities and structures of these enzymes? Are they conserved among diverse algal species? Can identifying the genes help predict an algal species capacity to synthesize DMSP? Recent advances in sequencing diverse algal genomes, creation of algal cDNA libraries, and development of genetic tools for algae can facilitate algal gene

discovery A combined comparative genomics and bacterial mutant complementation strategy to identify the enzymes responsible for DMSP biosynthesis will be outlined.

CSPP-9 **Mitochondrial-associated Class-2 PEP carboxylase complexes provide a novel mechanism of metabolic control in the castor-oil plant.** J. Park[1], B. O'Leary[1], N. Khuu[2], R. T. Mullen[2], and W. C. Plaxton[1]. [1]Dept. of Biology, Queen's Univ., Kingston, ON, K7L 3N6; [2]Dept. of Molecular and Cellular Biology, Univ. of Guelph, Guelph, ON, N1G 2W1

Phospho*enol*pyuvate carboxylase (PEPC) is a tightly controlled cytosolic enzyme situated at a pivotal branch point of plant carbohydrate metabolism. Two physically and kinetically distinct oligomeric classes of PEPC exist in plants and green algae. Our previous studies established that: (1) *Ricinus communis* (castor) Class-1 PEPC is a typical PEPC homotetramer composed of 107-kDa plant-type PEPC (PTPC) subunits, whereas the Class-2 PEPC is an unusual 910-kDa hetero-octamer arising from a tight interaction between Class-1 PEPC and distantly-related 118-kDa bacterial-type PEPC (BTPC) subunits; (2) BTPC functions as a catalytic and regulatory subunit of Class-2 PEPC and is subject to multi-site regulatory phosphorylation *in vivo;* (3) Class-1 PEPC is abundant throughout the castor plant, whereas Class-2 PEPC and its BTPC subunits are specifically expressed in rapidly growing tissues involved in active biosynthesis; *e.g.*, the endosperm of developing castor beans, as well as leaf buds and young expanding leaves. Class-2 PEPC is desensitized to allosteric inhibitors and has been hypothesized to function as a 'metabolic overflow' mechanism that could maintain a significant anaplerotic flux from PEP to oxaloacetate under conditions that would largely inhibit Class-1 PEPCs. The subcellular location and *in vivo* interaction of castor PTPC and BTPC were examined by imaging (via CLSM) various PEPC-fluorescent protein (FP) fusions in transiently-transformed tobacco suspension cells. This was complemented by immunogold-TEM imaging of PTPC vs BTPC in developing castor beans. Overall results indicate that: (1) castor BTPC and PTPC interact *in vivo* as a Class-2 PEPC complex on the surface of mitochondria, (2) BTPC's unique intrinsically disordered region mediates its tight association with PTPC, whereas (3) Class-1 PEPC is uniformly distributed throughout the cytosol. The interaction between divergent PEPC polypeptides within mitochondrial-associated Class-2 PEPC complexes adds another layer of complexity to the evolution, physiological functions, and metabolic control of this essential CO_2-fixing plant enzyme.

CSPP-10 **Further studies of carbon and nitrogen partitioning among shoots, roots and rhizospheric soil in double haploid genotypes *of Brassica napus* (cv. Polo x cv. Topas) varying in seed oil content by ^{13}C and ^{15}N dual labeling.** H. Fei, J. K. Vessey*. Department of Biology, Saint Mary's University, Halifax, NS, B3H 3C3, Canada

Oilseed rape (*Brassica napus* L.) is a promising crop for development into a major feedstock for biodiesel production because of its higher seed oil content potential (>50%) compared to other crops, e.g., soybean (18-20%). However, a concern in regard to using oilseed rape as a biodiesel feedstock is that it requires more N fertilizer than cereal crops. N fertilizer not only increases the cost of production, but also can contribute to greenhouse gas emissions. There is considerable interest to improve oil productivity in *B. napus* and manage partitioning of carbon and nitrogen among shoots, roots and the soil to optimize the crop as a feedstock for biofuel production. The extent to which partitioning of carbon and nitrogen within the plant and between the plant and rhizospheric soil changes in cultivars of *B. napus* varying seed oil content is unknown. In our previous work, four cultivars of *B. napus* (created from open pollinated population) varying in

seed oil content, i.e., cv. Topas (42-44%), cv. Sentry (a commercial canola cultivar, 45%), cv. Polo (47-48%) and cv. 04C204 (>50%), were selected to study carbon and nitrogen partitioning in shoots, roots and in rhizospheric soil, as well as nitrogen use efficiency. To confirm the previous study, three double haploid genotypes of *B. napus* created from tissue culture of F1 pollen produced by crosses between cvs. Polo and Topas were used to further study carbon and nitrogen partitioning among shoots, roots and rhizospheric soil. This was done by using ^{13}C and ^{15}N dual labeling techniques to identify superior genotypes of oilseed rape, in terms of higher seed oil content, lower greenhouse gas emission and higher nitrogen use efficiency.

CSPP-11 **Regulation of secondary cell wall biosynthesis in arabidopsis by poplar R2R3 MYB transcription factors.** S. Wang[1,2]*, E. Li[1], I. Porth[3], J-G. Chen[1], S.D. Mansfield[3], C.J. Douglas[1]. [1]Department of Botany, University of British Columbia, Vancouver, BC, Canada V6T 1Z4; [2]College of Life Sciences, Northeast Normal University, Changchun, Jilin, China 130024 (e-mail: wangshucai@yahoo.com); Department of Forestry, University of British Columbia, Vancouver, BC, Canada V6T 1Z4

Arabidopsis R2R3 MYB transcription factors control multiple aspects of plant growth and development. Several of them, including AtMYB20, AtMYB43, AtMYB45, AtMYB58 and AtMYB63 are involved in the regulation of secondary cell wall biosynthesis by directly or indirectly inducing the expression of secondary cell wall biosynthetic genes. To test if similar R2R3 MYB transcription factors in poplar also control secondary cell wall biosynthesis, we cloned poplar (*Populus trichocarpa*) homologues of the above mentioned Arabidopsis R2R3 MYB transcription factor genes including *PtrMYB018*, *PtrMYB021*, *PtrMYB028*, *PtrMYB152* and *PtrMYB192*, and studied their functions in Arabidopsis. When transiently expressed in an Arabidopsis protoplast expression system as fusions to the GAL4 DNA binding domain, all the poplar MYB transcription factors tested activated the expression of the reporter gene *GAL4-GUS*, indicating that they can all function as transcriptional activators. When overdressed in Arabidopsis, *PtrMYB021* driven by a *PtrCesA8* promoter, *PtrMYB192* driven by a *35S* promoter, and *PtrMYB152* driven by *PtrCesA8* promoter and *35S* promoter increased secondary cell wall thickness in inflorescence stems , which is likely caused by increased lignification and other changes in cell wall composition. However, plants overexpressing PtrMYB018 and PtrMYB028 do not exhibit any obviously phenotypes. In accordance with the phenotypes observed, RT-PCR results showed that PtrMYB158 and PtrMYB192 specifically induced the expression of several lignin biosynthesis genes, while PtrMYB021 induced the expression of both lignin biosynthesis genes and secondary wall associated cellulose synthesis genes, and PtrMYB028 did not induce any of those genes. These results suggest that selected poplar R2R3 MYB genes control secondary cell biosynthesis by inducing the expression of discrete sets of secondary cell wall biosynthesis genes.

CSPP-12 **Production of exogenous proteins in the seed coat mucilage secretory cells of *Arabidopsis thaliana* (L.) Heynh and *Brassica napus* (L.)**. U. K. Divi[1], A. A. Abdeen[1], and T. L. Western[1*]. Biology Department, McGill University, Montreal, Quebec, Canada H3A 1B1 (email: tamara.western@mcgill.ca)

Canola (*Brassica napus* (L.)) is a major crop cultivated for the oil that is contained in the embryo. The embryo is surrounded by a seed coat or hull which contributes ~16% of total seed mass in Canola. After extraction of oil from the embryo, the hull is usually discarded as waste. Converting the waste hulls to valuable co-products by production of

novel bioproducts can enhance the economic value of these crops. The mucilage secretory cells (MSCs) of the seed coat present an excellent tool for such manipulation. These cells produce large amounts of pectin and cell wall-related proteins during seed development that are released upon hydration. This would allow easy harvesting of the exogenous protein by wetting of the seed and extracting the water soluble fraction. This study aims at developing tools for targeting novel proteins to the MSCs of *Arabidopsis thaliana* (L.) Heynh (Arabidopsis) and *B. napus*, and determining parameters for maximizing their accumulation. Six Arabidopsis seed coat promoters, including those of two newly identified genes, are being analyzed for their expression in different tissues and various stages during seed development. For all the promoters, a secretable β-glucuronidase (GUS-Plus) reporter gene is used. Different signal sequences were also used to target the proteins to apoplast. Preliminary studies in Arabidopsis using three of the promoters with two different signal sequence combinations showed expression in seed coat for all the combinations. The activity of one of the promoter-signal sequence combinations was confirmed in the seed coat of transgenic *B. napus*. Further time course and quantitative studies using antibodies and enzymatic assays will identify a suitable promoter-signal sequence combination for exogenous protein production whose application for *B. napus* will be validated.

CSPP-13 **Bioactive *Streptomyces* species isolated from desert plant rhizosphere soil in Riyadh, Kingdom of Saudi Arabia: evaluation of their activity against plant pathogenic fungi, human pathogenic bacteria and yeast.** Ismet Ara1*, Mohammad Abdul Bakir1, Muneera Al-Othman1, and Najat A. Bokhari1.1Department of Botany and Microbiology, King Saud University, College of Science, Medical studies and Sciences Sections, Post Box 22452; Riyadh, 11495, Kingdom of Saudi Arabia (e-mail: ismetara@yahoo.com).

Gram-positive, filamentous, bioactive compound producing Streptomycetes group was studied in Riyadh desert plant rhizosphere soil and our data indicated that it is an eminently suitable ecosystem for diverse *Streptomyces*. Actinomycetes counts ranged from 50×10^2 cfu/g to 700×10^2 cfu/g in the 50 rhizosphere soil samples collected in Riyadh. The highest number of Streptomycetes group was found in rhizosphere soil samples collected from Al-Thumama desert. A total of 150 Streptomycetes were isolated and purified isolates exhibited a range of 16 diverse colony colors (such as, grey, dark grey, pale grey, white grey, grey white, white, off white (chalk white), blackish grey, pink white, red white, brown red, dark brown, brown white, cream white, yellow and yellow white) and among them, grey and off white series represented the most dominant color groups in our study. The selected potent *Streptomyces* strains were characterrized by biochemical tests such as, fermentation of citrate, starch hydrolysis, gelatin hydrolysis, casein hydrolysis, milk coagulation, triple sugar iron test etc. for their differentiation. Morphological observations were made using scanning electron microscopy and light microscopy and the data tentatively confirmed that almost all the selected strains belong to the dominant genus *Streptomyces* in the family *Streptomycetaceae*. Further preliminary and secondary screening for bioactivity test results indicated that about 60% of all the isolates have the ability to inhibit the growth at least one or more of the selected 17 human and phytopathogens when examined *in vitro*. The highest antimicrobial activity was recorded in the case of grey and off-white (chalky white) series. More intensive study will be conducted on the isolated potent actinomycetes to utilize as biocontrol agents and there is a new probability of finding new species in unexplored soil samples in Saudi Arabia as indicated by its unique diversity. Further, the presence of diverse bioactive *Streptomyces* strains in the desert plant rhizosphere ecosystem could show the way for the establishment of disease free desert seedlings in the nursery and in the field.

CSPP-14 **Photoperiodic adaptation at high-latitudes complicates adaptation of forests to future climate.** R.Y. Soolanayakanahally[1, 2*], R.D. Guy[2], S.N. Silim[1], and M. Song[3]. [1]Agri-Environment Services Branch, Agriculture and Agri-Food Canada, Indian Head, Saskatchewan, S0G 2K0, Canada; [2]Department of Forest Sciences, University of British Columbia, Vancouver, British Columbia, V6T 1Z4, Canada; and [3]Institute of Geographic Sciences and Natural Resources Research, Chinese Academy of Sciences, Beijing, 100101, China

Adaptation to adverse environmental conditions in widespread species is often achieved by genetic and/or plastic responses in numerous traits. In an attempt to better understand adaptation to north-temperate and boreal environments, we have studied variation in phenology and ecophysiology in an extensive range-wide collection of *Populus balsamifera* L. (balsam poplar) planted into common environments. When planted into outdoor common gardens at low-latitudes (Vancouver, BC and Indian Head, SK), northern trees accomplish much less height growth than southern ones and are severely dwarfed in height. However, when grown in a greenhouse without photoperiodic and resource limitations, the northern trees accomplish greater growth as a result of higher photosynthetic rates. Consequently, height growth among northern trees in the southern common gardens is not limited by intrinsic growth rate or photosynthesis, but by the shorter photoperiods experienced in Vancouver and Indian Head. Based on three years of observations at Vancouver, the mid-latitude and near-arctic trees from northern Canada set terminal bud in response to short-days that occur before the summer solstice. These genotypes, planted in the south, begin preparations for the next winter before spring even arrives in their native habitats. Some of the mid-latitude genotypes recover with a second flush, while southern trees maintain continuous height growth. Similar to bud set, leaf senescence also occurs earlier among northern trees. At Vancouver, however, "autumn" leaf senescence can occur as early as May in trees from the extreme northwest. Similar phenological mismatches may have important implications for human-assisted migration in response to climate change. It is possible that undesirable manifestations of phenological mismatch resulting from photoperiodic maladaptation might be avoided by moving trees along climate clines that have an east-west orientation, rather than from low latitude to high latitude.

CSPP-15 **Phytohormonal responses of soybean (*Glycine max* L.) to co-inoculation by *Azospirillum brasilense* and *Azotobacter chrococcum* under water deficit conditions.** M. R. Ardakani[1*], H. Zakikhani[1], A. Kashani[1], F. Rejali[2] and F.Paknejad[1]. [1]Department of Agronomy and Plant Breeding, Karaj Branch, Islamic Azad University, Karaj, Iran and [2]Soil and Water Research Institute, Iran. (email: mohammadreza.ardakani@kiau.ac.ir)

Drought stress is one of abiotic stresses which imposes serious constraints on soybean (*Glycine max L.*) particularly during flowering and pod filling stages. The present investigation was carried out to find the interrelationship between total plant nitrogen, accumulation of abscisic acid (ABA), proline and antioxidants enzymes such as superoxide dismutase (SOD), catalase (CAT) and glutathione peroxidase (GPX) during drought stress conditions with concurrent application of pure isolates of *Azotobacter* and *Azospirillum*. In this study five irrigation regimes (40 percent depletion of soil water ,60 and 80 percent depletion water during flowering, 60 and 80 percent depletion water during pod filling) and four bacterial application methods (no application , foliar application, seed inoculation, foliar-seed inoculation) were studied. The results showed

that drought stress and bacteria application during pod filling stage increased CAT and GPX activity, drought stress conditions increased singly the activity of SOD during pod filling stage, the accumulation of ABA and proline were increased under drought stress and bacteria application during flowering stage while total plant nitrogen enhanced under well water conditions concomitant with bacteria application. The close relation between levels of enzyme's activities and drought stress concurrent with bacteria presence indicated that antioxidant enzymes play an important role in alleviating the water stress destructive effects. Also, concomitant enhancement of ABA and proline could be positively linked and drought-induced ABA could induce proline accumulation and expression of antioxidants genes.

CSPP-16 **Endogenous and exogenous ethylene induces needle abscission and cellulase activity in postharvest balsam fir (*Abies balsamea* L.).** Mason T. MacDonald[1], Rajasekaran R. Lada[1*,] Martine Dorais[2], Steeve Pepin[3]. [1]Christmas tree Research Center, Department of Environmental Sciences, Nova Scotia Agricultural College, Bible Hill, NS, B2N 5E3; [2]Agriculture and Agri-Food Canada, Université Laval, Quebec, QC, G1V 0A6; [3]Horticultural Research Center, Université Laval, Quebec, QC, G1V 0A6

Post-harvest needle loss is a major problem for balsam fir and other Christmas tree species. Recent evidence has implicated ethylene as a signal responsible for post-harvest needle abscission, but enzymological changes remain unknown. The objective of this study was to identify and quantify cellulase activity associated with endogenous and exogenous ethylene-induced abscission. An experiment was designed with three treatments (control, endogenous ethylene, or exogenous ethylene) with five replicates. Key response variables include needle retention duration, xylem pressure potential, ethylene evolution rate, and cellulase activity. Two complimentary methods were used to assess cellulase activity: a cellulose plate digestion and zymography. The results confirm ethylene as a signal for post-harvest abscission and identify ethylene-induced cellulase. Ethylene evolution was typically between 15 and 16 $\mu L \bullet g^{-1} \bullet h^{-1}$, but there was no difference among the three treatments. However, exogenous ethylene significantly decreased needle retention by 60% and resulted in a 6-fold decrease in xylem pressure potential. In addition, cellulase activity increased by 8-fold and 12-fold in endogenous and exogenous ethylene-induced abscission, respectively, compared to the control. Identification of ethylene-induced cellulase activity has increased our understanding of the post-harvest needle abscission process and confirms ethylene's role as a signal molecule.

Canadian Phytopathological Society

Student Posters

CPS-S1 ***Verticillium dahliae* genes putatively involved in microsclerotium development and pathogenicity.** N.P Morales-Lizcano[1*] and K. F. Dobinson[1,2]. [1]Department of Biology, University of Western Ontario, London ON N6A 5C1, Canada; [2]Southern Crop Protection and Food Research Centre, Agriculture and Agri-food Canada, 1391 Sandford Street, London, ON N5V 4T3, Canada

Verticillium dahliae Kleb. is a soil borne fungus, causal agent of an economically significant vascular wilt disease. *V. dahliae* produces persistent resting structures, known as microsclerotia, which are the primary source of disease inoculum in the field. Microsclerotium development has been studied at the morphological level, but still little is known about the molecular mechanisms that govern development. Recent gene expression studies and analysis of the *V. dahliae* genomic sequence have identified a diverse number of genes that may be involved in microsclerotia development. This study focuses on the characterization of several genes, including one (provisionally designated *VdHyp04*) that encodes a "hypothetical protein", and four that encode hydrophobin-like proteins. Bioinformatics analyses suggest secretion of these hydrophobin-like proteins, and indicate that they are, like the previously characterized VDH1, class II hydrophobins. *VdHyp04* appears to be an intron-containing gene (with two non-consensus intron splice sites) that encodes a small, secreted protein. *Agrobacterium tumefaciens*-mediated transformation is being used to generate gene deletion mutants, and knock out (KO) strains have been produced for *VdHyp04* as well as one of the hydrophobin-like protein encoding genes (*VdH5*). Both gene KO strains show an amicrosclerotial phenotype, but no other defects have yet been identified. Generation of KO mutants for the other three hydrophobin gene homologues is in progress. Preliminary analyses of the *vdhyp04* and *vdh5* mutants is being done to determine if these genes are involved or not in microsclerotia development or in pathogenicity, and data from these studies will be presented.

CPS-S2 **Suppression of *Fusarium oxysporum* f. sp. *radicis lycopersici* and *Pythium ultimum* by fish effluent** D. Dey[1*], V. Gravel[1], G. W. Vandenberg[2], and M. Dorais[1]. [1]Agriculture and Agri-Food Canada, Horticultural Research Centre, Laval University, Quebec, QC, Canada G1V 0A6 and [2]Department of Animal Science, Laval University, Quebec, QC, Canada G1V 0A6

Tomato production is the number one vegetable greenhouse crop in Canada. *Fusarium oxysporum* and *Pythium ultimum* are two pathogens that seriously threaten greenhouse tomato production. Numerous studies reported that fish effluent represents an opportunity to provide nutrients for greenhouse tomato. However, little is known about the disease suppressiveness ability of fish effluents for horticultural crops. The objective of this study was to evaluate the effectiveness of fish effluent to reduce disease susceptibility of tomato plant to *F. oxysporum* and *P. ultimum*. An in vitro assay was conducted in order to determine the effect of fish effluent on mycelial growth of *P. ultimum* and *F. oxysporum.* Fish effluent or water was incorporated into PDA media (1 to 25%). In

addition, sterilized fish effluent effect on mycelial growth was evaluated by incorporating autoclaved or microfiltered fish effluent into PDA. A second experiment was conducted with tomato seedlings grown in peat mix under greenhouse conditions and irrigated with conventional nutrient solution (6–11–31; 15.5–0–0). A split-plot experimental design with 5 replicates was used. Twice a week, treated plants received 50 mL of fish effluent at concentrations of 1.0, 0.5 and 0.25. After 1 and 4 weeks of growth, half of plants inoculated with 100 mL of a suspension of *P. ultimum* ($1x10^6$ propagules/mL). The chlorophyll a fluorescence was measured every week. Growth parameters and root colonization by *P. ultimum* were evaluated two weeks after the last inoculation. In vitro assay revealed that there was no significant difference between 5 to 25% of fish effluent and showed 100% inhibition of mycelia growth of *P. ultimum.* In the case of *F. oxysporum*, 32% growth was suppressed using 25% of fish effluent on PDA medium. Significant difference ($P<0.05$) was observed at the 25% with other percentages of fish effluent (5 to 20%). Interestingly, inhibition effect was not observed when fish effluent was sterilized by autoclaving or by microfiltration. These results suggest that the microbial antagonists in the fish effluents have direct inhibition of mycelial growth. Bioassay is underway and results will be discussed in terms of disease supressiveness against these two plant pathogens.

CPS-S3 ***Fusarium graminearum* chemotypes and DON (deoxynivalenol) levels from winter wheat commercial fields across Ontario in 2010**. A. Muckle[1]*, A. Schaafsma[1], M.R McDonald[2], W.G.D. Fernando[3], L. Tamburic-Illincic[1]. [1]Department of Plant Agriculture, University of Guelph Ridgetown Campus, Ridgetown, ON N0P 2C0; [2]Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1; and [3]Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2

Fusarium head blight (FHB) caused by *Fusarium graminearum* (Schwabe) is an economically important wheat disease in Canada. FHB causes decreased yield and quality and the accumulation of mycotoxins including deoxynivalenol (DON). Different *F. graminearum* populations (chemotypes) produce either DON/15-ADON or DON/3-ADON and some parts of North America (not Ontario) are reporting a shift from the 15- to the 3-ADON chemotype. The objective of this study was to investigate the occurrence and frequency of 15-ADON and 3-ADON isolates of *F. graminearum* and DON levels from fields with and without fungicide application, across different counties and winter wheat cultivars. In 2010 grain samples were collected from 50 commercial fields across Ontario. Grain DON content was estimated for each location using the ELISA method. From each location, 60 kernels considered to be of low quality, were surface sterilized, then cultured and incubated on acidified potato dextrose agar to isolate the pathogen. The frequency of *Fusarium* spp. was determined and *Fusarium graminearum* chemotypes will be identified by PCR. DON levels ranged from none detected -1.8 ppm. The highest DON level (1.8 ppm) occurred in a commercial field with the variety 'Wentworth' and no fungicide application. The lowest DON level (none detected) occurred in two commercial fields with the varieties '25W43' and '25R47' both of which received fungicide application. Middlesex County had the highest DON level (0.9 ppm) based on the average of 7 commercial field locations, while Chatham-Kent, Lambton and Wellington counties had the lowest DON level (0.2 ppm), based on the average of 8, 2 and 6 commercial field locations, respectively. Middlesex County had the highest average percent *Fusarium* spp. (56.9%), while Lambton County had the lowest (15.8%).

CPS-S4 **Effect of nozzle type and orientation on fungicide efficacy against mycosphaerella blight in field pea.** R. Bowness[1,5*], B.D. Gossen[2], R.L. Conner[3], T. Wolf[2], K.F. Chang[4], C. Willenborg[4,5], and S.E. Strelkov[5]. [1]Alberta Agriculture and Rural Development (AARD), Lacombe, AB, Canada; [2]Agriculture and Agri-Food Canada (AAFC), Saskatoon, SK, Canada; [3]AAFC, Morden, MB, Canada; [4]AARD, Edmonton, AB, Canada; [5]University of Alberta, Edmonton, AB, Canada

Mycospharella pinodes (Berk. and Blox.) Vestergren causes substantial yield loss in field pea (*Pisum sativum* L.) across western Canada. Symptoms include necrotic lesions on the leaves, stems and pods. Epidemics are initiated at the base of the plant canopy, but quickly spread up the plants when conditions are cool and wet. The only effective strategy to manage mycosphaerella blight in most areas is the application of foliar fungicide. The effect of spray application options (nozzles producing different spray quality in various arrangements), on severity of mycosphaerella blight were assessed at field trials at Morden, Man. in 2008–2010, Saskatoon, Sask. in 2008 and 2009 and Lacombe, Alta. in 2009. The nozzles used included fine and coarse spray quality, single and double nozzle arrangements, a reduced application rate and a non treated control. Pyraclostrobin (Headline) fungicide was applied in 250 L/ha of water at early to late flowering depending on the timing of epidemic initiation. Across all years and sites, blight severity was lowest in the double nozzle system with either two fine droplet nozzles or a combination of a fine and coarse nozzle. Similarly, the highest yields were obtained using a double nozzle system, but differences were small and often not significant in individual trials. Blight severity was generally low during the study period, and mean yield was increased by only 4% over the single nozzle system and 13% over the control. It is likely that double nozzle systems improve canopy penetration and droplet retention at all levels in the canopy, but especially at the base of the canopy and on stems, where stem lesions increase lodging and so have a relatively large impact on yield.

CPS S5 **Importance of the microRNAs pathway in the interaction between *Arabidopsis thaliana* and necrotrophic pathogens.** S. El Mnouchi[1*] and K. Bouarab[1], [1]Centre en amélioration végétale, Département de Biologie, Université de Sherbrooke, QC, J1K 2R1, Canada (email: Kamal.bouarab@usherbrooke.ca)

Plants have evolved sophisticated mechanisms to sense and respond to pathogen attacks. Resistance against necrotrophic pathogens which need dead tissues to cause disease generally requires the activation of the jasmonic acid signaling pathway, whereas the salicylic acid signaling pathway is mainly activated against biotrophic pathogens that require live tissues to invade their host. MicroRNAs (miRNAs) have critical roles in most eukaryotes. They repress gene expression by acting on RNA to guide cleavage and translation repression. Their synthesis is processed by the ribonuclease III enzyme Dicer like 1. Mature miRNAs guide Argonaute–containing RNA-induced silencing complexes to inhibit gene expression at the transcriptional or posttranscriptional levels. Here we report our advances in the role played by this pathway in the interaction between *Arabidopsis thaliana* and necrotrophic pathogens.

CPS-S6 **The teliospore and meiosis as probes for investigating host influence of smut fungi development.** A. M. Seto*[1], C. E. Doyle[1] and B. J. Saville[1,2]. [1]Environmental & Life Sciences Graduate Program, Trent University, DNA Building, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada; [2]Forensic Science Program, DNA Building, Trent University, 2140 East Bank Dr Peterborough, ON K9J 7B8, Canada

Ustilago maydis D.C. Corda requires growth in the host plant *Zea mays* to complete its sexual cycle. A goal of the Saville lab is to investigate the influence of the host on *U. maydis* development using the teliospore as the probe. Teliospores are formed only during growth in the plant; they are the dormant dispersal agents, and the only cell type capable of meiotic division. It is reasonable to propose that genes expressed in the teliospore are involved in facilitating germination and the completion of meiosis. These genes are likely expressed in response to signals received from the plant. To investigate the role of these genes, we are following changes in their transcript levels during teliospore germination. Additionally, we will be determining the function of a gene putatively involved in the control of meiosis. Since teliospore germination is asynchronous, determining the timing of gene expression is difficult. We hypothesize that growth in a highly susceptible host, an inbred line of maize, along with harvesting teliospores from individual tumours, will result in increased germination synchrony. We will report on the level of germination synchrony assessed microscopically and through the change in transcript level of several genes with teliospore specific expression. To begin assessing the control of meiosis in *U. maydis* gene expression, *umNdt80,* an ortholog of the *Saccharomyces cerevisiae* meiotic control gene *Ndt80,* was deleted. Teliospores resulting from infection of corn with compatible *umNdt80* mutants germinate but do not complete meiosis. Genes that are possible downstream targets of *umNdt80* have been identified and will be characterized by comparing their levels of expression in teliospores produced from wildtype and *umNdt80* deletion strains. Together these investigations will identify genes that can be used as probes for following the influence of *Z. mays* on *U. maydis* development.

CPS-S7 **Characterization and functional analysis of an exo-β-1,3-glucanase from *Pyrenophora tritici-repentis*.** H.T. Fu*, R. Aboukhaddour , T. Cao, and S.E. Strelkov. Department of Agricultural, Food and Nutritional Science, 410 Agriculture/Forestry Centre, University of Alberta, Edmonton, AB T6G 2P5, Canada (e-mail: ***stephen.strelkov***@ualberta.ca)

Tan spot, caused by the fungus *Pyrenophora tritici-repentis*, is an important foliar disease of wheat worldwide. In a previous study, analysis by 2-dimensional gel electrophoresis revealed that the enzyme exo-β-1,3-glucanase was five times more abundant in the secretome of a pathogenic race 5 isolate of the fungus versus that of a non-pathogenic race 4 isolate. To learn more about the relationship of exo-β-1,3-glucanase and the virulence of *P. tritici-repentis*, the *glu* gene coding for the enzyme was characterized and silenced via a sense and antisense mediated silencing mechanism. Quantitative-PCR analysis revealed a depressed level of *glu* gene transcript in the silenced strains. One *glu* gene transformant (C1) showed significantly reduced growth and sporulation relative to the wild-type. Microscopic analysis revealed that the transformant C1 produced significantly lower numbers of germ tubes and appressoria than the wild-type isolate on susceptible wheat leaves. The same transformant also caused significantly less disease symptoms relative to the wild-type after inoculation onto a susceptible wheat genotype. These results suggest that exo-1,3-β-glucanase encoded by the *glu* gene may contribute to the development and virulence of *P. tritici-repentis.*

CPS-S8 **Chemical Genomics: Discovery of novel fungicides and their targets in the phytopathogen *Fusarium graminearum*.** C. D. Mogg[1,2]*, P. Barks[2], M. L. Smith[2], and G. Subramaniam[1]. [1]Eastern Cereal and Oilseed Research Centre, Agriculture and

Agrifoods Canada, Ottawa, Ontario, Canada K1A 0C6; and [2]Department of Biology, Carleton University, Ottawa, Ontario, Canada K1S 5B6

The ascomycete fungus *Fusarium graminearum* is a globally distributed cereal pathogen that is responsible for billions of dollars in annual worldwide economic losses. The infection of wheat with *F. graminearum* causes Fusarium Head Blight (FHB) resulting in grain quantity and quality degradation, and mycotoxin contamination. *F. graminearum* and other members of this genus have become important model organisms for biological and evolutionary research on account of their impact upon the economics of global food production. We have developed a high-throughput system and assessed the growth of *F. graminearum* in the presence of a chemical library and plant extracts. Out of 35 compounds discovered to inhibit fungal growth, four have been selected for closer investigation. Future research will be to: 1) Perform efficacy studies to counter FHB in wheat; 2) Use a *Saccharomyces cerevisiae* Synthetic Deletion Array to identify targets; 3) Functionally complement identified *S. cerevisiae* targets with *F. graminearum* gene homologues.

CPS-S9 **Resistance of soybean cultivars fed with silicon to soybean rust and genetic diversity of *Phakopsora pachyrhizi* strains.** G. Arsenault-Labrecque[1*], S. Hambleton[2], K.Oliver[2], E. Whitfield[2], J. Menzies[3], P. Dion[4] and Bélanger, R.R[1]. [1]Département de Phytologie, Centre de Recherche en Horticulture, Université Laval, Québec, Canada G1V 0A6 ; [2]Biodiversity (Mycology and Botany), Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa Canada K1A 0C6,; [3]Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, Canada R3T 2M9;and [4]Département de Phytologie, Faculté des sciences de l'agriculture et de l'alimentation, Université Laval, Québec, Canada G1V 0A6

Soybean rust caused by *Phakopsora pachyrhizi* is a major threat to soybean production throughout the world. Its control still represents a challenge as much remains to be understood in the interaction between the plant and the pathogen. In a first approach, we wanted to determine the susceptibility of different soybean cultivars to the rust pathogen and to evaluate if silicon (Si), a reported prophylactic agent against biotrophic fungi, had a repressing effect against the disease. Scanning electron microscopy and X-ray microanalysis mapping were used to determine Si deposition in soybean leaves of plants treated with 0 or 1.7 mM Si and rust severity was assessed daily. The Korean cultivar Hikmok sorip displayed a significantly higher Si concentration *in planta* than all others when fed with Si. At the same time, plants from this cultivar exhibited a near absence of disease symptoms when supplied with Si. This resistance appeared to be the result of hypersensitive (HR) reactions that were triggered when plants were fed with Si. These results suggest a potential role for Si as part of an integrated approach to control soybean rust. In a second approach, we were interested in characterizing some of the genetic diversity and virulence within *P. pachyrhizi* strains, and for this purpose, we analyzed 24 different isolates collected from experimental plots and farmers' fields at six different sites in Mozambique and Malawi. For each sample, DNA was extracted and a fragment encompassing the ITS1 and ITS2 regions was PCR-amplified using rust-specific primers. Forty-six different ITS sequences were collectively detected in the various samples. Of these, 16 ITS sequences occurred in at least two samples. The remaining 30 ITS sequences occurred in one sample only, with 15 out of the 24 samples yielding such a unique sequence. This high within-sample diversity calls for the establishment of monosporic cultures, to allow individual characterization with respect to virulence and ITS genotype. Virulence profiles coupled with DNA analyses may reveal a relationship

between genetic and phenotypic variation observed within the fungal population.

CPS – General Posters

CPS-1 **Screening for resistance to pasmo (*Septoria linicola*) in flax**. K.Y. Rashid. Agriculture and Agri-Food Canada, Morden Research Station, Unit 100-101 Route 100, Morden, MB R6M 1Y5, Canada

Flax (*Linum usitatissimum* L.) is the second major oilseed crop grown on 600,000 to a million hectares in western Canada. Flax pasmo disease, caused by the funguus *Septoria linicola* (Speg.) Garassini (sexual state *Mycosphaerella linorum* Naumov), is a stubble-borne pathogen that causes severe epidemics with disease severity of 20-60% foliage affected, and 10-30% yield losses. Methodologies for testing flax genotypes and screening for resistance under controlled growth room conditions have been developed. Several trials were conducted using various levels of inoculum concentrations, varying incubation periods with dew formation, and different light and temperature regimes. The most consistent results were obtained by using artificial inoculations of 3-wk old seedlings with single spore isolates and incubating in a dew chamber with a misting system for 48 hrs (N/D of 16/8 hr with 25/28°C, respectively). The inoculated plants were then moved into a growth room of similar N/D hrs and 20/25°C, respectively. Disease reactions on leaves and stems were assessed every 10 days for 40 days after inoculation. This methodology proved effective in identifying differential reactions among flax genotypes and *S. linicola* isolates for future identification of distinct races of this pathogen and specific resistance genes for resistant cultivar development.

CPS-2 **Molecular phylogenetic analysis, trichothecene chemotype Patterson, and varianht in aggressiveness among georgraphically diverse isolates of *Fusarium graminearum*.** A. Malihipour[1]*, J. Gilbert[1], M. Piercey-Normore[2], and S. Cloutier[1]. [1]Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada R3T 2M9; and [2]Dept. of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2

Fifty eight putative *Fusarium graminearum* isolates from Canada, Mexico, and Iran (isolated between 1996 and 2005) were used for chemotype analysis and to determine levels of aggressiveness on wheat. Phylogenetic relationships among the isolates were characterized using the *Tri101* gene sequencing data. All Canadian and Iranian isolates clustered in one group and were identified as *F. graminearum* lineage 7 (= *F. graminearum sensu stricto*) within the *F. graminearum* (*Fg*) clade. The isolates from Mexico were placed in *F. graminearum* lineage 3 (= *F. boothii*) within the *Fg* clade or in *F. cerealis* (= *F. crookwellense*). A PCR assay based on the *Tri12* gene revealed the presence of the three trichothecene chemotypes, 15-ADON, 3-ADON, and NIV among the isolates tested, with 15-ADON predominating. All *F. boothii* isolates from Mexico were identified as 15-ADON chemotype, while all *F. cerealis* isolates were determined to be the NIV chemotype. While the NIV chemotype was not found among Canadian isolates, this chemotype was predominant among the Iranian isolates. There was evidence of a shift from the 15-ADON to the more toxigenic 3-ADON chemotype among the Canadian isolates within the period 1996 to 2004. *Fusarium* isolates were individually inoculated on the susceptible wheat cultivar 'Roblin' under greenhouse conditions to measure disease spread within the spike as an indication of aggressiveness. Disease spread within the spike was rated as the percentage of diseased spikelets per spike 21 days after inoculation. A high variation in aggressiveness was observed among and

within the species tested, with isolates of *F. graminearum sensu stricto* being the most aggressive, followed by *F. boothii* and *F. cerealis*. An association was found between chemotype and aggressiveness with the observation that 3-ADON chemotypes were the most aggressive, followed by the 15-ADON and NIV chemotypes.

