

Genetic-Environment Associations Across the Range of *Pinus strobus*¹

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Because of rapid global warming, it is critical for us to better understand the capacity of forest trees to adapt to a changing climate, especially species such as five-needle pines that are particularly at risk to threats because of fire suppression, population fragmentation, and pests. In this study, we used several methods to disentangle the effects of local adaptation (isolation by environment, IBE) from those of isolation by distance (IBD) and isolation by colonization (IBC) in *Pinus strobus*. For this reason, 153 SNPs from 103 genes, including 44 candidate genes for growth and phenology, were genotyped in 133 populations across the range of *P. strobus*. IBD and IBC were found to be significant drivers of population structure. STRUCTURE analyses identified two distinct southern and northern genetic groups that likely originated from different glacial lineages. IBE did not significantly explain population structure when controlling for IBD and IBC. However, genetic-environment association (GEA) methods and F_{ST} outlier tests detected 33 (21.6 percent) outlier SNPs, indicating that local adaptation took place in the presence of high gene flow. We combined results across GEA and F_{ST} outlier methods and identified six highly supported candidate genes for local adaptation. Local adaptation was further tested by a dendrochronological analysis on a subset of mature *P. strobus* trees representative of the species range and established in a provenance trial. Cumulated radial growth decreased with increasing difference in mean annual temperature between the population origin and the trial location. Many of the highly supported SNPs identified by GEA and F_{ST} outlier tests were also associated with growth tolerance to summer drought and heat constraints in the provenance trial.

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