

Macrofungal Diversity in Successional Douglas-fir Forests

Robert E. Countess, Bryce Kendrick, Department of Biology,
University of Victoria, P.O. Box 3020 Stn. CSC, Victoria, British
Columbia, Canada, V8W 3N5

and

J.A. Trofymow, Pacific Forestry Centre, Canadian Forest Service,
Natural Resources Canada, 506 West Burnside Road, Victoria, British
Columbia, Canada, V8Z 1M5

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Natural Resources Canada
Canadian Forest Service
Pacific Forestry Centre
506 West Burnside Road
Victoria, British Columbia
V8Z 1M5
Canada

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Robert E. Countess, Bryce Kendrick, Department of Biology, University of Victoria, P.O. Box 3020 Stn. CSC, Victoria, British Columbia, Canada, V8W 3N5

and **J.A. Trofymow**, Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada, 506 Burnside Road West, Victoria, British Columbia, Canada, V8Z 1M5

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Introduction

Currently in British Columbia, old-growth forests are being cut down and replaced with managed forests that will be harvested when they are mature; i.e. the managed forest will never reach the old-growth stage. An entire stage in the life-cycle of the forest is being eliminated with potentially devastating effects on biodiversity and ecosystem functioning. Only 45 % of the mature old-growth forest on Vancouver Island remains (BCMOF 1991). We must strive to understand the impacts of forestry before these reservoirs of biodiversity are lost.

Macrofungi are essential to forest ecosystems as nutrient-cyclers and mycorrhizal symbionts of the trees, yet the macrofungi of British Columbia are poorly characterized (Redhead 1997) and the impacts of forestry on macrofungal diversity have been little studied. The primary objective of this study is to determine these impacts by characterizing the macrofungal diversity on three east Vancouver Island (CWHxm) chronosequences (Trofymow et al. 1997) each containing stands of four age classes: regeneration (mean age=10 years), immature (mean age=44 years), mature (mean age=95 years), and old growth (mean age=288 years). Some preliminary findings are reported in this abstract.

Methods

Macrofungal sporocarps were sampled monthly on 20 quadrats, each 4 x 4 m per sere per site. The quadrats were spaced 4 m apart along a pre-existing brushed trail in the shape of a 40-m square. In the fall of 1995 the South Vancouver Island Mycological Society conducted a survey on these same trails. Monthly sampling for this study began in October 1996 and continued until November 1997 except for December through February. Sporocarps greater than 2 cm (cap diameter for agarics) were sampled on the 4x4-m quadrats and

macrofungi smaller than 2 cm and as small as 3 mm were sampled on 1.25x1.25-m quadrats nested within the larger quadrats. The number of sporocarps of each taxon was estimated and the substrate noted. The presence of a taxon in a quadrat was considered as a single occurrence or fruiting for diversity calculations, regardless of the number of sporocarps. Specimens that could not be identified in the field were collected and taken to the lab where they were stored at 4°C until identified. Specimens were identified to genus and to species, when possible, according to the available literature. Voucher specimens will be deposited at the Pacific Forestry Centre.

Results and Discussion

From the period of October 1996 to November 1997 over 5300 observations of macrofungal sporocarps were made and 362 species of macrofungi from 124 genera were identified, some tentatively. Many species will be new records for British Columbia and/or Vancouver Island. The most abundant genera were *Mycena* (795 occurrences), *Cortinarius* (692), *Russula* (443), *Inocybe* (312) and *Lactarius* (235). *Mycena* is a genus of saprotrophic, primarily litter decomposing agarics, and the other four genera are all almost exclusively ectomycorrhizal. Figure 1 shows the diversity trends across seral stages in terms of genus richness with data from all months from March to November 1997 pooled. Genus richness drops markedly from the old growth (mean=50) to the regeneration age (mean=27) but returns to pre-harvesting levels in the immature (mean=51) and mature (mean=47) ages. Only the regeneration is significantly different from the old growth ($p < 0.05$) using Tukey's post-hoc comparisons. The abundance data for the same period show a similar pattern (Figure 2) and again only the regeneration is significantly different from the old growth ($p < 0.05$) using Tukey's post-hoc comparisons. Fungi have excellent dispersal ability due to their airborne spores and the