CPS-3 ***Fusarium avenaceum*: a causal agent of Fusarium head blight and its population s structure in western Canada.** T. Gräfenhan[1*], S. K. Patrick[1] and R. M. Clear[(1)]. [1]Canadian Grain Commission, Grain Research Laboratory, Winnipeg, Manitoba, Canada R3C 3G8 (e-mail: tom.graefenhan@grainscanada.gc.ca)

Out of three *Fusarium* species commonly associated with Fusarium head blight (FHB) on wheat in Canada, usually *Fusarium avenaceum* is considered least important. Fusarium damaged kernels (FDK) from western Canadian durum wheat are commonly infected by *F. avenaceum*, which is known to be incapable of producing Fusarium trichothecenes such as nivalenol (NIV) or deoxynivalenol (DON, vomitoxin). The spectrum of secondary metabolites formed by *F. avenaceum*, however, encompasses several "emerging" mycotoxins, e.g. moniliformin and enniatins. In 2010/11, ca. 500 producer samples of various wheat classes were plated and tested for their causal agents of FDK. Numerous pure cultures of *F. avenaceum* and *F. acuminatum* were isolated from incubated seeds based on macro- and micro-morphological criteria. Of these, a selection of strains was analyzed further employing DNA cycle sequencing of two phylogenetic markers, namely the translation elongation factor 1 alpha (*tef1*) and the ATP citrate lyase I (*acl1*). Phylogenetic analyses of the DNA alignment revealed a rather simple population structure of the *Fusarium avenaceum* morphological species in the Prairie Provinces.

CPS-4 **Assessment of fusarium head blight in oat mid-season and at maturity.** A. Tekauz*. Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, R3T 2M9 (e-mail: andy.tekauz@agr.gc.ca)

Fusarium head blight (FHB) in oat and other cereals is monitored annually in Manitoba to document disease occurrence, prevalence, and severity. In a growing oat crop there usually is scant visual evidence of FHB. However, when immature kernels are examined, some of these are normally infested by various *Fusarium* species, suggesting FHB is developing. FHB can also be assessed at maturity, as done routinely by agencies such as the Canadian Grain Commission, to determine levels of fusarium damaged kernels (FDK), *Fusarium* infestation of seed, and the presence and amounts of the mycotoxin deoxynivalenol (DON). To compare results between such assessments, and their implications, in 2010, ten commercial oat crops in southern Manitoba were sampled both mid-season (ZGS 78-85) and at maturity. The average mid-season Fusarium head blight index or FHB-I (overall visual FHB severity) was 0.3% (range 0-1.3%), a typical low value. *Fusarium* kernel infestation averaged 10.2% (range 0-24%), and involved four main species, *F. graminearum* Schwabe (7.0%), *F. poae* (Peck) Wollenw. (1.4%), *F. avenaceum* (Fr.) Sacc. (1.0%) and *F. sporotrichioides* Scherb. (0.6%). At maturity, kernel infestation levels doubled to 23.6% (range 11-34%), but now *F. poae* predominated (12.5%), followed by *F. graminearum* (8.6%), *F. avenaceum* (0.9%) and *F. sporotrichioides* (0.7%). FDK levels averaged 8.3% (range 1-27%) while mean DON contamination (determined using ELISA) was 1.9 ppm (range 0.5-3.3 ppm). The results indicate that while mid-season data provide useful information, such as the onset of FHB and the causal *Fusarium* species involved, sampling at maturity is needed to determine final FDK and DON levels. These influence grade, end-use options or indicate a health

risk, and, total *Fusarium* kernel infestation levels that could impact seed quality. Both assessments provide necessary data, but each must be interpreted in context.

CPS-5 **Development of FHB in wheat, barley and oat inoculated with *Fusarium graminearum*, *F. poae* and *F. sporotrichioides*.** A. Tekauz[1]*, and D. Gaba[2]. [1]Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, Manitoba, R3T 2M9 (e-mail: andy.tekauz@agr.gc.ca); and [2]Grain Research Laboratory, Canadian Grain Commission, Winnipeg, Manitoba, R3C 3G8

Cereal crops on the Canadian prairies often are affected by fusarium head blight (FHB). The disease reduces yields, lowers grade, and may contaminate grain with harmful mycotoxin(s). *Fusarium graminearum* Schwabe is the recognized principal causal agent of FHB, but other *Fusarium* species also are implicated, especially in oat and barley. To assess FHB produced by *F. graminearum*, *F. poae* (Peck) Wollen. and *F. sporotrichioides* Scherb., one wheat, two barley and three oat cultivars were grown in southern Manitoba in 2010 in field plots treated with *Fusarium*-infested corn kernels of the individual species. At maturity, levels of FDK, seed-borne *Fusarium*, and mycotoxins (using GC-MS) were determined. FDK levels for each pathogen were similar (7-15%) in oat and barley, but twice as high (40%) for *F. graminearum* in wheat vs. the others. Recovery of *F. poae* from seed was low (0-9%) in wheat and barley and moderate in oats (15-28%). Recovery of *F. sporotrichioides* was similar in all cereals (25-34%). Recovery of *F. graminearum* was very high (>80%) in wheat and barley, and moderate (35-50%) in oat. The principal mycotoxins detected were deoxynivalenol (DON) and HT-2. The latter was detected in *F. sporotrichioides*-treated samples of all cereals. The highest level (~1.5 ppm) occurred in wheat. DON levels were very high (23-37 ppm) in wheat and barley treated with *F. graminearum*, but low (0.6-1.4 ppm) in oat. Trace levels of nivalenol were occasionally detected in barley, but not associated with a particular *Fusarium*. Apparent high amounts of natural *F. graminearum* inoculum led to substantial levels of this species being isolated from seed in all treatments. This likely influenced results, which must be interpreted accordingly.

CPS-6 **The incidence and severity of loose smut and surface borne smuts of barley on the Canadian Prairies: 1972-2009.** J.G. Menzies*; P.L. Thomas. Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, R3T 2M9

The barley pathogens *Ustilago nuda* (Jensen) Kellerman & Swingle, the cause of loose smut, *U. nigra* Tapke., the cause of false loose smut, and *U. hordei* (Pers.) Rostr., the cause of covered smut, were likely introduced to Canada on seed by early settlers. This report summarizes the survey data collected annually from 1972 to 2009, which have monitored the incidence and severity of these pathogens in barley fields on the Canadian Prairies. Barley fields to be surveyed were selected at random at intervals of at least 10 to 15 km. The presence of disease and an estimate of the percentage infected plants (plants with sori) were determined while walking an ovoid path of approximately 100 m in each field. Samples of smutted heads were collected for accurate identification of the pathogen in the laboratory. The data were separated into loose smut incidence and severity (*U. nuda* infects developing embryos) and surface borne smut incidence and severity (combining data for *U. nigra* and *U. hordei*, which infect germinating seedlings) for analysis. The three pathogens are ubiquitous in barley fields on the Canadian Prairies, but their areas of greatest incidence and severity were in Manitoba and northern crop districts of Saskatchewan and Alberta. The incidence of loose smut has declined since 1985, when 90% of all barley fields were infested. Since 2004, 20 to 40% of barley fields

were infested with loose smut. The surface borne smuts have also declined since 1977, when 95% of barley fields were infested, to the point where few infested fields were found after 1999. The average severity of loose smut and surface borne smuts has been low. The highest average severity of loose smut occurred in 1975 at 1.6% and for surface borne smuts, in 1987 at 2.3%. Since 1998, the average severity of loose smut has been below 0.5%, and for surface borne smut, the severity was below 0.1%.

CPS-7 **Stripe rust resistance among western Canadian wheat and triticale cultivars.** D. A. Gaudet*, H. Randhawa, B. J. Puchalski, R. J. Graf, A. Goyal, T. Despins, and A. Laroche. AAFC Lethbridge Research Center, Box 3000, Lethbridge, Alberta, Canada T1J 4B1 (e-mail: denis.gaudet@agr.gc.ca)

Stripe rust (*Puccinia striiformis* Westend.) is an important pathogen of wheat in western Canada. Infections generally originate from urediniospores blown in from the Pacific Northwest U.S.A. during the spring and early summer. One hundred and four spring wheat and triticale and ten winter wheat cultivars were evaluated for resistance to stripe rust in nurseries at Lethbridge and Creston, B.C. Infection levels in all nurseries were high. Resistance occurred in all tested varieties in the triticale, amber durum, extra strong and soft white spring classes. Within the red Canada Prairie Spring (CPS) class, newer varieties were resistant but many of the older varieties were susceptible. Among the white CPS wheats, 'Vista' is resistant whereas 'Snowhite 475' and 'Snowhite 476' are susceptible. Among the hard white wheats, only 'Karma' was resistant whereas 'Snowstar' and 'Snowbird' were susceptible. Fifty-nine percent of the hard red spring wheats (HRS) were resistant; much of the resistance was attributed to the presence of the *Yr17* and *Yr18* resistance genes. Susceptible HRS varieties that are extensively seeded in western Canada include 'Barrie', 'Superb', 'BW881' and 'BW415'. Sixty percent of the varieties belonging to the Hard Red Winter class were resistant. Effectiveness of the *Yr10* gene in 'Radiant' has been lost due to the apparent occurrence of a new race. The cultivars were tested for the presence of markers for *Lr34/Yr18, Yr17, Yr36* and *Yr10* genes.

CPS-8 **The effect of leaf rust on 'Thatcher' near-isogenic wheat lines.** B.D. McCallum[1*], G. Humphreys[1], R. DePauw[2], and C. Hiebert[2]. [1]Agriculture & Agri-Food Canada, Cereal Research Centre, 195 Dafoe Rd., Winnipeg, Manitoba, Canada R3T 2M9; and [2]Agriculture & Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, P.O. Box 1030, Swift Current, Saskatchewan, Canada S9H 3X2

Wheat leaf rust, caused by *Puccinia triticina* Eriks., is a serious production problem in Canada and other countries. Genetic resistance has been effective in controlling wheat leaf rust. A series of near-isogenic wheat lines (NILs) were developed, by the late Dr. Peter Dyck, each with a different resistance gene or gene combination, using the susceptible cultivar 'Thatcher'. In 2002 and 2003, 30 'Thatcher' NILs and six hard red spring wheat cultivars were grown in yield trials at Glenlea, Morden and Brandon MB which all had high natural levels of leaf rust, and Swift Current SK, which had very low leaf rust incidence. Agronomic characters such as maturity, height, lodging, and grain yield were evaluated along with the leaf rust reaction. Quality of the harvested grain was assessed on samples from Glenlea and Swift Current by measuring test weight, 1000 kernel weight, grain protein content, grain hardness, and sedimentation volume. Under leaf rust pressure, many of the 'Thatcher' NILs with effective resistance genes exhibited reduced levels of leaf rust and yielded significantly more than 'Thatcher'. In the absence of leaf rust pressure, most NILs were equivalent to 'Thatcher' in terms of agronomic

performance and quality, although some lines were inferior. These results demonstrated the effectiveness of many of these genes in controlling leaf rust and protecting grain yield under leaf rust pressure, while having no apparent deleterious effects on agronomic performance or end use quality in the absence of the disease.

CPS-9 **Identification of a stem rust resistance gene in wheat line Tr129 with an introgression from *Aegilops triuncialis* genome.** H. Ghazvini*, C. Hiebert, T. Zegeye and T. Fetch Jr. Cereal Research Centre, Agriculture & Agri-Food Canada, 195 Dafoe Road, Winnipeg, MB, Canada R3T 2M9. (Habibollah.Ghazvini@agr.gc.ca)

Stem rust, caused by the fungus *Puccinia graminis* f. sp. *tritici*, is a devastating disease of wheat worldwide. The last stem rust epidemic in North America's wheat fields occurred in the early 1950s, when race 15B became prevalent for the first time in North America. Since then, deployment of effective stem rust resistance (Sr) genes in wheat breeding programs has controlled stem rust damage in North America as well as other parts of the world. Stem rust on wheat caused by race Ug99 (TTKSK) is currently spreading across Africa and into the Middle East. This race has virulence to most Sr genes that have been employed for decades in wheat breeding programs across the world, as well as most of Canadian spring wheat cultivars. A preliminary study indicated that line Tr129, which contains an **Aegilops triuncialis** introgression, is resistant to race Ug99. F_2 progeny lines from a cross (RL6071/Tr129) were inoculated with a local *P. graminis* race (MCCFR) to characterize inheritance of resistance in the line Tr129. Results showed that segregation of the F_2 population fitted both a single dominant gene ratio ($p = 0.222$) and a two gene (one dominant and one recessive) ratio ($p= 0.237$). F_2 lines are being increased to the F_3 generation and will be inoculated with races MCCFR and TTKSK (Ug99) to clarify number of genes in line Tr129 and to confirm if gene(s) provide resistance against both strains. Molecular studies are in progress to determine the chromosomal location of these resistance gene(s). Preliminary evaluation of the parents showed that 19 wheat SSR markers, located in different chromosomes, had null alleles in Tr129 which are often indicative of alien segments. Markers will be used to locate and map the stem rust resistance transferred from **Ae. triuncialis.**

CPS-10 **First report of *Phytophthora palmivora* Butler causing root rot on avocado (*Persea americana* Mill.) in Cuba.** M. Machado[1], C. Collazo[1], M. Peña[1], M.-A. Renaud[2], M.O. López[3], O. Coto[1], V. Zamora[1], R.I. Cabrera[1], M. Arauguren[4] and G.J. Boland[2*]. [1]Instituto de Investigaciones en Fruticultura Tropical. 7ma., No.3005, PO 11300, La Habana, Cuba; [2]School of Environmental Sciences, University of Guelph, Guelph, Ontario, Canada. N1G 2W1; [3]Instituto de Investigaciones de Sanidad Vegetal. 110 e/5A y 5F, Playa, La Habana, Cuba; [4]Unidad Científico-Técnica "Felix Duque-Guelmes", Matanzas, Cuba.

During 2007-2008, avocado trees showing root rot symptoms were observed in Jagüey Grande, Alquízar, and Havana city, Cuba. We conducted pathogen isolation by plating diseased roots and fallen fruit directly, and avocado fruit tissues baited from rhizosphere soil onto selective V8 agar (PARPH) or carrot agar. Direct plating of infected and baited tissues yielded pure cultures that developed white, stellate colonies with sparse aerial mycelia. Hyphal growth was completely inhibited above 35°C. Single, terminal sporangia on simple sympodium sporangiophores formed abundantly in agar and liquid media. Sporangia were 20 to 80 µm (48.4 ± 9.2µm) long and 17.5 to 52.5 µm (31.6 ± 5.5µm) wide, caducous, with short pedicels and prominently papillated. Sporangia were variable in shape, mostly ovoid-ellipsoid, obpyriform, spherical and distorted, with a narrow (6.4 ± 1.7 µm) exit pore. The isolates were heterothallic; and hyphal swellings and terminal

and intercalary globose chlamydospores were also observed. PCR amplification using Pa11s/Pa12a primers, specific to *Phytophthora palmivora* , yielded a band of the expected size (648 bp). BLAST analysis of the nucleotide fragments of about 900 bp from Cuban isolates (FJ666090, GU073390, and GU073391) amplified using ITS5/ITS4 generic primers showed a 98-99% identity with *P. palmivora* isolates from India (AM422704 and EU515173) and Colombia (GQ398157). Multiple sequence alignment by VectorNTI program revealed a 98.8% of identity. Pathogenicity tests were performed using pieces of lateral branches from mature avocado trees and resulted in rapidly developing (within 72 h), sunken, necrotic lesions around the sites of wound inoculation. The causal agent was consistently re-isolated from necrotic tissues. This is the first report of *P. palmivora* affecting avocado trees in Cuba.

CPS-11 **Multilocus genotyping of a worldwide collection of *Phytophthora ramorum*, the sudden oak death pathogen.** M.-J. Bergeron[1]*, G. J. Bilodeau[2], C. A. Lévesque[3], and R. C. Hamelin[1]. [1]Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, Stn. Sainte-Foy, Quebec, Quebec, Canada G1V 4C7; [2]Canadian Food Inspection Agency, 3851 Fallowfield Rd, Ottawa, Ontario, Canada K2H 8P9; and [3]Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, Ontario, Canada K1A 0C6

Phytophthora ramorum Werres, De Cock & Man in't Veld, the causal agent of sudden oak death and ramorum blight, is responsible for extensive mortality of *Quercus* spp. and *Lithocarpus densiflorus* in native forests of the western United States. *Phytophthora ramorum* has over 100 reported plant hosts that exhibit different symptoms of infection. Three clonal lineages have been reported to date in forests, nurseries and gardens of North America and Europe: the NA1 and NA2 lineages are currently only known in North America whereas the EU1 lineage, although initially found in Europe, is also found in North America. Here we examine the genetic variation within 13 nuclear genes from a worldwide collection of 100 *P. ramorum* isolates in order to better understand the evolutionary history of this introduced pathogen. The complete genome of *P. ramorum* provided us with a resource of approximately 16000 predicted genes from which polymorphic regions were identified. Eighty-six single nucleotide polymorphisms (SNPs) and five insertion/deletion changes were uncovered over the 6158 base pairs we sequenced. Fifteen multilocus genotypes (MLGs) were observed within the European population (n=72) compared with five within the North American population (n=28), among which two were shared between both populations. As expected, more diversity is observed in Europe. Moreover, phylogenetic relationships among the *P. ramorum* genetic variants show that the 15 MLGs associated with the European population cluster together and correspond to the EU1 lineage. The five MLGs associated with the North American population split up into three groups, corresponding to the NA1, NA2 and EU1 lineages.

CPS-12 **Efficacy of fungicide, seeding date and seedling age on seedling emergence, clubroot severity, and yield of canola.** S.F. Hwang[1*], T. Cao[2], Q. Xiao[2], H. Ahmed[1], V.P. Manolii[2], G. Turnbull[1], S.E. Strelkov[2], B.D. Gossen[3], and G. Peng[3]. [1]Crop Diversification Centre North, Alberta Agriculture and Rural Development, Edmonton, AB, Canada T5Y 6H3; [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, , Edmonton, AB, Canada T6G 2P5; and [3]Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, Canada S7N 0X2

Infestation of canola seed by *Plasmodiophora brassicae* Woronin could result in seedborne transmission of clubroot to fields where the pathogen (or a particular pathotype) does not yet occur. The effect of the seed treatment fungicides Dynasty 100 FS, Helix Xtra, Nebijin SSC, Prosper FX, and Vitavax RS on seed transmission of clubroot were evaluated under greenhouse conditions using artificially infested canola seeds. Each of the fungicides significantly reduced clubroot levels relative to the control, but Dynasty 100 FS and Nebijin SSC were the most effective, reducing disease severity by 75 and 80%, respectively. However, in trials planted in fields where *P. brassicae* was already present, none of the treatments evaluated (Cruiser, Helix Xtra, Dynasty, Prosper and Sedaxane) applied alone or in combination reduced clubroot severity or increased seedling emergence and yield. It appears that while seed treatments may be effective at removing seedborne inoculum, they may not be sufficient to protect the crop when sown in a field where a *P. brassicae* infestation is already established. In seeding date experiments conducted under field conditions, clubroot severity was higher and seed yield was lower in late-seeded canola (clubroot severity 1.30; seed yield 0.91 t/ha) compared to the early-seeded (clubroot severity 0.65; seed yield 1.18 t/ha) crop in one of three site-years. In another study, the impact of seedling age and cultivar resistance on clubroot severity, plant height and yield was evaluated under greenhouse conditions. Clubroot was more severe and plant height and yield were lower in younger seedlings versus older seedlings of both resistant and susceptible canola cultivars. We conclude that early seeding has promise for use as part of an integrated program for clubroot management.

CPS-13 **Infection of canola by secondary zoospores of *Plasmodiophora brassicae* produced on ryegrass.** J. Feng[1*], Q. Xiao[2], S. F. Hwang[1], S. E. Strelkov[2], and B. D. Gossen[3]. [1]Crop Diversification Centre North, Alberta Agriculture and Rural Development, Edmonton, AB, Canada T5Y 6H3 (e-mail: sheau-fang.hwang@gov.ab.ca); [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5; and [3]Agriculture and Agri-Food Canada, Saskatoon, SK, Canada S7N 0X2.

Clubroot caused by *Plasmodiophora brassicae* has a two-stage infection process. In the initial phase, root hairs are infected by primary zoospores from resting spores in the soil. In the second phase, secondary zoospores released from the root hairs fuse and then infect the root cortex. Although the initial phase occurs in many plant species, the second phase only continues to completion (pathogen development and symptoms) in susceptible hosts. As part of a larger study of clubroot pathogenesis, secondary zoospores collected from infected root hairs of canola (a susceptible host) and ryegrass (a nonhost) were inoculated onto healthy roots of both plant species. The treatments consisted of all possible combinations of the two plant species and the two sources of resting spores used as inoculum. At 5 days after inoculation, levels of both root hair infection and secondary plasmodia in the root cortex were similar on plant roots in all of the treatments. At 5 weeks after inoculation, typical large galls developed on canola inoculated with secondary zoospores derived from canola and no galls developed on ryegrass, regardless of inoculum source. However, tiny galls developed on canola inoculated with zoospores from ryegrass. These results indicate that there are distinct components in pathogen pathogenicity and plant resistance that correspond to the stages of the pathogen life cycle.

CPS-14 **Quantification of cortical infection by *Plasmodiophora brassicae* using Assess image analysis software**. K. Sharma[1*], B. D. Gossen[2], M. R. McDonald[3]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1 Canada; [2]Agriculture and

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The life cycle of *Plasmodiophora brassicae* Woronin, which causes clubroot of canola (*Brassica naups* L.) and other crucifers, consists of a primary phase (infection and development in root hairs), and a secondary phase (cortical infection and clubbing). The objective was to develop a histological technique to quantify cortical infection using Shanghai pak choy (*B. rapa* subsp. *Chinensis*) as a model crop. Individual 3-day-old seedlings of pak choy in soil-less mix were inoculated with 1 x 10^8 resting spores and maintained at 25º C. Cortical infection and clubroot severity were assessed on four plants per date at 4-day intervals from 10 to 42 days after inoculation (DAI). A 0.5-cm root segment from the top 0–1 cm of each main root was dehydrated in an ethanol series, embedded in paraffin, and 6-µm-thick cross-sections were cut and stained using methylene blue. This top of the taproot was selected because infection occurs first in this region and has a large impact on subsequent plant development. Four stains (periodic acid schiff, fast green, haematoxylin + eosin and methylene blue) were assessed. Methylene blue was selected for the analysis because it provided consistent results that were compatible with image analysis (Assess software, American Phytopathological Society). Five digital images per root at 125x magnification were collected and used to estimate the mean proportion of the area of each field of view that stained for *P. brassicae*. Cortical infection (CI) was 2.4% at 10 DAI but increased to 37% by 42 DAI. CI was strongly and positively correlated with disease severity ($r = 0.98$; $P < 0.001$). The Assess software readily separated infected and noninfected areas, and so provided a rapid technique for assessing cortical infection. This approach would be particularly useful where large numbers of samples are assessed. We conclude that assessment of cortical infection can be a useful supplement to other parameters of pathogen quantification, such as qPCR. Assessment of CI at 30 DAI at 25º C would be optimum for many studies because this ensures a high CI in susceptible lines in a relatively short time.

CPS-15 **Effect of fertilizer on components of the disease cycle of *Valdensinia heterodoxa* in lowbush blueberry**. P.D. Hildebrand*, W.E. Renderos, S.A.E. Fillmore, and B.A. Walker. Atlantic Food and Horticulture Research Centre, Agriculture and Agri-Food Canada, 32 Main Street, Kentville, NS B4N 1J5 (email: Paul.Hildebrand@agr.gc.ca)

Valdensinia leaf spot has become a serious disease in lowbush blueberry that causes premature leaf drop in the crop and sprout phases of production. In this study, we examined the effect of fertilizer on various components of the disease cycle of *Valdensinia heterodoxa* Peyronel. Two-year old potted plants were obtained from a nursery that had been grown outdoors until mid-December of the second year when they were placed into cold storage at 1 C until the following season. The plants were pruned to simulate commercial practices and fertilized once with 15-15-18 (N-P-K) at 20 kg N/ha or weekly at this rate (6 applications). After 6.5 weeks of re-growth in a greenhouse, the foliage was inoculated with conidia of *V. heterodoxa* and incubated at 20 C for 24 h when the incidence of infected leaves, lesions/leaf and lesion size were assessed. Infected leaves were collected and incubated in Petri dishes with moist filter paper in a growth chamber at 20 C with a 16 h photoperiod. After 8 days, released conidia on lids were counted, leaf area was measured and leaves were then further incubated at 20 C in darkness for 12 days when incidence of leaves with sclerotia and their length in the mid-vein were assessed. The incidence of infected leaves was not affected by fertilizer, but lesions/leaf increased by 19.8%, lesion size increased by 21.8%, conidia/cm^2 leaf tissue

increased 3.4 times, incidence of leaves with sclerotia increased 4.1 times and size of sclerotia increased 7.9 times with 20 Kg N/ha compared with the nontreated control. The high rate of fertilizer further stimulated these components. During the last 10-15 years, growers began to routinely fertilize fields with up to 24-31 kg N/ha. This study showed that an application of just 20 Kg N/ha can dramatically stimulate this disease and may help to explain its recent increase in blueberry fields.

CSA-1 **Improved Salt Tolerance of *Arabidopsis thaliana* Plants.** F. Bayat [*1], B. Shiran[2], D. V. Belyaev[3]. [1]Department of Plant Breeding, Faculty of Agriculture, Persian Gulf University, Booshehr, Iran. [2]Department of Plant Breeding, Faculty of Agriculture, University of Shahrekord, Shahrekord, Iran. [3]Timiryazev Institute of Plant Physiology, ul. Botanicheskaya 35, Moscow 127276 Russia.

Salt tolerance is a complex trait which control with multiple gene and numerous biochemical and physiological mechanisms. One possible mechanism to avert Na^+ toxicity in the cytosol is compartmentalizing Na^+ away from the cytosol via vacular Na^+/H^+ antiporters. The compartmentation of Na^+ into the vacuole more than cytosol toxicity elimination, allows the plants to use Na^+ as an osmoticum, maintaining an osmotic potential that drives water into the cells. V-type H^+-ATPase and H^+-PPase generate the necessary proton gradient required for activity of Na^+/H^+ antiporters. In the present work full-length *HvNHX2* open reading frame (ORF), a vacuolar Na^+/H^+ antiporter gene from barley, was cloned into *Bam*HI and *Sac*I sites of pBI121 binary vector. Resulted vector were introduced into *Agrobacterium* and transgenic *Arabidopsis* plants overexpressing *HvNHX2*, were regenerated via transformation with *Agrobacterium tumfaciens* by floral dipping method. The T3 progenies homozygous for kanamycin resistance have been assayed for salt tolerance. These transgenic plants were able to grow normally in presence of 200 mM Nacl in pots, while wild type *Arabidopsis* plants showed necrosis. Transgenic plants overexpessing *HvNHX2*, accumulated more Na^+ in the shoots, and had longer root in early seedling stage in MS medium plus NaCl. These result show that improved salt tolerance could be achieved by compartment of Na^+ into vacuole.

CSA-2 **A comparison of preharvest sprouting responses in Canadian hard red, hard white and CIMMYT hard white spring wheat.** D.G. Humphreys. Agriculture and Agri-Food Canada, Cereal Research Centre, 195 Dafoe Road, Winnipeg, Manitoba, Canada R3T 2M9 (email:gavin.humphreys@agr.gc.ca)

Preharvest sprouting is a perpetual threat to wheat production, particularly in the shorter season or higher rainfall areas. Sprouted grain can result in significant harvest losses for the producers and downgrading due to sprouting can cause wheat to lose up to 40% of its value. Sprouted grain has low falling numbers which are associated with poor baking and noodle quality. White seeded wheat is more susceptible to preharvest sprouting than red seeded wheat. The objective of this study was to compare Canadian hard red, hard white and CIMMYT hard white spring wheat varieties for their sprouting response. Preharvest response was measure over two years using sprouting scores and Hagberg falling number tests. Falling numbers were higher in 2009 compared to 2010, which is not unexpected because 2010 had wet, cool harvest conditions while 2009 was warmer and drier. Generally, Canadian hard red wheat had the lowest sprouting scores and highest falling numbers. Among Canadian white seeded wheat lines, Snowstar and HW005 had significantly lower sprouting scores and higher falling numbers than Minnedosa. CIMMYT wheat showed generally low levels of sprouting resistance with the exception of PHS-06 (Milan/Munia) which had high falling numbers and low sprouting scores. PHS-06 may be useful as a parent to improve preharvest sprouting resistance in hard white wheat.

CSA-3 **Soyasaponin B concentrations in 20 soybean genotypes**. P. Seguin[1]*, G. Tremblay[2], D. Pageau[3], and W. Liu[1]. [1]Department of Plant Science, McGill University, Macdonald Campus, Sainte-Anne-de-Bellevue, Québec, Canada (email: philippe.seguin@mcgill.ca) ; [2]CEROM, Centre de Recherche sur les Grains Inc., Saint-Mathieu-de-Beloeil, Québec, Canada; and [3]Agriculture et Agroalimentaire Canada, Centre de Recherche et de Développement sur les Sols et les Grandes Cultures, Normandin, Québec, Canada

Soybean is an important source of health-beneficial compounds including saponins. Soyasaponins B have been implicated in the cholesterol-lowering effect of soy products. Studies were conducted in four environments in southwestern Québec, Canada to determine the soyasaponins B concentration in 20 locally adapted genotypes. Soyasaponins B were hydrolyzed into non-DDMP soyasaponins during the extraction process resulting in the quantification by HPLC of soyasaponins I, II, III, IV, and V. Among all soyasaponins B, soyasaponin I was found in greatest proportion. Interactions between genotypes and environments (G × E) were observed for soyasaponins I and IV, and for total soyasaponins B, none being observed for soyasaponins II, III and V. Differences between genotypes were observed for all soyasaponins in all environments. Despite the presence of G × E interactions, ranking of most genotypes was generally consistent across environments. Total soyasaponins B averaged 3.93 µmol g^{-1}, ranging between 2.70 and 5.69 µmol g^{-1} across four environments for the 20 genotypes. Highest concentrations were observed in the cultivar 'Toki' in all 4 environments. Selection of high soyasaponins B soybean cultivars thus appears possible.

CSA-4 **Inheritance of biomass quality traits in barley for a 'Falcon'x'Tyto' cross**. P. Juskiw[1*], M.L. Swift[1], J.H. Helm[1], J. Nyachiro[1], M. Oba[2], and W. Pitz[3]. [1] Field Crop Development Centre, Lacombe AB Canada T4L 1W8 (patricia.juskiw@gov.ab.ca); [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB Canada T6G 2P5; [3] Parkland Laboratory, Red Deer AB Canada T4N 4B7

Digestibility of biomass is an important quality trait of silage used in ruminant rations. The digestibility of biomass when taken for silage production has been found to differ between genotypes of barley (*Hordeum vulgare* L.). While growth stage at harvest and environmental conditions during growth may confound genotypic difference, 'Falcon' barley has on average 8% higher *in vitro* fibre digestibility (IVFD 30 hr) than 'Tyto'. The cross between Falcon and Tyto was made to determine what traits between these two hulless, six-rowed, semi-dwarf, barley cultivars may account for this difference in quality. Two hundred recombinant inbred lines were created by single seed decent advancement to the F_5 generation. The following generations were grown out as hill plots in the growth room (20/15 C 16/8hr) and as small plots in the field at Lacombe AB. Hills and small plots were harvested either by hand or using the silage harvester when plants were as close to the soft-dough stage as possible by staggering harvests into three batch times. Quality traits measured at Parkland Laboratory (Red Deer, AB Canada) were acid detergent fibre (ADF), neutral detergent fibre (NDF), and protein while lignin and IVFD were done by Cumberland Valley Analytical Services, Inc. (Hagerstown, MD USA) and starch was done by Dr. Oba at the University of Alberta (Edmonton, AB, Canada). Two- and three-gene ratios were fitted to the data for these traits. The number of genes controlling starch, lignin and IVFD differed between the growth room and the field. For populations grown in the growth room, lignin was a dominant trait while in the field it was recessive. When stepwise analyses were conducted with this population, for

plants grown in the growth room IVFD was related to NDF and starch. However for plants grown in the field, lignin and protein were the most important traits associated with IVFD. This complex interaction of environment on trait expression will complicate our discovery of the underlying mechanisms controlling this trait.

CSA-5 **Evaluation of newly developed alfalfa varieties for adaptability under fall and spring waterlogging.** Yousef A. Papadopoulos[1], K.E.Glover[2], M. Gruber[3], S.A.E. Fillmore[4], M. McElroy[2], K.B. McRae[4], W.G. Thomas[5], M.A. Price[6], D.G.Mason[7], R.G. Thompson[8], and C. McLean[6] [1]Agriculture and Agri-Food Canada, 100-5 Haley Institute, PO Box 550, Truro, N.S. Canada B2N 5E3; [2]Nova Scotia Agricultural College, Truro, N.S; [3]Agriculture and Agri-Food Canada, Saskatoon SK; [4]Agriculture and Agri-Food Canada, Kentville, N.S; [5]AgraPoint, Nova Scotia Agricultural College, Truro, N.S. [6]N.B. Dept. Agriculture, Fredricton, N.B; [7]Agriculture and Agri-Food Canada, Nappan, N.S; [8]Mount Allison University, Sackville, N.B

Plants tolerant to fall and spring waterlogging within alfalfa cultivars have been observed. This investigation sought to determine the selection gain for tolerance to fall and spring waterlogging following one selection cycle. New synthetics and their parents were planted in root-retainers and placed in plywood boxes that accommodated flooding treatments under field conditions. Two flooding treatments, 'fall' and 'fall and spring', were initiated in mid October. At the end of the fall flooding (6 weeks), boxes were drained and then lined and covered with sheets of 5-cm Styrofoam bead board to simulate snow cover during the winter. Spring flooding for the second treatment was initiated in April for a 6-week period. After flooding, boxes were drained and the plants moved to a greenhouse, where they were kept under natural day length. Top growth was harvested twice, at 6-week intervals. Before each harvest, stage of development, persistence and dry matter (DM) yield were recorded. Fall flooding did not result in a significant reduction in number of plants for all populations studied. Excellent plant acclimation in the fall and effective simulated snow cover conditions ensured that, on average, 87.5% of the control plants survived. Visible stress symptoms were observed when the entries were subjected to fall and spring waterlogging treatment, with decreased herbage DM yield and delayed flowering. The fall and spring flooding treatment reduced the number of surviving plants for all populations. Source versus selected populations was not significant for DM yield, but all two- and three-way interactions were highly significant. Variations for fall and spring waterlogging tolerance were evident among and within the newly developed populations, indicating that further selection gains are possible with advanced cycles of recurrent selection.

