

ECOLOGY AND EVOLUTION OF A TREE SPECIES CHALLENGED BY DUAL THREATS

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Abstract

We are studying the ecological and evolutionary processes affecting the geographical distribution of southwestern white pine (SWWP; *Pinus strobiformis*), an important tree species of the Southwestern USA and Mexico. Southwestern white pine viability is threatened by changing climate and an invasive tree disease, white pine blister rust (caused by the fungal pathogen, *Cronartium ribicola*). Rapid climate change is negatively affecting SWWP by increasing heat and drought stress, and thus challenging its ability to adapt. White pine blister rust causes extensive tree decline and mortality, including in SWWP. The dual threats of climate change and invasive species make forecasting future tree distributions at continental scales an urgent challenge. The goal of our project is to determine how gene movement among populations, adaptation to disease and drought, heritable changes beyond DNA mutations, and a changing environment interact to govern the success of SWWP. We are utilizing and developing tools to help forecast and manage the future of the species, including those from genomics, common gardens, tree disease resistance testing, engineering, and technology innovation to measure drought tolerance and physiological response. Results will be synthesized and included in cutting-edge landscape genomics models to meet our overarching goal. We will present our framework and current project status, including results. Completed products include development of landscape genomic models, a species distribution model incorporating climate change, and adaptive trait, phenotype plasticity, and genomic variation analyses. Continuing work incorporates these aspects in addition to transgenerational plasticity research and a genome-wide association study.

Broad Project Goals:

1. Find genetic resistance to white pine blister rust
2. Find adaptive traits using common gardens
3. Find adaptive genes using next generation sequencing
4. Link phenotypes to genotypes using remote sensing technology
5. Model gene flow, adaptive variation, and climate change across the landscape

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Cone, seed, and foliage source locations (Figure 1).

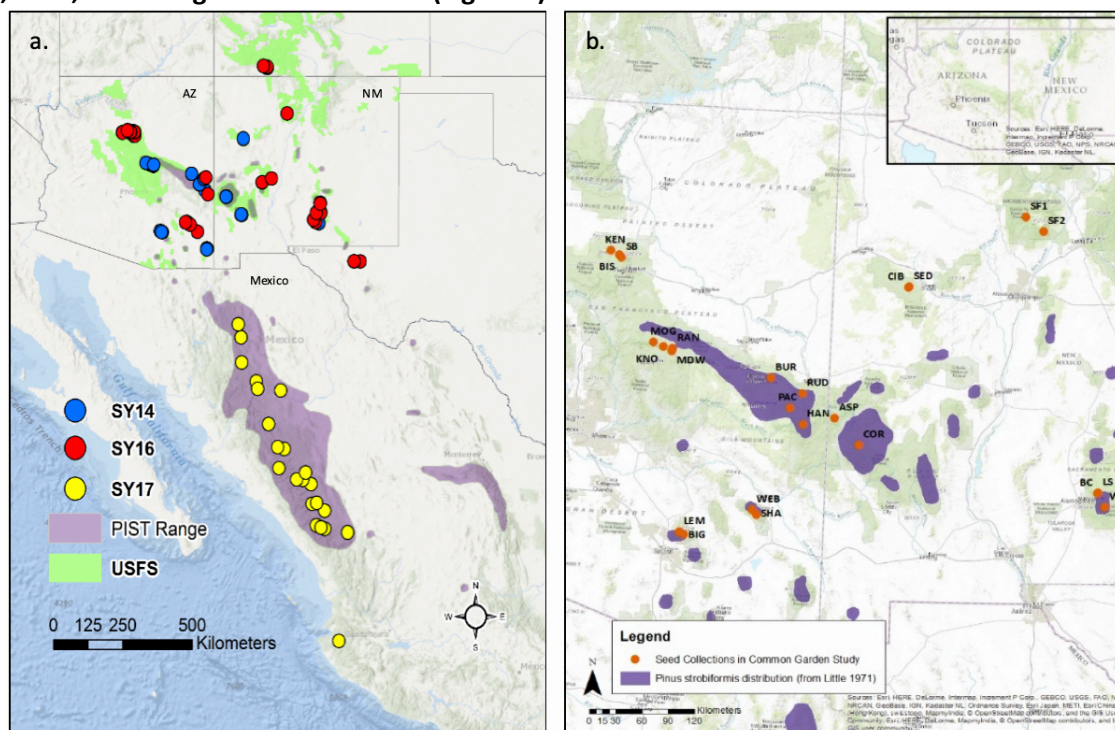


Figure 1: *a.* Sow year 2014, 2016 and 2017 source population locations. *b.* Sow year 2015 source population locations.