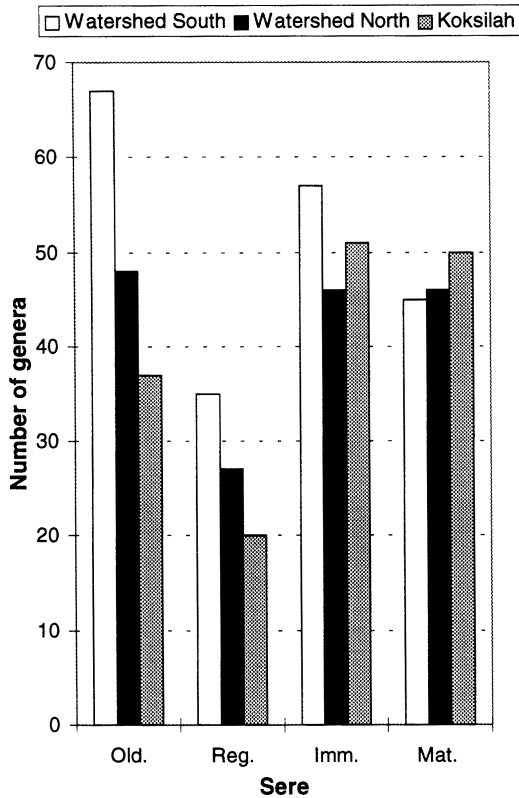


Figure 1. Macrofungal genus richness by site and seral stage for three Vancouver Island chronosequences in the CWHxm biogeoclimatic subzone.

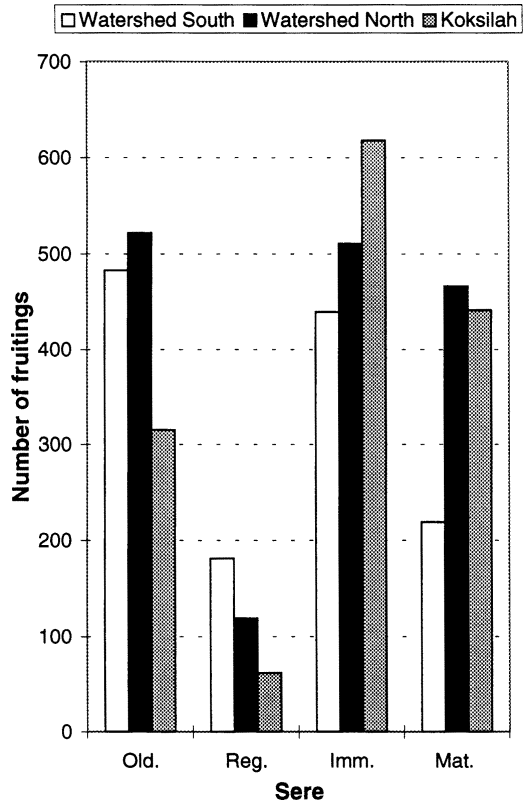


Figure 2. Macrofungal abundance by site and seral stage for three Vancouver Island chronosequences in the CWHxm biogeoclimatic subzone.

return in diversity in the later seral stages is most likely due to re-colonization by spores from nearby old-growth stands rather than to the persistence of fungi in the soil. This return in diversity should be interpreted cautiously, it is a return in generic diversity only. Species diversity may present a much different picture. The non-regeneration plots have high proportions of *Cortinarius* and *Inocybe*, two difficult and diverse genera that could not be adequately characterized during this study. A more detailed long-term study must be undertaken in order to truly understand the effects of clearcutting on fungal diversity and species composition. Future plans for this study include more detailed analysis with some species level data and separate analyses for the different functional compo-

nents of the fungal community. Genus and species composition will be analysed using ordination techniques. Relationships between fungal diversity, abundance, and other factors such as vegetation diversity, habitat structure, soil moisture, and air humidity will be examined using canonical correlation.

With the significant decrease in fungal genus richness and abundance after harvesting it appears that re-colonization of young forests by some fungal species depends upon the proximity of older stands as sources of inoculum. The size of stand to leave and how these stands should be distributed across the landscape are questions which still need to be answered.

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