CSA-6 **Effect of zinc and partial substitution of urea with ESN and ammonium sulphate on silage corn yield, feed quality and residual fertility.** T. S. Sahota*, Thunder Bay Agricultural Research Station (TBARS), 435 James St. S, Thunder Bay, Ontario, Canada, P7E 6S7 (e-mail:tarloksahota@tbaytel.net)

Optimum rate of N application to silage corn is usually considered to be 150 kg N ha^{-1}. Corn takes longer than cereals to mature; part N applied from a slow release fertilizer could prolong N supply to corn till maturity. Field experiments were conducted at TBARS, Thunder Bay, during 2007-2009 to confirm this hypothesis and to study corn's response to zinc; often considered critical for corn. The treatments included urea @ 100 kg N ha^{-1}, urea @ 79 kg N ha^{-1} + ESN @ 21 kg N ha^{-1}, and urea @ 79 kg N ha^{-1} + ammonium sulphate (AS) @ 21 kg N ha^{-1}, each with Zn @ 0, 7, 14, and 21 kg ha^{-1}, and an absolute check; without N or Zn. All treatments, replicated four times in completely

randomized block design, got manure @ 50 kg N ha^{-1}. Averaged over years, application of N increased the silage corn dry matter yield (DMY) by > 2.5 Mg ha^{-1}. Partial substitution of N from urea, by ESN (Environmentally Smart Nitrogen, Agrium Inc.'s brand name for polymer coated urea) or by AS, didn't improve the silage corn DMY (12.5 Mg ha^{-1} with part N from AS to 13.1 Mg ha^{-1} with all N from urea). Application of Zn @ 7-21 kg ha^{-1} didn't increase the silage corn DMY as compared to the check (12.8 Mg ha^{-1}). Treatments' effect on the feed quality wasn't discernible. Post harvest soil analysis (0-30 cm) revealed that the residual nitrate N (29.7 ppm) and total mineral N in soil (33.0 ppm) were highest with urea + ESN, whereas ammoniacal N (5.3 ppm) and sulphate S (10.3 ppm) were highest with urea + AS. Partial substitution of urea N therefore improved residual soil fertility!

CSA-7 **Analysis and interpretation of nitrogen efficiency in breeding trials**. Y. Anbessa and P. Juskiw*, Field Crop Development Centre, Alberta Agriculture and Rural Development, Lacombe, AB, T4L 1W8 (*presenter, E-mail yadeta.kabeta@gov.ab.ca)

Genetic improvement in nitrogen use efficiency (NUE) is important to reduce input costs and the negative impact of excessive N on water and air quality. NUE is assessed as grain yield per unit of N supply (soil N + applied) and by this computation, genotype assessment within a breeding program for NUE would identify those lines that are higher in grain yield. However, NUE based on yield would not distinguish if it was actually to do with more efficient use of N nutrition or other factors such as water, radiation, other nutrients, etc. In grain crops, a more precise measurement of the efficiency of use of N nutrition is the ratio of grain N yield to N supply hereafter referred to as N efficiency (NE). NE reflects the proportion of N recovered in the economic yield grain and specific to N nutrition. The objective of this study was to determine if NE could discriminate between relatively efficient and inefficient lines of spring barley (*Hordeum vulgare* L.). Twenty-five genotypes, assembled from different sources, were evaluated under low (120 kg N ha^{-1}) and normal (170 kg N ha^{-1}) fertility regimes at Lacombe, AB in 2010. Data were collected on grain yield, grain N concentration and other agronomic traits. NE was computed as grain N yield divided by total N supply (soil N + applied), where grain N yield was the product of grain yield and grain N concentration. Analysis of variance revealed significant differences among the genotypes in NE under both low and normal fertility regimes. Averaged over the two N regimes, the best genotypes, including I09501, I09502, I09505, I09507, and I08128, had NE of over 0.6 kg grain N per kg N supply while the inefficient check F09438 had less than 0.4 kg grain N per kg N supply. The top NE lines also out yielded F09438 by 160% or more. In conclusion, these preliminary results indicate that selection based on NE would be effective and can be used to simultaneously improve total N recovery in the grain and grain yield.

CSA-8 **Nutrient management for Saskatchewan organic cropping systems.** J.D. Knight*, *Department of Soil Science, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK

Many challenges associated with growing organic crops on the Canadian prairies are unique to the region. Climatic extremes limit the length of the growing season for crops as well as crop diversity options. Furthermore, drought is frequently more limiting to crop growth than are nutrients. Further challenges arise because the majority of farms are stockless. Even farms that have livestock tend not to have enough animals to replenish nutrients farm-wide. Farms without sufficient animal stocks cannot economically rely on

manure for nutrient additions. Research addressing alterative nutrient sources for organic production will be discussed in the context of organic dry-land agriculture in Saskatchewan.

CSA-9 **Effect of different levels of zinc and copper on germination and seedling growth of Oat (Avena *sativa* L.)** R. Amirnia[1*], M. Ghiyasi[1], and M. Tajbakhsh[1.1] Department of Agronomy and Plant Breeding, Faculty of Agriculture, Urmia University, Iran, (r.amirnia@urmia.ac.ir)

Heavy metals such as zinc and copper are released into the environment by both natural and anthropogenic sources. With the exception of soils derived from the physical and chemical weathering of parent materials containing increased levels of trace elements (e.g. black shales and basic igneous rocks), the presence of elevated metal concentrations in the environment is mostly related to man's activities. The objective of this work was to study different levels of copper and zinc on germination and seedling growth of Oat (*Avena sativa* L.) under laboratory conditions. The experiment design was conducted as a completely randomized design (CRD) with three replications. Treatments comprised of control (deionized water), 4, 6, 8 and 10 ppm of cu^{2+} and zn^{2+}. The results showed both metals significantly decreased the germination and seedling growth parameters except for 4 ppm of metals.

CSA-10 **The challenges of irrigating with reclaimed water in sod production.** P. Schwieder[1*], K. Dunfield[2], E.M. Lyons[1] and K.S. Jordan[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1; [2]School of Environmental Science, University of Guelph, Guelph, ON, N1G 2W1

Irrigating with reclaimed water is not a common practice in Canada and particularly in Ontario. The potential contamination of agricultural food crops is a major obstacle to overcome in the public perception of wastewater reuse. An alternative crop with economic benefit to both Ontario and Canada is sod. As this crop is not consumed and public access to the production site can be limited, it offers a means to reuse wastewater in a relatively safe manner. However, in Ontario there is a lack of information on the benefits and pitfalls of using reclaimed water irrigation when producing sod. This poster is designed to illustrate some of the information that has been found to date in our study of reclaimed water irrigation when producing Kentucky Bluegrass sod (*Poa pratesis* L.). Examined were four different sources of reclaimed water with differing chemical properties for their sod growing potential and environmental impact. This was carried out by means of two greenhouse experiments, one set up in a completely random design and the other as a randomized complete block. Differences in the turf health and the amount of nitrates leaching through the soil were found between the different reclaimed water irrigation treatments.

CSA-11 **Relative adaptability for various pulse types and cultivars in semiarid northern latitude areas.** X. Y. Wang[1*], Y. T. Gan[1], [1]Agricultural and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Gate#3, Airport Road East, Swift Current, SK, S9H 3X2

Global warming has become increasingly evident in recent decades. The impacts of climate changes on agricultural production and crops phonological characteristics are visible, especially in the cooler, high latitude regions of the earth. This study determined the relative adaptability and crop performance of various pulse types and cultivars grown

in semiarid northern latitude areas. A total of 6 green and yellow pea (*Pisum sativum* L.), 6 desi and kabuli chickpea (*Cicer arietinum* L.), 11 large green, small green, small red, and clear-field red lentil (*Lens culinaris* Medik.) cultivars, along with fababean (*Vicia faba)*, drybean (*Phaseolus vulgaris*) and lupin (*Sundial lupine*) were tested at southwest Saskatchewan, Canada, 2008-2010. Pea produced the greatest seeds and biomass yield among the pulses. Dry rainfall condition in 2009 lowered seeds and biomass yield for all pulse crops. In the high rainfall 2010, seeds yield of Desi and Kabuli chickpeas significantly decreased due to their indeterminate natures. Cultivar difference of seeds yield only showed in red lentil with CDC Rouleau producing higher seeds than any others in three years. Duration of vegetative growth stage was less affected by rainfall variations and similar between pulse crops while the duration of reproductive growth stage differed between pulses with chickpea and fababean had longer duration than others. Overall, lower GDD was required to complete reproductive physiological development stage in the low rainfall year compared to moderate and high rainfall years. Favourable rainfall condition prolonged reproductive growth stage of "warm-season" crop chickpeas, then greater GDD required. In semiarid Canadian prairies, continued global warming, coupled with genetic enhancement of pyramiding earlier-maturing genes to cultivars, integrated crop management like early seeding may provide more promises for chickpea better adapted to the high latitude regions of the world.

CSA-12 **Water use and distribution profile for various pulse types and cultivars in semiarid northern latitude areas.** X. Y. Wang[1*], Y. T. Gan[1], [1]Agricultural and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Gate#3, Airport Road East, Swift Current, SK, S9H 3X2

Pulse crops have been increasingly used to replace conventional summerfallow and diversity cropping systems in semiarid northern latitude areas. Understanding of water use characteristics and its distribution patterns in the soil profile is essential for optimizing cropping systems aimed at improving water use efficiency. This study was to depict soil water distribution profile at various soil depths and determine water use (WU), water use efficiency (WUE), post harvest residual soil water (PHRSW) for various types of pulses and different cultivars grown in semiarid northern latitudes. A total of 6 green and yellow pea (*Pisum sativum* L.), 6 desi and kabuli chickpea (*Cicer arietinum* L.), 11 large green, small green, small red, and clear-field red lentil (*Lens culinaris* Medik.) cultivars, along with fababean (*Vicia faba)*, drybean (*Phaseolus vulgaris*) and lupin (*Sundial lupine*) were tested at southwest Saskatchewan, Canada, 2008-2010. Overall, water use mainly occurred in the top 30-cm depth, which averaged to 19 mm in 2008 and 2009 and < 4 mm in 2010 for all pulses, respectively. Desi and kabuli chickpea used the greatest amount of water evaluated. Water use profile differed only between lentils cultivar in 2009 with CDC Glamis used the greatest amount of water and CDC Richlea and CDC Blaze used the least. Pea had the highest WUE in three years. Pea left the greatest amount of water in the soil at harvesting while chickpeas left the least in both 2008 and 2009 suggesting subsequent crops may receive more benefit from the water reserved in the soil by a pea crop than by a chickpea crop in a normal to dry year but this effect may diminish in a high rainfall year. Similar water use distribution profile or water use between individual dry pea and chickpea cultivars suggested that a large progress has not been made, if any, in pulse breeding programs targeting at the improvement of water use efficiency. Global climate change is becoming more evident in semiarid northern latitudes, challenges to improve water use efficiency in newly released pulse cultivars should be on pulse breeders' top agenda.

CSA-13 **High-resolution mapping of QTL controlling root anatomical traits in maize (*Zea mays L.*).** Patompong Saengwilai[1], Amy L. Burton[2], Shawn M. Kaeppler[3], Kathleen M. Brown[2], and Jonathan P. Lynch[2]*. [1]Intercollege Program in Plant Biology, Pennsylvania State University, University Park, PA 16802, USA; [2]Department of Horticulture, Pennsylvania State University, University Park, PA 16802, USA (email: jpl@psu.edu) and [3]Department of Agronomy, University of Wisconsin, Madison, WI 53706, USA

Root anatomical traits influence the acquisition and transport of water and nutrients, the metabolic cost of root growth and maintenance, and the mechanical strength of the root system. A number of experiments have shown significant benefits of root anatomical traits under biotic and abiotic stresses. The combination of high-throughput phenotyping and genotyping with advanced statistical techniques has permitted high-resolution mapping of maize root anatomical traits. This makes possible crop improvement by Marker-Assisted Selection (MAS). In this study, Quantitative Trait Loci (QTL) controlling root anatomical traits of the public maize intermated B73 x Mo17 (IBM) population grown in the greenhouse and in the field under controlled condition were identified and compared. In addition, the phenotypic variation of root anatomical traits of 26 parents of the Nested Association Mapping (NAM) population was observed. Based on percent Root Cortical Aerenchyma (RCA) and plant vigor of the parents, 9 populations were selected for further joint linkage analysis and genome-wide association mapping.

CSA-14 **Functional characterization of cinnamic acid 4-hydroxylase, a key candidate in characterizing the process of after-cooking darkening in potatoes.** T. Borza*, A. Schofield, Y. Wu, G. Wang-Pruski. Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3 (e-mail: gwangpruski@nsac.ca)

After-cooking darkening (ACD) occurs when cultivated potatoes (*Solanum tuberosum*) are exposed to air after processing (boiling, baking, frying, or dehydration). ACD in potatoes is caused by the formation of a colorless ferrous-chlorogenic acid complex, which upon exposure to air oxidizes to form a dark compound, the ferri-dichlorogenic acid. In the last years, a wide array of methods including bioinformatics, proteomics and QTL mapping have been used to identify candidate genes; one of the genes likely to be involved in controlling ACD in potatoes encodes for cinnamic acid 4-hydroxylase (*c4h* gene). A *c4h* gene was cloned and its expression analysed in potato tubers several years ago by this group. However, new data resulting from the sequencing of the diploid relative *Solanum phureja* suggested that two *c4h* genes are likely to be present in the genome of *S. tuberosum.* Using *S. tuberosum* EST data and genomic information from *S. phureja*, we generated more sequence data for both *S. tuberosum c4h* genes including a comprehensive single nucleotide polymorphism (SNP) map of exons. The expression pattern of the two *S. tuberosum c4h* genes was analysed in leaf, tuber, stem and flower samples by quantitative RT-PCR. Two different plasmid constructs, one over expressing a *c4h* gene and the other one suppressing the expression of *c4h* genes (interference RNA-mediated suppression) have been engineered to produce transgenic *S. tuberosum* plants.

CSA-15 **Effect of plant growth regulators on crop growth, maturity and seed yield of CDC Frontier chickpeas in southern Alberta.** M. S. Bandara[1*]; P. P. Lokuruge[2] ; A. Kruger[1], R. J. Howard[1]; T. Harms[1] ; N. Chaudhary[3] ; B.Taran[2]. [1]Crop Diversification Centre South, 301 Horticultural Station Road East, Brooks, AB, T1R 1E6; [2]Department of Plant

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Late and uneven crop maturity, caused mainly by indeterminate growth habit is one of major impediments for the production of high quality chickpeas on the Canadian Prairies. Plant growth regulators (PGRs) with growth inhibitory properties have been successfully used to control excessive growth of annual cereals and pulses. A field study was conducted to examine the impact of three PGRs (Chlormequate chloride=A, Prohexadione-Ca=B and Trinexapac-ethyl = C) on crop maturity, seed yield and quality of CDC Frontier chickpeas under rainfed and supplementary irrigated conditions at two locations in southern Alberta. PGRs were applied at four rates (1000, 2000, 4000 and 6000 ppm for A and C, and 750, 1500, 3000 and 4500 ppm for B) at 10, 20 or 30 days after first flowering (DAF), either as a mixture with a fungicide or separately. Treatments were arranged in a split-plot randomized complete block design with three replicates at each location. Only PGR B and C reduced plant heights significantly. The 2010 season was wet and cool, thus the crop maturity was inconsistent. In general, yield improvement was more apparent when treatments were applied at 20 DAF, indicating that PGR has a potential to improve seed yield and quality in chickpeas.

CSA-16 **Herbage composition and methane production of switchgrass grown in eastern Canada**. A. Claessens[1*], G. Bélanger[1], P. Savoie[1], G. Parent[1], A. Bertrand[1], G.F. Tremblay[1], D. Massé[2], Y. Gilbert[2], D. Babineau[3]. [1]Soils and Crops Research and Development Centre, Agriculture and Agri-Food Canada, Québec, Canada (e-mail:annie.claessens@agr.gc.ca); [2]Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Canada; and [3]Groupe EBI, Berthierville, Canada

Switchgrass (*Panicum virgatum* L.) is a warm-season grass recognized as a potential biomass crop for energy production in North America. However, little information exists on the effect of stage of development on herbage composition and methane production of switchgrass cultivated in eastern Canada. Our objective was to determine how harvest date and frequency affects switchgrass herbage characteristics and to relate these to specific methane yield. Switchgrass, seeded in 2002 and 2006, was harvested as a one cut system on three dates (late July, early September, and early October) in 2007. The regrowth of herbage harvested in late July was also harvested in early October as a two-cut system. At each harvest, herbage non structural carbohydrate (NSC), neutral detergent fiber (NDF), and acid detergent fiber (ADF) concentrations, along with *in vitro* true digestibility (IVTD) of dry matter (DM), *in vitro* digestibility of NDF (dNDF), and DM yield were determined. Switchgrass herbage samples (35% DM) were ensiled at each harvest. Silage pH and concentrations of NH_3-N, NSC, lactic acid, and volatile fatty acids (VFA) were determined after 60 days of fermentation; all harvests produced good silage (pH < 4.4; NH_3-N < 38 g kg^{-1} of total N). Silage samples were anaerobically digested in mesophilic batch reactors to measure methane production. In a one cut system, delaying harvest from late July to early September increased herbage DM yield (9.0 to 11.5 Mg DM ha^{-1}) and herbage NSC concentration (51 to 85 g kg^{-1} DM), delaying harvest from late July to early October decreased IVTD (720 to 582 g kg^{-1} DM), dNDF (590 to 409 g kg^{-1} DM), specific methane yield (0.288 to 0.207 L g^{-1} volatile solids), and had little effect on ADF and NDF concentrations. The two-cut system and the single harvest in early September produced the highest biomass yields (11.5 and 11.9 Mg DM ha^{-1}), however, the two-cut system produced more methane per unit area (3.17×10^6 L

CH_4 ha^{-1} vs 2.53×10^6 L CH_4 ha^{-1}) because of greater IVTD, dNDF, and specific methane yield.

CSA-17 **Effect of lime and wood ash on barley productivity and available nutrients.** T. S. Sahota*, Thunder Bay Agricultural Research Station (TBARS), 435 James St. S, Thunder Bay, Ontario, Canada P7E 6S7 (e-mail: tarloksahota@tbaytel.net)

Earlier work at TBARS, Thunder Bay, established that wood ash could substitute lime for amelioration of acidic soils and increased crop productivity. The ash is delivered free of cost by Abitibi Bowater at farmers' fields. It was not known how late or how soon farmers would need a second application of lime/wood ash. A long term field experiment on lime, wood ash and wood ash + lime (both at 50% of lime requirements) at different frequencies of application (after a gap of 2-8 years), with a check treatment was initiated in acidic soil (pH 5.9) of medium fertility at TBARS in 2004. Lime/wood ash were applied to meet the lime requirements in 2004 and at constant rates of 4 and 10 t/ha, respectively, for the later applications. Results from barley (2007-2010), second crop in rotation, are reported here. Both lime and wood ash increased the soil pH by 0.8-0.9, and available Ca, whereas only wood ash (applied after every two years) improved available P, K, Zn, Mn, and B. Barley grain yields (mean 2007-2010) were in the order of lime + wood ash (4,139 kg ha^{-1}) ≥ wood ash (4,089 kg ha^{-1}) ≥ lime (3,871 kg ha^{-1}) ≥ check (3,673 kg ha^{-1}). Wood ash improved the grain protein content by 1 % point and lime by 1.5 % point. Frequency of lime/or wood ash application (after 2 or 4 years), especially the latter, didn't affect the barley grain yield. It may be concluded that while both wood ash (also permitted for organic crop production) and lime could be used to overcome soil acidity, wood ash could be preferred to lime because of its better effect on improving soil fertility.

CSA-18 **Effect of solid dairy manure, wood ash, N, P, K and Mn on barley productivity and available nutrients.** T. S. Sahota*, Thunder Bay Agricultural Research Station, 435 James St. S, Thunder Bay, Ontario, Canada, P7E 6S7 (e-mail: tarloksahota@tbaytel.net)

A long term experiment on alfalfa (4 years)-barley (3 years)-soybean (3 years) was initiated in split plot design at Thunder Bay in a medium-high fertility soil in 2004. The treatments included solid dairy manure @ 50 t ha^{-1}, wood ash at liming requirements in 2004 and @ 10 t ha-1 in later years, manure + wood ash, and a check (no manure or wood ash) in the main plots split for N, N + P, N + P + K, and N + P + K + Mn. Manure and wood ash were applied after a gap of every two years. This paper reports treatment effects on barley (2008-2010). Interactions between the main and sub plot treatments were not significant, which means that manure or wood ash didn't affect nutrients requirement of barley. Both manure and wood ash significantly increased the barley grain yield; the effect of wood ash/ or manure + wood ash was better than manure. Average grain yield responses were 514, 788 and 768 kg ha^{-1} yr^{-1} with manure, wood ash, and manure + wood ash, respectively. Grain protein varied little (11.1-11.6 %) with these treatments. Improvement in soil pH, organic matter, Ca, Mg, Zn, Mn, and B by wood ash was more than that with manure, whereas reverse was true for P and K. Application of N @ 70 kg ha^{-1} significantly increased barley grain yield (770 kg ha^{-1} yr^{-1}) and protein content (by 1.1 % point) as compared to the check. Addition of P or PK or PK and Mn in addition to N, increased the grain yield only marginally (200-300 kg ha^{-1} yr^{-1}), but not the grain protein content. Application of nutrients increased only the soil Ca and K and didn't affect other nutrients, soil pH or organic matter.

CSA-19 **The study of genetic variability in related to efficiency of zinc uptake in different genotypes of *Triticum aestivum.*** Abdollah Hassanzadeh Gorttapeh[1]* and Javad Mozafari[2]. [1]Agricultural and Natural Resources Research Institute, West Azarbaijan,Urmia Iran. E_Mail: ahassanzadeh_g@yahoo.com, Phon: +989143465485,

Fax:+984412771253.and [2]Seed and Plant Improvement Institute, National Plant Genetic Resources, Iran

Nutrient efficiency in wheat is very complex. It includes nutrient acquisition efficiency and nutrient use efficiency. 26 winter wheat genotypes were used to investigate the interactive effects between genotypes and the use efficiencies of the Zn micronutrient by the grain. The results obtained in this study indicate that nutrient use efficiency of the Zn varies widely within wheat genotypes. Some genotypes were identified as being Zn use efficiency. These are considered low-input genotypes. It appears that a special breeding programmer of crop cultivars for low Zn nutrient and stress condition could be successful. Improved cultivar response to Zn nutrient will help to reduce inputs and hence protect the environment.

CSA-20 **Heat tolerance of Bt and non-Bt cotton (*Gossypium hirsutum* L.) under varying nitrogen rate.** M. F. Saleem[1]*, M. A. Cheema[1], A. Shakil[2], H. Z. Khan[1], and M. F. Bilal[1]. [1]Department of Agronomy, University of Agriculture, Faisalabad, Pakistan (mfsuaf@yahoo.com) and [2]Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

To determine the effect of temperature differences and varying nitrogen application rates on cell membrane thermo stability and yield of Bt and non-Bt cotton, an experiment was laid out on Agronomic Research Area in University of Agriculture, Faisalabad during Kharif 2009. The experimental area is located at 73.09^{o} East longitude, 31.25^{o} North latitude and at an altitude of 183 meters above sea level. The experiment was laid out in randomized complete block design (RCBD) with split-split arrangement and replicated thrice. Two cotton cultivars; FH-113 (Bt) and CIM-496 (non-Bt) were planted at two different times (mid March and mid May) using three nitrogen levels (115 kg ha^{-1}, 145 kg ha^{-1} and 175 kg ha^{-1}). Planting times were placed in main plots, varieties in sub plot and N levels in sub sub plots. Plot size was same for each treatment. The length of plot was 6 m and width was 3 m having four rows per plot with row to row spacing of 0.75 m and plant to plant spacing of 0.30 m. Maximum cell membrane thermo stability (58.88) was observed in FH-113 at mid March planting and minimum cell membrane thermo stability (30.77) was observed in CIM-496 at mid May planting while performance of CIM-496 at mid March planting and FH-113 at mid May planting was at par with mid March planting in FH-113. Statistically maximum seed cotton yield per plant (63.15 g) was observed in mid March planting and minimum seed cotton yield per plant (51.89 g) was recorded in mid May planting, while among varieties FH-113 gave maximum seed cotton yield per plant (62.32) and minimum seed cotton yield per plant (52.72 g) was observed in CIM-496; amongst the nitrogen levels maximum seed cotton yield per plant (64.85 g) was recorded with 145 kg ha^{-1} which was at par with 175 kg ha^{-1} and minimum (46.91 g) was recorded with 115 kg ha^{-1}. R^2 value (0.175) for cell membrane thermo stability vs. seed cotton yield per plant (g) was non significant.

CSA-21 **Influence of Seeding Rates and Harvesting Methods on the Determination of Optimum Population Density in *Amaranthus Cruentus*.** F.O. Odeleye[1*] and A.O. Olufolaji [2]1.Dept. of Crop Protection & Environmental Biology, University of Ibadan, Ibadan, Nigeria, 2. National Horticultural Research Institute, Jericho, Idi-ishin, Ibadan, Nigeria *Corresponding/presenting author: gbengaodeleye2@yahoo.com

Two field trials were carried out at the National Horticultural Research Institute, Ibadan, Nigeria, to determine the optimum population density for cultivating *Amaranthus*

cruentus using varying seeding rates and two harvesting methods (uprooting and pruning at 15 cm plant height). Seeds were drilled at 25 cm apart on 1m wide beds at the seeding rates of 1.0, 3.0. 6.0 and 9.0 kg ha^{-1} and the two standard methods were used to evaluate crop performance. The experimental design was split-split-plot with varieties as main plot seeding rate as the sub-plot and harvesting methods as the sub-sub-plot. Data were taken on total number of established plants, the total number and area of leaves and other yield components and analyzed using ANOVA and means separated using LSD (P=0.05). Results indicate that, seedling establishment increased with increase in seeding rates up to 6kg ha^{-1} after which plant population and yield became similar but highest at the 6 and 9 kg ha^{-1} seeding rates. Pruning engendered the regeneration of more leaves but the newly regenerated leaves were smaller in size than the leaves of uprooted plants. The cumulative yield of pruned plants was superior to those uprooted. Drilling at 6kg ha^{-1} seeding rate, the determinate early maturing NHAc3 variety of *A. cruentus* gave optimal plant performance with established population densities of 1.76 million uprooted plants ha^{-1} and a corresponding yield of 26.7 t ha^{-1} On the other hand, the intermediate late maturing ED82/1040A variety established 1.24 million plants ha^{-1} which with regular pruning gave shoot yields of 32.7 t ha^{-1}. The early maturing variety was therefore best suited for harvesting by uprooting while the late maturing variety gave higher yields by regular pruning.

CSA-22 **Evaluation of Mussel Sediments as Soil Amendment and/or Weed Suppressant**

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The mussel industry in Atlantic Canada produces large quantities of sediments as a by-product, for which there is no readily available means of recycling. With rising waste disposal costs and increased attention toward sustainable management, investigating alternative methods of handling these wastes is necessary. The objectives of this study were to (i) investigate the fertility value of shellfish sediments for crop production, and (ii) evaluate potential weed inhibitory properties of the shellfish sediments. The bioavailability of nutrients in mussel sediments was evaluated by testing tomato (T) and annual rye (AR) responses in a randomized and replicated greenhouse study. Treatments included control (impoverished soil with no amendment), three rates of mussel sediments [14,000 (S14), 28,000 (S28), 42,000 (S42) L/ha wet weight basis], and synthetic fertilizers (NH_4NO_3, triple superphosphate and KCl) (F). The weed inhibitory properties of the shellfish sediments were evaluated by testing responses of two dominant weed species (dandelion and lamb's quarters). The effect of sediment application (28000 L/ha wet weight basis) on weed germination and at an early stage of weed growth was tested and compared with control conditions. Sediment application increased both T and AR total dry biomass. Higher rates of application resulted in increased biomass. The highest rate of mussel sediments (S42) resulted in 5.5 and 1.9 times greater biomass production for T and AR compared with the infertile control treatment, respectively, and was almost half of the F treatment (48% and 44% for T and AR, respectively). Nitrogen uptake in T was equivalent to 14.3, 20.7 and 35.4 kg/ha for S14, S28 and S42, respectively, while N uptake in AR for the same treatments was 25.8, 36.6 and 54.6 kg/ha, respectively. Overall, 30% of total N supplied by mussel sediments was available to T, and 40% to AR. There was no evidence in this experiment to confirm the weed inhibitory effect of mussel sediment application for dandelion or lamb’s quarters, when sediments were applied before or after germination.

CSA- 23 **Animal performance and incidence of bloat in mixed alfalfa/sainfoin grazing.** E. Sottie[2], S. Acharya[1], A. Iwaasa[3], T. McAllister[1], Y. Wang[1] and J. Thomas[2]. [1] AAFC Research Centre, Lethbridge, AB, T1J 4B; [2] University of Lethbridge, Lethbridge, AB, T1K 3M4; [3]AAFC, Swift Current, SK, Canada, S9H 3X2

Beef cattle production can be maximized through the use of alfalfa (*Medicago sativa*) as a monoculture or dominant species in a forage mixture. However, pasture bloat discourages grazing of alfalfa-based pasture despite the high growths that are obtainable. Sainfoin (*Ononbrychis viciifolia*) is known to lower the incidence of pasture bloat when grown in mixed stands with alfalfa, but currently available cultivars are not suitable for the purpose. Three new sainfoin populations (LRC05-3900, LRC05-3901 and LRC05-3902) developed for their improved ability to survive with alfalfa and grow back quickly after cutting were established with 'Nova' in replicated mixed stands with alfalfa for simulated grazing at Lethbridge in 2008. In this trial the three new populations had higher total biomass yields than alfalfa in the stands after three cuts. The yields of LRC05-3900 and LRC05-3902 were significantly ($p<0.05$) higher than alfalfa and they both had yields about 25% more than Nova. The alfalfa samples collected from these plots had higher crude protein (24.3g/kg DM) compared to the sainfoin populations (18 – 21g/kg DM). Eighty Hereford steers of mean weight 362±3.5kg were divided among the 16 mixed paddocks established with three new and Nova sainfoin. Animals were rotationally grazed for a total of 43 days comprising of two grazing periods. Due to wet weather conditions grazing started when alfalfa was about 75% in bloom and sainfoin was at 100% bloom for the first round of grazing. The second round of grazing was carried out at the vegetative stage of both alfalfa and sainfoin. During the first 32 days of grazing the ADG among the sainfoin populations in the mixture varied between 0.60 to 0.75kg/d and during the second grazing the ADG was 1.20 to 1.45kg/d, but the differences among sainfoin populations in the mixture were not significant. No bloat incidence was observed during the grazing trial.

CSA-24 **Agronomics of Miscanthus varieties in coastal BC.** Shabtai Bittman[1], Derek Hunt[1], Margaret Gruber[2] and Tom Canam[2] Agriculture and Agri-Food Canada, Research Branch, Agassiz, BC[1] and Saskatoon, SK[2]

There is growing interest across Canada in low-cost biomass crops for a range of uses including soil improvement, livestock bedding, and energy feedstocks for combustion pyrolysis and cellulosic ethanol. Tropical grasses, such as *Miscanthus x giganteus* and *Panicum virgatum*, are high yielding and require less inputs than temperate grasses. There is a need for species and varieties that will persist and grow well in Canada. Two cultivars of the species *Miscanthus sinensis,* and *M. x giganteus parent,* were studied over two years in coastal BC. Under favourable moisture, a well established stand of *M. sinensis* yielded up to 20 t dry matter/ha with relatively little effect on yield from applications of mineral fertilizers (N-P-K-S-Mg). In autumn, the moisture content of the crop was too high for storage without prior curing. In winter, the moisture content dropped to 10-15%, suggesting that the crops could be harvested and stored with little or no additional curing. However, yield loss over winter varied with year and variety, reaching 30- 50% in the worst case. The proportion of yield loss seems to be related to the amount of leaves left on the crop in fall since most leaves are lost over winter. In general, the variety 'Blutenwunder' had lower moisture content, lower winter yield loss and lower nutrient removal, and is therefore likely to be a more suitable choice as a biofuel than the leafier variety 'Gracillimus'. Winter-harvested Blutenwunder removed

less than 3 and 10 kg/ ha for P and K, respectively, but removed 45-55 kg/ha of N. Leaf litter in winter contained as much N, K and other nutrients as the standing harvestable stems indicating the importance of not removing leaves from the plots to promote nutrient cycling. *M. x giganteus* followed similar patterns as Blutenwunder but produced around 30 t DM/ha under favourable moisture and there was little yield loss over winter. Offsetting factors of yield, DM content and mineral removal should be assessed with economic optimization analysis to select the best biomass crops.

CSA-25 **Phenotypic variation of side-oats grama grass collections from Canadian prairie.** M.P. Schellenberg*, B. Biligetu, G. J. McLeod. Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada. Swift Current, SK, Canada S9H 3X2 *Email: schellenberg@agr.gc.ca

The climate for the Canadian prairies is predicated to become warmer and drier due to the changing climate. Development of drought tolerant forage is necessary for sustainability of forage production under this changing climate. Side-oats grama grass (*Bouteloua curtipendula* (Michx.) Torr.) is a drought tolerant grass with desirable forage characteristics, and is distributed in Canadian prairies. Understanding ecotypic variability of this species is a prerequisite for developing populations suitable for drier region of western Canada. A field plot was established in 2005 near Swift Current (50°25' N, 107°44' W), Saskatchewan using 9 seed collections from Manitoba (MB) and Saskatchewan (SK). Seed yield, tiller number, plant height, and crown width of individual plants were measured for each collection in the summers of 2007 and 2010. The flowering date was also recorded for each collection. The collections from Sydney, MB and Wolsley, SK ranked the highest for most measured variables, indicating a greater potential for further population development. However, there was no clear ranking of these variables among other collections. Based on flowering date, collections from Minto, Coulter, and Glenboro, MB were classified as late flowering group, and the rest were as early flowering group.

CSA-26 **Responses of N, P accumulation, grain yield and dry matter accumulation of wheat and hulless and hulled oats to N supply**. B. L. Ma*[1], D. K. Biswas[1], and C. Ren[2]. [1] Agriculture and Agri-Food Canada, Ottawa, ON, Canada K1A 0C6 (e-mail: Baoluo.ma@agr.gc.ca); [2] Baicheng Academy of Agricultural Sciences, Baicheng, Jilin, China

Understanding of the crop source-sink balance in response to nutrient supply is important for cultivar improvement of cereal crops. A field experiment with spring wheat, hulless and hulled oats supplied with three levels of N fertilizer was conducted for three years in Ottawa, ON. Biomass samples were taken at 7-10 d intervals from seedling to maturity. Plant and component N and P concentrations of the dry matter samples were analyzed. Lodging scores, harvest index and grain yield were determined. Grain yield of wheat AC Brio was significantly greater ($P < 0.05$) than of hulless VAO-2 and Hulled Gosling across all N treatments and years. Moderate to severe plant lodging occurred in both hulless and covered oats, and this effect was magnified by increasing N fertility levels. Under non-N limiting conditions, lower P concentration and larger N:P ratios at early grain filling and maturity stages appeared to be associated with higher lodging scores and lower yield in oats than in wheat.

CSA-27 **Relationships between forage productivity, quality, legume fixed nitrogen and soil phosphorus fertility on organic dairy farms.** M. H. Main[1], D. H. Lynch[1], R. P.

Voroney[2], K. Schneider[2], and A. Ward[1]. [1]Department of Plant and Animal Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3 (e-mail: mmain@nsac.ca); and [2]Department of Land Resource Science,University of Guelph, Guelph, Ontario, Canada N1G 2W1

Roberts et al. (2008, CJSS **88**: 107) showed farm P deficits on many Ontario organic dairy farms, raising concerns about potential P limitation of forage N fixation. To address this, soil P, forage yield, tissue P and N fixation were examined on transects across 25 fields on organic dairy farms in Ontario and Nova Scotia in 2008 and 2009. Field legume content averaged 53% in Ontario and 24% in NS (range of 1 to 84%). Measured N fixation in harvested forage (estimated using the ^{15}N natural abundance technique) ranged between 10 and 150 kg ha^{-1}, representing 40 to 94% of the harvested N. Average forage yield was 5.8 T ha^{-1} (range of 2.4 to 8.8 T ha^{-1}). Plant tissue P concentration correlated with soil-test P in both provinces, with an obvious inflection in response at 8-10ppm P Olsen soil test (ON) or 12-14 ppm P Mehlich 3 (NS), with relatively flat tissue P response above the inflection point. In both provinces, there was no correlation between soil-test P and N fixation or forage yield over a range of 10 to 53 ppm P Mehlich (very low to moderate, NS), or 4-16 ppm Olsen P (very low to moderate, Ontario), when assessing data collectively from all points. However, on 1/3 of Ontario farms, a weak positive correlation between soil-test P and yield response could be observed on data from points within the farm. Two NS fields with soil-test of 6.5-8 ppm P (Mehlich 3) had very low yields and legume content, with tissue P content between 0.11 to 0.17%. At almost all points otherwise, tissue P levels were between 0.2 and 0.4%, which is generally above previously cited critical minimums of 0.2 to 0.25%. There was no overall correlation between forage yield and tissue P concentration. Organic and total P showed no correlation to plant responses. The study did not produce conclusive evidence that soil P availability (as measured by standard soil tests) is currently a major or consistent limitation to legume forage performance on organic dairy farms in Canada.