Goal 1: Find genetic resistance to white pine blister rust

Resistance screening is taking place for both major gene resistance (MGR) and quantitative resistance. Results are preliminary, with ongoing inspections and results being updated multiple times annually. We have identified new maternal trees with MGR in Arizona and New Mexico plus a potential source tree in Mexico. Early results indicate that genetic resistance is greater in more southern US populations, but these are preliminary (Figure 2). Additionally, clustering of genetic resistance in south-central New Mexico corresponds to the general area white pine blister rust was first identified in southwestern white pine, providing the most time for natural selection against susceptible families to occur.

Goal 2: Find adaptive traits using common gardens

We are using three common gardens within the (SEGA) (Figure 3) to grow progeny side by side, simulate climate warming using an elevational gradient, and compare adaptive traits across families and populations. Starting in 2018, half of the seedlings are subject to a drought experiment during the growing season. Each SEGA site is equipped with a full weather station, fencing to protect from browse damage, and irrigation system. Seedlings were planted in a complete randomized design, in raised bed boxes in 10 rows of 10 during late summer, in 2015, 2016, and 2017. Seedlings are measured bi-annually to assess growth (height and diameter), phenology, and mortality. A subsample has been included in seedling physiology research as well.

Unpublished results: Mortality has been highest in the high elevation garden but similar between the mid and low elevation gardens. Results from seedling physiological studies indicate some plasticity in response to increased temperature (carbon isotopes and stomatal densities) at the low elevation garden and a drought avoidance water use strategy.

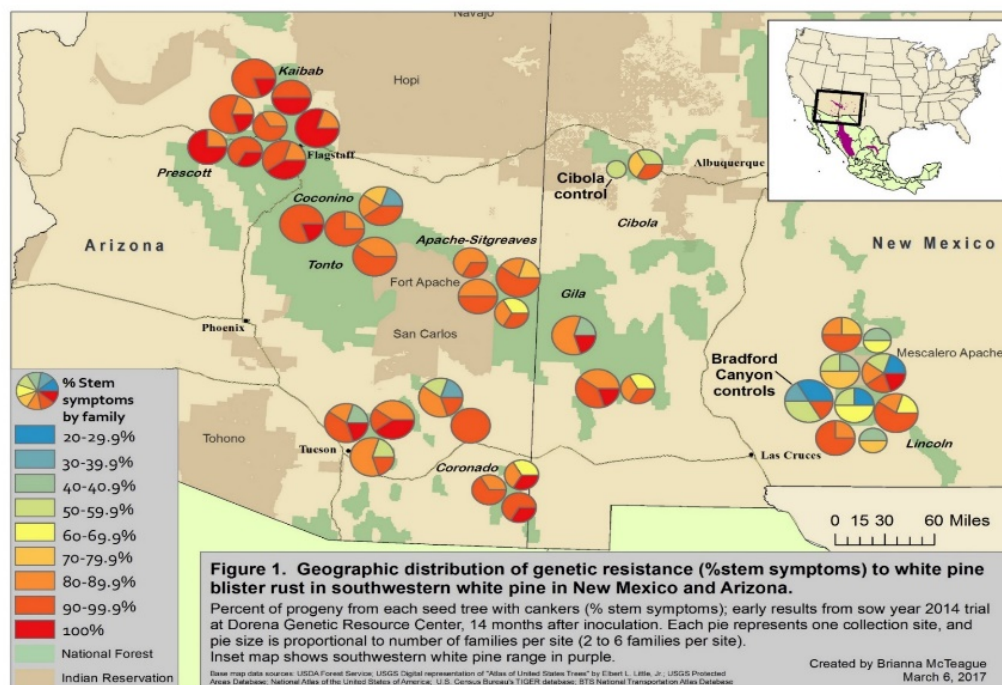


Figure 2: Preliminary results (March 2017) indicating geographic locations of genetic resistance in the US Southwest. Unpublished data, Dorena Genetic Resource Center, Cottage Grove, Oregon.

