Genetic Resistance to *Cronartium ribicola* in Limber Pine (*Pinus flexilis*)

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Limber pine (*Pinus flexilis*) is being threatened by the lethal disease white pine blister rust (WPBR) caused by the nonnative pathogen *Cronartium ribicola*. The types and frequencies of genetic resistance to the rust in native populations before invasion are likely to determine the potential success of restoration or proactive measures.

The first extensive inoculation trials using individual tree seed collections from more than 100 limber pine trees confirm that genetic segregation of a stem symptom-free trait to blister rust is consistent with inheritance by a single dominant resistance gene (*Cr4*) and the resistance allele appears to be distinct from the *Cr2* allele in western white pine (*P. monticola*) (Schoettle et al. 2014). The frequency of the *Cr4* allele across healthy and recently invaded populations in the southern Rocky Mountains was unexpectedly high (5.0 percent, ranging from 0 to 13.9 percent), and northern Colorado (USA) appears to be a hotspot. Other tests by us and others suggest that the *Cr4* allele may be absent in populations in the U.S. northern Rockies and California. An ongoing inoculation trial of 74 limber pine families confirms the low frequency of bark reaction and resistance mechanisms for slow canker development.

Genetic resistance is present in limber pine populations and occurs at frequencies that are detectable even in populations that have not yet been invaded by the pathogen (i.e., sampling without the benefit of putative resistance phenotypic selection in the field). The limber pine seed trees that our trials reveal to have the *Cr4* allele will serve as monitors for the evolution of the *vcr4* virulent allele in *C. ribicola* (Schoettle et al., in press). To date, the *Cr4* trees in populations sampled here and exposed to WPBR for more than 20 years remain disease-free. The combination of low stand densities and open canopies of southern Rocky Mountain limber pine stands and the lack of a strong relationship between proximity to *Ribes* and disease incidence in limber pine suggest long-distance transport of *C. ribicola* spores in these ecosystems. The atmospheric mixing of spores from multiple *C. ribicola* populations over extensive landscapes may reduce localized selection pressure on *C. ribicola* and, therefore, slow the proliferation of virulence. However, relying on *Cr4* alone to sustain limber pine populations into the future in the presence of increasing WPBR pressure is not recommended and investigations to identify other more durable types of resistance to WPBR in limber pine are underway. The identification of *Cr4* and other types of resistance in native populations of limber pine early in the invasion process in this region provides useful information for predicting near-term impacts and structuring long-term management strategies (Schoettle and Sniezko 2007).

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