CSHS-1 **A new non-destructive rapid method to select strawberry lines rich in polyphenols: a preliminary study.** L. Fan[1,2], C.Q. Fang[1], C. Dubé[2], N. Tremblay[2] and S. Khanizadeh[2*]. [1]Research Institute of Pomology, Chinese Academy of Agricultural Sciences, Xingcheng, Liaoning, P.R. China 125100, [2] Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, St-Jean-sur-Richelieu, Quebec, Canada J3B 3E6

Fruit total phenolic content (TPC) and total antioxidant capacity (TAC) are usually assessed by destructive wet chemistry. Yet, for precision agriculture and recent breeding programs, more rapid and non-destructive methods are needed. A new portable device, Dualex, is used to access the epidermal polyphenol content of leaves in order to select seedlings with good fruit quality. A field experiment was conducted to investigate the potential of Dualex, applied to fruit breeding, on four selected strawberry genotypes ('Kent', 'Jewel', 'Saint-Pierre' and 'SJ8976-1') of known quality. Our results showed that Dualex readings, either from the adaxial side (upper side, DUAD), abaxial side (lower side, DUAB), sum of DUAD and DUAB (Phen), soluble solids content (SSC), titratable acidity (TA), TPC and TAC of 'Jewel' and 'Kent' were significantly higher than those of 'SJ8976-1' and 'Saint-Pierre'. There were positive correlations between DUAD, DUAB and Phen vs. SSC, TA, TPC and TAC. The use of Dualex in strawberry breeding programs might be useful to estimate TA and SSC along with TPC and TAC to select for high fruit quality in a seedling population, which consequently reduces the time from crossing to naming and reduce field costs.

CSHS-2 **Arbuscular mycorrhiza improves the performance of selected strawberry cultivars under salt stress.** L. Fan[1,2], C. Fang[1], C. Dubé[2], M. Deschênes[2], Y. Dalpé[3], S. Khanizadeh[2*]. [1]Institute of Pomology, Chinese Academy of Agricultural Sciences, Xingcheng, Liaoning Province, P. R. China 125100, [2]Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Blvd, St-Jean-sur-Richelieu, Quebec, Canada J3B 3E6, [3]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, Ontario, Canada K1A 0C6

Salt stress is one of the most important environmental factors limiting plant growth and yield. This limitation can be overcome using several cultural practices including high tunnel plastic culture and use of arbuscular mycorrhizae (AM). It has been shown that AM fungi not only stimulate the growth of plants but also contribute in enhancing plant tolerance to abiotic and biotic stresses such as salinity. A greenhouse experiment was conducted at Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, to evaluate the performance of three elite strawberry (*Fragaria×ananassa* Duch.) cultivars ('Kent', 'Jewel' and 'Saint-Pierre') subjected to two NaCl levels (30 and 60mM), in addition to the control (0mM), inoculated and non-inoculated (control) with AMF *Glomus irregulare* DAOM 197198. Mycorrhizal root colonization significantly reduced by increasing salinity, with the highest point at 58.1% and the lowest at 33.6%. Salinity significantly reduced the plant dry weight (23.10%) but the addition of AM fungi increased significantly the plant dry weight (20.99%) compared to the control. Cultivars responded differently to AM fungi treatment, with or without salt, indicating an interaction between these factors. Regardless of salinity, 'Jewel' showed more plant dry

weight than 'Saint-Pierre' when colonized by AM fungi. The highest AM plant growth benefit was observed for 'Kent' with 60 mM salt treatment, while 'Jewel' benefited best from AM with 30 mM salt treatment. 'Saint-Pierre' had the least AM dependency under salt treatments and seemed to be more resistant to salinity. Overall, the results indicated that the AM fungus was capable of alleviating the damage caused by salt stress on strawberry plants and promoted plant growth.

CSHS-3 **Nutrient uptake of selected strawberry cultivars in response to arbuscular mycorrhizal fungi under salinity.** L. Fan[1,2], C. Fang[1], Y. Dalpé[3], C. Dubé[2] and S. Khanizadeh[2*]. [1]Institute of Pomology, Chinese Academy of Agricultural Sciences, Xinghai Road, Xingcheng, Liaoning, P. R. China 125100, [2]Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Blvd, St-Jean-sur-Richelieu, Quebec, Canada J3B3E6, [3]Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, Ontario, Canada K1A0C6

Soil salinity is becoming an increasing threat to agro-ecosystems in arid and semi-arid regions. Under saline conditions, development, growth and productivity of the plants are adversely affected. Arbuscular mycorrhizal fungi (AMF) are symbiotic associations between plant roots and fungi that occur widely in natural biotic communities, and this highly dynamic interaction affects many aspects of the host plant physiology. A greenhouse experiment was conducted at Agriculture and Agri-Food Canada, L'Acadie Experimental Farm, in L'Acadie, Quebec, Canada, to evaluate the nutrient uptake of four commonly grown strawberry (*Fragaria* × *ananassa* Duch.) cultivars ('Kent', 'Jewel', 'Glooscap', and 'Saint-Pierre') along with an advanced line ('SJ8976-1'). All genotypes were subjected to three NaCl levels (0, 30 and 60mM) with or without inoculation with AMF *Glomus irregulare* DAOM 197198. Strawberry leaves were collected and N, P, K, Ca, Mg, Cu, Fe, Mn, Zn and B contents were measured after three months growth. Generally speaking, salinity significantly reduced the N, P, K, Mg, Cu and Zn uptake but the addition of AM fungi significantly increased the N, P and Zn uptake compared to the control, on strawberry leaves. There were significant differences between genotypes on N, Fe and Zn content of strawberry leaves. Genotypes responded similarly to AMF and salt treatments, on all the elements measured, indicating no interactions between these factors with an exemption of N and Ca. Our results showed that the AM fungus was capable of enhancing the nutrient uptake of strawberry plants under salt stress and promoting plant growth. Hence, the use of AMF might be a biological and practical way to alleviate the unfavourable effects of salinity stress on plant growth.

CSHS-4 **The effect of three production systems on the postharvest quality and phytochemical composition of 'Orléans' strawberry.** L. Fan[1,2], C. Yu[3], C. Fang[1], M. Zhang[4], M. Ranieri[5], C. Dubé[2] and S. Khanizadeh[2*]. [1]Research Institute of Pomology, Chinese Academy of Agricultural Sciences, Xingcheng, Liaoning, P.R. China 125100, [2]Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, St-Jean-sur-Richelieu, Quebec, Canada J3B 3E6, [3]Industrial Crops Institute of Hubei Academy of Agricultural Sciences, Wuhan, Hubei, P.R. China 430064, [4]Pomology Institute, Jilin Academy of Agricultural Sciences, 303 Kemao Street, Gongzhuling, Jilin, P.R. China 136100, [5]Agriculture Research Council – Fruit Culture Research Unit, Forlì, Italy 47100

The effect of two production systems, plastic mulch (PM) and plastic mulch with row covers (PMRC) versus the commonly used matted-row system (MRS) was evaluated on postharvest fruit quality and chemical composition of 'Orléans' strawberry, during 2008

and 2009, including shelf life, fruit weight loss, juice leakage, fruit glossiness and postharvest disease caused by grey mould (*Botrytis cinerea* Pers.). PMRC accelerated fruit maturity by 7 to 10 days and produced larger fruits compared to the MRS. Production systems significantly changed the total phenolic content (TPC) and total antioxidant content (TAC), but the effect varied during the harvest season. TPC was significantly higher for PMRC than MRS and PM at early harvest, but the effect was similar to PM at mid and late harvests. TAC was significantly higher for PMRC compared to MRS and PM, at all stages of fruit production, especially at late harvest. Fruit weight loss, juice leakage and presence of grey mould during storage were lower and fruit glossiness was higher for those harvested under PMRC compared to those from MRS. No significant differences were observed for firmness, pH, titratable acidity (TA) and soluble solids content (SSC) between the three production systems. TA and SSC of PMRC were slightly higher than those from MRS and PM but were not significantly different. It seems that PMRC not only accelerates ripening but also have a significant effect on pre- and postharvest fruit quality and on chemical composition of the harvested fruits.

CSHS-5 **Drought tolerance of Cumin (*Cuminum Cyminum* L.) as affected by seed priming.** M. Ghiyasi[1], R. Amirnia[*] and M. Tajbakhsh. Department of Agronomy and Plant Breeding, Faculty of Agriculture, Urmia University, Iran

Poor seed germination and crop stand are major problems in dry lands. However, seed performance might be able to alleviate the negative effects of drought. This study carried out to test germination and seedling growth of Cumin (*Cuminum Cyminum* L.) primed seeds under drought stress condition. Seeds treated with KNO_3 and KH_2PO_4 solutions had -1.2 MPa osmotic potential and hydropriming for 18 h. Seed samples were evaluated under four levels of osmotic potential 0 (control), -0.3, -0.6, -0.9 and -1.2 MPa induced by polyethylene glycol (PEG 6000) as drought stress. Drought stress significantly affected germination and seedling growth parameters in all seed samples, while at the control treatments drought stress was more severe than primed seeds. All priming treatments improved germination and seedling growth characters. Results of this study indicated that seed priming could be a suitable seed invigoration treatment under drought-prone environments.

CSHS-6 **Effect of pre-sowing seed treatment with NaCl on germination and seedling growth of cumin (Cuminum Cyminum L.) seeds under saline condition**. R. Amirnia[1]*, M. Giyasi[1], M. Tajbakhsh[1] and A. Hassanzadeh Gorttappeh[2]. [1]Department of Agronomy and Plant Breeding, Faculty of Agriculture, Urmia University, Urmia, West Azerbaijan, Iran, [2]Urmia Research Institute of Agricultural and Natural Resources, West Azarbaijan, Iran.

Germination is a major factor limiting the establishment of plants under stress condition. Seed priming is one of the seed enhancement methods that might be resulted in increasing seed germination and emergence under different conditions. The objective of this study was to evaluate the effects of osmopriming on germination and seedling growth of Cumin (*Cuminum Cyminum* L.) under salinity stress condition. The experiments were conducted as a completely randomized design (CRD) with three replications. Seeds primed with NaCl solution (1mM) were examined at different salinity levels (0, 2, 4, 6 and 8 dSm^{-1}) in relation to early growth stage. Results indicated that

osmopriming with NaCl (1mM) increases salt tolerance in the cumin seeds during germination and seedling establishment phases compared with non-treated seeds.

CSHS-7 **Composts and Forestry Industry Waste as Peat Moss Substitute in Greenhouse Growth Media**. M. K. Islam[1], C. Marshall[2]* and D. Lynch[2]. [1]Department of Environment Science, Parthenope University of Naples, Centro Direzionale, Isola- C4, 80143 Napoli, Italy, [2]Department of Plant Science, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3.

The horticulture industry is looking for alternatives to peat based greenhouse growth media due to its decreasing availability and the environmental implications of peat harvesting. Combinations of composts and forestry industry wastes were evaluated as potential sources of peat replacement in greenhouse growth media. The performance of 21 blends; obtained from 4 different types of compost, 2 types of wood wastes, peat, and perlite; with or without chemical fertilizer were compared against Promix®, a commercial peat moss substrate, on tomato (*Solanum lycopersicum* var. Scotia) seedling growth and nutrient content. The experiment was conducted at the greenhouse of the Nova Scotia Agricultural College, Truro NS, Canada during 2011 and consisted of a split-plot design with four replications. Growth media blend comprised the main plots while supllemental soluble NPK fertilizer (+/-) comprised the suplots. The physical and chemical properties of the raw materials used as well as all blends were analyzed. After 4 weeks of growth, the tomato seedlings were harvested and shoot height, leaf number, and biomass of roots and shoots were recorded. Nitrogen and carbon content of tomato shoots and roots were analyzed. Significant interactions between blend and fertilizer were found with respect to shoot and root biomass ($p=0.0010$). Fertilizer addition increased shoot and root biomass ($p<0.0001$), but blends containing fresh softwood waste did not respond as strongly to fertilizer addition. The N content of tomato roots (p=00160) was also significantly affected by the fertilizer and blend interaction. Tomato plants grown in blends with wood wastes had lower root N compared to other blends in the fertilizer treatment. The results suggest that adding wood wastes to growth media as a peat substitute may divert nutrients away from the plant, but the testing of different amounts and types of wood waste may lead to a suitable peat substitute.

CSHS-8 **Virtual experiments: sensitivity analysis for identification of crucial agro-ecological factors affecting the yield quality of processing carrots**. S. Muthuswamy, A. Thiagarajan* and R.R. Lada. Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Virtual experimentation saves time and money and would allow examination of resilience on the parameters of interest. However, in order to increase the efficiency and accuracy of the virtual experimental platform, the sensitivity of the parameters must be understood. Yield and root grades of processing carrots are a consequence of interactions between several factors such as, cultivar traits, agroclimatology and crop agronomy. Mathematical models to predict various yield components of three carrot types (baby, diced and sliced) were developed using seeding date and rate, harvest date, cumulative degree days (CDD), cumulative rainfall (CR), cumulative high and low temperature, and plant density (PD) as input parameters using multiple linear regression (MLR) and artificial neural network (ANN) platforms. Of all the input parameters, the independent parameters, viz, CDD, CR and PD were selected for sensitivity analyses. Sensitivity analysis was performed on both the platforms (MLR and ANN) to identify the sensitive parameters. Predictions of the different yield components were performed by changing one or two input parameters

and maintaining the other parameters constant (averages). The analyses identified CDD and CR as the sensitive parameters affecting baby carrot yields and CDD and PD as the sensitive parameters for diced and sliced carrot types. This analysis also identified the input combination that predicts the maximum yield for baby (1300-1350 CDD, 200-250 mm, 50-60 plants per meter); diced (1300-1400 CDD, 250-300 mm, 30-40 plants per meter) and sliced (1500-1600 CDD, 100-110 plants per meter) carrot types.

CSHS-9 **Genetic structure of Prince Edwards Island wild rosehip ecotypes as revealed by single nucleotide polymorphisms**. K. Ghose*[1,2], K. Sanderson, C.W. Kirby[1], J. McCallum[1] and B. Fofana[1]. [1]Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, C1A 4N6, PEI, Canada, [2]Biology Department, University of Prince Edward Island, 550 University Avenue, Charlottetown, PEI, Canada C1A 4P3

Wild roses are widespread throughout North America and Atlantic Canada. Rosehips, the fruits of wild roses are renowned for their high levels of vitamin C and essential fatty acids. Phylogenetic studies have examined boundaries between the North American and Asian roses and defined the Rosa sections within the North American roses. However, micro evolutionary studies in North American roses at the regional and local levels, in terms of genetic structure, are scarce. Here we report on the genetic diversity within a collection of 30 Prince Edward Island wild roses ecotypes. Microsatellite genotyping, single nucleotide polymorphisms (SNPs) analysis using a chloroplast intergenic region UCP11 and the nuclear gene GAPDH were performed to infer phylogenies and allelic variants analysis in this polyploid rose collection. Our data showed that confounding effect due to inter and intra population crossing lead to increased hybridity between founder species, contributing blurring the species determination. The UCP11 SNP diversity data suggest that *R. nitida* and/or *R. blanda* are possibly the maternal diploid progenitors for the majority of the PEI wild roses investigated. GAPDH allelic sampling revealed 9 haplotypes groups as a result of SNP, deletions and insertion mutational events. Although true *R. virginiana* specimens were identified in the collection, no *R. Carolina* specimens could be authentified. Instead, most of the ecotypes appeared to be natural hybrids between *R. Carolina* and *R. virginiana*. The implication and correlations for this genetic diversity in terms of bioactive metabolites diversity and bioactivity are being investigated.

CSHS-10 **Impact of fall cover crops on processing tomato yield, quality, pest pressure, nitrogen availability, and profit margins.** L. L. Van Eerd[1,2*], C. Trueman[2], S. A. Loewen[2] and R. J. Vyn[2,3]. [1]School of Environmental Sciences, University of Guelph, Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0, [2]University of Guelph Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0, [3] Department of Food, Agricultural and Resource Economics, University of Guelph Ridgetown Campus, Ridgetown, Ontario, Canada N0P 2C0

To improve management practices, a field experiment was designed to evaluate the effect of fall cover crops on subsequent processing tomato (*Solanum lycopersicum* L.) production. The trial was a split-split-plot factorial design with cover crop as main-plot factor and ammonium nitrate fertilizer rate (10 or 150 kg N ha^{-1} preplant broadcast incorporated) and tomato crop cultivar (early 'TSH18' or late 'CC337') as sub-plot factors. Cover crops were seeded after spring wheat (*Triticum aestivum* L.) harvest; treatments were no cover crop control, oat (*Avena sativa* L.), fall rye (*Secale cereale* L.), oilseed radish (OSR) (*Raphanus sativus* L. var. *oleiferus* Metzg Stokes), and mix of OSR

and rye (OSR+Rye) drilled at 80, 67, 16, and 9+34 kg ha^{-1}, respectively. The following spring, the trial was disked twice and tomatoes transplanted two weeks later. During the 2010 growing season, cover crop type did not influence the level of damage caused by two insect pests ($p \geq 0.2842$) or the incidence and severity of one fungal and three bacterial diseases ($p \geq 0.3098$). At harvest, processing tomato fruit quality (rots, insect or disease damage, Agtron colour, pH or soluble solids) was not affected by cover crop type ($p \geq 0.1505$). Cover crop type ($p=0.0601$) and variety ($p<0.0001$) had a significant effect on marketable processing tomato yield but there was neither an N rate effect ($p \leq 0.1970$) nor any two-way or three-way interactions ($p \geq 0.1835$). Marketable yield and profit margins were 13.1 t ha^{-1} and 1400 \$ ha^{-1} higher with OSR+rye than rye but none of the cover crops were different from the no cover crop control. At tomato harvest, plant available N (PAN: soil mineral N to 60 cm depth plus plant N content) was significant for cover crops, N rate and cultivar ($p \leq 0.046$) but there were no interactions ($p \geq 0.3673$). Cereal cover crops had approximately 43 kg N ha^{-1} lower PAN than OSR at tomato harvest but the other two cover crop treatments were not different than any other treatment. Thus, based on a systems-based approach, preliminary results suggest that the cover crops tested had no negative impact on processing tomato productivity or profit margins.

CSHS-11 **Organically-grown greenhouse tomato under supplemental lighting – optimization of the light distribution**. M. Dorais[1], S. Pepin[2*], L. Gaudreau[2], C. Ménard[1], R. Bacon[1] and M. Lemieux[3]. [1]Agriculture and Agri-Food Canada, Université Laval, Québec, QC, Canada G1V 0A6, [2]Horticulture Research Centre, Department of Soil and Agri-Food Engineering, Univ. Laval, Québec, QC, Canada G1V 0A6, [3]Serres Sagami, Chicoutimi, QC, Canada G7H 5B3

Organic cultivation has long been seen as key to improving the sustainability of greenhouse tomato production systems. Yet, few organic systems have been established because of concerns about yield and fruit quality being lower in organic than in conventional productions. As light is a key limiting factor related to plant productivity and fruit quality, supplemental lighting (SL) under organic farming could constitute a promising alternative to satisfy Canadian consumer demand for organic vegetables. Hence, the purpose of this study was to adapt an organic growing system to supplemental lighting. A split-plot experiment was performed in a commercial greenhouse (Serres Sagami, Chicoutimi, QC) to determine the effects of row spacing (main plots: 3 rows per bay vs. 4 rows) and growing system (sub-plots: conventional vs. organic) on tomato yield, plant growth parameters and fruit quality. A conventional system was used to establish a baseline for the productivity that can be reached with an organic crop under SL when nutrient availability may also be a limiting factor. Seedlings of *Lycopersicon esculentum* (cv Heritage grafted on Beaufort) were transplanted in 15-liters coco coir slabs vs. containers with organic soil and grown under supplementary lighting (HPS lamps) for six months. Plant density was similar between row spacing treatments and the irrigation management was based on soil matric potential measured at 15 cm depth using wireless tensiometers and an irrigation set point of –2.8 kPa. Measurements of supplemental light at plant height (~1.7 m from HPS) and near the 5th leaf (~2.5 m from HPS) with a line Quantum showed no significant difference in PPFD (mean: 95 and 82 mmol m^{-2} s^{-1}, respectively) between the two row spacings. There were no significant differences in measured plant growth parameters between the growing systems or the row spacing treatments. Tomato yield was similar between the organic and conventional crop system. Our results will be discussed in term of light distribution and potential yield reached under a sustainable greenhouse tomato production.

CSHS-12 **Seasonal changes in photochemistry, light use efficiency and net photosynthetic rates of wild blueberry (*Vaccinium angustifolium* AIT.).** D. Percival[1*], J. Kaur[1], L. Hainstock[1] and J.P. Prive[2]. [1]Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3, [2]Senator Hervé J. Michaud Research Farm, Agriculture and Agri-Food Canada, Bouctouche, New Brunswick, Canada

The seasonal variation of carotenoid concentration, chlorophyll a and b levels, dark (Fv/Fm) and light adapted (Fv'/Fm') dark and light adapted variable to maximal chlorophyll fluorescence (an indication of the quantum efficiency of PSII photochemistry) and net photosynthesis of the wild blueberry (*Vaccinium angustifolium* Ait.) was examined in the vegetative and cropping phases of production. Chlorophyll levels ranged from 2.0 to 12 $\mu g \cdot cm^{-2}$ and 0.042 to 1.4 $\mu g \cdot cm^{-2}$ for chlorophyll a and b respectively, were significantly lower in the cropping phase of production, and were also lower in the latter stages of the growing season. Similarly, carotenoid concentrations ranged from 0.67 to 4.1 $\mu g \cdot cm^{-2}$ and were lower in the cropping phase of production. However, carotenoid concentration and dark and light adapted variable to maximal chlorophyll fluorescence (Fv/Fm and Fv'/Fm') decreased marketably at the mid-point of the growing season presumably as a result of photoinhibition. Net photosynthetic values of upright stems ranged from 2.1 to 7.6 $\mu mol \cdot m^{-2} \cdot s^{-1}$, were substantially higher in the vegetative phase of production and also decreased significantly in the latter part of the growing season. Results from this investigation indicate that the wild blueberry has a relatively low photosynthetic rate, may be prone to photoinhibition and is carbohydrate supply (i.e., source) limited when compared to other temperate fruit crops.

CSHS-13 **Slow-release nitrogen fertilizers in carrot production.** K. Sanderson[1], B. Dickson[1], S. Wyand[1] and S. Fillmore[2]. [1]Agriculture and Agri-Food Canada, Crops and Livestock Research Centre, Charlottetown, Prince Edward Island, Canada C1A 4N6, [2]Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Kentville, Nova Scotia, Canada B4N 1J5

The impact of nitrogen management using slow release fertilizers has not been examined for carrot production in this region. To assess the effects of such products, we evaluated five slow release fertilzers over a 3-yr period. Treatments consisted of sulphur coated urea (SCU) (42-0-0), isobutylidene diurea (IBDU) (31-0-0), methylene urea (Nutralene) (40-0-0), urea formaldehyde (Sirflor) (38-0-0), Uflexx (46-0-0) compared to ammonium nitrate (Control) (34-0-0). All treatments were balanced to supply N at 50 kg ha^{-1} pre-plant. PCA analysis shows that score 1 accounted for 74% and score 2 accounted for 18% of the variation. The biological yield in 2006 (99 t ha^{-1}) was very high compared to 2005 (69 t ha^{-1}) and 2007 (72 t ha^{-1}). The control treatment performed similar to IBDU, SCU, and Sirflor. Nutralene and Uflexx had a very similar yield response with higher yield and was different from the other fertilizers. Higher biological yields were associated with lower petiole N concentration at harvest. Petiole N determined by LECO was highly correlated to GreenSeeker®. Petiole N levels measured by Cardy was not as strong a correlation to LECO and GreenSeeker®.

CSHS-14 **Effect of plant species and Benomyl on Pb concentration and removal from Pb enriched soil.** V. D. Zheljazkov[1] and T. Astatkie[2*]. [1]University of Wyoming, Sheridan Research and Extension Center, 663 Wyarno Road, Sheridan WY 82801, U.S.A., [2]Nova

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Some agricultural soils in Nova Scotia are lead (Pb) enriched as a result of the application of lead arsenate ($PbHAsO_4$) insecticide in apple orchards several decades ago. Controlled environment experiment was conducted with Pb enriched Canning soil series to evaluate the remediation potential of 10 plants (Allysum, black mustard, Clary Sage, garden sage, Indian mustard, Swiss chard, thorn apple, white mustard, yellow poppy, and Geranium) in combination with the fungicide Benomyl to suppress mycorrhizae. Overall, the highest biomass was provided by yellow poppy followed by Indian mustard and thorn apple. The application of Benomyl increased Pb concentration in thorn apple tissue but not in the other crops. The phytoremediation potential (or Pb removal with the harvested biomass) was greatest with Clary sage, Allysum, garden sage and Indian mustard with benomyl treatments, and lower in the Swiss chard, thorn apple without Benomyl, and in the Geranium with Benomyl treatments. This study demonstrated that some plants can be used for phytoremediation of mildly Pb contaminated soils in Nova Scotia.

CSHS-15 **Study on shrimp waste water and vermicompost as a nutrient source for bell peppers.** V. D. Zheljazkov[1] and T. Astatkie[2*]. [1]University of Wyoming, Sheridan Research and Extension Center, 663 Wyarno Road, Sheridan WY 82801, U.S.A., [2]Nova Scotia Agricultural College, Department of Engineering, P.O. Box 550, Truro, NS, B2N 5E3, Canada

Aquaculture industry generates significant amount of nutrient-rich waste water that is released into streams and rivers causing environmental concern. The objective of this controlled environment study was to evaluate the effect of waste shrimp water (SW), vermicompost (VC, at rates of 10, 20, 40, and 80% by volume) alone, or in combination with SW, controlled release fertilizer (CRF), and water soluble fertilizer (WSF) on bell peppers (*Capsicum annuum* L.) cv. X3R Red Knight. Application of VC at 80% or SW alone increased yields relative to the unfertilized control. Combined applications of VC and SW increased yields compared to VC. Overall, total yields were highest in the chemical fertilizer treatments (CRF and WSF) and lowest in the unfertilized control. SW and VC increased growth medium pH relative to the unfertilized control or to the chemical fertilizer treatments. In pepper fruits, highest N content was found in the CRF treatment, although it was not different from the VC at high rates or the WSF treatments. P concentration in peppers was highest in the CRF treatment, lower in all VC or SW treatments but not different from the unfertilized control or WSF treatment. Fe, Mg, and Zn concentrations in peppers were highest in the CRF treatment, but not different from the control or WSF treatments. Overall, N accumulation in peppers was negatively correlated to the growth medium pH and Ca, P in peppers was negatively correlated to growth medium pH, Ca, and Na, while K in peppers was negatively correlated to the growth medium P, Mg, and Na. The results indicated that: (1) SW can be used as a viable nutrient source for peppers; (2) SW can provide similar nutrient supply as VC; (3) chemical fertilizers can provide greater pepper yields compared to SW or VC, alone or in combination.

CSHS-16 **Characterization and evaluation of twelve oregano genotypes cultivated in the main areas of production of Argentina.** L. E. Torres, P.C. Brunetti*, A. G. Chaves, S. F. Ocaño, Y. Massuh and M. S. Ojeda. Facultad de Ciencias Agropecuarias, Universidad Nacional de Córdoba. Av. Valparaíso s/n, Ciudad Universitaria, CP:5000, Córdoba, Argentina

In Argentina, oregano (*Origanum* spp.) is one of the most important aromatic species, which leaves and flowering tops are used as seasoning, targeting the retail consumer, industrial and less to export. Local production has low average yields due to the variability of cultivated material, the vegetative propagation methods used and the lack of knowledge and adaptive experimentation on advanced cultivation practices. In order to characterize the germplasm of oregano used in Argentina and to determine the inter and intra-population variation existing for traits of agronomic importance, the collection of clones of oregano grown in the country was carried out. Conditions for the establishment of *in vitro* culture, sanitation by meristems culture and micropropagation for 19 clones of oregano were adjusted. It was possible to recover clones of oregano, which due to the successive cycles of vegetative propagation, were disappearing from the fields of production. It was also possible to generate a collection of germplasms *in vitro* consisting of 12 clones of oregano of different origins. These clones were field evaluated at three different locations, showing genotype x environment interaction for the most of the variables. Regardless of growing location, the quantitative variables with more discriminating value were essential oils yield, internode length, length of the longest branch, fresh weight, dry weight of leaf and stem, leaf/stem ratio and leaf area. With regard to qualitative variables, those with the largest discriminant value were leaves color, stem color, color of bracts, flower color, growth habits, flowering time and spike length. Depending on the variables analyzed oregano clones could be classified into four groups. Finally, it was determined that the evaluated clones belong to three different taxa: *Origanum vulgare* ssp *vulgare*, *Origanum vulgare* ssp *hirtum* and *Origanum x majoricum* (hybrid). Within each group, the clones belong to the same taxon.

CSHS-17 **Oxygenation of soils in container-grown organic greenhouse tomato**. V. Gravel[1,2*], C. Ménard[1,2], M. Dorais[1,2] and S. Pépin[1,3]. [1]Centre de recherche en horticulture, Université Laval, Québec, Québec, Canada G1V 0A6, [2]Agriculture and Agri-Food Canada, Université Laval, Québec, Québec, Canada G1V 0A6, [3]Département des sols et de génie agroalimentaire, Université Laval, Québec, Québec, Canada G1V 0A6

Activating the soil biological activity is a key element in optimizing fertilisation in organic greenhouse crops. Also, adequate plant growth often relies on a sufficient mineralization rate synchronized with plant needs. Unfortunately, this is not usually observed under normal organic greenhouse conditions. Oxygen input directly in the soil is thought to improve tomato plant growth in soil bound crops. An experiment was undertaken to evaluate the effect of oxygenation of six soils with different physical properties on the growth of organic greenhouse tomato plants. These soils were: 1) loam, 2) sandy loam, 3) sandy soil, 4) muck soil, 5) reconstituted organic soil with 40% air porosity and 6) peat soil amended with sawdust. Oxygen was injected periodically through the soil at the bottom of the container over a period of 2 months. The effect on plant growth, fruit yield and soil biological activity was evaluated. Overall, #1 fruit yield was significantly lower for plants in the oxygenated soils compared to the control. The soil biological activity, evaluated by measuring the CO_2 efflux from the soil surface, was significantly higher in oxygenated soils. No significant difference was observed in the fruit organo-leptic quality (lycopene content, antioxidant capacity and acidity) between oxygenated and non-oxygenated soils.

CSHS-18 **Use of ampelographic methods in the identification of Nova Scotian grape (*Vitis spp.)* cultivars.** L.A. Wiser and D.N.Kristie*. Department of Biology, Acadia University, Wolfville, Nova Scotia, Canada, B4P 246

In recent years the evaluation of suitable grape (*Vitis spp*.) cultivars for the Nova Scotia grape growing and wine industries has become increasingly important. Despite this, little material exists documenting the morphological characteristics of grape cultivars grown in Nova Scotia. This lack of material could make identifying unknown cultivars in a vineyard problematic. The objectives of this study were to describe grape cultivars based on several ampelographic characteristics proposed by Pierre Galet (1979), and to evaluate these characteristics to determine their usefulness in identification. Twenty-nine cultivars that are currently grown in Nova Scotia were described based on morphological characteristics such as leaf colour, hair type, tendril placement and tooth size and shape. Leaf measurements, such as vein length ratios, leaf size and sinus depth, were also used to describe cultivars. Results demonstrated which characteristics were useful in identification and which were not. For instance, indument, or hairiness, was useful as it allowed all cultivars to be divided into numerous small groups, and in some cases narrowed down the identities of single cultivars, such as Einset and KW96-1. Other characteristics, such as tendril placement, were less useful as all sampled cultivars showed an identical pattern. In many cases vein length ratio measurements were also of little use, as these measurements tended to differ little between cultivars. The results of this study provided a preliminary means of cultivar identification and an approach to identification that did not previously exist for Nova Scotian viticulture. However, future work is required to test this proposed method of identification. Additional cultivars and characteristics should also be included in future work.

CSHS-19 **Innovative agronomic techniques for growing profitable high quality organic sweet corn.** J. Owen* and S. LeBlanc. Agriculture and Agri-Food Canada, Bouctouche, Canada NB E4S 2J2

Sweet corn is a high input, high value vegetable crop popular across Canada. In the Maritimes, sweet corn is commonly sold for $6 per dozen, and organic sweet corn is in high demand and may fetch as much as $12 per dozen. Nonetheless, growing organic sweet corn is challenging because the crop requires high levels of fertility timed with key growth stages, as well as intensive pest management techniques to control weeds and insects which cause reductions in crop quality and yield. In the context of a long term organic rotations experiment at AAFC in Bouctouche, New Brunswick, innovative techniques for growing organic sweet corn are being developed. These include: 1) using transplants instead of direct seeding; 2) planting into zone-tilled established red clover plantings; 3) use of narrow over-zone biodegradable organic “mini-mulches”; 4) drip irrigation beneath the mulches; 5) a fertility regime using organic compost pre-planting soluble organic fertigation; and 6) insect pest scouting and control using organic pesticides. This very intensive system was developed as a context for studying nutrient dynamics in companion plantings in organic rotational systems, and may be regarded by some as prohibitively expensive outside a research setting. However, a cost analysis was conducted comparing input costs and revenues from this intensive organic system with input costs and revenues from commercial Maritime conventional sweet corn growers. The results show that the risk profile differs vastly between systems, yet profitability is equal or greater with the organic system. Costs, revenues, risks, risk-mitigation suggestions and considerations for future efficiencies are discussed.

CSHS-20 **Black chokeberry productivity in Northern Quebec.** J. Lajeunesse and R. Drapeau. Agriculture and Agri-Food Canada Research Farm, 1468 Saint-Cyrille St., Normandin, QC, Canada G8M 4K3

The Saguenay-Lac-Saint-Jean area (Northern Quebec) is host of a variety of wild fruit species that are well adapted to the climatic conditions of this region. Some of these species, like blueberries and cranberries, are grown and contribute greatly to the economy of the region. Also, there is growing interest in the cultivation of indigenous fruits and some species, as *Aronia floribunda* (black chokeberry), seem to offer a high potential for production and marketing. The objective of this study was to evaluate the adaptation, the development and the productivity of *A. floribunda* in a Northern agricultural area. The mother plant was located in the town of Girardville (Québec) and multiplied by seedlings.Two plantations of black chokeberry were established in 2001 and 2002 on clay loam Labarre at the AAFC research farm in Normandin (climatic zone 2b). For each plantation, twenty-eight plants were planted. Plot consisted in seven plants. Within-row spacing was 1 meter. The row spacing was 3 m for a total of 21 m^2 per plot. With the variety used, the results showed that black chokeberry is well adapted to cold and humid area and average fruit yields could be as high as 15 000 kg ha^{-1}.

