

A Microsatellite Assessment of Population Architecture and Gene Flow in Fraser Fir

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Fraser fir (*Abies fraseri* (Pursh) Poir. is a coniferous tree species endemic to a handful of the highest ridge systems in the Southern Appalachians of North Carolina, Tennessee and Virginia. In addition to its ecological importance, Fraser fir is a species with great economic significance in the region, where it is the foundation of North Carolina's \$100 million annual Christmas tree industry.

The six major and three minor disjunct natural populations of Fraser fir have been isolated since the end of the late-Wisconsin glacial period more than 10,000 years ago. Using microsatellite markers designed specifically for this species, we found a relatively small amount of genetic differentiation among most Fraser fir populations (average F_{ST} per locus ≈ 0.04). This may indicate the presence of fairly extensive gene flow among populations, in the form of pollen wind dispersal over long distances (5-60 km). Alternatively, it may suggest that inadequate time has passed to allow for significant genetic separation among the populations.

Several results appear to point to the presence of pollen-mediated gene flow between populations, the effect of which decreases as the distance between populations increases:

- 1) Pairwise F_{ST} and genetic distance values showed that populations nearer to each other were generally, but not always, more genetically similar than those more distant.
- 2) The mean number of alleles per locus was negatively correlated with population isolation.
- 3) The most isolated population, Mount Rogers in Virginia, was the most genetically differentiated and had the smallest mean number of alleles per microsatellite locus.

These results will be useful in the assembly of a gene conservation plan for Fraser fir, which has experienced severe mortality from the infestation of the balsam woolly adelgid (*Adelges piceae* Ratz.), an exotic insect from Europe.