

**Comparative genetic structure and patterns of genetic variation among populations for white spruce (*Picea glauca*) and eastern white pine (*Pinus strobus*) in eastern Canada**

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Genetic structure and patterns of genetic variation among populations are required for sound gene resource management. A sample of 63 and 66 populations with family structure for white spruce and eastern white pine were used in nursery tests to compare their genetic structure and patterns of genetic variation among populations. Data were collected on seedling heights, branch number and bud phenology. For white spruce populations and families within populations accounted for similar amounts of the genetic variability (6.7% and 6.4% of the total variance, respectively), while for eastern white pine the variance due to populations (23%) was more than twice that due to families within populations (9%). Two principal components summarized 87% and 77% of the total variation for all characters for white spruce and eastern white pine, respectively. Patterns of genetic variation among populations were examined by regressing principal component scores and individual characters with geographical locations (latitude, longitude and elevation) of the sampled populations. Regression equations explained 16% to 65% of genetic variation for different characters for the two species. Patterns of genetic variation among populations differed between white spruce and eastern white pine. Data on total height and survival rate from field tests were used to validate regression models describing patterns of the among-population variation developed from seedling characters. For white spruce the models performed fairly well in predicting relative risk of seed transfer. For eastern white pine the models were less successful, which is likely due to the field planting of the tested trees under protected hardwood bands. The disclosed genetic structure and patterns of genetic variation among populations could be used in designing gene conservation programs, guiding seed transfer in reforestation and delineating breeding zones.

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