Liston, A. M. Parker–Defeniks, J. Syring, A. Willyard, and R. Cronn (2007) *Interspecific phylogenetic analysis enhances intraspecific phylogeographic inference: A case study in* Pinus lambertiana. Mol. Ecol. 16: 3926–3937.

Abstract

Pinus lambertiana (sugar pine) is an economically and ecologically important conifer with a 1600km latitudinal range extending from Oregon, USA, to northern Baja California, Mexico. Like all North American white pines (subsect. *Strobus*), sugar pine is highly susceptible to white pine blister rust, a disease caused by the fungus Cronartium ribicola. We conducted a chloroplast DNA (cpDNA) survey of *Pinus* subsect. *Strobus* with comprehensive geographical sampling of P. lambertiana. Sequence analysis of 12 sugar pine individuals revealed strong geographical differentiation for two chloroplast haplotypes. A diagnostic restriction site survey of an additional 72 individuals demarcated a narrow 150-km contact zone in northeastern California. In the contact zone, maternal (megagametophtye) and paternal (embryo) haplotypes were identified in 31 single seeds, demonstrating bidirectional pollen flow extending beyond the range of maternal haplotypes. The frequencies of the *Cr1* allele for white pine blister rust major gene resistance, previously determined for 41 seed zones, differ significantly among seed zones that are fixed for the alternate haplotypes, or contain a mixture of both haplotypes. Interspecific phylogenetic analysis reveals that the northern sugar pine haplotype belongs to a clade that includes Pinus albicaulis (whitebark pine) and all of the East Asian white pines. Furthermore, there is little cpDNA divergence between northern sugar pine and whitebark pine (dS =0.00058). These results are consistent with a Pleistocene migration of whitebark pine into North America and subsequent chloroplast introgression from whitebark pine to sugar pine. This study demonstrates the importance of placing phylogeographical results in a broader phylogenetic context.