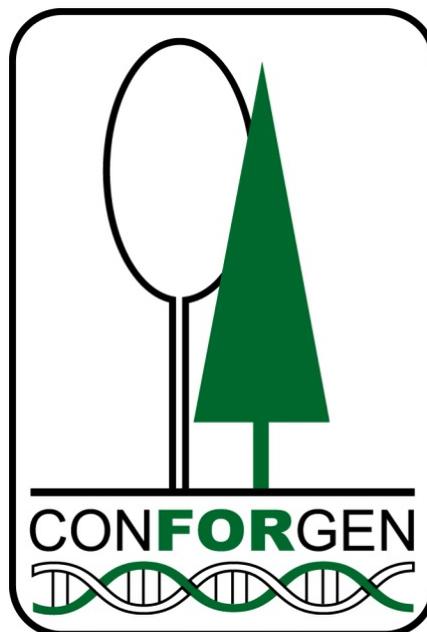


Fourth Forum on the Conservation of Forest Genetic  
Resources

“Contribution of Genomics to Developing  
Forest Genetic Resource Conservation  
Strategies”

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**ABSTRACTS**



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# Ecological Genomics of Eastern White Spruce (*Picea glauca*) in Relation to Climatic Variation

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White spruce is a dominant species of the Canadian boreal forest and it is also important at the economic level. Previous studies reported significant quantitative trait differentiation among populations from eastern Canada for traits related to growth and phenology as well as local adaptation at the molecular level, suggesting climate-driven adaptation. Because of ongoing climate change, identifying genetic polymorphisms related to climate adaptation becomes critical for the management and conservation of genetic resources and for genomic-assisted tree improvement programs in a rapidly changing environment.

The objective of the study was to detect genes carrying polymorphisms (SNPs) significantly associated to climatic factors in eastern white spruce. To do so, 41 populations from eastern Canada distributed along climatic gradients of temperature and precipitation were sampled. Their genomes were scanned for 11,085 SNPs located in 7,819 expressed genes, which represents nearly one-third of the known transcriptome. Two outlier-detection and two correlation methods were used to identify SNPs showing selection signatures where allele frequency variation was related to variation in mean annual temperature and total precipitation or both.

The union of the four detection methods resulted in around 10% of the genes that carried SNPs significantly differentiated or associated with climatic factors. A sizeable proportion of the genes were related to more than one climatic factor, suggesting pleiotropic effects. Sequence alignments with gene ontologies (GO) and protein domains (Pfam) databases revealed that these genes represented a great diversity of putative molecular functions and gene families. Gene families such as kinase domain, caspase domain, lipoxygenase or ferredoxin were significantly

enriched with genes carrying significant SNPs. A few genes carried SNPs detected independently by the four methods used, providing very strong evidence of the adaptive role of these genes. One such gene putatively codes for a tubulin/FtsZ GTPase domain, for which expression has been shown to be repressed by cold in *Arabidopsis thaliana*. Work on identifying potential epistatic effects and gene networks is underway.

# Conservation Strategies Under Climate Change: Accounting for Adaptive Potential and Migration Capacity in Tree Species

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A number of assumptions underpinning the use of species distribution models to predict biological responses to climate change are violated for temperate and boreal tree species that are widespread, long-lived, and genetically adapted to local climate conditions. To address this situation we propose a methodology to account for the potential effects of genetic structure, adaptive potential, and limited migration capacity.

For 24 North American tree species, we calculated geographic distances between similar climate habitats in the past, present, and future, with a k-sample nearest neighbor algorithm. Secondly, we employed biological response scenarios to evaluate the potential effects of genetic adaptation to local environments and the capacity of species to adapt and migrate.

In two case studies for western Canada, we demonstrated how the approach can be used to evaluate the adequacy of a protected areas system, and reforestation guidelines to ensure the maintenance of forest genetic resources. We found that between 35% and 85% of locally adapted populations in protected areas are maintained under a median climate change scenario until the end of the century.

Nevertheless, we found that on average populations already lag behind their optimal climate niche by approximately 130 km in latitude, or 60 m in elevation. For the 2020s we expect an average lag of approximately 310 km in latitude or 140 m in elevation, with the most pronounced geographic lags in the Rocky Mountains and the boreal forest.

We propose that this approach can provide important information to effectively allocate limited resources available for conservation of genetic resources and to guide seed transfer in reforestation programs.

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# Genetic Conservation in the Anthropocene: The Case for Assisted Gene Flow in Forest Trees

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Assisted migration is being evaluated and in some cases already being used as a tool for maintaining resource production or conserving species as climates change. However, there is a lack of scientific consensus on this subject. Much of the debate arises from a lack of a common definition for assisted migration. To some, it primarily refers to the human movement of seed or individuals within existing species ranges, which we define here as *assisted gene flow (AGF)*. To others, assisted migration primarily refers to species introductions outside of their historical range. In order to evaluate the risks and benefits of assisted migration, it is necessary to consider AGF and assisted migration outside of native ranges separately. AGF has greater genetic implications for existing native populations than assisted migration outside of native ranges as existing recipient populations will be altered, while assisted migration into novel areas has greater ecological implications than AGF as species will be introduced to ecosystems. Here we focus on the genetic effects of AGF.

To provide a more nuanced perspective on the potential for AGF to facilitate adaptation to climate change, we have evaluated genetic risks and potential benefits through a review and synthesis of the theoretical and empirical literature in combination with simulation modeling of populations. AGF can increase average fitness in a population through introducing or increasing the frequency of pre-adapted alleles or genotypes. However, AGF may result in outbreeding depression due to the disruption of co-adapted gene complexes, called intrinsic outbreeding depression. AGF may also disrupt local adaptation to non-climatic factors such as soil properties, photoperiod, or the presence of other organisms such as competitors, pathogens or mutualists through hybridization of residents and immigrants, termed extrinsic outbreeding depression. AGF may result in lineage swamping and the loss of local populations; however, it may also maintain genetic lineages from rear-edge populations that are likely to be extirpated if left *in situ*.

Many tree populations have large effective population sizes, experience relatively high levels of gene flow among populations, and are locally adapted to climate, thus are ideal candidates for AGF. Intrinsic outbreeding depression is unlikely to occur unless populations have been long isolated, and evolution should resolve weak outbreeding depression in a few generations due to epistasis. Similarly, natural selection should resolve mild extrinsic outbreeding depression due to adaptive differences in large populations. To weigh the risks of maladaptation to climate change against the risks of AGF for a given species requires information on the extent of local adaptation to climate versus other environmental factors, and the patterns of gene flow. We conclude that AGF should be a powerful tool for the management and conservation of many widespread tree species that show historical adaptation to local climatic conditions.

Funding acknowledgement: This research is part of the AdapTree Project, funded by Genome Canada, Genome BC, Alberta Innovates Bio Solutions, the Forest Genetics Council of British Columbia, the BC Ministry of Forests, Lands and Natural Resources Operations, Virginia Tech, the University of British Columbia, and the University of California, Davis.

### **Reference**

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