Nucleotide diversity and neutrality testing in genes involved in adaptation in Douglas-fir

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Douglas-fir (*Pseudotsuga menziesii*) is one of the predominant timber-producing species in North America. One of the problems for wood production is the loss of annual growth through frost damage to actively growing tissues. Natural populations of Douglas-fir however exhibit tremendous variation in response to low temperature suggesting substantial underlying genetic control. This is supported by findings of QTL mapping studies over the last decade which have highlighted that multiple genomic regions contribute to the variation in genecological traits. The specific genes involved however are still largely unknown. In contrast, association genetics is proving to be a powerful approach for dissecting complex traits into their individual gene components. Our goal is to use this method to detect association between SNPs from candidate genes and the variation in cold tolerance phenotypes.

We have resequenced 128 Douglas-fir homologs to candidate genes for cold tolerance based on similarity to genes in Arabidopsis. These amplicons were analyzed using a panel of 24 diverse trees from across the Washington-Oregon region, and 684 SNPs were identified in total. We report the estimation of nucleotide diversity and tests for departures from neutrality in these candidate gene sequences. From these, 384 SNPs are being genotyped in the remaining association population of c.900 trees using the Illumina GoldenGate Assay platform.

The ability of plants to adapt to environmental fluctuation is critical to survival, and more so now in the face of global climate change. Douglas-fir is a good model for studying the molecular basis of adaptation, and resources are continuing to be invested to further understand the individual genes involved in this response. The information gained will also be transferable, helping to build genomic resources in less well-studied conifers, and enable a better understanding of adaptation in these important tree species.