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GENETIC STRUCTURE OF EASTERN WHITE PINE POPULATIONS IN GREAT LAKES - ST-LAWRENCE REGION

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The genetic structure of natural eastern white pine (*Pinus strobus* L.) populations was investigated using allozyme variants. Ten populations were sampled in the eastern section of the Great Lakes and St-Lawrence forest region in the province of Quebec. Cones were collected on 30 trees within each population. Electrophoretic analyses were carried out on the megagametophyte haploid tissue. Twelve isozyme systems involved in the metabolic pathway and coding for 18 loci were assayed. Cellulose acetate gel method with overlay staining was used. Thirteen loci were found to be polymorphic at the 95% criterium level. Mendelian segregation of alleles was observed at all loci but two (PGI-1 and PGI-2). Four genetic parameters were calculated at the species as well as within-population level to measure genetic variation. Results show that the mean number of alleles per locus at the species level is 1.96. The percentage of polymorphic loci is 50.6% and the observed and the expected levels of heterozygosity are 0.176 and 0.180 respectively. Fixation indices were also calculated for each polymorphic locus and averaged over the thirteen loci. Results indicate an overall slight excess in homozygotes with an average F_{IT} of 0.022. A low average value of 0.002 for F_{IS} suggests that populations are virtually panmictic. Population structure seems to be the main factor for the observed heterozygote deficiency.