CSHS-21 **An automated yield monitoring system for commercial wild blueberry harvester**. Q. Zaman[1]*, Young-Ki Chang[1], A. Farooque[1], A. Schumann[2] and D. Percival[1]. [1]Nova Scotia Agricultural College, Truro, Nova Scotia Canada B2N 5E3, [2]Citrus Research and Education Centre, University of Florida, USA

Blueberry fruit yield maps could be used to generate prescription maps for site-specific application of fertilizer to improve crop productivity. An automated yield monitoring system (AYMS) consisting of two ÿEye color cameras, differential global positioning system, custom software, and a ruggedized laptop computer was developed and mounted on a specially designed Farm Motorized Vehicle (FMV) for real-time fruit yield mapping. Custom software was developed in C++ programming language to acquire and process image in real-time from both camera and store the blue pixel ratio in ruggedized laptop computer. Two wild blueberry fields were selected in central Nova Scotia to evaluate the performance of the AYMS for fruit yield mapping. Calibration was carried out at 20 randomly selected data points, 19 in each field. The ripe fruit was hand-harvested out of a 2.2 x 0.8 m quadrant at each selected point and camera images were also taken from the same points to calculate the blue pixel ratio (fraction of blue pixels in the image). Linear regression analysis was performed to calibrate the actual fruit yield with percentage blue pixels. Real-time yield mapping was carried out with AYMS. Custom software was developed to acquire and process the images in real-time. The estimated yield per image along with geo-referenced coordinates was imported into ArcGIS 9.3 software for mapping. The linear regression results showed highly significant relationship between blue pixel ratio and actual fruit yield in field 1 (R^2 = 0.95; $P < 0.001$) and field 2 (R^2 = 0.94; $P < 0.001$). The correlation between actual and predicted fruit yield (validation, using the equation from field 2) in field 1(R^2 = 0.94; $P < 0.001$; RMSE = 0.23 Mg/ha) and field 2 (validation, using the equation from field 1) (R^2 = 0.95; $P < 0.001$; RMSE = 0.83 Mg/ha) was also highly significant. Maps showed substantial variability in fruit yield in both fields. The bare spots coincided with no or low yielding areas in the fields. This information could be used to implement site-specific management practices within the blueberry fields to optimize productivity while minimizing the environmental impact of farming operations.

CSHS-22 **Development and evaluation of a green ratio based algorithm for the detection of weeds in mowed wild blueberry fields.** Y. K. Chang[1*], Q. Zaman[1], T. Esau[1], A. W. Schumann[2] and D. C. Percival[3]. [1]Engineering Department, Nova Scotia Agricultural College, Truro, Nova Scotia, B2N 5E3, Canada, [2]Citrus Research and Education Centre, University of Florida, Lake Alfred, FL33850, USA, [3]Environmental Sciences Department, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

A weed detection algorithm was developed and evaluated for spot-specific agrochemical delivery in mowed wild blueberry fields with the aim of reducing the cost of agrochemicals and environmental contamination. Clear green contrast between weed and other areas was used to develop a robust and effective algorithm. A custom built C^{++} program was made to acquire images from µEye-1220SE cameras mounted in front of an all-terrain vehicle (ATV). Exposure time and digital gain were automatically controlled by auto exposure shutter / auto gain control (AES/AGC) to adjust for variable outdoor light conditions (> 50 $\mu m^{-2}s^{-1}$) during image acquisition. Maximum auto exposure shutter was set to 4 ms to prevent image blurring. MATLAB® Image Processing Toolbox was used for image processing including converting the 24-bit Red-Green-Blue (RGB) images to normalized green ratio images, segmentation by threshold values, and counting over-threshold pixels. Optimum threshold value and number of over-threshold pixel were investigated. Green ratio based algorithm was compared with excessive green index algorithm. The green ratio algorithm was evaluated with visual inspected images taken from different field situations. Results will be presented in the paper.

CSHS-23 **Effect of seaweed extract application on surrounding soil microbial community of strawberry.** M. Z. Alam[1]*, G. Braun[2], J. Norrie[1] and D. M. Hodges[2]. [1]Acadian Seaplants Ltd. 30 Brown Avenue, Dartmouth, Nova Scotia, Canada, B3B 1X8, [2]Atlantic Food and Horticulture Research Centre, Agriculture and Agri-Food Canada, 32 Main Street, Kentville, Nova Scotia, Canada B4N 1J5

Effects of applying a water soluble seaweed extract powder (SSEP) were evaluated on the rhizospheral microbial communities of four varieties of strawberry (‘Albion’, ‘Chandler’, ‘Camarosa’, and ‘Festival’) produced under greenhouse and field conditions during 2009 and 2010. Seaweed extract was applied twice per week, once per week or once per two weeks at rates of 0 (control), 1, 2 or 4 g/l during the first 7-9 weeks of strawberry production. Microbial colony counts, microbial respiration and carbon substrate metabolic activities of microbes were examined. Seaweed extract treatment increased total number of microbes both in greenhouse and field. Maximum colony counts were recorded at 4 g/l SSEP in the greenhouse. In the field, maximum colony counts were recorded at 1 and 2 g/l SSEP, and 4 g/l appeared to slightly suppress microbial growth. Seaweed extract treatment also increased microbial respiration at 1 and 2 g/l SSEP, and 4 g/l reduced microbial reduced. The carbon substrate metabolic activity of the soil microbes showed that SSEP application increased microbial activity in the soil. In the greenhouse, maximum AWCD, H, E, and S responses were recorded at 4 g/l SSEP; in soil treated with 1 and 2 g/l SSEP applications, microbial activity were similar, though higher than the control. However, in field trials, AWCD, H, E, and S responses to extract treatment showed successive increases at 1 and 2 g/l SSEP, but reduced responses at 4 g/l. Among the microbes isolated, the majority (49%) were primarily pseudomonads (King’s B Agar), about 3% were fungi (Rose Bengal Agar) and about 2% were streptomyces (Triptic Soy Agar). Seaweed extract treatment (1 and 2 g/l) increased pseudomonad populations (KBA) by about 55% and general bacteria by about 35% (TSA). While fungal and streptomycete populations were doubled. This study provides

clear evidence that SSEP applications increased rhizosphere microbial diversity and physiological activity.

CSHS-24 **Impact of groundcover and fruit zone manipulation on the microclimate, berry yield and must composition of 'De Chaunac' grapevines.** D. Percival, Department of Environmental Sciences, Nova Scotia Agricultural College, P.O. Box 550, Truro, Nova Scotia, Canada, B2N 5E3 (e-mail: dpercival@nsac.ca)

A study examining the main and interactive effects of fruit zone leaf removal, reflective row covers and polyethylene sleeves on canopy microclimate, plant growth and development, berry yield and must composition of the interspecific hybrid grape cultivar De Chaunac (Seibel 9549) was completed during the 2007 and 2008 growing seasons in Gaspereau, Nova Scotia. A 2^3 factorial experimental design was used consisting of applications of reflective groundcover between the rows at the start of the growing season (-/+), polyethylene sleeves at bud break (-/+) and fruit zone leaf removal at fruit set (-/+). Application of the polyethylene sleeves stimulated shoot growth early in the season with anthesis occurring 7 and 9 days earlier in the 2007 and 2008 growing seasons respectively. Although the reflective groundcover increased fruit zone light intensity, it also decreased mid-day soil surface temperatures. Fruit zone leaf removal increased cluster exposure and decreased the number of interior leaves and leaf layer number. However, there was no significant effect of any of the factors on berry yield, and only the application of the polyethylene sleeves were observed to influence must composition with soluble solids, titratable acidity, total anthocyanin and total phenolic levels being increased by 11.2, 10.8, 12.6 and 5.27%. Therefore, results from study have indicated that the use of polyethylene sleeves can advance berry growth and development and improve must composition of late maturing red grape cultivars such as 'De Chaunac.'

CSHS-25 **Vitamin A and Lutein Levels in Dried Leaves of *Moringa Oleifera***. G. Ndayikeza, and P. Angers*, Department of Food Science and Nutrition, Université Laval, Québec, QC, G1V 0A6

Leaves of Moringa oleifera, a tropical plant used in Burundi as food against malnutrition, is high in lutein and vitamin A. The leaves are consumed as dry powder that people store in their home at room temperature. As such, content in vitamin A and lutein may decrease over time and affect the amonts that are ingested. In order to assess such a decrease, we performed HPLC quantification of lutein and vitamin A in powdered dry leaves of *Moringa oleifera* over a six month period, in both young and mature leaves. Young and mature leaves were also harvested in July and August. The results show that levels in lutein and in β-carotene were generally higher in leaves harvested in July compared to those harvested in August, whereas no dfferences were observed for *cis*-β-carotene. Levels in lutein (0.66 mg/g +/- 0.29, on average) and in *cis*-β-carotene (0.033 mg/g +/- 0.020, on average) decreased rapidly over the first month, with values near 0 after this period. Content in β-carotene (0.17 mg/g +/- 0.01, on average) showed a 50% decrease during the first month, and reached nearly 0 after two months. In conclusion, dried leaves of *Moringa oleifera* should be consumed within the first month after they have been harvested and dried, in order to benefit from their content in lutein and in β- and *cis*-β-carotenes.

CBA-1 **Floral development of *Urospatha*: merosity & phylogeny in the Lasioideae (Araceae).** D. Barabé[1,2], C. R. Lacroix[3]*, and M. Gibernau[1]. [1]CNRS-UMR 8172, Ecologie des Forêts de Guyane, BP 709, 97387 Kourou, France; [2]Institut de Recherche en Biologie Végétale, Université de Montréal, Jardin Botanique de Montréal, 4101 rue Sherbrooke Est, Montréal (Québec), Canada H1X 2B2; [3]Department of Biology, University of Prince Edward Island, 550 University Avenue, Charlottetown, PE, Canada, C1A 4P3 (e-mail: lacroix@upei.ca)

The merosity of flowers of *Urospatha* is investigated within the framework of a resolved phylogeny of the Araceae. We analyse how a transition from dimerous or tetramerous merosity to a pentamerous or hexamerous merosity can occur developmentally in the Lasioideae. In *Urospatha*, the initiation of floral primordia along the inflorescence is acropetal while the development of flowers is basipetal. This indicates the presence of two distinct phases in the development of the *Urospatha* inflorescence. The first phase corresponds to the initiation of flowers and the establishment of the phyllotactic pattern and the second phase to the differentiation of floral organs. *Urospatha* is characterized by the presence of trimerous, tetramerous, pentamerous, and rarely hexamerous flowers. In all types of flowers, the stamens are closely associated and opposite to the tepals. Pentamerous flowers are formed by the addition of a sector consisting of a stamen and a tepal. Likewise, in the case of hexamerous flowers, two sectors are added. In the Lasiodeae, the increase in the number of tepals and stamens is linked with two developmental processes that have appeared independently in the subfamily: 1) the addition of one or two stamen-petal sectors (*Anaphyllopsis* and *Urospatha*); and 2) the independent increase in the number of tepals and stamens on whorls more or less organized and inserted in an alternate position (*Dracontium*). Tetramerous whorls as they occur in basal Lasioideae would be homologous to two dimerous whorls from an evolutionary point of view.

CBA-2 ***Stigonema* in the cephalodia of *Stereocaulon condensatum* differs between Canada and the U.K.** P. D. Crittenden[1] and M. D. Piercey-Normore[2]*. [1]Department of Biology, University of Nottingham, Nottingham, U. K., NG7 2RD; and [2]Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada, R3T 2N2 (pierceyn@cc.umanitoba.ca)

Stereocaulon condensatum Hoffm. is a crustose lichen that grows on sandy substrata in North America and Europe. It produces short pseudopodetia on a persistent crustose primary thallus with granular phyllocladia containing a green alga (*Trebouxia*) and rough cephalodia containing a cyanobacterium (*Stigonema*). Nitrogen fixation by *Stigonema* has been shown to vary seasonally for cephalodia of other species of *Stereocaulon*. Numerous studies have described genetic variation in *Nostoc* associated with lichen fungi, but little is known about the variation in *Stigonema*. The main goal of this study was to seek evidence for a link between genetic variation and variation in nitrogen fixation rates. Other objectives were to examine whether cephalodia of *S. condensatum* from North American and European populations have similar nitrogen fixation levels, and to examine genetic variation of *Stigonema* between populations of cephalodia for two continents. Five soil crust samples each about 3cm x 3cm were collected from four locations

(populations) in each of Wales, U.K. and Manitoba, Canada. Nitrogenase activity in excised cephalodia was assayed by acetylene reduction and genetic variation of cephalodia was determined by nucleotide sequences of the trnL(Leu) gene and its intron using cyanobacterial primers. Mean nitrogenase activities (± 1 SE) for the U.K. (collected and assayed in June) and Canadian (collected August, assayed September) populations were 749 ± 113 (n = 64) and 433 ± 46 (n = 188) pmols mg^{-1} h^{-1}. Neither activity per unit mass nor total acetylene reduced was related to cephalodium mass. Preliminary results of sequence variation showed that the North American and the European samples have two different intron sequences. There was less overall sequence variation but more variation between crusts in the European than the North American populations. trnL sequences of all cephalodia within a soil crust were identical. We will discuss the extent of the interaction between genotype and nitrogen fixing capacity between the North American and European strains of *Stigonema* that associate with *S. condensatum*.

CBA-3 **Communicating traditional ecological knowledge (TEK).** S. Barnes; J.P. Young*. Ecosystem Science and Management Program, University of Northern British Columbia, 3333 University Way, Prince George, British Columbia, Canada V2N 4Z9

Traditional ecological knowledge (TEK) is defined as a body of knowledge built up by a group of people through generations of living in close contact with nature, and is traditionally communicated and disseminated orally. The knowledge accumulated by knowledge holders represents vast amounts of information about a specific locale and is part of the culture of the community. Because TEK is part of culture, it cannot be understood without a sociocultural context of the knowledge and the knowledge holder. Once knowledge holders share TEK, the dissemination, with permission, of this knowledge is an important step in its effective transference and preservation. The present study involves a critical analysis of the different ways one can transmit TEK, including dissemination via technical reports, books, atlases, oral presentations, DVDs/videos, audio clips, CD-ROMs, academic journals, community booklets, and websites. Each format has assets and limitations, and the choice of communication methodology is of utmost importance for creating useful, accessible, and appropriate deliverables for both community and non-community members.

CBA-4 **Assisted Migration Adaptation Trial of lodgepole pine and Douglas-fir: A tale of survival and their ectomycorrhizal associates.** J.C. López-Gutiérrez[1], B.J. Pickles[1], L.E. Tackaberry[1], G. O'Neill[2], M. Gorzelak[1], D.S. Green[1], H.B. Massicotte[1*] and K.N. Egger[1]. [1]Ecosystem Science and Management, University of Northern British Columbia, 3333 University Way, Prince George, BC V2N 4Z9, Canada (e-mail:hugues@unbc.ca); [2]Kalamalka Research Station, BC Ministry of Forests, Lands and Natural Resource Operations, 3401 Reservoir Road, Vernon, BC V1B 2C7, Canada

Climate change presents many challenges for plant species and, consequently, for ecosystem management. In western North America a long term study, the Assisted Migration Adaptation Trial (AMAT), aims to understand the climatic tolerances of reforestation materials in western North America in order to better match seedlings with current and future climate of plantations. Populations from 15 tree species will be planted at 48 test locations encompassing a wide range of climates. As part of this large study, we planted 10 seedlings from each of 5 populations of lodgepole pine (*Pinus contorta* Dougl. Ex. Loud. var. *latifolia*) and Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco var. *glauca*) at 7 recently harvested forest sites in southern British Columbia. Seedlings planted in June 2009 were harvested in October 2010, after two field growing seasons.

Survival and ectomycorrhiza (ECM) fungal-root associates (characterized by morphotyping) were compared between hosts, populations, and sites. Overall survival was 20.9 ± 4.4% for pine and only 2.0 ± 0.8% for Douglas-fir; survival ranged from 0% (both species: Riske Creek 52°00'N) to 10 ± 3.2% (Douglas-fir: Kalamalka 50°14'N) to 58.0 ± 12.0% (lodgepole pine: Lynx Creek 49°08'N). Low survival, which may be attributed to above average summer temperatures and low rainfall during both successive growing seasons, limited ECM characterization and analyses to pine seedlings; these included 3 populations each at 3 sites where survival exceeded 25%. Ectomycorrhiza formation was significantly lower for Kalamalka seedlings (72.4 ± 9.4%) compared to Deep Creek (92.7 ± 1.4%: 50°33'N) and Lynx Creek (89.9 ± 3.0%). Ectomycorrhiza diversity (richness and Simpson's index) was also significantly lower at Kalamalka; seven ECM morphotypes were identified for Kalamalka seedlings compared to 10 each from Deep Creek and Lynx Creek. *Thelephora*, *Cenococcum* and *MRA* ECM abundance was significantly lower at the Kalamalka site. Lodgepole pine populations did not vary in terms of ECM community structure (with the exception of one population that had higher abundance of *Thelephora*), and analysis using morphotype data as well as fungal hyphae exploration type did not identify any specific patterns linked to survival of lodgepole pine.

CBA-5 ***In vitro* androgenesis as a source of haploid pepper (*C. annuum* L.) plants.** A. Kisiała[1*], and P. Nowaczyk[2]. [1]Department of Biology, Nipissing University, North Bay, Ontario, Canada P1B 8L7; and [2]Department of Genetics and Plant Biotechnology, University of Technology and Life Sciences, Bydgoszcz, Poland.

In vitro induced androgenesis is the formation of sporophyte from immature pollen grains through anther or isolated microspore cultures. It is a fast and efficient method of obtaining haploid plants, widely applied in breeding of many vegetable and ornamental species. Haploids with a single set of chromosomes in somatic cells, and fully homozygous doubled-haploid lines (DH lines) of *Capsicum annuum* L. are used to speed up breeding for resistance traits, improve agronomically important plant characters, and to construct species genetic linkage maps. The effectiveness of pepper anther culture depends on many factors, optimalization of which is the important condition of obtaining high yield of androgenic embryos. The main goal of the presented research was to determine reaction of selected Polish *C. annuum* L. genotypes on *in vitro* anther culture conditions. The results of performed experiments indicate that the crucial factor determining the effectiveness of androgenic embryos development was the genotype of donor plants. The effectiveness of androgenesis ranged from 1.43% to 33.8%, which means the tested pepper forms differed considerably in spite of their androgenic response. Additionally, it was found that androgenic response of the anthers was strongly modified by the stage of microspore development at which anthers were excised and the age of anther-donor plants. It depended also on the culture media composition. Ploidy level of androgenic regenerants was determined cytometrically and the effective method of colchicine treatment was established. Isosyme analysis and the characteristics of plants morphology were applied to determine microspore origin of the regenerants. On the base of performed experiments it was stated that Polish breeding lines, cultivars, and hybrid genotypes of pepper, cultivated in local climate and soil conditions, can be a source of haploid plants and fully homozygous DH lines. The possibility of the application of *in vitro* induced androgenesis in pepper breeding programs may highly increase genetic variability of *C. annuum* germplasm.

CBA-6 **Development of a new research project for undergraduate plant physiology and sustainability courses: Seasonal changes in photosynthesis and transpiration rates of evergreen and deciduous trees.** M.S. Kaile[1], J. Mehroke[1], and S. Singh[1*]. [1]Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4 (email: santokh.singh@botany.ubc.ca)

By analyzing the effect of seasonal changes in the photosynthesis and transpiration rates of evergreen and deciduous trees, we can determine which trees should be promoted for future plantation projects, to develop a greener and more sustainable future. Trees exhibiting higher photosynthesis rates under various environmental conditions and growing seasons could reduce the rapidly increasing concentration of CO_2 in our atmosphere, and global warming. Evergreen and deciduous trees differ in their leaf senescence patterns through seasonal variations. Photosynthesis and transpiration rates were measured in leaves of two evergreen species, Western Red Cedar (*Thuja plicata*), and Lawson Cypress (*Chamaecyparis lawsoniana*), and two deciduous species, Red Maple (*Acer rubrum*), and Red Oak (*Quercus rubra*) during July 2010 - February 2011. Environmental factors such as light intensity, temperature, and the amount of precipitation were also recorded with observational data provided from Environment Canada's Historical Weather Database. Results so far show higher photosynthetic and transpiration rates amongst the evergreen species during the fall/winter period, when compared to the deciduous species, as deciduous leaves undergo a senescence process due to environmental changes. Furthermore, specific protein analysis by gel electrophoresis and Western Blotting also showed higher levels of key photosynthesis proteins, light harvesting complex of photosystem II (LHCIIB), and the ribulose-1,5 bisphosphate carboxylase/oxygenase (RUBISCO) in evergreen species when compared to deciduous ones during the fall/winter period. Photosynthesis and transpiration data will be discussed in relation to environmental parameters such as light intensity, temperature, and the amount of precipitation. The findings of this study will contribute to our knowledge about the role of these trees in CO_2 absorption and sustainable development. The results of this investigation form basis of new laboratory research projects in our third year plant physiology course.

CBA-7 **Development of a new undergraduate plant physiology laboratory research project on the effects of plant hormones on auxin spatial distribution in *Arabidopsis thaliana.*** D. S. Kumar[1], J. Mehroke[1], and S. Singh[1*], [1]Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4 (e-mail: santokh.singh@botany.ubc.ca)

Plant hormones are signaling molecules that control plant development via their spatiotemporal concentration gradients. Understanding how different plant hormones regulate plant growth and development by interacting with each other is an important aspect of plant hormone biology. Auxin, an important plant hormone, is synthesized in the shoot apex and is transported through the plant by auxin-transport proteins. It affects lateral organ development, cell elongation, and can also interact with other plant hormones to influence cell division and shoot elongation. In our study, we aimed to understand the effect of auxin transport inhibitors, such as tri-iodobenzoic acid (TIBA), on the spatial expression pattern of auxin in 6 day old DR5::GUS transformed *Arabidopsis thaliana* plants. Secondly, we wanted to understand the influence of other hormones such as brassinosteroids and gibberellin on auxin distribution in these plants. The DR5::GUS construct used in this study, contains an auxin-response element that is sensitive to increasing endogenous auxin concentrations and allows us to visualize auxin

distribution within the plant. It was found that endogenous auxin was concentrated at root tips, cotyledons, lateral root primordia, apical meristem, and the leaf margins. TIBA resulted in complete inhibition of auxin expression and ultimately lead to plant death. Brassinosteriods amplified endogenous auxin expression in the roots and leaf vascular tissues. Lastly, increasing gibberellin concentrations reduced auxin expression at the root tip. Information gained from this study could lead to a better understanding of the mechanisms by which different hormones interact to influence plant growth, development and productivity. The results of this investigation form the basis of new laboratory research projects on auxin transport in our third year plant physiology course.

CBA-8 **Effects of phytohormones, auxin, cytokinin, abscisic acid, and brassinosteroid on spore germination, protonema elongation and morphology in moss *Leptobryum pyriforme*.** S. Liang[1], J. Mehroke[1], S. Ellis[1], and S. Singh[1*]. [1]Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4 (e-mail: santokh.singh@botany.ubc.ca)

Phytohormones play an essential role in plants, governing growth and regulating physiological responses. Although the influence of phytohormones on vascular plants has been studied extensively, research on bryophytes is limited to a few species, in spite of their extensive biodiversity. The moss *Leptobryum pyriforme* was chosen for this study because it is ubiquitous in British Columbia, yet its response to phytohormones has not been studied. In order to understand the exact role of phytohormones on moss *L. pyriforme*, this study examined the effect of various phytohormones, e.g. cytokinin (CK), auxin, naphthaleneacetic acid (NAA), brassinosteroid, *epi*brassinolide (*epi*BL) and abscisic acid (ABA)] on spore germination, protonema elongation and morphology. The mature spores of *L. pyriforme* were cultured under aseptic conditions in Petri dishes containing minimal medium. The count of germinated spores, protonema length, and branching patterns and/or bud formation were compared with the control. Only CK was found to induce the formation of buds while NAA and *epi*BL promoted spore germination. ABA was observed to function as an inhibitor for germination, growth, and bud formation. Hormone concentration was also found to be important in determining the response of *L. Pyriforme*. Supra-optimal concentrations of exogenous phytohormones were observed to reduce growth of the moss. The results of this investigation indicate that the various phytohormones have specific roles in the growth and development of *L. pyriforme*. Further study is needed to establish the effect of phytohormone interaction on the development and growth of this moss.

CBA-9 **Development, anatomy and ultrastructure of the floral nectary of disk florets of Echinacea purpurea (Asteraceae).** Dr. Xiaohui Zhang*, Dr. Vipen Sawhney, Dr. Art Davis. Department of Biology, University of Saskatchewan

Development, anatomy and ultrastructure of the floral nectary of disk florets of Echinacea purpurea (Asteraceae) X.H. Zhang1,2*, V.K. Sawhney1 and A.R. Davis1 1Department of Biology, University of Saskatchewan, Saskatoon, SK; 2College of Life Sciences, Shaanxi Normal University, Xi'an, China. We are investigating the structure of ten developmental stages of the floral nectaries of Echinacea purpurea, which occur as multicellular disk-shaped outgrowths surrounding the style base atop the inferior ovary of each of the capitulum's central disk florets. A combination of light, fluorescence, scanning-electron and transmission-electron microscopy has revealed important features of the origin and location of vascular tissue within the nectary interior. Phloem alone enters the nectary tissue, following the initiation of stomata on the gland surface.

Interestingly, phloem in the subepidermal layer of the nectary tissue has been confirmed to originate from periclinal divisions of nectary epidermal cells, thus signifying a rare role of the epidermis in formation of precursor cells that yield sieve tube elements and companion cells immediately below the epidermis. These specialized cell types of phloem connect with phloem traces that traverse the nectary interior, thus providing a network of sieve tubes for transport of nectar sugar to the nectary exterior, where nectar can be collected by potential insect pollinators.

CBA-10 **Investigation of carbon gain of autotrophic, mixotrophic and myco-heterotrophic species at three sites in north-central British Columbia.** Rebecca Bowler[1], Dr. Art Fredeen[2]*, Dr. Hugues Massicotte[2]. [1]Ecosystem Science and Management (ESM) Program, UNBC, Prince George, BC, Canada V2N 4Z9. [2] ESM Program; NRESI, UNBC, Prince George, BC, Canada V2N 4Z9

Most terrestrial vascular plants rely to some degree on mycorrhizal fungi for obtaining mineral nutrition. A subset of these plants also rely on their mycorrhizal partner(s) for some (mixotrophy) or all/most (myco-heterotrophy) of their carbon. Many pyroloids (Pyroleae tribe of the Ericaceae family) and some 'green' orchids (Orchidaceae) are mixotrophs. By contrast, leafless orchids of the genus *Corallorhiza* are thought to be exclusively myco-heterotrophic. We conducted a pilot project where we assessed the photosynthetic competence of autotrophic, mixotrophic and myco-heterotrophic species growing in three sub-boreal forest sites in north-central British Columbia. Gas exchange properties of each species were non-destructively measured *in situ* at least once a month during the growing season (May to September) of 2010 using a portable gas exchange system (LI-6400, LiCor Inc.). Individuals of each species were also replanted in the Enhanced Forestry Lab at UNBC for further analysis. After approximately one month of acclimation to non-forest light levels, light response curves of each transplant were measured using the same methods as *in situ* measurements with the exception of an artificial light source. We will highlight the current implications of our results and our future plans for this study.

CBA-11 **Changes in the spatial relationships between trees, shrubs, moss and lichens across the Canadian forest-tundra ecotone.** Karen Harper[1*], Luise Hermanutz[2], Ryan Danby[3], Keith Lewis[4], Andrew Trant[5], Danielle De Fields[6], and Brian Starzomski[7]. Dalhousie University, Halifax, NS Canada[1], Memorial University, Newfoundland and Labrador, Canada[2], Queens University, Ontario, Canada[3], Memorial University, Newfoundland and Labrador, Canada[4], Memorial University, Newfoundland and Labrador, Canada[5], Dalhousie University, Nova Scotia, Canada[6], and University of Victoria, British Columbia, Canada[7].

The forest-tundra ecotone may be shifting due to climate change, affecting both regional biodiversity. We were interested in how this could affect the spatial pattern of vegetation. Here we present the results of our investigtation into the relationship between trees, shrubs, moss and lichens across the forest-tundra ecotone in Yukon, Manitoba and Labrador. Our objectives were to describe trends in the pattern of shrubs, saplings, mosses and lichens across the forest-tundra ecotone and to investigate how the relationship between different categories of vegetation changes with scale and position along the ecotone. Cover of trees, shrubs, moss and lichens was estimated in contiguous quadrats along transects up to 100 m long at different locations along the forest-tundra gradient at each site. Spatial pattern analysis was used to estimate patch size, scale and amount of aggregation, as well as the negative or positive bivariate correlation at

different scales. Initial results show that lichen and moss cover were more aggregated in the tundra compared to the ecotone and forest. In the Yukon, trees tended to be negatively correlated with nonvascular plants at very fine (1-3 m) and larger scales (20-24 m) but positively correlated at intermediate scales. In Manitoba and Labrador, trees seemed to be more negatively associated with lichens at intermediate distances but more positively associated with mosses at further distances in the forest compared to the ecotone. In the Yukon and Labrador, shrubs and nonvascular plants tended to have negative correlations towards the forest and positive correlations away from the forest. However, most of the results were complex and indicate that local factors appear to be strongly affecting processes within the forest-tundra ecotone. Any predictions for the effects of climate change on vegetation within the forest-tundra ecotone will necessarily be site-specific.

CBA-12 **Ponderosa pine forest dynamics at the northern extent of the species range.** André Arsenault, Atlantic Forestry Centre, Canadian Forest Service, Natural Resources Canada, P.O. Box 960, Corner Brook, Newfoundland and Labrador, Canada, A2H 6J3

Ponderosa pine forests reach their northern limit in British Columbia where they are considered at risk due to the cumulative effects of anthropogenic disturbances, urban encroachment and agriculture. Surprisingly, very little research has been done on the dynamics of this unique Canadian ecosystem. The drought of 2003 and a subsequent severe bark beetle outbreak are rapidly changing the Ponderosa pine forests of southern British Columbia. We studied the effect of the beetle outbreak and the historical dynamics of Ponderosa pine forests using age distributions in 12 one kilometre transects in the Thompson valley west of Kamloops. Mountain pine beetle mortality was severe with over 95% of ponderosa pine larger than 30 cm in diameter killed on all transects over a three year period. Two distinct age structures were discernible. Most of the areas that were easily accessible by roads or trails had a cohort of trees that regenerated between 1880 and 1910 suggesting there was widespread severe disturbance. This is supported by historical records which indicate that there was logging throughout the range of ponderosa pine in the province at that time. However the stands that were in more remote locations exhibited an all-age distribution. Stands with little regeneration will likely shift to a grassland phase, while adjacent patches of grasslands with Ponderosa pine trees encroaching on them will likely be the future Ponderosa pine forest. We propose that Ponderosa pine forests and adjacent grasslands may form a shifting ecotone mosaic, alternating in dominance through space and time as a result of complex responses to variation in climate and disturbance history.

CBA-13 **Forests and climate change: An unique training program at the University of Victoria.** C. P. Constabel, Centre for Forest Biology and Department of Biology, University of Victoria, Victoria BC, cpc@uvic.ca

Forests are an important part of the global carbon cycle and play a crucial role in mitigating and adapting to climate change. Temperate forests are a vital carbon sink for the biosphere, and contain more than twice the mass of carbon than is found in atmospheric CO_2. Since forests cover almost half the land area of Canada, they are particularily significant for Canada's terrestrial carbon budget and global carbon cycle. The importance of forests as mediators of climate change is the focus of a new interdisciplinary training program the University of Victoria. Forests. This program aims to address the role of forests in climate change and in mitigation strategies, with projects in the following major research areas: 1. How can we maximize carbon sequestration in forest stands through optimal regeneration practises for selection of fast-growing and C-

rich species or genotypes. 2. What are the pathways and controls that determine to what pool carbon is allocated in the tree? Can genes responsible for these control points be identified? In particular, non-structural phenolic compounds would be interesting targets as they are typically highly plastic trait. 3. What biological and ecological factors determine greenhouse gas absorption or emission from forest soils? How does plant species, genotype and chemical phenotype impact soil microbes, mycorrhizal associations and nutrient cycling? This NSERC-funded program will train students in collaborative research in these areas, and will enable them to contribute to future mitigation and adaptation strategies.

CSPP-17 **Auxin efflux-carrier gene expression and vascular development is influenced by GA3ox1 overexpression in pea.** A.D. Wickramarathna[1]; J.A. Ozga[1]; L.V. Kurepin[2]; R.P. Pharis[2] and D.M. Reinecke[2]. [1] Plant BioSystems Group, Dept of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5; [2] Dept of Biological Sciences, University of Calgary, Calgary, AB, Canada T2N 1N4

In order to further determine how auxins and gibberellins (GAs) interact during stem elongation, we determined whether increased levels of the growth effector GA, GA_1, were modulating auxin efflux-carrier gene expression during rapid stem growth. Our experimental system involved monitoring the expression of the putative auxin efflux-carrier genes *PsPIN1* and *PsPIN2* in transgenic pea lines that overexpress *PsGA3ox1*. When transcript levels of *PsPIN1* and *PsPIN2* were compared in elongating internodes 2 to 9 (all internodes harvested when at 15% full-length), most internodes of the *PsGA3ox1*-overexpressor lines had higher transcript levels when compared to the controls (transgenic null lines), though some unusual patterns were observed. Specifically, in the *PsGA3ox1*-overexpressor lines, *PsPIN1* and *PsPIN2* transcript levels were reduced in elongating internode 3 relative to a marked increase of these transcripts in the elongating internode 4. This same pattern occurred, though to a lesser extent, in the control lines. For the *PsGA3ox1*-overexpressor lines, the *PsPIN1* transcript abundance was similarly reduced in the elongating internode 7 whereas an increase in *PsPIN1* transcript abundance occurred in the elongating internode 8. When transcript levels of the putative auxin efflux-carrier genes were reduced, there was a coincidental increase in IAA concentration (measured in internodes 6 and 7). A histological assessment showed that vascular re-patterning events occurred in the internodes of pea lines where the reduced *PsPIN* transcript abundance was observed. These data suggest that bioactive GA can modulate the expression levels of auxin efflux-carries genes, and in some cases stimulate vascular re-patterning events in the stem.

CSPP-18 ***Tri6* is defined as a broad domain transcription regulator in the phytopathogen *Fusarium graminearum*.** G. Subramaniam, C.N. Nasmith, S. Walkowiak, L. Wang. AAFC-Canada, 960 Carling Avenue, Ottawa, ON, K1A0C6, subramaniamra@agr.gc.ca.

In *F. graminearum*, the transcriptional regulator *Tri6* is encoded within the trichothecene gene cluster and regulates structural genes involved in the synthesis of the secondary metabolite deoxynivalenol (DON) Targeted disruption of *Tri6* confirmed its role as a positive regulator of trichothecene genes and designates *Tri6* as a narrow transcriptional regulator, responsive to specific pathway signals. The Tri6 protein with its Cys_2His_2 zinc-finger may also conform to the class of broad-domain transcription regulator. This class of global transcriptional regulators mediate various environmental cues and generally responds to the demands of cellular metabolism. To address this issue directly, we sought to find gene targets regulated by *Tri6* by chromatin immunoprecipitation followed by Illumina sequencing (ChIP-Seq). In addition to identifying six genes within the trichothecene gene cluster, *Tri1, Tri3, Tri6, Tri7, Tri12* and *Tri14*, the ChIP-Seq also identified 192 additional targets potentially regulated by *Tri6*. Functional classification revealed that among the annotated genes ~40% are associated with cellular metabolism and transport and the rest of the target genes fall into the category of signal transduction

and regulating gene expression. ChIP-Seq data also revealed Tri6 has the highest affinity toward its own promoter, suggesting that this gene could be subject to self-regulation. Electro mobility shift assays (EMSA) performed on the promoter of *Tri6* using a purified Tri6 protein identified a minimum binding motif of GTGA repeats as a consensus sequence. Finally, expression profiling of *F. graminearum* grown under nitrogen-limiting conditions revealed that 26 out of 198 target genes are differentially regulated by *Tri6*. The identification of potential new targets together with deciphering novel binding site for Tri6, casts new light into the role of this transcriptional regulator in the overall growth and development of *F. graminearum*.

