Long, slow lives facing rapid change: Climate adaptation in conifers

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Conifers are ancient plants that still dominate one third of forests globally. While conifer species diversity is low, many conifers have large geographic distributions spanning wide climatic ranges. Their longevity makes classical genetic experiments intractable, and their large genomes are unwieldy and difficult to assemble. Despite these challenges, we are using genomic tools to understand local adaptation to climate, to understand genetic and demographic dynamics during species range migration, and to evaluate the potential role of somatic mutations in generating new variation for adaptation. Climate adaptation is highly polygenic, and involves a trade-off along temperature gradients between competitive growth rates and adequate cold hardiness. There is considerable convergence in loci associated with local adaptation to low temperatures between lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca, P. engelmanni* and their hybrids) despite 140 million years of independent evolution. We have combined dendrochronology and genetic analyses of Sitka spruce (*Picea sitchensis*) to understand colonization of Kodiak Island over 500 years. After initial long-distance dispersal, genetic and demographic factors contribute to a pronounced lag in population expansion, suggesting species shifts in response to climate change will be slow. Finally, to determine if somatic mutations could compensate to some extent for long generations in conifers by generating additional genetic variation, we sequenced DNA from the bottom and top of exceptionally tall Sitka spruce to estimate the somatic mutation rate. While this species has a high somatic mutation rate per generation (2.7×10^{-8} per bp), the rate per year is among the lowest reported for any species (7.4×10^{-11} per bp per year).