

Integrating genomic and climate data to understand local adaptation of trees in a changing world

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Predicting the capacity of populations to adapt to climate change and adapting management strategies for new climates requires knowledge of population differentiation, geographic patterns of local adaptation, and environmental drivers of adaptive variation. In the AdapTree Project, we have explored whether population genomic approaches can generate this knowledge in the conifers lodgepole pine (*Pinus contorta*) and the interior spruce complex (*Picea glauca*, *P. engelmannii*, and their hybrids). We analyzed genotype-environment associations and conducted genome-wide association studies of climate-related traits on hundreds of populations of each species grown in seedling common garden experiments. The primary driver of local adaptation in these species is low temperature, as revealed by parallel results between genomic approaches and long-term field experiments. Pine and spruce use 47 of the same genes to locally adapt to low temperatures. Neither species is strongly locally adapted to summer temperatures or precipitation. Phenology, growth and cold hardiness traits that are locally adapted to temperature are highly polygenic. Collectively, these results indicate that genomic approaches provide rapid, accurate knowledge of the extent and nature of local adaptation to climate in these non-model organisms.