CSPP-19 **Association mapping of seed phenolics in common bean (*Phaseolus vulgaris* L.).** Y. Reinprecht*, D. Frey, T. H. Smith and K. P. Pauls. University of Guelph, Department of Plant Agriculture, Guelph, ON N1G 2W1, Canada (e-mail: yreinpre@uoguelph.ca)

Dry beans contain nutraceutical phytochemicals such as lignans, isoflavones and phenolics. These compounds, synthesized by phenylpropanoid pathway, have potential to promote human health, and have important functions in the plant to increase disease resistance, determine seed coat colour and enhance nodulation. The information about the genes involved in this important pathway is incomplete in bean. In our previous studies, 35 phenylpropanoid pathway genes have been identified and 22 were mapped in the Bat93 x Jalo EEP558 population, which is a core mapping resource for *P. vulgaris*. However, an association between these genes and different seed phenolics is not available. The major objective of this study was to map QTL for seed phenolics and agronomic traits in an association mapping population. The population is composed of 42 cultivars/lines belonging to different bean market classes (seed colour, size and shape) from the University of Guelph dry bean breeding program. The aim of this work was also to confirm the positions of the phenylpropanoid pathway genes mapped in the Bat93 x Jalo EEP558 population, and to map additional 13 phenylpropanoid pathway genes identified in a previous study. The beans were analyzed for a variety of agronomic and seed characteristics, including the levels of phenylpropanoid pathway compounds in developing seed. Bean phenylpropanoid pathway microarray was used to test the activities of the phenylpropanoid pathway genes in these germplasm. The differences in gene expression among bean cultivars from different market classes will be used to map expression quantitative trait loci (eQTL). Genotyping with phenylpropanoid pathway gene-specific, whole bean genome, bean SSR and soybean SSR markers is underway. In an initial analysis with 29 bean SSR markers, an allele sharing-based UPGMA dendrogram consists of 2 major branches separating association population into Mesoamerican (e.g. Bat93) and Andean (e.g. Jelo EEP558) gene pool. Association between markers and seed phenolics (and other traits) will be tested with TASSEL software taking into account population structure and relative kinship. The identification of key factors in biosynthesis of seed phenolics will facilitate rapid introgression of genes coding for proteins directing the synthesis of these important secondary metabolites into new dry bean cultivars.

CSPP-20 **Study of *Brassica villosa* trichomes and trichome-related genes.** N.K. Nayidu, X. Li, and M.Y. Gruber. Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, Saskatchewan, S7N 0X2, Canada. Nagabushana.Nayidu@agr.gc.ca

Trichomes are single cell epidermal structures of importance in plant defence that provide a mechanical barrier against damaging insect pests or synthesize repellent compounds. *Brassica napus*, Canada's most important oilseed crop (canola), has very few trichomes

and seedlings are highly susceptible to feeding damage by *Phyllotreta* flea beetles. In contrast, the Sicilian mountain species, *Brassica villosa*, is a flea beetle resistant perennial weed with dense trichome coverage over the leaves, stems, and flowers. Arabidopsis seedlings also are covered (moderately) in trichomes, which deter flea beetle feeding compared with *glabrous* mutant lines. In order to determine sequence differences between trichome genes of these three plant species, five major trichome regulating genes (*GLABROUS 1*, *GLABROUS 2*, *GLABROUS 3*, *TRANSPARENT TESTA GLABRA 1* and *TRYPTOCHON*) were isolated from *Brassica villosa* and substantial sequence similarity was found between these sequences compared with Arabidopsis and *B. napus* (*GL3* sequence information is not available from *B. napus*). Additionally to determine whether insect resistance in *B. villosa* is due strictly to the mechanical barrier or to additional phytochemical feeding deterrents, we isolated trichomes from the leaves of *B. villosa* grown in a greenhouse and extracted polar compounds. Processed trichome-reduced leaves also were collected and used as a control sample. Filtered methanol extracts were analyzed by HPLC/UV, followed by UPLC/MS and 1D- and 2D-NMR analysis. NMR results indicated several peaks unique to trichomes, one corresponding to inorganic compound(s) and several corresponding to disaccharide derivatives. The poster will focus on sequence variation for the 5 trichome regulatory genes and structure elucidation of the trichome-specific compounds and their potential application to the development of "Hairy Canola" lines with enhanced trichome coverage and resistance to insect pests.

CSPP-21 **Antimicrobial peptide from a rhizobacterial isolate antagonistic to *Clavibacter michiganensis* susbp. *michiganensis*: isolation and partial purification.** F. Mabood*, A. Souleimanov, and D. L. Smith. Department of Plant Science, Macdonald Campus of McGill University, 21,111 Lakeshore Road, Ste Anne de Bellevue, Quebec, Canada, H9X3V9 (fazli.mabood@mail.mcgill.ca)

Clavibacter michiganensis subsp. *michiganensis* (Cmm) causes bacterial canker of tomato. The aim of the study was to isolate and characterize anti-cmm compound(s) produced by a novel rhizobacterial isolate antagonistic to Cmm. A novel rhizobacterial strain showing strong antibacterial activity against Cmm was isolated from the rhizosphere. Using an agar well diffusion assay, activity of the cell free supernatant was studied. The compound(s) were isolated, from bacterial culture, with n-butanol and further fractionated with HPLC. Purified fractions were subjected to SDS-PAGE analysis. Our results demonstrate that the antibacterial compound was produced during the late growth phase of the culture. Initial studies have shown that the antimicrobial compound is proteinaceous in nature and thus is a bacteriocin. SDS-PAGE of the bacteriocin shows that the molecular weight of the compound is less than 4 KDa. Further work on characterization of the compound(s) is underway.

CSPP-22 V**iruses as trigger of DNA damage in host plants.** L. Andronic, Institute of Genetics and Plant Physiology of the Academy of Sciences of Moldova, Padurii str.20, Chisinau, RM, MD 2002; andronic.larisa@yahoo.com

The diseases caused by viral agents in susceptible host induce a wide spectrum of structural and functional destroys accompanied by the disturbances of the process of cells division. The microsporogenesis assessment in tomato (Lycopersicon esculentum, syn. Solanum lycopersicum, cultivars Fachel, Nistru and Prizior) infected with Tomato aspermy virus (TAV) or Potato virus X (PVX) showed deviations in the conjugation of homologues chromosomes, segregation of genetic material, expressed in disruption of chromatin cohesion between homologous chromosomes. The evidence of meiotic

recombination in targeted genotypes indicates the effect of viral infection on chiasmata number and position, promoting the redistribution of chiasmata. On the bases of cytological study in early diakinesis were established significant changes and in induction of additional exchanges offset by asynapsis. Different parameters, determined at particular stages of meiosis, such as chromosome aberration and the mean percentage of abnormal pollen mother cells served as cytogenetic evaluation of microsporogenesis in virus infected tomato cultivars. The study of the meiotic stability in anaphase and telophase I and II revealed a significant increase in different type of abnormalities: eliminations or/and lagging chromosomes, formation of chromosome and chromatid bridges with or without fragments. The results of cytogenetic examination of cell division in barley (Hordeum vulgare L., cultivars Galactic, Sonor, Unirea) roots showed that Barley stripe mosaic virus (BSMV) inhibits the mitotic activity and induces micronuclei, C-metaphases and chlorophyll mutations. The analysis of sister chromatid exchange (SCE), considered as a definite cytogenetic test showing DNA damages or alterations of the replication processes, indicated a significant increase of SCE frequencies in the virus infected plants. Reviewed examples provide data regarding the genetic rearrangements in host plants as a response to viral infection.

CSPP-23 **Characterization and quantification of proanthocyanidins in saskatoon fruits (*Amelanchier alnifolia* Nutt.) during development and at maturity.** A. Jin[1]; J.A. Ozga[1]; J. L. Koerner[2]; J.A. Kennedy[3]; C.P. Constabel[4]; and D.M. Reinecke[1]. [1]Plant BioSystems Group, Dept of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada, T6G 2P5; [2]Dept of Food Science and Technology, Oregon State University, Corvallis, OR, 97331, USA; [3]Dept of Viticulture and Enology, California State University, Fresno, CA, USA, 93740-8003; [4]Dept of Biology and Centre for Forest Biology, University of Victoria, Victoria, BC, Canada, V8W 3N5

Proanthocyanidins (PAs) are oligomeric and polymeric flavan-3-ols. As one of the main subclasses of flavonoids, PAs are widely distributed in many types of fruits, where they provide flavour and astringency to the fruit when consumed. Additionally, recent research suggests that PAs may also have beneficial effects on human health. In order to further understand the potential health beneficial effects of consuming saskatoon fruits (a small fruit native to North America), we have identified and quantified the PAs in mature saskatoon fruits. PA subunit composition and degree of polymerization were characterized and quantified using a method of acid hydrolysis of the PAs followed by phloroglucinol derivatization. Detection of the reaction products was performed by reverse-phase HPLC-diode array detection. Both A-type and B-type PAs were found in saskatoon fruits, and epicatechin was the most abundant PA subunit. In general, PA concentration decreased as the fruits matured. Using histochemical analysis to localize PAs in saskatoon fruit tissues, we found that most fruit tissues contained PAs early in development. However, as the fruit developed, PAs were mainly localized to the epidermis, placental, and seed coat tissues.

CSPP-24 **Efficacy of new environmentally-friendly, sustainable weed control methods using the University of British Columbia campus as a living laboratory.** A. S. Sidhu[1], T. Kheirandish[1], J. Mehroke[1], and S. Singh[1]*. [1]Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4 (email: santokh.singh@botany.ubc.ca)

In pursuit of sustainability in agriculture and urban landscaping, there is now a greater push to develop and test new environmentally friendly agricultural practices. Using the

University of British Columbia (UBC) campus as a living laboratory in collaboration with the UBC Social, Ecological, Economic Development Studies (SEEDS) program and the UBC Building operations department, this study examines the efficacy of environmentally friendly, natural organic acid-based herbicides i.e. Topgun™ (fatty acids) and Ecoclear™ (acetic acid) for control of Canada thistle (*Cirsium arvense*), Morning glory (*Calystegia sepia*), and Horsetail (*Equisetum arvense*). These weed species were investigated on 8 different sites at UBC, where the weed species were treated with various combinations ($C_{100\%}$, $C_{50\%}$), and mixtures ($M_{100\%}$, $M_{50\%}$) of Topgun™ and Ecoclear™. At the physiological level, an almost complete inhibition of the photosynthesis and transpiration rates was observed within few hours of the organic herbicide application. Between Topgun™ and Ecoclear™ solutions, Topgun™ worked the best on every site, as it induced rapid and more drastic changes in the plants. The results of this study indicated that the combination and the mixture of the Topgun™ and Ecoclear™ were the most effective treatments in rapidly killing these weeds and inhibiting their re-growth. In particular, Morning glory and Horsetail were completely eradicated after two cycles of treatment. The organic herbicide-treated leaves of these species showed greater protein degradation. The likely mechanisms of organic herbicide –induced death of weed species will be discussed.

CSPP-25 **Insecticidal activity of flucythrinate acetone derivative as a new insecticide of synthetic pyrethroid.** M.A. Marzouk. Department of Pest Control and Environmental Protection, Faculty of Agriculture, Damanhour University, Al-Gomhouria Street, Damanhour, Al-Behera, Egypt; e-mail: mmarzouk2003@yahoo.com

The α-isopropyl position in flucythrinate (acid moiety) reacts readily with acetone to give a 1:1 adduct, α-cyano-3-phenoxy benzyl-1-(2,2-dimethyl-2-hydroxylethyl)–1-isopropyl-p-difluoromethoxy phenyl acetate. The yield product of adduct was 96%. Structural confirmation using N.M.R. and I.R. was carried out to confirm the structure of the acetone derivative. The N.M.R. spectra showed loss of proton from the α- isopropyl position at 5.20 ppm, addition of two methyl groups from acetone at 1.35 and 1.60 ppm, and introduction of a proton from the hydroxyl group at 0.6 ppm. I.R. spectra revealed the presence of "$C(CH_3)_2$" group at 1360-1380 cm^{-1} (two bands) and "COH" group at 1050 cm^{-1}. The toxicity of flucythrinate and its acetone derivative was evaluated against the 4th instar larvae of cotton leafworm, *Spodoptera littoralis* and female adults of house fly, *Musca domestica*. Results showed that the acetone derivative of flucythrinate is more toxic than its parent compound by 32 and 33 % against *Spodoptera littoralis* and *Musca domestica,* respectively.

CSPP-26 **Hormonal regulation of senescence and longevity of fresh-cut Chrysanthemums flowers.** O. Shi[1], J. Mehroke[1], and S. Singh[1]*. [1]Department of Botany, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4 (email: santokh.singh@botany.ubc.ca)

Fresh-cut flowers of a variety of plant species generally become fully senesced within two weeks if placed in water. The role of plant hormones in retarding senescence and enhancing the shelf-life of cut flowers of Chrysanthemums has not yet been thoroughly researched. The purpose of this study is to examine the hormone-induced delay in Chrysanthemum petal senescence and to use hormones to prolong the shelf-life of these fresh-cut flowers, which would ultimately benefit the consumer and flower industry. Fresh-cut chrysanthemums were treated with various concentrations of plant hormones such as auxin, gibberellin, cytokinins, and abscisic acid. The hormone-treated flowers

were then closely monitored for signs of senescence including wilting of petals. Samples of the hormone-treated flowers were taken during different senescence periods for protein analysis, especially ATP synthase by Western Blot. ATP synthase is a membrane-bound enzyme of plant cells and it gets degraded as the plant ages. In addition, the effects of pH, nutrients, and senescence-inhibitors such as silver ions were also tested. The results have shown that a synthetic cytokinin, thidiazuron (TDZ) at a concentration of 10^{-5} M is the most effective hormone treatment to retard senescence. ATP synthase was most prominent in petals of TDZ treated Chrysanthemum flowers. Silver ion, an inhibitor of ethylene, was found to be moderately effective in delaying senescence. Furthermore, the optimum pH for fresh-cut chrysanthemums flowers was found to be between 7 and 8. Finally, a combination of TDZ, silver ions, and Johnson nutrient solution at a pH of 8 was found to be the most effective treatment in delaying the petal senescence in cut flowers of Chrysanthemum.

CSPP-27 **Extract of *Ascophyllum nodosum* (L.) Le Jolis applied during nursery culture stimulates spring root development in *Pinus contorta* Dougl. var. *latifolia* Engelm. seedlings after winter storage.** J.E. MacDonald[1*], J. Hacking[1], Y. Weng[2], and J.Norrie[3]. [1]Natural Resources Canada, Canadian Forest Service – Atlantic Forestry Centre, P.O. Box 4000, Fredericton, New Brunswick, Canada E3B 5P7 (email: Joanne.MacDonald@NRCan-RNCan.gc.ca); [2]Tree Improvement Office, New Brunswick Department of Natural Resources, 3732 Route 102, Island View, New Brunswick, Canada E3E 1G3. [3]Acadian Seaplants Limited, 30 Brown Avenue, Dartmouth, Nova Scotia, Canada B3B 1X8

Ensuring successful reforestation under a changing climate is important to maintaining the sustainability and competitiveness of Canada's forest sector. Vigorous root development immediately after spring planting is crucial to ensuring a well-developed root system before the occurrence of extreme heat and drought events. Stratified *Pinus contorta* var. *latifolia* (lodgepole pine) seed were sown in containers on 13 April. Seedlings were cultured following standard regional regimes. On 1 September, 19-week-old seedlings were root drenched with *Ascophyllum nodosum* extract in finisher fertilizer at rates of 1:750, 1:500, 1:250, and 1:125. Applications were made three or six times on non-fixed dates, coinciding with irregular irrigation events. After treatment, seedlings were cultured until lifting in December, then freezer stored. No significant treatment effect on root dry weight of seedlings was observed in December. The following May, seedlings were potted and placed in environmental conditions favorable for growth. After 21 days, root development was assessed by excising and counting the number of white roots emerging from the peat plug. Three applications of extract had no significant effect on root development whereas six applications had a significant effect ($P < 0.05$). Further analysis revealed the response varied with rate. The 1:500 rate produced the greatest stimulation, significantly ($P < 0.05$) increasing the number of roots that were ≤ 1 cm, > 1 cm ≤ 5 cm, and > 10 cm long, but not the number of roots > 5 cm ≤ 10 cm long. These findings suggest a benefit in using *Ascophyllum nodosum* extract during nursery culture of lodgepole pine seedlings to promote vigorous root development immediately after spring planting.

CSPP-28 **Intracellular transport logistics and plant cell morphogenesis.** A. Geitmann[1*], C. van Oostende[1], F. Bou Daher[1], D. Guillet[2], and P. Wiseman[2]. [1]Institut de recherche en biologie végétale, Département de sciences biologiques, Université de Montréal, Montréal, Québec, Canada H1X 2B2 (e-mail: anja.geitmann@umontreal.ca); [2]Physics Department, McGill University, Montréal, Québec, Canada

Cellular growth and cell division in plants implicate the assembly of new cell wall surface. The targeted deposition of the material necessary for the assembly of new surface - cell wall polymers and membrane - is therefore a crucial regulatory feature in plant development. The intracellular delivery of this material is generally performed by vesicles, but how is the logistics of this transport process regulated in space and time? Monitoring and quantifying the dynamics of these vesicles in the living cell is severely challenged by the small size of these organelles which is below the diffraction limit of the optical microscope. Particularly in situations when vesicles move rapidly and/or in dense clouds, conventional particle tracking methods are therefore powerless. By combining high temporal and spatial resolution confocal laser scanning microscopy with advanced imaging techniques originally developed for the analysis of molecular movements (STICS, spatio-temporal image correlation spectroscopy), we monitored the intracellular dynamics of vesicles in two plant cell systems displaying intense material delivery activity: the growing pollen tube and dividing BY-2 cells. We used these motion data to generate dynamic profiles for these systems and we aim at modeling mathematically the principal mechanisms governing intracellular trafficking.

CSPP-29 **Expression changes controlling regrowth during vegetative dormancy emergence in potato shoot apical meristems.** Jessica R. Sheldon[1], Julieta Werner[2], Michael G. Broere[3], Marlena Tassone[4], Lauren C. Sinnemaki[5], R. David Law[3]. [1]Department of Microbiology and Immunology, University of Western Ontario, London, Ontario, N6A 5C1, Canada; [2]DST Consulting Engineers, Inc., 605 Hewitson Street, Thunder Bay, Ontario, P7B 5V5, Canada; [3]Department of Biology, Lakehead University, 955 Oliver Road, Thunder Bay, Ontario, P7B 5E1, Canada; [4]Northern Ontario School of Medicine, West Campus, 955 Oliver Road, Thunder Bay, ON, P7B 5E1, Canada; [5]Faculty of Medicine, University of Manitoba, Faculty of Medicine, Winnipeg, Manitoba, R3E 3P5, Canada

Similar to shoot apical meristems (SAMs) that develop during embryogenesis in seeds, potato (*Solanum tuberosum* L.) SAMs form and then temporarily cease growth when the tuber is mature. After a period of endodormancy, the meristems then resume growing during bud break. It is unknown whether the molecular events leading to regrowth are similar to those of seed germination. Potato shoots were thus cultured in vitro and used to form microtubers. SAMs removed from microtubers at various timepoints after harvest and storage at 4°C exhibited endodormancy similar to that seen in field tubers. The expression of several genes linked to seed dormancy and germination and SAM identity was determined by real-time polymerase chain reaction. ABI5 and PKL expression declined during dormancy emergence. By contrast, both expression of the meristem-specific STM, WUS and CLV3 genes, and de novo DNA synthesis increased significantly between 7 and 11 weeks after harvest, indicating that potato SAMs emerge from dormancy at this time. Southern blotting and cDNA sequencing indicated the presence of 2 isoforms of the STM gene, similar to that in tomato. These data indicate that microtubers are an excellent model system to use for studying potato SAM development in vitro, and that important differences exist between potato and *Arabidopsis* shoot development.

CSPP-30 **Cellular and nuclear dynamics during germination and collet hair formation in *Arabidopsis thaliana* (L) Heynh.** E. Sliwinska[1*], J. Mathur[2,] G. W. Bassel[3] and J. D. Bewley[2], [1]University of Technology and Life Sciences, Bydgoszcz, Poland (e-mail:

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Using laser-scanning confocal microcopy of fluorescent-labeled *Arabidopsis* embryos during and following germination, several movies were made which show the cellular changes that occur during emergence of the radicle and the dynamics of collet hair growth and nuclear migration therein. Germination is completed by expansion of cells of the root-hypocotyl transition zone (the collet) that is immediately behind the radicle. This region is also definable by the accumulation of carbohydrate bodies during germination and distinct GFP expression of GAL-4-GFP in enhancer-trap lines. From the collet region there is the simultaneous initiation of hairs following the completion of germination; their growth is accompanied by the synchronous migration of nuclei at a short fixed distance behind the tip. Following cessation of hair growth, the nuclei migrate to the base of the cell; thereafter their movement is limited and asynchronous. This is due to the inability of most nuclei to migrate past large vesicles (pre-vacuoles) that form in the mature hairs. Changes in nuclear dynamics are accompanied by an increase in nuclear DNA content due to endoreduplication. Perturbation of the microtubules allows tip growth despite complete disturbance of nuclear movement, thus dissociating the relationship between the two phenomena. Actin disruption allows the nuclei to enter the developing hairs, although their movement is less synchronous than in control hairs and is not at a fixed distance from the tip. The collet plays an important role in germination and in the early establishment of the seedling; it has largely been ignored in research into both of these events.

CSPP-31 **Inflorescence architecture and reproduction development are affected by heterologous expression of a conifer MADS-box gene.** J.-J. Liu, Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada, Victoria, British Columbia, Canada V8Z 1M5 (Jun-Jun.Liu@NRCan-RNCan.gc.ca)

Plant architecture and the allocation of growth resources are key factors that will determine plant adaptability under global climate change. Phenotypic traits important to tree architecture and biomass growth are supposed to be controlled genetically. However, little information is available on these specific traits in forest conifer species. Understanding of the genetic basis/genomic networks for tree growth form and carbon allocation between vegetative and reproductive growths is thus essential for effective tree improvement through molecular breeding and biotechnology. Plant MADS-box genes of the *AG/PLE* subfamily are known to control the identity of plant sexual organs, but very few MADS-box genes have been characterized in forest conifer species. In the present study, an *AG* homologous gene (*PrAG1*) was cloned from conifer *Pinus radiata*. *PrAG1* transcript was detected only in the female and male strobili. Dominant negative mutation analysis was used to investigate regulatory function of the gene during reproductive development using a binary vector for overexpressing a truncated PrAG1 protein with deletion of both C and K domains under control of the CaMV 35S promoter (35S::PrAG1-MI) in transgenic tobacco. Phenotypic analysis revealed that 23.8% of the 35S::PrAG1-MI transgenic lines displayed altered inflorescence architecture and variety of floral development changes, including transgenic male sterility. These results suggest that *PrAG1* may be a *P. radiata* AG-homologous gene with C-function and it plays a role in the determination of meristem identities in both inflorescence and flower organs. Expression of a truncated AG-MI gene could be useful in diminishing plant pollen and seed formation, as well as increasing inflorescence branching and flower production, providing a novel genetic engineering strategy for sterility of transgenic plants, as well as

potential application in molecular breeding of flowering plants for modified Inflorescence architecture.

CSPP-32 **Ring-type E3 ligases, XBAT34 and XBAT35, play essential roles in embryo and vegetative development in *Arabidopsis thaliana.*** H. Liu; S. Stone. Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada B3H 4R2

Ubiquitin-mediated protein modification plays a key role in many growth and developmental processes in plants. The Arabidopsis *XBAT34* and *XBAT35* genes encode for ankyrin repeat containing RING-type E3 ligases of unknown function. Analysis of *xbat34* or *xbat35* mutants did not reveal any phenotypic difference compared to wild type controls. Amino acid sequence comparison shows 68% identity and 73% similarity between XBAT34 and XBAT35. In addition, *XBAT34* and *XBAT35* show the same subcellular localization pattern. This information suggests that both genes may be redundant. Therefore, we attempted to generate *xbat34* and *xbat35* double mutants. However, we were unable to recover *xbat34 xbat35* as well as *xbat34 XBAT35/xbat35* seedlings. *XBAT34/xbat34 xbat35* displayed a number of mutant phenotypes including severe growth retardation, defects in lateral root production, differences in leaf color and shape, delayed flowering, short siliques and reduced seed set. Segregation analysis of selfed *XBAT34/xbat34 xbat35* plants and *XBAT34/xbat34 xbat35* crossed with *xbat34* indicate that mutant alleles can be transmitted through both the male and female gametophyte, suggesting that the inability to recover *xbat34 xbat35* and *xbat34 XBAT35/xbat35* seedlings is due to embryo lethality. To further characterize the *XBAT34/xbat34 xbat35* plants, hormone analyses were carried out and we found that the lateral root defect of *XBAT34/xbat34 xbat35* can be partially rescued by exogenous auxin. Interestingly, overexpression of *XBAT35* but not *XBAT34* led to cell death in tobacco transient expression system. These results provide evidence that *XBAT34* and *XBAT35* play possibly overlapping and distinct roles in plant growth and development.

CSPP-33 **Plant invasion, soil pH, and epigeal springtails: implications for nutrient recycling in temperate forests.** A.B. Alerding* and R.M Hunter. Department of Biology, Virginia Military Institute, Lexington, VA, 24450, USA

A common response to plant invasion is thinning of the litter layer, which is attributed to increased rates of decomposition. Whether this thinning is facilitated by abiotic changes resulting from invasion or to alterations in decomposer communities is unknown. In North American forest understories, invasion by the herbaceous biennial, garlic mustard (*Alliaria petiolata*, M. Bieb.) produces near-monocultures that have displaced native herbs and woody plants. Thus, litter inputs both above- and below-ground have dramatically changed in these forests. Since Collembolans (i.e. springtails) serve an important role as detritivores of epigeal litter, we hypothesized that their populations would increase in response to garlic mustard invasion, expediting decomposition rates of litter inputs from this invader. To test this hypothesis, we obtained epigeal cores from neighboring invaded and uninvaded sites in an early-invasion temperate forest in Virginia. Springtails were extracted from cores by high-gradient dynamic extraction and identified to family. Over a two-month sampling period in early summer 2010, springtails from the family Entomobryidae were found to be twice as abundant in sites invaded by garlic mustard, but this effect was mollified by the co-presence of the invasive grass, *Microstegium vimineum* (Trin.). Interestingly, sites dominated by juvenile rosettes produced higher pH soils (5.6 versus 5.3), which in our study explained 20% of the

variation in springtail abundance. These results point to a complex relationship between plant invaders, soil chemistry, and decomposer abundance.

CSPP-34 **Somaclonal Selection for Phytonutrient Improvement in 'Russet Burbank' Potato.** Atef M.K. Nassar[1,2,3*], Stan Kubow[2], Yves N. Leclerc[4], and Danielle J. Donnelly[1]. [1]Plant Science Dept. (e-mail: danielle.donnelly@mcgill.ca), [2]School of Dietetics and Human Nutrition, Macdonald Campus of McGill University, 21,111 Lakeshore Rd., Sainte Anne de Bellevue, QC, H9X 3V9, Canada. [3]Pest Control and Environmental Protection Dept., Faculty of Agriculture, Damanhour University, Damanhour, Al-Beheira, Egypt. [4]McCain Foods Canada Ltd., 107 Main Street, Florenceville, NB, Canada E7L 1B2

Screening of > 800 somaclones of 'Russet Burbank', North America's leading French fry cultivar, for improved yield and processing quality, lead to the selection of 25 advanced lines. Three replicates of at least three tubers each from advanced somaclones were assessed for nutritional attributes, a subject of great modern interest among dieticians, plant breeders, and consumers. Phytonutrients and antioxidant capacity per serving (150 g FW) varied significantly among tubers (5 months storage) of the 25 somaclones as well as between these and control plants ('Russet Burbank' field tuber-derived). For example, ascorbic acid ranged > 3-fold (81.47 to 304.60 mg) among somaclone tubers with some lines greater than control tuber level (173.14 mg). Similarly, several polyphenolics (chlorogenic acid, caffeic acid, ferulic acid), and the flavonoid rutin ranged in concentration from 10- to 100-fold among the somaclone tubers. In each case, there were some somaclone lines that exceeded control tuber concentrations by up to 3-fold. Antioxidant capacity estimated using 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulphonic acid) (ABTS, mM Trolox equivalent/serving), ranged up to 5-fold for somaclones, from 2,121.30 to 11,163.10. Most somaclones (16/25) had greater antioxidant capacity than control (5,113.90) and these corresponded to lines with increased ascorbic and chlorogenic acids. Somaclonal selection appears to offer clear benefits for phytonutrient improvement in potato.

CSPP-35 **Targeted expression of an antimicrobial peptide gene in potato tubers to reduce post-harvest diseases.** D. P. Yevtushenko* and S. Misra. Centre for Forest Biology, Department of Biochemistry & Microbiology, University of Victoria, Victoria, British Columbia, V8W 3P6, Canada (e-mail: dmytro@uvic.ca)

Precise control of transgene expression is crucial for the successful engineering of crops with reduced post-harvest losses. An efficient promoter-transgene system with a suitable level of organ-specific expression is a prerequisite for practical applications of this technology. In our study, comparative analyses of different promoters in plants using ß-glucuronidase (GUS) reporter gene system revealed that the promoter of luminal binding protein from Douglas-fir (*BiP Pro1-1* promoter) exhibited high activity in potato tubers. This prompted us to evaluate the use of this promoter for accumulation of an antimicrobial peptide MsrA2 (a derivative of dermaseptin B1 that displays high activities against a variety of phytopathogens) in storage organs of potato. The MsrA2 peptide (32 amino acids) belongs to a diverse group of small membrane-active molecules that are components of the innate defense system of all multicellular organisms. Its powerful antimicrobial activity, combined with low toxicity to mammalian and plant cells, presents great potential for engineering plants with increased disease resistance. The plant-optimized nucleotide sequence encoding MsrA2 was transcriptionally fused to the *BiP Pro1-1* promoter, and introduced into potato via *Agrobacterium*-mediated transformation. Stable transgene integration into the plant genome was confirmed with Southern analysis.

Growth characteristics and the morphology of transgenic potato were identical to untransformed controls. Western blot analysis showed high level of MsrA2 accumulation in tubers of transgenic plants. Moreover, *in vitro* bioassays revealed that the expression level of the MsrA2 peptide in potato tubers, regulated by the *BiP Pro1-1* promoter, was sufficient to confer resistance to bacterial soft rot disease caused by plant-pathogenic species of *Erwinia* (*Pectobacterium carotovorum*). Thus, the tuber-specific expression of MsrA2 enables the development of soft rot resistant potato plants, thereby reducing tuber losses in the post-harvest system. This research was supported by a grant from the Advanced Foods and Materials Network to S.M.

CSPP-36 ***Arabidopsis thaliana*** **(L.) with partially-suppressed mitochondrial pyruvate dehydrogenase kinase show enhanced productivity at high CO_2 and altered patterns of fatty acid synthesis.** S.M. Weraduwage[1], S.A. Rauf[1], M.C. Micallef[1], E-F Marillia[2], D.C. Taylor[2], B. Grodzinski[1] & B.J. Micallef[1*]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, N1G 2W1, Canada. [2]NRC-PBI, Saskatoon, Saskatchewan, S7N 0W9, Canada

Sink limitations in plants can limit photosynthesis and productivity particularly under conditions that support greater source activity such as high-CO_2. *Arabidopsis* with partially-suppressed mitochondrial pyruvate dehydrogenase (mtPDH) kinase (mtPDHK), a negative post-translational regulator of mtPDH, show increased seed weight and oil content per seed at ambient CO_2, suggesting that these transgenics have greater sink activity. In the present study, we hypothesized that *Arabidopsis* having suppressed mtPDHK and an apparent greater sink activity will display a greater productivity enhancement at high-CO_2. *Arabidopsis* having either constitutive or seed-specific expression of antisense mtPDHK were grown at either ambient or high CO_2, and growth and oil parameters, mtPDHK transcripts, and mtPDH activities were measured. Elevated CO_2 significantly increased seed and oil yield both on a seed and whole plant basis for control and transgenic lines. The greatest productivity (up to 3 times) was found for constitutive lines grown at high CO_2 that also showed the highest suppression of mtPDHK expression and enhanced mtPDH activity. Reduced feedback on net C exchange was also found for constitutive lines. The fatty acid content per 100-seeds showed a significant positive correlation with Very Long Chain Fatty Acid (>C20, VLCFA) content and a negative correlation with Long Chain Fatty Acid (C16-18) content; the highest VLCFA content was found for constitutive lines grown at high CO_2. The polyunsaturated (mainly 18:2, 18:3 and 22:2) and monounsaturated (mainly 18:1) fatty acid content showed a positive and negative correlation, respectively, with the fatty acid content per 100-seeds at high CO_2. These data support a role for mtPDH in supplying carbon skeletons for fatty acid synthesis in the endoplasmic reticulum. Collectively, the data show that enhanced and not decreased respiratory activity can increase plant productivity under conditions that support greater source activity such as high CO_2.

CSPP-37 **Ureide metabolism and differential regulation of allantoinase genes in soybean.** V. A. Duran and C. D. Todd* Department of Biology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5E2 (email: chris.todd@usask.ca)

Biological nitrogen fixation in plants occurs in partnership with bacteria able to convert atmospheric dinitrogen (N_2) into a form usable by the plant. The bacterial partner provides nitrogen, in the form of ammonia, to the plant and the plant provides the

bacteria carbon as an energy source. Ammonia is assimilated by the plant, converting it to other forms for immediate utilization and/or export. In many legumes nitrogen is exported from the nodule to the rest of the plant as amino acids. Soybean (*Glycine max* (L.) Merr.), and related tropical legume species, export ureides, rather than amino acids, from the nodule during active nitrogen fixation. In ureide-exporting legumes the enzyme allantoinase plays a dual role in ureide synthesis in the nodule as well catabolism in leaves and other sink tissues. In order to better understand the role of allantoinase in ureide metabolism we determined ureide content, allantoinase activity and allantoinase gene expression in seedlings, in N_2-fixing vegetative soybean and in non-fixing soybean plants at the same developmental stage. In soybean there are four which appear to have arisen through gene duplication and whole genome duplication. In all the tissues examined, *GmALN1* and *GmALN2* transcripts were generally more abundant than those of *GmALN3* and *GmALN4*; however, *GmALN3* and *GmALN4* were highly up-regulated in nodules, pointing to a possible role in allantoate synthesis during nitrogen fixation. This specialization may point to a mechanism allowing ureide exporting legumes to adopt this pathway for nitrogen transport.

CSPP-38 **Activation and repression of genes involved in cytokinin biosynthesis and degradation through root application of soluble *Ascophyllum nodosum* extracts in *Arabidopsis thaliana.*** O.S.D. Wally,[1*], A. T. Critchley[2], D. Hiltz[2], B. Prithiviraj[1]. [1] Department of Environmental Sciences, Nova Scotia Agriculture College, Truro, Canada(E-mail: owally@NSAC.ca);[2] Acadian Seaplants limited, Dartmouth, Canada

There is a long held belief that seaweeds and their extracts contain the same plant growth regulators (PGRs) as land plants. With these PGRs stimulating growth and enhancing the plants responses towards abiotic and biotic stresses. Recent PGR analysis and quantification of a variety of seaweed extracts revealed levels of PGRs that would be insufficient to cause any beneficial effect on treated plants. However, components within the seaweed extracts may activate plants innate pathways for the biosynthesis PGRs, in particular cytokinins. Therefore, gene expression profiles for cytokinin biosynthetic and catabolic pathways were determined following the application of soluble seaweed extract powder (SSEP, Acadian Seaplants limited) of the brown macro algae *Ascophyllum nodosum*, to roots of *in vitro* grown Arabidopsis plants at a rate of 100 mg l^{-1}. Quantitative real time PCR was used to determine the change of gene expression, from total RNA isolated at various time points from the rosettes of SSEP or mock treated Arabdiopsis. Genes involved in the initial steps towards cytokinin production *isopentenyl transferase (IPT3*, *4*) and *CYP735A2* are upregulated 2, 4and 5 fold respectively after 24h of SSEP treatment, further increasing to 2, 5 and 4.5 fold after 48 h before returning to control levels by 96h. Conversely the key gene *cytokinin oxidase/dehydrogenase 4* (*CKX4*) that initiates the degradation of cytokinins is down regulated more than 5-fold at 24 and 48h following treatment, returning to control levels after 96h. Taken together these findings may indicate rapid stimulation of endogenous cytokinin accumulation within SSEP treated plants.