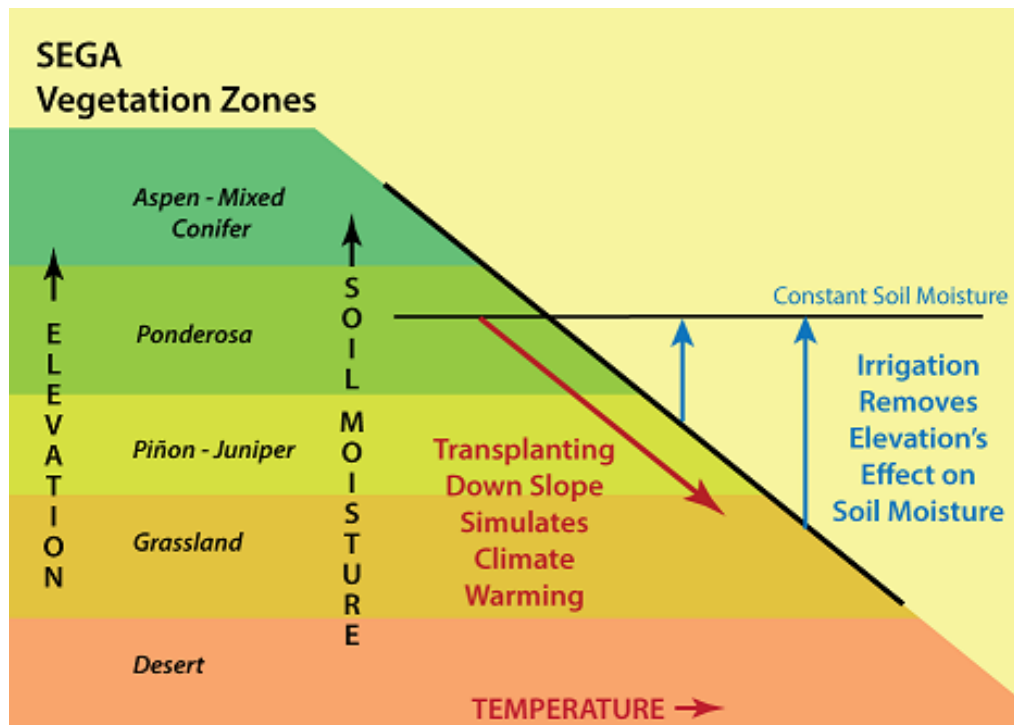


Figure 3: Environmental gradients and experimental design of the Southwest Experimental Garden Array (SEGA). This study is utilizing the aspen-mixed conifer (high elevation), ponderosa (mid elevation), and piñon-juniper (low elevation) common garden sites.

Goal 3: Find adaptive genes using next generation sequencing

Research related to this goal has thus far been focused on investigating the genetic relationship between *Pinus flexilis* (limber pine) and *P. strobiformis* (SWWP). The US populations of SWWP primarily fall into a hybrid zone, with trees containing genes from both species (weighted toward SWWP) (Figure 4, from Menon et al. 2018). Additional research found evidence that the hybrid zone is shifting north (Menon et al. 2019).

Goal 4: Link phenotypes to genotypes using remote sensing technology

The team is using a multispectral sensor to image white pine blister rust inoculated and un-inoculated seedlings to determine if disease infection can be detected remotely. Preliminary results were positive and led to a successful Special Technology Development Program proposal to expand this component of the research.

Goal 5: Model gene flow, adaptive variation, and climate change across the landscape

To date, the landscape genomics models have been updated and validated, and in the coming year, data from the other four goals will be used to initiate the model. Additionally, we predicted the distribution of southwestern white pine under the changing climate (Figure 5); the species distribution model will also be a component of this modeling effort.

