Whitebark Pine (*Pinus albicaulis*) Assisted Migration Trial

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Abstract—Assisted migration—the translocation of a species into a climatically-suitable location outside of its current range—has been proposed as a means of saving vulnerable species from extinction as temperatures rise due to climate change. We explore this controversial technique using the keystone wildlife symbiote and ecosystem engineer, whitebark pine (*Pinus albicaulis*). Species distribution models (SDMs) predict that whitebark pine will be extirpated from most of its current range over the next 70 years. However, the same models indicate that a large quadrant of northwestern British Columbia is climatically suitable for the species under current conditions, and will remain so beyond the 21st century. To test the accuracy of this model, as well as the capacity of treated (x-rayed, stratified and nicked) and untreated whitebark pine seeds to germinate, survive and grow relative to geographic, climatic, microsite and genetic factors, we planted seeds from seven populations in eight trial locations ranging from 600 km southeast to 800 km northwest of the northern boundary of the species range. During the first two growing seasons, germination occurred in all locations, with treated seeds germinating at three times the rate and a year earlier, relative to untreated seeds. Seed weights and x-ray-based viability estimates helped predict germination rates among populations for both seed treatments. Earlier snowmelt dates and corresponding warmer early-growing-season temperatures positively influenced untreated, but barely affected treated, seed germination. Seedling survival, health and growth were also positively influenced by earlier snowmelt dates, with better-developed seed stocks performing best. Our experiment provides initial verification of SDM predictions for whitebark pine, and informs the creation of scientific and ethical guidelines for assisted migration prior to a time of critical need.

Keywords: climate change, common garden, quantitative genetics, species distribution models, species range, genecology