CSPP-39 **Genotype Effects on Physico-thermal Properties of Soybean Stem Fibres in Composite Materials.** M. Arif[1]*, Y. Reinprecht[1], L. Simon[2] and K. P. Pauls[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G [2]W1(marif@uoguelph.ca); and [2]Department of Chemical Engineering, University of Waterloo, Waterloo, Ontario, Canada N2L 3G1

The current study was initiated to investigate the influence(s) of plant genotype on the performance characteristics of fibres extracted from soybean stems after incorporation into a polypropylene (PP) matrix. Soybean stem fibres from a recombinant inbred (RI) population (from a RG10 x OX948 cross) of 50 lines that were grown in 2008 in Harrow and Woodstock in Ontario. The stem fibres were incorporated into PP at 20% (wt/wt) by extrusion at 190□C and 40 rpm with a conical twin-screw extruder. Test samples were injection moulded at a barrel temperature of 190□C and a tool temperature of 50□C with injection period of 15 sec at 100 psi. The samples were annealed at 150□C for 10 minutes in air circulating oven and cooled to room temperature. The composites were tested for their flexural, tensile, impact and thermo-gravimetric properties. The composites prepared with fibres from different genotypes had significantly different flexural, tensile, modulus and impact properties. In general, PP had a higher impact value (28 J/m) than the composites but some of the composites had better impact values (up to 31 J/m) than PP. Soy stem fibre composites had significantly better flexural properties than pure PP. For example, composite flexural strength values ranged from 42 to 51 MPa and flexural modulus values were from 1.2 to 1.4 GPa in comparison to PP which had 39.3 MPa and 0.9 GPa flexural strength and modulus values, respectively. In addition, soy stem fibre composites prepared from the different genotypes had ultimate strength values ranging from 33 MPa to 38 MPa and tensile strength values from 28 MPa to 35 MPa tensile strength at break point, compared to PP which had ultimate tensile and tensile strength at break point values of 34.5 MPa and 32.2 MPa, respectively. Thermo-gravimetric analysis (TGA) of the soybean stem fibre composites showed that the fibres extended the degradation profile by 37°C (from 425°C for pure PP to 462°C for the composites). This study will provide information required by plant biologists to identify fibre-related genes and breed soybean varieties with fibres that produce superior composites.

CSPP-40 ***In vitro* androgenesis as a source of haploid pepper (*C. annuum* L.) plants.** A. Kisiała[1*], and P. Nowaczyk[2]. [1]Department of Biology, Nipissing University, North Bay, Ontario, Canada P1B 8L7; and [2]Department of Genetics and Plant Biotechnology, University of Technology and Life Sciences, Bydgoszcz, Poland

In vitro induced androgenesis is the formation of sporophyte from immature pollen grains through anther or isolated microspore cultures. It is a fast and efficient method of obtaining haploid plants, widely applied in breeding of many vegetable and ornamental species. Haploids with a single set of chromosomes in somatic cells, and fully homozygous doubled-haploid lines (DH lines) of *Capsicum annuum* L. are used to speed up breeding for resistance traits, improve agronomically important plant characters, and to construct species genetic linkage maps. The effectiveness of pepper anther culture depends on many factors, optimalization of which is the important condition of obtaining high yield of androgenic embryos. The main goal of the presented research was to determine reaction of selected Polish *C. annuum* L. genotypes on *in vitro* anther culture conditions. The results of performed experiments indicate that the crucial factor determining the effectiveness of androgenic embryos development was the genotype of donor plants. The effectiveness of androgenesis ranged from 1.43% to 33.8%, which means the tested pepper forms differed considerably in spite of their androgenic response. Additionally, it was found that androgenic response of the anthers was strongly modified by the stage of microspore development at which anthers were excised and the age of anther-donor plants. It depended also on the culture media composition. Ploidy level of androgenic regenerants was determined cytometrically and the effective method of colchicine treatment was established. Isosyme analysis and the characteristics of plants

morphology were applied to determine microspore origin of the regenerants. On the base of performed experiments it was stated that Polish breeding lines, cultivars, and hybrid genotypes of pepper, cultivated in local climate and soil conditions, can be a source of haploid plants and fully homozygous DH lines. The possibility of the application of *in vitro* induced androgenesis in pepper breeding programs may highly increase genetic variability of *C. annuum* germplasm.

CSPP-41 **RAPD assessment for identification of genetic stability of *in vitro* propagated cotton sedge (*Eriophorum vaginatum* L.) plants.** A. Kisiała[1], M. Rewers[1], and E. Cholewa[1*]. [1]Department of Biology, Nipissing University, North Bay, Ontario, Canada P1B 8L7

Eriophorum vaginatum L. (cottongrass; Cyperaceae), an ecologically important tussock-forming perennial graminoid, is the most abundant herbaceous species in Northern Hemisphere peatlands and circumpolar tussock tundra. It possesses a high adaptability to a broad range of environmental conditions, and is widely distributed in nutrient-poor sites. Additionally, cotton sedge can colonize habitats that are damaged by metal contamination or extensive anthropogenic exploitation (e.g. vacuum-mined peatlands), demonstrating its potential use in phytoremediation and wetlands restoration. However, propagation of *E. vaginatum* on a large scale is problematic due to seed dormancy and limitations in reproduction by rhizomes. Therefore, *in vitro* micropropagation systems appear to be the alternative method of successful production of *E. vaginatum* plants. Genetic fidelity of tissue cultured regenerants is of utmost importance for commercial utilization of the technique for large scale production of true-to-type plants. Thus, because common consequence of *in vitro* plant regeneration can be genome sequence variations, tools must be used to examine any genetic changes that might be induced by *in vitro* culture conditions. In the presented study genetic uniformity of the *in vitro* micropropagated *E. vaginatum* plants of callus origin was determined using Random Amplified Polymorphic DNA (RAPD) analysis. 20 arbitrary 10-base primers were successfully used to amplify DNA from *in vitro* regenerants and control plants collected from their natural habitat. A total of 156 scorable fragments were amplified with the average of 8.21 bands per primer. The PCR amplification products were monomorphic across all the analysed plant materials, thus no somaclonal variation was detected. Lack of polymorphism observed within the regenerants reveals that callus obtained from *in vitro* cultured seeds could be used as an alternative source material of genetically stable *E. vaginatum* plants. This is the first report on the application of molecular methods in the research on this species. Currently, RAPD analyses are applied to test genetic variability between the populations of *E. vaginatum*, originated from different sites across Canada.

CPS-16 **Prevalence, distribution and epidemiology of Godronia canker on highbush blueberry in the lower mainland of British Columbia.** S. Sabaratnam[1], S. Chatterton[2], R. You[2], K. Sakalauskas[2], and M. Sweeney[1]. [1]Abbotsford Agriculture Centre, Ministry of Agriculture, Abbotsford, British Columbia, Canada V3G 2M3 (e-mail: siva.sabaratnam@gov.bc.ca); and [2]British Columbia Blueberry Council, Abbotsford, British Columbia, Canada V2T 1W5

Godronia canker, caused by *Godronia cassandrae* Peck (anamorph *Fusicoccum putrefaciens* Shear), is one of the major diseases on highbush blueberry (*Vaccinium corymbosum* L.), grown in the lower mainland of British Columbia. Studies conducted in 2009 and 2010 reveal that the disease is prevalent in all blueberry growing regions in the lower mainland of British Columbia. Initial symptoms appear early in the spring as small, brown coloured lesions on one- and two-year-old stems, mostly at the base of leaf and floral buds and leaf scares at nodes. Young canker-lesions expand rapidly, producing elliptically shaped cankers that often girdle the stem resulting in flagging and dieback of stems. Pycnidia on mature cankers release conidia throughout the crop season. However, high number of conidia can be found from spring to early summer months (April to June) and fall months (September to October), that coincided with rain events in year 2009 and 2010, indicating that the pathogen is actively producing spores during cool, wet months of the year. This suggests that blueberry plants are more vulnerable to infection during spring and fall months than dry summer months. Furthermore, the appearance of symptoms in early spring suggests that the initial infection of blueberry plants is most likely taking place in the fall, when temperature and moisture requirements are conducive for the germination of conidia and subsequent infection process by the pathogen. Further studies will be conducted to determine the time of the year and environmental conditions that are most conducive for the pathogen to infect plants and, thus, appropriate disease management strategies will be developed.

CPS-17 **Differential gene expression responses of *Pythium aphanidermatum* within plant hosts during root rot disease development.** K. Bala[1,2]*, C.A. Lévesque[2], and B. Saville[1].[1]Forensic Science Program and Environmental and Life Sciences Graduate Program, Trent University, Peterborough, ON, Canada, K9J 7B8(e-mail: kanak.bala@agr.gc.ca); and [2] Biodiversity, Agriculture and Agri-Food Canada, Ottawa, ON, Canada, K1A 0C6

Pythium aphanidermatum is a root rot pathogen and a major agricultural threat. It causes heavy losses in greenhouse vegetable and cereal crops worldwide. While pathogenicity and virulence studies have been carried out with this pathogen, no information is available on the *P. aphanidermatum* transcript level changes during growth within its plant hosts. Tracking the dynamic interplay between this pathogen and hosts at the early stages of infection will provide a substantial gain in understanding *Pythium*-host interactions. To provide context for deep transcriptome analysis, the timing of the pathogenic development in distinct hosts must be determined. This is being accomplished through the development of novel pathogenesis assay protocols and the use of these to assess the progression of disease development. The three hosts selected were cucumber, wheat and corn. The progression is being followed microscopically, through

determining the relative concentrations of nucleic acids from the host and pathogen during infection by monitoring changing transcript levels of housekeeping genes, and by following the levels of selected *P. aphanidermatum* pathogenesis genes. RNA samples were pooled from the infected plant root tissue exposed to the zoospores of *P. aphanidermatum* at different time intervals. Quantification of transcript levels was assessed using quantitative reverse transcriptase RT-PCR. The results showed that the root-rot disease progression is consistent with the relative increase in the pathogen biomass to the total root mass. Progress in determining transcript levels of pathogenicity genes and the correlation with pathogen biomass at different times in pathogenesis will be presented. This work sets the stage for a comparative deep transcriptome investigation of *P. aphanidermatum* disease development on three agronomically important plant hosts.

CPS-18 **Analysis of aerobiological data: a new approach to model the influence of weather on dynamics of airborne spores.** O. Carisse[1]*, V. Morissette-Thomas[2] and D. C. Morissette[3]. [1] Horticulture Research and Development Centre, Saint-Jean-sur-Richelieu, Quebec, Canada J3B 3E6 (email:odile.carisse@agr.gc.ca); [2]Department of Mathematics, Sherbrooke University, Sherbrooke, Québec, Canada, J1K 2R1; [3]Phytodata Inc., Sherrington, Quebec, Canada J0L 2N0

Aerobiology is the science which studies the spatial and temporal dynamics of biological particles and their relationships with the environment and organisms. In plant pathology, aerobiology mainly deals with the atmospheric plant pathogen spores in relation to the weather and the diseases they cause. Atmospheric spores are monitored with various devices such as volumetric or impaction spore samplers. Traditionally, the amount of spores caught was determined by microscopic observations. The advances in molecular biology now allow spore quantification with techniques such as quantitative PCR. Nevertheless, the analysis of aerobiological data poses statistical problems. By nature, the weather variables are highly correlated, which cause multicolinarity that should be addressed when modeling a response variable as a function of weather variables. Furthermore, the quantity of airborne inoculum at any given time is influenced by weather conditions on the current day and for some period of time prior to the current day. Polynomial distributed lag regression analysis, followed by linear mixed model analysis, was used to identify the weather variables that are most influential on the abundance of airborne conidium concentration of *Erisyphe necator* Schwein (ACC), the causal agent of grape powdery mildew; to determine the time window over which each weather variable influenced ACC and to determine the form of the relationship between each weather variable and ACC. Only few weather variables allowed prediction of ACC with a lag of 7 and 10 days. Daily maximum temperature, maximum vapour pressure deficit, wind velocity and occurrence of high humidity periods significantly influenced ACC. Various models based on 3 of these variables predicted 95% of the variation in ACC.

CPS-19 **Isolation and evaluation of soil microorganisms for control of clubroot on canola.** G. Peng, S.M. Boyetchko*, R.K. Hynes, L. McGregor, K. Sawchyn, and D. Hupka. Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7J 0X2

Clubroot, caused by the plasmodiophorid pathogen *Plasmodiophora brassicae* Woronin, is an emerging threat to canola (*Brassica napus* L.) production in western Canada. During the 2008 and 2009 crop seasons, canola roots were collected from the Black Soil

Zone of Alberta and Saskatchewan for isolation and screening of indigenous microorganisms against clubroot. Under laboratory conditions, soils removed from the root surfaces were suspended in sterile water (SW), and plated on acidified potato dextrose agar amended with antibiotics or on nutrient agar (NA) for isolation of rhizosphere fungi and bacteria, respectively. Additional root samples were surface sterilized in 70% alcohol for 30 s, 0.12% hypochlorite for 5 min, cut into 1-cm pieces after rinsing, and placed on the same media for 2-6 wks to isolate endophytes. A total of 5,152 isolates were obtained, and screened for antagonism initially against an indicator pathogen (*Pythium ultimum* Trow) *in vitro*. About 440 antagonistic isolates were selected and tested against clubroot on canola using a bioassay in which the microbial candidates were applied as a soil drench (25 ml) immediately after seeding to saturate the growth medium that had already been infested with *P. brassicae* at 2×10^6 resting spores/g. For fungal isolates, the suspension was adjusted to about 10^6 spores or propagules/ml and for bacteria, the lawn of a culture on NA from three Petri plates (10-cm-diam) was scraped and suspended in 200-ml SW. Treated plants were kept in a growth cabinet at 23/18ºC for 4 wks, and clubroot development assessed using a 0-3 scale where 0 indicated no clubroot symptoms and 3 represented greater than 75% of the root affected. Seven plants (replicates) were used for each microbial candidate, and plants which received water only were included in each test as controls. Overall, only three bacterial isolates resulted in greater than 75% of reduction in clubroot severity relative to controls. These bacteria were identified tentatively as *Bacillus* sp. and *Pseudomonad* spp. and the *Bacillus* sp. isolate appeared to be an endophyte capable of colonizing canola roots. These isolates are being further investigated for their practicality in clubroot control on canola.

CPS-20 **Rapid detection and identification of five pathogens associated with tomato corky root rot by real-time PCR.** K. Wang[1*], G. Patterson[1], J. A. Traquair[2], and G. Larzarovits[1]. [1]A&L Biologicals, Agroecology Research Services Centre, 2136 Jetstream Road, London, Ontario, Canada N5V 3P5 (e-mail: kwang@alcanada.com) and [2]Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 1391 Standford Street, London Ontario, Canada N5V 4T3

Early diagnosis of tomato corky root rot, a commercially important disease emerging in Ontario processing tomato production, is complicated and time consuming using traditional methods, since it is associated with five different pathogens including *Fusarium oxysporum*, *Colletotrichum coccodes*, *Rhizopycnis vagum*, *Pyrenochaeta terrestris*, and *Pyrenochaeta lycopersici* as well as their interactions. For the rapid and reliable detection and identification of these pathogens, oligonucleotide primers and probes were designed on the basis of alignment of internal transcribed spacer (ITS) sequences (ITS1-5.8S-ITS2) for a TaqMan real-time quantitative polymerase chain reaction (qPCR) assay. Specificity of species-specific primer pairs and probes was confirmed by using 15 different fungal pathogens. Under optimum conditions, the sensitivity of the qPCR assay was as little as 0.05 pg of target genomic DNA. The DNA standards and an internal control were also developed for quantification of these pathogens. The qPCR has been successfully used to detect and quantify pathogens present in soil and asymptomatic tomato roots. This technique provides an accurate, reliable and fast method for identification and quantification of pathogens associated with Ontario tomato corky root rot in etiological studies and in disease control strategies.

CPS-21 **Methods of inoculating pea plants with *Peronospora viciae* f. sp. *pisi*.** K.F. Chang[1]*, J.F. Liu[2], S.F. Hwang[1], S.E. Strelkov[2], B.D. Gossen[3], D.J. Bing[4], and G.D. Turnbull[1]. [1]Crop Diversification Centre North, Agriculture and Rural Development, Edmonton, AB, Canada T5Y 6H3; [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5; [3]Agriculture and Agri-Food Canada (AAFC), 107 Science Place, Saskatoon, SK, Canada S7N 0X2; and [4]AAFC, Lacombe, 6000 C & E Trail, AB, Canada T4L 1W1

Downy mildew, caused by the obligate parasite *Peronospora viciae* (Berk.) de Bary f. sp. *pisi*, causes substantial losses in field pea (*Pisum sativum* L.) crops when environmental conditions are conducive to its development. The distribution of downy mildew from field to field and year to year in central Alberta is highly variable, and reliable assessments of pea resistance are often necessary, in which plants must be inoculated to ensure uniform levels of exposure to the pathogen. Inoculum must consist of viable spores or mycelium of *P. viciae*. Three inoculation methods were compared for their ability to consistently induce symptoms of downy mildew in growth chamber trials with 24 pea cultivars: 1) Seedlings at the 4-leaf stage were inoculated by inserting a 2x3 mm^2 piece of diseased leaf tissue between the bud-leaves of the top shoot; 2) Systemically infected plant tissues were ground to a powder, suspended in distilled water, and then poured (2 mL volume at $2x10^4$ oospores/mL) over each pea seed before planting; and 3) The 2 mL inoculum suspension in 2) was also added to the top soil as a drench after seeding. The plants were rated for disease severity (DS) 2 and 4 weeks after inoculation using a 0-4 rating sale. The mean DS was 0.07, 0.43 and 0.69 on a five-point scale using methods 1, 2 and 3, respectively. Therefore, the 3rd soil drench method appears to be the most reliable for assessing pea resistance to downy mildew.

CPS-22 **Detection of mutagenic secondary metabolites produced by entomopathogen fungus, *Metarhizium robertsii*.** D. Errampalli [1]*, M.C. Gienow[1], T. Mugadza[1] and T. Laengle[2]. [1]Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON Canada L0R 2E0 (e-mail: Deena.Errampalli@agr.gc.ca). [2]Pesticide Risk Reduction Program, Pest Management Centre, Agriculture and Agri-Food Canada, 308 Brookfield Road, PO Box 39088, St. John's, NL A1E 5Y7.

The fungal entomopathogens, *Metarhizium anisopliae* and *M. robertsii* cause fatal mycosis to agricultural arthropod pests. The objective of this study is to determine if any of the secondary metabolites are produced by two isolates of insect pathogenic fungi, *M. robertsii* ARSEF 2575 and *M. anisopliae* BIPESCO 5 were mutagenic. Liquid culture broth was inoculated at a concentration of 2.5 x 10^5 spores/ml of *M. robertsii* ARSEF 2575 and *M. anisopliae* BIPESCO 5 and incubated at 160 rpm at 25C for 8 days. The secondary metabolites produced in liquid culture media by these insect pathogenic fungi were extracted with dichloromethane and ethyl acetate solvents, and concentrated by rotoevaporation. Resulting oily brown residue was dissolved in dimethyl sulphoxide (DMSO) and tested using TA98 and TA100 isolates of *Salmonella typhimurium* in the Ames MPF Penta I microplate format mutagenicity assay. The *S. typhimurium* TA98 detects 2-nitrofluorene (2-NF) while *S. typhimurium* TA100 detects 4-nitroquinoline N-oxide (4-NQO) without S9 (Aroclor-induced rat liver enzymes). Both TA98 and TA100 detect 2-aminoanthracene (2-AA) when tested in the presence of S9 (Aroclor-induced rat liver enzymes) which causes metabolic activation of the mutagenic compounds. The results from the Ames MPF Penta I assay showed that the positive control *M. robertsii* ARSEF 2575 produced two mutagenic metabolites, while *M. anisopliae* BIPESCO 5

tested negative for mutagenic metabolites. The negative control DMSO tested negative. The *M. robertsii* ARSEF 2575 and *M. anisopliae* BIPESCO 5 tested negative for mutagenic metabolites with *S. typhimurium* TA98 in the absence of S9. The negative result for the metabolite using the *S. typhimurium* TA98 tester strain indicates that the mutagens that can be detected by *S. typhimurium* TA98 was not produced by both *Metarhizium* species. All the experiments were repeated four times. The detection of mutagenic metabolites produced by the positive control, *M. robertsii* ARSEF 2575, with the Ames MPFTM Penta I microplate format mutagenicity assay (Xenometrix) suggests that the mutagenic metabolites were produced only by *M. robertsii* ARSEF 2575 but not by *M. anisopliae* BIPESCO 5.

CPS-23 **Relationships between plant phenology and the development of bacterial leaf spot of lettuce.** V. Toussaint, M. Ciotola, A. Dallier, M. Cadieux and G. Bourgeois. Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, St-Jean-sur-Richelieu, Québec, Canada J3B 3E6 (e-mail: Vicky.Toussaint@agr.gc.ca)

In this study, the effect of the growth stage of lettuce (*Lactuca sativa* L.) on the development of the bacterial leaf spot caused by *Xanthomonas campestris* pv. *vitians* (Brown 1918) Dye 1978b (*Xcv*) was investigated. In 2011, three trials were conducted under controlled conditions using a growth chamber equipped with a misting system. Growth stages were obtained by seeding plants (cv. Paris Island Cos) over time, once a week for 5 weeks for first and second trials and 4 weeks for the third one respectively. One week after the last seeding date, the number of leaves were recorded for each plant and then inoculated with a suspension of *Xcv* (strain B07-07) adjusted to 10^8 CFU/mL. Plants were placed in conditions known to be conducive to disease development with a mist settled to spray fine droplets of water 20 sec every 15 minutes. One week after inoculation, symptoms were rated for each leaf of each plant using the Horsfall-Barratt scale. Analysis of variance was conducted to compare disease incidence (percentage of affected leaves per plant) and the non-parametric Kruskall-Wallis test was used to compare disease severity for the different growth stages. The incidence did not significantly differ for the different growth stages amongst trials, but the severity of the affected leaves was higher on older plants than younger ones. The next steps to this study are to elucidate the mechanisms in the lettuce phenology that influence disease development.

CPS-24 **Effect of cover crops as mulches in the development of diseases in Spaghetti squash.** V. Toussaint* and M. Ciotola. Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, St-Jean-sur-Richelieu, Québec, Canada J3B 3E6 (e-mail: Vicky.toussaint@agr.gc.ca)

In a context of sustainable agriculture, the use of cover crops as mulches is gaining in popularity because it promotes soil conservation, increases microbial diversity and activity, reduces weed infestation and was reported to reduce the incidence of some plant diseases. In this study, the impact of cover crops as mulches on diseases of cucurbits was investigated. The study was conducted three times from 2008 to 2010 at the Agriculture and Agri-Food Canada experimental farm in Frelighsburg, Qc. Cover crop plots, rye (*Secale cereale* L.) and wheat (*Triticum* L.), were seeded in a randomized complete block design fashion the preceding fall. The other treatments were conventional tillage cropping (control) and dried mulch using wheat straw. In June, cover crops were destroyed using a roller crimper and herbicides when required. Spaghetti squash (*Cucurbita pepo* L.) seedlings were transplanted in the different treatments. Disease

development, growth and yield were determined for each treatment. In 2008, the disease pressure was high and the percentage of healthy fruits was significantly higher for the rye and wheat treatments (P=0.003; F=13.096). The bacterial disease caused by *Pseudomonas syringae* (van Hall 1902) and scab caused by *Cladosporium cucumerinum* (Ellis & Arthur 1889) were significantly reduced. In 2009 and 2010, the disease pressure was low and the percentage of healthy fruit was equivalent in all treatments. For 2008 and 2009, the number of squash was equivalent in all treatments. In 2010, the number of squash was significantly lower in both rye and wheat treatments compared to the control (P=0.03, F=5.085) and the foliar analysis showed a N deficiency. In conclusion, cover crops can reduce the incidence of diseases in cucurbits; the next steps are to verify how the cover crops act as a disease control method by studying the impact on the microclimate, soil and plant microbiology and on the plant itself.

CPS-25 **Heterobasidion populations in Canada are separated geographically and resemble *H. irregulare* and *H. occidentale* based on sequence analysis of housekeeping genes.** X. Li[1]; S. Shamoun[2]; J. Nie[1]; D.L. Hammill[1]; and S.H. De Boer[1*]. [1]Canadian Food Inspection Agency, Charlottetown Laboratory, Mount Edward Road, Charlottetown, PE, Canada, C1A5T1 (email: sean.li@inspection.gc.ca); [2]Canadian Forest Service, Pacific Forestry Centre, Victoria, BC, Canada V8Z 1M5

Heterobasidion annosum species complex, the causal agent of root and butt rot of coniferous trees, is comprised of five fungal species. *H. annosum, H. parviporum* and *H. abietinum* are widely distributed in European countries while *H. irregulare* and *H. occidentale* occur in different regions of North America. Morphological differentiation among species remains a long standing challenge for classification of these plant pathogenic fungi despite recent progress. In this study, we collected 26 isolates from the provinces of British Columbia and Ontario. Eight housekeeping gene markers were selected for genetic analysis of heterobasidion populations isolated in Canada. Specific gene fragments were amplified and purified, and sequenced for each of the fungal isolates. The targeted genes were transcription factor, glutathione-S-transferase, internal transcribed spacer region, NADH dehydrogenase (subunit 5), elongation factor 1 (α subunit), ATP synthase (subunit 6), glyceraldehyde 3-phosphate dehydrogenase and mitochondrial rDNA insertion element. Phylogenetic analysis of sequences from the 26 isolates along with those from 226 other strains isolated in Europe, Asia, and North America, based on the partial elongation factor sequences, revealed that isolates from British Columbia formed a cohesive cluster resembling *H. occidentale*, and shares high sequence homology with isolates from regions west of the Rocky Mountains, such as California and Idaho in the USA. Another 16 isolates from regions east of the Rocky Mountains exhibited various degrees of sequence variation, and shared a close phylogenetic relationship with *H. irregulare* isolates from Quebec and Ontario in Canada, and Montana, Georgia, and Alabama in the USA. We are currently analysing the sequence data obtained from the additional housekeeping genes of the 26 isolates for multi-loci sequence typing.

CPS-26 **Identification and specific detection of *Pectobacterium wasabiae* associated with blackleg-like disease of potato.** L.J. Ward, S.H. De Boer*, and X. Li. Charlottetown Laboratory, Canadian Food Inspection Agency. 93 Mount Edward Road, Charlottetown, PE, C1A 5T1, Canada

Pectobacterium atrosepticum, the pathogenic bacterium usually associated with the potato blackleg, was readily detected in most potato stems with symptoms of the disease

collected from commercial potato fields in Canada during 2007-2010. However, *Pectobacterium wasabiae* was identified as the sole or companion pectobacterial species detected in some symptomatic stems and tubers. Purported *P. wasabiae* isolates did not grow at 37ºC and did not produce reducing substances from sucrose or have phosphatase activity, but acid production from α-methylglucoside was variable. Sequence analyses of individual and concatenated housekeeping genes (*acnA*, *gapA*, *icdA*, *mdh*, *pgi* and *proA*) by a neighbour-joining algorithm *sensu* Ma *et al.* 2007 (Phytopathology 97:1150-1163) showed that on this basis these strains clearly grouped with the *P. wasabiae* clade which included the type strain of the species, a Japanese isolate from horseradish. A *P. wasabiae*-specific PCR test was designed based on the phytase gene which in blast analyses of Genbank data was shown to have only an 82-89% sequence similarity to analogous gene regions of *P. atrosepticum* and *P. carotovorum*, and only short segment similarities with the genome of *Dickeya* spp. In PCR using primers based on the phytase gene (PhF: GGTTCAGTGCGTCAGGAGAG; PhR: GCGGAGAGGAAGCGGTGAAG) a 100 bp species-specific amplification product was obtained at an annealing temperature of 62ºC. The sequences of cloned PCR products from seven Canadian *P. wasabiae* isolates were identical to the published sequence except for occasional deviation in the number of repeats in a repetitive TC region, which was probably due to sequencing errors common for such repetitive regions. Pathogenicity of *P. wasabiae* isolates on potato was confirmed by stem inoculation and tuber vacuum infiltration experiments conducted respectively, in the greenhouse and a growth chamber. By both methods symptoms induced by *P. wasabiae* were indistinguishable from those induced by *P. atrosepticum*.

CPS-27 **The effect of bacteria on the reproduction and pathogenicity of pinewood nematode (*Bursaphelencus xylophilus*).** S.H. Kim* and M.W. Hyun. Department of Microbiology and Institute of Basic Sciences, Dankook University, Cheonan, Chungnam 330-714, The Republic of Korea (e-mail: piceae@naver.com)

Pinewood nematode (PWN, *Bursaphelenchus xylophilus* (Steiner et Burhrer)) is one of several serious pine pests that cause pine wilt disease. Recently, we isolated and identified a few bacterial species from the nematode that infested Japanese black pine in Korea. To understand their ecological relationships with the nematode, we investigated their effect on the reproduction and pathogenicity of PWN. *Pseudomonas geniculata* and *Serratia nematodiphila* selected from the few isolated bacterial species were used for the investigation. For the reproduction test, wild type PWN, axenic PWN and axenic PWN with the two bacteria were prepared and each of these PWN was inoculated, respectively, onto *Botrytis cinerea* (De Bary) Whetzel mats pregrown in plates containing potato dextrose agar (PDA), and the inoculated plates were then incubated for 7 to 14 days. When compared with wild type PWN, axenic PWN did not reproduce much. However, axenic PWN with *P. geniculata* and *S. nematodiphila* reproduced to about 80% of the level of the wild type PWN reproduction. This result showed that the two bacterial species assisted PWN's reproduction. In a pathogenicity test, axenic PWN itself did not cause wilting symptoms on healthy seedlings of Japanese black pine, but when it was inoculated with *P. geniculata* and *S. nematodiphila,* axenic PWN could generate wilting symptoms on healthy seedlings like wild type PWN did. Our results demonstrate that bacteria have a role in the reproduction and pathogenicity of PWN.

CPS-28 ***In vitro* antagonistic effects of bacteria on the potato late blight-causing agent *Phytophthora infestans*.** P. Audy[1]*, S.M. Boyetchko[2], C. Le Floch-Fouéré[3], and K. Sawchyn[2]. [1]Soils and Crops Research and Development Centre, Agriculture and Agri-Food Canada, Quebec, QC G1V 2J3, Canada (email: Patrice.audy@agr.gc.ca);

[2]Saskatoon Research Centre, Agriculture and Agri-Food Canada, Saskatoon, SK S7N 0X2, Canada; and [3]Institut national de la recherche agronomique (INRA), Agrocampus Ouest, UMR1253, F-35000 Rennes, France.

Late blight of potato (*Solanum tuberosum* L.), caused by *Phytophthora infestans* (Mont.) de Bary, is the world's single most economically important food crop disease with crop losses estimated worldwide at more than $3.0 billion annually. Multiple applications of chemical fungicides are required to control the disease, but the public's demand for environmentally friendly pest control products and preference for pesticide-free foods are driving the need to develop biological control options. Fifty-four bacterial strains, initially selected for *in vitro* screening against two mating types (A1 and A2) of *P. infestans* by measuring zones of inhibition, exhibited various degrees of antifungal activity. Incorporation of bacterial supernatant into agar (50%, v/v) was also used to measure the strength of the inhibition and/or suppression of *P. infestans* by monitoring mycelial growth rate after 7 days. The majority of the bacterial strains exhibited near complete inhibition of mycelial growth of both mating types, despite variable solubility of the secondary metabolites in agar. From these bacteria, *in vivo* tests were conducted with nine strains by dipping detached potato leaves in a 24 h bacterial culture suspension, followed 24 h later by dipping in a suspension of *P. infestans* (1000 zoospores/ml) of each mating type, and incubating in the dark for 6 days. Disease progression on the detached leaves was measure 4, 5, and 6 days post-inoculation. Preliminary results indicated that two bacterial strains delayed the progression of disease by the A1 mating type isolate, while five bacterial strains delayed disease progression by the A2 isolate. These bacterial strains appear to be promising for biological control. These results are remarkable considering that the experimental conditions favored the pathogen and disease progression, including optimum environmental conditions for the disease, susceptibility of the potato cultivar, and pathogen inoculum. Further testing is required to determine optimum conditions for maximizing growth and survival of the bacteria for biological control, including formulation.

CPS-29 **Identification of potential pathogenicity factors and host defense genes in the *Sclerotinia homoeocarpa* – turfgrass pathosystem using transcriptome analysis.** A. M. Orshinsky[1], J. Hu[1], R.C. Venu[2], T.K. Mitchell[1], and M.J. Boehm[1]. [1]Department of Plant Pathology, The Ohio State University, Columbus, Ohio, 43210 (email: Orshinsky.1@osu.edu) and [2]Dale Bumpers National Rice Research Center, Stuttgart, AR, 72160

Dollar spot disease is one of the most predominant and destructive diseases of cool-season turf on golf courses worldwide. Biweekly applications of fungicides are often required to manage the disease, leading to high levels of fungicide resistance to a variety of fungicide classes. To date, research on the dollar spot pathogen, *Sclerotinia homoeocarpa*, has primarily focused on applied management strategies and the genetic structure of populations. There is a large gap in our understanding of the molecular nature of the *S. homoeocarpa* – turfgrass pathosystem. Advances in whole transcriptome shotgun sequencing have made defining specific pathogen-host interactions at the transcriptional level more accessible to research scientists and were utilized in the current study. Six RNA-sequence (RNAseq) libraries were constructed using 454 and SBS sequencing technologies. The libraries included a non-inoculated creeping bentgrass control, *S. homoeocarpa* PDA control, a creeping bentgrass-*S. homoeocarpa* interaction library, and *S. homoeocarpa* grown in liquid broth at 2, 4, and 6 days post inoculation. The RNAseq libraries were used to identify genes and pathways that are likely important

during the dollar spot disease process. The resulting analysis identified 31,830 contigs unique to the interaction library with 7,283 of the contigs of fungal origin and 11,184 contigs of creeping bentgrass origin. Fungal genes of interest that were upregulated in the infection library included those encoding xylanases (up to 485 % increase), polygalacturonases (up to 586 % increase), and various polyketide synthases (up to 671 % increase). Oxalate oxidase (75 % increase) and chitinase (PR1) (134 % increase) were among the creeping bentgrass genes upregulated during fungal infection that likely play a role in plant defense. In the fungal broth culture, genes that were upregulated over the course of a 6 day incubation encoded glyoxyl oxidase (321 % increase) and extracellular, serine-rich proteins (up to 168 % increase), both of which have been associated with pathogenicity of other fungal plant pathogens. This analysis provides an extensive overview of the *S. homoeocarpa*-turf pathosystem at the molecular level, and has identified key genes and pathways that are currently being characterized in more detail.

CPS-30 **Host-parasite interactions in the response of sclerotia of *Sclerotinia sclerotiorum* to freezing and parasitism by *Coniothyrium minitans*.** J.E. Cowan* and G.J. Boland, School of Environmental Sciences, University of Guelph, Guelph, Ontario, Canada N1G 2W1

Sclerotinia sclerotiorum (Lib.) de Bary is a worldwide pathogen of several economically important crops. The small, black sclerotia produced by the fungus enable it to survive adverse environmental conditions, such as Canadian winters. The effects of freezing on sclerotia of *S. sclerotiorum* are not well documented and previous literature conflicts with the high incidence of Sclerotinia diseases in Canada. Our research examined the effects of freezing (-12°C and a 10°C control) on cell damage and carpogenic germination (CG) of sclerotia from two isolates of *S. sclerotiorum*, and how those effects interacted with the mycoparasite *Coniothyrium minitans* Campbell (Contans® WG) in organic soils (Experiment 1). Additionally, sclerotia of nine isolates were cut in half, placed cut-side up in 1% water agar in a controlled environment (22°C with 200 µmol m^{-2} s^{-1} lighting), and evaluated for their rate of re-melanization and susceptibility to *C. minitans* ($3x10^2$ conidia cm^{-2}) before (day 0) and after (day 6) the cut surface re-melanized (Experiment 2). Using a ninhydrin test in Experiment 1, there was an isolate effect (P=0.05) of freezing on damage to sclerotia, with 7% and 0% cell damage occurring in isolates 274 and ZQ35-10, respectively. Regardless, freezing did not reduce CG of either isolate relative to their unfrozen controls. However, freezing damage in isolate 274 increased its subsequent susceptibility to parasitism by *C. minitans*, with CG of the freeze-damaged sclerotia reduced by up to 99% vs. 62% for the unfrozen sclerotia. In contrast, CG of isolate ZQ35-10 was not reduced by *C. minitans*, suggesting resistance to the mycoparasite. In Experiment 2, cut sclerotia of all isolates succumbed rapidly to *C. minitans*; however, both an overall decreased susceptibility and an isolate-specific susceptibility to *C. minitans* became prominent after sclerotia re-melanized. These results suggest that increased susceptibility resulting from freezing or wounding cell damage may be temporary and associated with the melanization characteristics of individual isolates. It appears that only biotic antagonism of sclerotia immediately following seasonal freezing would be capable of exploiting freezing damage in sclerotia, and this effect may be limited to a subset of isolates of *S. sclerotiorum* within a field.