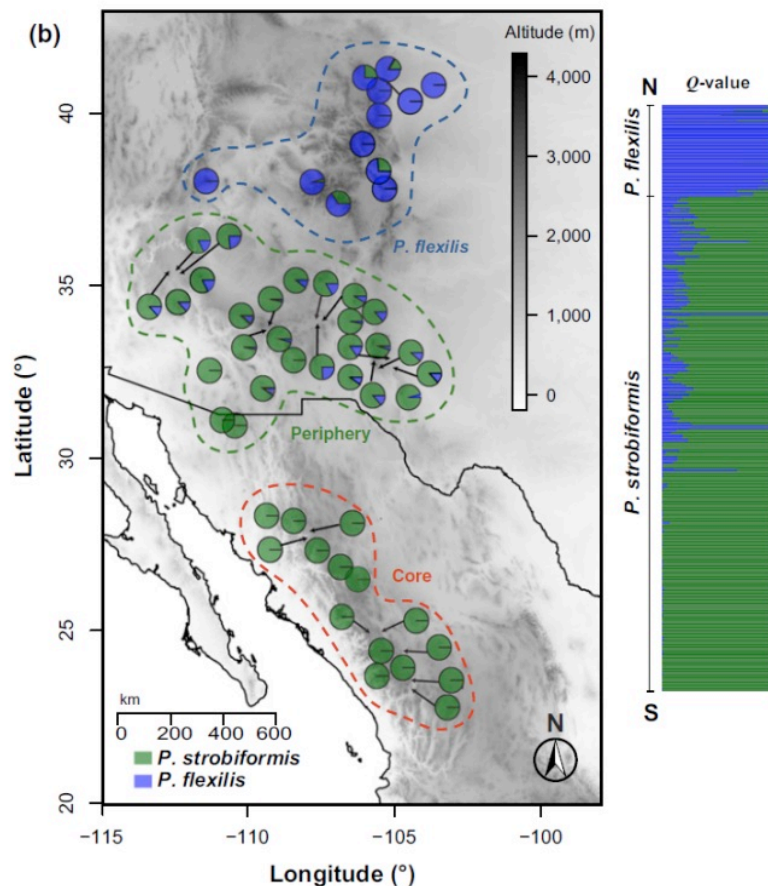


Figure 4: Geographic locations of core southwestern white pine populations (red dashed line), peripheral populations in the hybrid zone (green dashed line), and limber pine populations (blue dashed line). Pie charts represent ancestral proportions of *P. strobiformis* (green) and *P. flexilis* (blue); also represented by the Q-value bar chart on the right. From Menon et al. 2018.

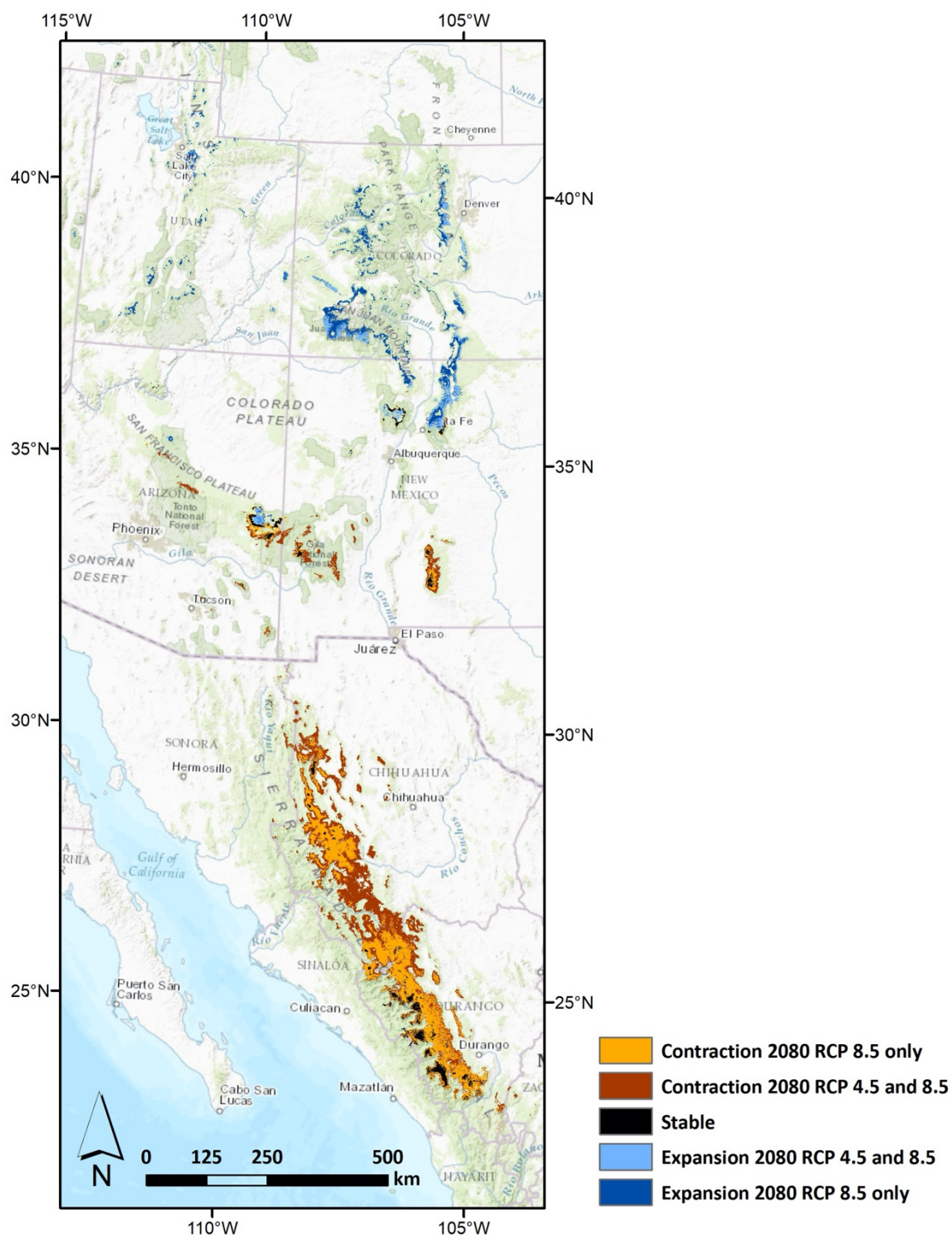


Figure 5: Predicted areas of southwestern white pine range expansion, stability, and contraction in 2080 under two climate scenarios. From Shirk et al. 2018.

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