CPS-31 **Suppression of *Sclerotinia* stem rot in soybean by field application of *Bacillus subtilis* strains SB01 and SB24.** J.X. Zhang, A.G. Xue*, and M.J. Morrison. Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, Ontario, Canada K1A 0C6 (allen.xue@agr.gc.ca)

Sclerotinia stem rot (SSR), caused by *Sclerotinia sclerotiorum* (Lib.) de Bary, is a major disease of soybean in Canada. In previous studies, *Bacillus subtilis* strains SB01 and SB24 have been identified as antagonists against *S. sclerotiorum* in suppressing mycelial growth and soybean SSR under controlled conditions. The objective of this research was to determine the efficacy of SB01 and SB24 in suppressing SSR under field conditions, as affected by time between the application of *B. subtilis* strains and inoculation with *S. sclerotioum*. Cell suspensions of the two strains were more effective than the cell-free filtrates, but the effectiveness decreased as the time between the bacterial application in the field and *S. sclerotiorum* inoculation increased. The *B. subtilis* cell suspensions applied on soybean leaves for up to 10 days under field conditions were able to provide a significant ($P < 0.01$) reduction in disease severity by approximately 20 to 90% at 5 days after the *S. sclerotiorum* inoculation. When rated 15 days after inoculation with *S. sclerotiorum*, plants treated with bacterial cells for ≤ 6 days reduced SSR severity by 15 to 70 %. The best effectiveness was provided by the cell suspensions living on soybean leaves for < 3 days under field conditions, which significantly ($P < 0.01$) reduced disease severity by 40 to 70% during 15 days. In comparison, the cell-free filtrates remaining on leaves for < 6 days significantly ($P < 0.01$) reduced disease severity during the first 5 days after the inoculation, while the best cell-free filtrate treatments was those with ≤ 1-day intervals, which significantly ($P < 0.01$) reduced disease severity by 10 to 40% at 15 days after the inoculation. The effectiveness of *B. subtilis* was reduced when it rained after application.

CPS-32 **Compost for organic control of apple replant disease**. G. Braun*, E. Bevis and S.A.E. Fillmore, Agriculture and Agri-Food Canada, 32 Main St., Kentville, NS. Canada B4N 1J5 (Gordon.Braun @agr.gc.ca)

Apple replant disease (ARD) is a serious soil-borne disease managed by soil fumigation in conventional agriculture, but remains a significant problem in organic production systems. Many studies on composts for ARD control have been published but with inconsistent results. In this study, large volumes of compost were equivalent to fumigation with Telone C17 in alleviating symptoms of ARD in 'Honeycrisp' apple trees in two locations. Compost increased trunk cross-sectional area by more than 40%, tree height by up to 20% and branch length by more than 100% in the second year. Hog manure compost (HMC) and municipal waste compost (MWC, household kitchen and garden waste) were equally effective in increasing tree growth in ARD soil. Soil bacterial counts were only slightly reduced by fumigation and remained constant in all treatments over a 16 week period. Fungal population numbers were significantly decreased by fumigation. Bacterial and fungal population numbers were consistently larger in HMC compared to MWC while the fumigated and non-treated control (NTC) soils had the lowest population numbers. Soil respiration was significantly greater in the compost treated soils than the fumigated or NTC. Fumigated soils had the lowest organic matter content, the lowest fungal and bacterial populations, the lowest respiration rates but among the highest tree growth parameters that were equivalent to compost treatments. Nitrogen content was higher in MWC than HMC but leaf nitrogen was highest in the NTC. Phosphorus was double in HMC compared to MWC and phosphorus was greater in leaf samples from HMC treated trees. However, growth responses were equal for HMC and MWC treated trees. Therefore, nutrients or minerals in the compost do not appear to explain the differences in tree growth in response to compost applications. No obvious relationship between soil microbial populations and improved growth response of apple trees in ARD soil could be found. Since the response to compost was not specific to the

type of compost, the physical dilution of root pathogens from the tree rhizosphere with large volumes of compost may have played the most significant role in ARD control in this study.

CPS-33 **Evaluation of dry bean lines for resistance to common bacterial blight.** J.G. Boersma[1*], R.L. Conner[1], P. Balasubramanian[2], C.L. Gillard[3], and A. Hou[1]. [1]Agriculture and Agri-Food Canada, Morden Research Station, Morden MB R6M 1Y5; [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB T1J 4B1; [3]University of Guelph, Ridgetown, ON. N0P 2C0

Common bacterial blight (CBB) caused by the bacterial pathogen *Xanthomonas axonopodis* pv. *phaseoli* (Smith) is a serious seed-borne disease affecting dry bean (*Phaseolus vulgaris* L.) production throughout the world. The bacteria attacks all plant aerial parts, first causing water soaked lesions on the plant leaves and later infecting pods and seeds. Infected seeds may exhibit a brown to butter-yellow discoloration or be small and shrivelled, resulting in poor marketability. One way of controlling CBB is to breed resistant varieties. To date this has largely been conducted by screening of field-inoculated plants for those displaying the least symptoms i.e., little or no leaf and pod lesions, since leaf disease and seed infection rates tend to be highly correlated. Seed discoloration is rarely if ever examined when breeding for CBB resistance. In two recent trials conducted at Morden it was found that the level of leaf disease was not always indicative of the level of seed infection. For instance, the cultivar 'Envoy' is reputed to be more susceptible to CBB than the cultivar 'Navigator' on the basis of incidence and severity of CBB on the leaves. However, our trial results showed that even though 'Envoy' had equal or higher levels of leaf disease incidence (70%) than 'Navigator' (68%), the percentage of diseased seeds was only half (18%) that of 'Navigator' (36%). Similar trends were seen in a backcross population derived from a cross between 'OAC Rex' and 'Morden003'. In this population, leaf disease incidence ranged from 5 – 40%. The minimum number of diseased seed gradually increased over this interval from approximately 3% at 10% leaf disease incidence to 5% at 40% leaf incidence. The maximum number of diseased seed was approximately 13% across most of this range. Two exceptions at 15% and 20% leaf disease incidence had diseased seed numbers exceed 15%. Further investigations are underway.

CPS-34 **Diversity of rare and novel bioactive compound producing actinomycetes in mangrove plant rhizosphere.** I. Ara[1,2*], M. A. Bakir1[2], T. Kudo[2]. [1]Department of Botany and Microbiology, King Saud University, Riyadh, Saudi Arabia (e-mail: ismetara@yahoo.com); [2]Microbe Division / Japan Collection of Microorganisms, RIKEN BioResource Center, 2-1 Hirosawa, Wako, Saitama 351-0198, Japan

Mangroves, the coastal equivalent of tropical forests on land, and also called "salt water forests", have provided livelihood for a lot of local people of Bangladesh. The survival of environmental isolates of filamentous actinomycetes introduced with the mangrove plants in the rhizosphere was studied. The diversity of rare actinomycetes in the mangrove ecosystem were analysed from rhizosphere soil samples of *Rhizophora* sp., *Avicennia* sp. and *Sonneratia* sp. A total of 500 strains were isolated from 20 mangrove plant rhizospheres and distribution of rare actinomycetes was varied in each soil sample. In this study, *Micromonospora* (37.7%) was the dominant genus in almost all the tested soil samples including other genera *Actinomadura* (17.2%); *Microbispora* (8.6%); *Nocardiopsis* (3.7%); *Catellatospora* (3.7%); *Streptosporangium* (3.3%); *Nonomuraea* (2.4%); *Sphaerisporangium* (2.4%); *Rhodococcus* or *Gordonia* (1.6%); *Nocardia* (1.6%);

Saccharomonospora (1.2%); *Nonomuraea* or *Actinomadura* (1.2%); *Luedemannella* (1.2%); *Virgisporangium* (0.8%); *Catellatospora* or *Virgisporangium* (0.8%); *Actinoplanes* (0.8%); *Longispora* (0.4%); *Krasilnikovia* (0.4%); *Pseudosporangium* (0.4%) and unknown actinomycetes (10.6%) were observed. Further, the polyphasic taxonomic studies of 22 unknown isolates indicated that the 15 strains were proposed as new species which belonged to the genera *Micromonospora*, *Catellatospora*, *Nonomuraea*, *Actinomadura*, *Microbispora*. Among the unidentified rare actinomycete isolates, 4 novel genera were also proposed as *Luedemannella* gen. nov., *Krasilnikovia* gen. nov., *Pseudosporangium* gen. nov., in the family *Micromonosporaceae* and *Sphaerisporangium* gen. nov., in the family *Streptosporangiaceae*. A number of selected actinomycete isolates have been examined with regard to their ability to produce antimicrobial compounds. This study provides further evidence of significant biodiversity of actinobacteria in mangrove habitats, revealed by previous studies, and suggests that new strains from the mangrove rhizosphere soils of Chittagong, Cox`s Bazar, Bangladesh might represent a valuable source of biologically active compounds with antimicrobial activity. Further, the presence of rare actinomycetes in the mangrove ecosystem could pave the way for the establishment of disease free mangrove seedlings in the nursery and in the field. Efforts also have been undertaken to find out the bioactive potential of mangrove rhizosphere actinomycetes for the treatment of dreadful human diseases.

CPS-35 **High-throughput isolation of glyphosate-degrading bacteria from agricultural soil and monitoring degradation of glyphosate in bacteria-enriched soil using LC-MS/MS.** X. Yang*, K. Wang, and G. Patterson . A&L Biologicals, Agroecology Research Services Centre, 2136 Jetstream Road, London, Ontario, Canada N5V 3P5

Glyphosate, commonly known as Roundup, is the world's most extensively used herbicide in the control of grasses and herbaceous plants. This broad-spectrum herbicide can be systematically transferred throughout the plant after spray application on plant shoots, resulting in high levels of residues in food and animal feed or being released into the rhizosphere and bound onto soil particles. Glyphosate is not only poisonous to animals acutely and chronically, but is also detrimental to plants and environments through direct toxicity or indirectly altering microbial community dynamics or reducing micronutrient availability. To decontaminate soils and feeds contaminated with glyphosate, we developed a high-throughput method for isolation of bacterial strains from agricultural soil for efficient degradation of glyphosate herbicide. Twenty soil samples from different agricultural fields heavily polluted with glyphosate were initially screened for the presence of glyphosate-degrading bacteria by monitoring degradation level of glyphosate using LC-MS/MS. Glyphosate-degrading bacteria were then isolated based on LC-MS/MS analysis of pooled cultures on a selective medium with glyphosate as the sole phosphorus source from the identified soil. Further chemical characterizations associated with glyphosate degradation efficiency of the bacterial isolates are in progress.

CPS-36 **Potential of *Ascocoryne sarcoides* to immunize *Picea mariana* against root decay**. M.T. Dumas[1*], A.M. Dumas[2] and N. W. Boyonoski[1]. [1]Natural Resources Canada, Canadian Forest Service – Great Lakes Forestry Centre,1219 Queen Street East, Sault Ste. Marie, ON P6A 2E5 and [2]ETH Zürich, Laboratorium Für Organische Chemie, Wolfgang-Pauli-Str.10, 8093 Zürich, Switzerland

Ascocoryne sarcoides (Jacquin ex S.F. Gray) Groves and Wilson is a fungal endophyte which inhibits the growth of decay fungi. A seed coating method was developed to introduce inhibitory strains into *Picea mariana* (Mill.) BSP seedlings prior to planting.

The mode of action of *A. sarcoides* appears to be through the production of antifungal compound(s). To date polyporic acid has been tentatively identified as one of the compounds produced by *A. sarcoides*.

CPS-37 **Enhanced gene replacement frequency in *KU70* disruption strain of *Stagonospora nodorum*.** J. Feng[1]*, W. Li[2], S. F. Hwang[1], B. D. Gossen[3], and S. E. Strelkov[4]. [1]Crop Diversification Centre North, Alberta Agriculture and Rural Development, Edmonton, AB, Canada T5Y 6H3 (e-mail: sheau-fang.hwang@gov.ab.ca); [2]Yunnan Academy of Agricultural Sciences, Kunming, Yunnan, P. R. China 650223; [3]Agriculture and Agri-Food Canada, Saskatoon, SK, Canada S7N 0X2; and [4]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5

To improve the efficiency of gene disruption in *Stagonospora nodorum* (Berk.) E. Castell. & Germano, the putative *KU70* gene encoding the Ku70 protein involved in the nonhomologous end-joining double DNA break repair pathway was identified and deleted. The *KU70* disruption strain showed no apparent defect in vegetative growth, conidiation and pathogenicity on wheat and barley compared with the wild-type strain. The effect of the absence of *KU70* on gene replacement frequency was tested by disruption of *TOXA* encoding toxin A and *LIP2* encoding a putative lipase. Frequency of gene replacement for both genes was dramatically increased in the *KU70* disruption strain, compared with the low frequency in the wild-type recipient.

CPS-38 **Avirulence genes of the soybean root rot pathogen *Phytophthora sojae*.** D. Qutob and M. Gijzen*. Agriculture and Agri-Food Canada, London, Ontario, Canada, N5V 4T3 (e-mail: mark.gijzen@agr.gc.ca)

Root rot of soybean caused by *Phytophthora sojae* was first discovered in the 1950s in Ontario and the mid-western USA. Since then the disease has been reported in all major soybean growing regions throughout the world. Management of the disease relies in part on the development and proper deployment of soybean varieties with cultivar-specific resistance traits. Strain-specific virulence in *P. sojae* is controlled by avirulence (*Avr*) genes that interact with cultivar-specific resistance (*Rps*) genes in soybean. We have recently identified the *P. sojae Avr* genes *Avr1a*, *Avr3a*, *Avr3c*, and *Avr5*. All of these *Avr* genes encode so-called RxLR effector proteins that are targeted for delivery into host cells. We have shown that *Avr3a* and *Avr5* from *P. sojae* represent a single gene, *Avr3a/5*. This highly polymorphic locus displays copy number variation (CNV), sequence polymorphisms, and transcriptional differences among *P. sojae* strains. Transcriptional differences among strains are sufficient to account for virulence differences on *Rps*3a but not on *Rps*5, as there are *P. sojae* strains that express *Avr3a* but are virulent on *Rps*5. In *P. sojae* strains with differential virulence towards *Rps*3a and *Rps*5, it is variation in amino acid sequence within the effector domain of Avr3a/5 that determines recognition by *Rps*3a or by *Rps*5. We also found that the *Avr1a* and *Avr3c* genes occur in tandem arrays of duplicated DNA segments. Comparison of *P. sojae* strains indicates there is copy number variation for *Avr1a* and *Avr3a*, whereas *Avr3c* did not display CNV but showed evidence of sequence exchanges between adjacent copies. Gain of virulence mutations for *Avr1a* included gene deletions and transcriptional polymorphisms, while amino acid changes were sufficient to account for virulence differences determined by *Avr3c*. We expect that the identification of *P. sojae Avr* genes will find practical application, by providing new tools for breeding and disease management in soybean, which is among the largest crops on the globe.

CPS-39 **Efficacy of fungicides to reduce the impact of Sclerotinia head rot in sunflower**. K.Y. Rashid. Agriculture and Agri-Food Canada, Morden Research Station, Unit 100-101 Route 100, Morden, MB R6M 1Y5, Canada

Sunflower (*Helianthus annuus* L.) is a major crop in the USA and Canada and is grown on about 1 million ha in the USA and 100,000 ha in Canada. Head rot and mid-stem rot caused by ascospore infections of *Sclerotinia sclerotiorum* (Lib.) de Bary, are major diseases affecting sunflower in North America and worldwide. In Manitoba, 50-90% of sunflower crops are affected annually, and yield reduction is estimated at 10-20% in most years, and up to 80% in some fields. Field trials were conducted to study the efficacy of 18 fungicides on reducing the disease severity of head rot using artificial inoculation with ascospores under a misting system to ensure infections and disease development. Several fungicides were effective in significantly reducing disease incidence by up to 50- 80% and significantly improved yield by up to 40-100% of the diseased control treatment. Fungicide application at flowering was more effective than after flowering, and two fungicide applications were more effective than one.

CPS-40 **New races of *Plasmopara halstedii* causing sunflower downy mildew in Manitoba**. K.Y. Rashid. Agriculture and Agri-Food Canada, Morden Research Station, Unit 100-101 Route 100, Morden, MB R6M 1Y5, Canada

Sunflower (*Helianthus annuus* L) is grown in western Canada on 80,000 ha mainly in Manitoba. The confection types are for in-shell and de-hulled kernels, while the oilseed types are mostly for the birdfeed market. Downy mildew (DM) caused by the fungus *Plasmopara halstedii* (Farl.) Berl. & De Toni is a major disease affecting sunflower worldwide. DM affects 15-80% of sunflower crops annually in Manitoba causing an estimated 10-20% yield reduction in most years, and up to 40% in some crops. Isolates of *P. halstedii* were collected from infected plants from sunflower fields between 2005 and 2010, and tested on 9 differential sunflower lines to identify the prevalent races. New race-groups 700 and 300 were more frequently collected than the 100 and 500 race groups traditionally reported in Canada. The specific races 720, 730 and 770 were very frequent over the last few years, and are virulent on most commercial sunflower hybrids grown in Canada.

CPS-41 **First report of *Fusarium equiseti* as the causal organism of cumin wilt disease in India.** S. R. Suthar[1] and P. N. Bhatt[2]. [1]Department of Biotechnology, P. S. Science and H. D. Arts College, kadi-382517. KSV University, Gujarat, India; and [2]Sun Agrigenetics P. Ltd, Vadodara, India. (E-mail:-ram_v2@yahoo.com)

Cumin (*Cuminum cyminum*) is an important spice in the world. Cumin is highly beneficial as anti-fungal, liver protection, DNA protection, powerful antioxidant, anti-cancer agent, brain and nerve booster, digestion. Wilt of cumin disease generally appears in patches and is characterised by wilting of affected plants. After the appearance of wilting, the whole plant dries up. In January 2009 and 2010, 324 samples (wilted plants) were collected from different areas of Gujarat. Total of 108 cumin fields in 25 locations of 7 districts were sampled during disease season. Isolations from the roots and stems of diseased plants yielded fungus characterised by the development of abundant white aerial mycelium which turns pinkish by keeping in daylight on potato dextrose agar medium. The colonies produced macro- and micro-conidia within 3-4 days at 25 ±2 °C. Microconidia are single-celled, hyaline, non-septate and ovoid. Macroconidia are 2-3 septate, straight or slightly curved at apex. The size of macro-conidia was in the range of

28.0-30.5 × 3.5-5.25 µm and the micro-conidia were in the range of 9.5-12.5 × 3.5-5.25µm. The pathogen culture was identified on the basis of colony and spore morphology as *Fusarium* and the identification was confirmed by the Fungal Identification Service, Mycology and Plant Pathology Group, Agharkar Research Institute, Pune. The culture was deposited under accession number NFCCI 2157. Our findings were confirmed NFCCI 2157 showed 99% sequence similarity with genus *Fusarium* Link (1809) species *F. equiseti* (NCBI Accession HM130559.1). For pathogenicity tests, sterilized soil was inoculated with conidial suspension (10^5 conidia of *F. equiseti* per ml of distil water) obtained from 7-days old fungal culture in 10 pots, followed by planting of one month old healthy cumin plants in each pot. Five pots with uninoculated plants served as controls. All pots were placed in a moist chamber at 25 ±2 °C. Every inoculated plant showed symptoms within 10-12 days and on re-isolation yielded the original fungus. The control plants remained healthy. Cumin wilt disease is caused primarily by *Fusarium oxysporum* but other *Fusarium* species have been implicated. This is the first report of wilt of *C.cyminum* caused by *F. equiseti* in India.

CPS-42 **Effect of Salt Solutions on Control of Fungal Diseases in Lettuce** (*Lactuca sativa* L.) **Plants.** H. M. El-Nabi [1], E. M. El-Far[2],and S. Ragab[2]. [1] Suez Canal University, Faculty of Agriculture, Ismailia,Egypt**;** and [2] Plant Pathology Research Institute, Agricultural Research Center, Giza, Egypt

Lettuce (*Lactuca sativa* L.) is one of the most important leafy vegetables in Egypt. Lettuce is cultivated for its high nutritional value (vitamin A, B_1, B_2 and C) as well as calcium and iron. Lettuce is subject to stand injury and yield loss due to fungal diseases such as a white mould (*Sclerotinia sclerotiorum*), gray mould (*Botrytis cinerea*) and downy mildew (*Bremia lactucae*). Different concentrations of six mineral salts (sodium bicarbonate, calcium chloride, calcium sulfate, potassium sulfate, mono-potassium phosphate, and dibasic potassium phosphate) were investigated to evaluate their ability to reduce the severity of fungal diseases. The experimental material was comprised of two cultivars of lettuce namely 'Romaine' and 'Balady'. Experiments were implemented under greenhouse conditions. Two cultivars of lettuce plants treated with potassium sulfate, calcium chloride, and sodium bicarbonate appeared more tolerant to all tested fungal diseases coupled with high level of enzymes in plants specially polyphenoloxidase and peroxidase.

CPS-43 **Field performance of *Brassica napus* L. spring canola hybrids with improved resistance to Sclerotinia stem rot.** Igor Falak[1], Winnie McNabb[2], [1]Pioneer Hi-Bred Production LP, Spring canola breeding, Caledon, Canada, [2]Pioneer Hi-Bred Production LP, Spring canola breeding, Carman, Canada

Sclerotinia stem rot (SSR) is an important disease of spring canola caused by *Sclerotinia sclerotiorum (Lib.) de Bary*. Foliar fungicides are applied to manage this disease with variable success despite the use of disease forecasting checklists and improved fungicide products. The first canola hybrid with improved field resistance to SSR developed by Pioneer Hi-Bred was Pioneer Brand ® 45S51 registered in 2008. A further improved hybrid, Pioneer Brand® 45S52, was registered in 2010. SSR testing of 45S51 was conducted in both large scale on farm trials under natural field conditions and in small replicated research yield plots at multi-locations exposed to either artificial or natural inoculum and in some cases were irrigated to stimulate disease development. Fungicide efficacy comparisons were instituted to determine a fit of such genetics in the market. The main objective of these studies was to quantify SSR reaction and yield of resistant

and susceptible canola products as well as compare results to plot trial results. A second objective was to quantify the impact of fungicide efficacy on SSR and yield. Data on disease incidence and disease severity were collected from which a disease index calculation SSFS (Sclerotinia sclerotiorum field severity) was performed. Extensive field testing of 45S52 was initiated in 2008 research trials. Large scale on farm trials over four years in Western Canada indicated a >50% overall reduction of SSFS in 45S51 vs. susceptible canola products. Field resistance was a function of reduced disease incidence and disease severity. Research plot trials under semi-natural conditions showed a similar reduction of SSFS in 45S51. While 45S51 field resistance did not match efficacy of fungicide control in the field, field resistance of 45S52 was notably higher. The best control of Sclerotinia was attained by applying fungicide on products with improved Sclerotinia resistance. Genetic resistance has benefits stretching from the farm level, pest management programs, fungicide efficacy and further.

CWSS-1 **Weed suppression and soil nitrogen benefits associated with legume cover crop-winter wheat intercrops.**R. E. Blackshaw* and J. R. Moyer, Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada T1J 4B1.

There is increasing interest in including legume cover crops in cropping systems to reduce fertilizer inputs and improve soil quality. A multi-year field study was conducted to determine the benefits of establishing alfalfa (*Medicago sativa* L.), red clover (*Trifoliumpratense* L.), and Austrian winter pea (*Pisumsativum* L.) cover crops in fall or in spring with winter wheat (*Triticumaestivum* L.). Spring-planted legumes emerged well within the winter wheat crop but their growth was limited by the already established wheat crop under these semi-arid conditions. Fall-planted red clover experienced severe winter kill in two of three experiments and thus had limited productivity. Fall-planted winter pea survived the winter and was very productive but winter wheat yield was reduced by 23 to 37% compared to monoculture winter wheat. However, fall-planted alfalfa exhibited excellent winter hardiness, suppressed weed growth without negatively affecting winter wheat yield, and contributed an extra 40 kg ha^{-1} of available soil N to the following spring canola (*Brassica napus* L.) crop. This resulted in fall-planted alfalfa increasing the yield of succeeding canola in two of three experiments. Further research is needed under a wider range of environmental conditions to better understand the agronomic and economic benefits of alfalfa-winter wheat intercrops in western Canada.

CWSS-2 **An investigation into cultural approaches for weed control in pesticide-free home lawns.** K.L. Dodson[1*], F.J. Tardif[1], E.M. Lyons[1], K.S. Jordan[1].[1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario Canada N1G 2W1

In Ontario traditional pesticides are not permitted on home lawns. Without the use of pesticides, a greater emphasis must be placed on cultural practices to maintain healthy turfgrass swards. A renovation study and a species transition study are being conducted to determine how cultural practices impact plant species composition and weed pressure in simulated home lawn environments at the Guelph Turfgrass Institute. The renovation study includes renovation techniques, and post-renovation maintenance practices. Renovation methods without the use of pesticides were performed both in the spring and fall. The four treatments are aeration, roto-tilling, scalping, and seeding into an existing lawn. Post renovation practices include fall core aeration, spring power raking, fall core aeration + spring power raking, a positive herbicide control of 2,4-D / dicamba /mecoprop, and a negative control of no maintenance practices. The various lawn maintenance methods are being performed in conjunction with overseeding. Renovation in the spring increases the number of annual weeds in the roto-tilled plots, while fall roto-tilling has no annual weeds present. Overall weeds are initially reduced by renovation practices. The species transition study is examining how seeding of various turfgrass mixtures, combined with varying irrigation and fertility treatments, will affect species composition and weed pressure. Plots were seeded in May 2010 and May 2011, and irrigation is being added at two frequencies when weekly precipitation rates are <2.5 cm to the irrigated plots. We are also testing the effects of adding typical home lawn fertilizers to half the plots in fall 2010 and spring 2011. The plots that received fertilizers have faster spring green-up, and better overall quality than the non-fertilized plots. Within non-irrigated plots, overseeding with a high percentage of fine fescue resulted in

lower weed totals than other overseeding treatments. Plots receiving irrigation once a week had the highest percentages of total weeds compared to non-irrigated plots and plots irrigated lightly three times a week.

CWSS-3 **Velvetleaf responses** to **temperature and light quality.**K. Slauenwhite[1*] and M. M. Qaderi[1]. Department of Biology, Mount Saint Vincent University, Halifax, Nova Scotia, Canada B3M 2J6

Few studies have considered the combined effects of temperature and light quality on weed growth and physiology. We determined the interactive effects of light quality and temperature on growth and some physiological properties of velvetleaf (*Abutilon theophrasti* Medic.) plants grown in controlled-environment growth chambers. One-week-old seedlings, grown from seeds, were subjected to two temperature regimes (24/20^{o}C and 30/26^{o}C, day/night) and three light qualities (white, as control; higher red: far red and lower red: far red) for two weeks. We measured stem height and diameter; leaf number, area and moisture; leaf, stem and root dry mass; and growth index. We also measured carbon dioxide assimilation, chlorophyll fluorescence, photosynthetic pigments and ethylene evolution. Anatomical features of stem and root transverse sections were examined by microscopy. Overall, higher temperatures increased root mass, but decreased shoot: root ratio, water use efficiency, and chlorophyll *a:b* ratio. Plants were taller under both lower and higher red: far red than under white light. All plant parts had greater mass under white and higher red: far red than under lower red: far red. Both lower and higher red: far red lights decreased specific leaf weight and leaf mass ratio, but only lower red: far red increased leaf area ratio and shoot: root ratio. Net carbon dioxide assimilation decreased under lower red: far red light. Both lower and higher red: far red decreased chlorophyll *a*, chlorophyll *b*, carotenoids and total chlorophyll, and only lower red: far red reduced chlorophyll *a:b*. Although temperature and light quality significantly affected some plant properties, no significant interactions of these factors were found.

CWSS-4 **Development and evaluation of a green ratio based algorithm for the detection of weeds in mowed wild blueberry fields.** Y.K. Chang[1]*, Z. Qamar[1], T. Esau[1], A. Schumann[2] and D. Percival[3], [1]Nova Scotia Agricultural College, Truro, Nova Scotia, Canada, B2N 5E3, [2]Citrus Research and Education Centre, University of Florida, Lake Alfred, FL, USA, 33850 and [3]Environmental Sciences Department, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada, B2N 583

A weed detection algorithm was developed and evaluated for spot-specific agrochemical delivery in mowed wild blueberry fields with the aim of reducing the cost of agrochemicals and environmental contamination. Clear green contrast between weed and other areas was used to develop a robust and effective algorithm. A custom built C++ program was made to acquire images from µEye-1220SE cameras mounted in front of an all-terrain vehicle (ATV). Exposure time and digital gain were automatically controlled by auto exposure shutter /auto gain control (AES/AGC) to adjust for variable outdoor light conditions (> 50 µm-2s-1) during image acquisition. Maximum auto exposure shutter was set to 4 ms to prevent image blurring. MATLAB® Image Processing Toolbox was used for image processing including converting the 24-bit Red-Green-Blue (RGB) images to normalized green ratio images, segmentation by threshold values, and counting over-threshold pixels. Optimum threshold value and number of over-threshold pixel were investigated. Green ratio based algorithm was compared with excessive green index algorithm. The green ratio algorithm was evaluated with visual inspected images taken from different field situations. Results will be presented in the paper.

CIFST-1 **Apple peel extracts as inhibitors of lipid oxidation in a meat model system.** P. Kathirvel and H.P.V. Rupasinghe. Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Apple peel, a by-product of the apple processing industry is a natural source for the extraction of polyphenolic antioxidants. The efficacy of apple peel extracts in inhibiting lipid oxidation in comminuted muscle model systems remains unexamined. In this study, mechanically separated chicken (MSC) was used as a meat model system to examine the effect of antioxidants on the kinetics of lipid oxidation. MSC contains high amounts of heme and unsaturated fatty acids that makes it particularly susceptible to lipid oxidation. In this study, we compared the effectiveness of two ethanolic apple peel extracts (0.1% APE 1 (crude extract) and 0.1% APE 2 (sugar removed)) in inhibiting lipid oxidation in MSC with comparison to synthetic antioxidant mixture (200 ppm BHT and BHA) mixture and 0.1% natural rosemary extract. The most abundant flavonoids determined by LC/MS in APE 1 and APE 2 were quercetin-3-*O*-galactoside, quercetin-3-*O*-rhamnoside and (–)-epicatechin, but the total phenolic content in APE 2 was 105 times higher than that of APE 1.The antioxidants mixed MSC samples were stored at 6°C and the lipid oxidation was determined at 0, 2, 5, 8 and 10 days. When thiobarbituric acid reactive substances (TBARS) assay was used to determine the levels of secondary lipid oxidation products in MSC during storage, incorporation of APE 2 in MSC was effective in inhibiting TBARS formation compared to the control and APE 1 ($p<0.001$). The differences in the antioxidative ability of the apple peel extract in MSC could be attributed to the high phenolic content of the extracts. Also, the inhibition of lipid oxidation in MSC by APE 2 was similar to the synthetic BHA/BHT mixture and rosemary extract. Thus, APE 2 has a great potential to be used as a natural food antioxidant in meat systems and could be of significant interest to the meat industry as well as the consumers.

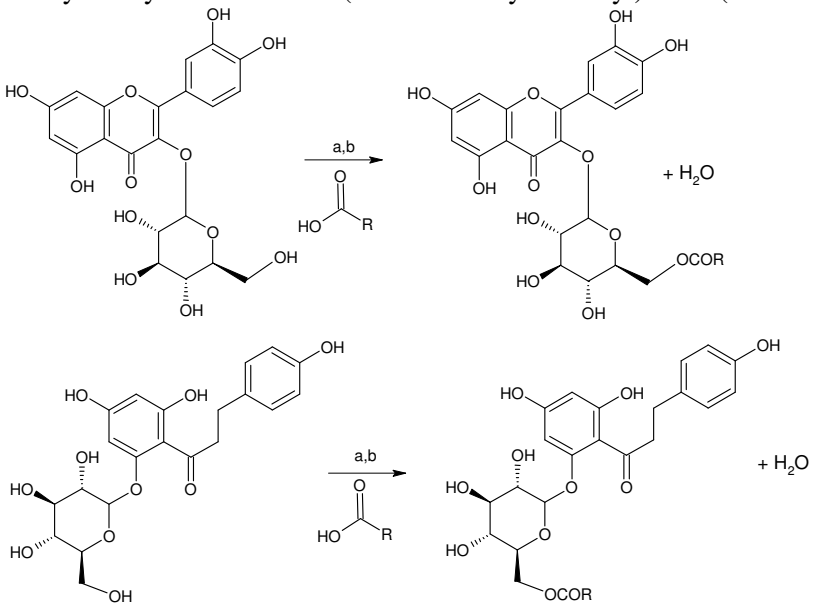
CIFST-2 **Effect of Acidification on Quality and Shelf-life of Carrot Juice.** L. J. Yu[1*], and H.P. V. Rupasinghe[1]. [1]Department of Environmental Sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, Canada B2N 5E3

Acidification is a practical method to extend the shelf-life of fruit and vegetable juices. This study compared the effects of different acidification methods: blanching of carrot with 2 to 4 mg kg^{-1} of citric acid, 2 to 4 mg kg^{-1} of lactic acid and blending carrot juice with cranberry juice in the 80:20 and 70:30 ratios on the quality in terms of pH, TA, total soluble solids (TSS), turbidity, ferric reducing antioxidant power (FRAP) and beta-Carotene, and shelf-life of carrot juices in terms of total aerobic count (TAC). Water blanched carrot juice was selected as the control instead of untreated carrot juice because blanching is the necessary processing step for carrot juice processing. During the 21-day storage, the pH, TA, TSS and turbidity values were much more stable for all acidified juices than water blanched juices. The highest stability and value of antioxidant capacity (FRAP value) belonged to carrot-cranberry juice blends in 70:30 ratios compared with water blanched juices after the 21-day storage. For beta-Carotene results, carrot-cranberry juice blends in 80:20 ratios and water blanched juices gave the maximum stability compared with other juice samples. However, the highest beta-Carotene value on day 21 belonged to 4 mg kg^{-1} of lactic acid blanched juices. All acidification methods could

effectively prolong the shelf-life of juices in terms of TAC value. Blanching with 4 mg kg^{-1} of lactic acid and 4 mg kg^{-1} of citric acid were among the most effective methods for expending the shelf-life of carrot juices.

CIFST-3 **Enzymatic Esterification of Flavonoids With Fatty Acids in Organic Solvents/Room Temperature Ionic Liquids.** Ziaullah*, H.P. Vasantha Rupasinghe, and Emily Fraser, Tree Fruit Bio-Product Research Laboratory, Department of Environmental sciences, Nova Scotia Agricultural College, Truro, Nova Scotia, B2N 5E3

Our present investigation describes the regioselective enzymatic acylation of Phloridzin and Quercetin-3-glucoside in high yields with different long chain saturated, mono- and poly-unsaturated fatty acids using immobilized lipase B from *Candida antartica* (Novozym 435^{R}) in acetone at 45 ^{o}C as well as in room temperature Ionic liquid (Trioctylmethylammonium bis(trifluoromethyl sulfonyl)imide ($TOMATF_2N$) at 60 ^{o}C.



a) Acetone, 4 ^{o}MS, Novozyme 435, 45 ^{o}C, stirring, 2-days

b) RTIL, 4 ^{o}MS, Novozyme 435, 60 ^{o}C, stirring, 24 h

R= Oleic, Stearic, Linoleic, Linolenic, Eicosapenataenoic, Docosahexaenoic Acids

The synthesized esters will be evaluated for their different biological activities such as antioxidant, antihypertensive, cytotoxicity etc[1-4].

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Notes

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