

A Population Genetic Model for High-Elevation Five-Needle Pines: Projecting Population Outcomes in the Presence of White Pine Blister Rust

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The slow growth and long generation time of the five-needle pines have historically enabled these trees to persist on the landscape for centuries, but without sufficient regeneration opportunities these same traits hinder the species' ability to adapt to novel stresses such as the non-native disease white pine blister rust (WPBR). Increasing the frequency of resistance to WPBR is the foundation for options to sustain five-needle pine species in the presence of the pathogen. Depending on the condition of the ecosystems, increasing resistance can be achieved via outplanting resistant seedling stock and/or stimulating natural regeneration (Schoettle and Snieszko 2007). As the objective of management intervention in the high elevation ecosystems is often to promote multiple generations of sustainability, greater understanding of the regeneration cycle and the potential for increasing the frequency of resistance are needed. This is especially critical for the WPBR pathosystem as WPBR kills trees of all ages and therefore impacts multiple stages of the regeneration cycle of five-needle pines.

We are developing a population genetic model, parameterized for high elevation five-needle pines, to improve our understanding of pine population dynamics in the presence of WPBR and to identify key processes that could be manipulated with management to sustain high elevation pines over multiple generations. This model allows us to address questions such as: (1) What frequency of resistance to WPBR is enough to sustain a population? (2) What regeneration densities will be sufficient to promote increased frequency of resistance over time? (3) During what state of infestation and impact by WPBR is intervention most effective? The matrix model includes 6 age classes (cohorts): seeds, primary seedlings (1-4 yrs old), secondary seedlings (5-20 yrs), saplings (21-40 yrs), young adults (41-90 yrs), and mature adults (>90 yrs) (Fig. 1). The model includes non-linear functions for the effects of competition (leaf area index) on germination and cone production. Population size, incidence of infection by WPBR and frequency of a simply inherited dominant WPBR resistance gene by age class over time are all included in the model output. This model can examine the interactions between regeneration and resistance under different WPBR infection probabilities and their effects on population dynamics and changes in the frequency of the resistant allele over time.

Early evaluations of the population genetic model reveal realistic disease incidence and demographic dynamics (Field and others, submitted). The model predicted a similar

pattern of disease incidence among the age classes that is commonly observed in the field (i.e., higher disease incidence in the older cohorts than the younger cohorts). One interpretation of this pattern is that the young seedlings present such a small target for infection that they escape infection resulting in the low observed rust infection incidence. However, our model output revealed the same pattern even when a uniform probability of infection was applied across all cohorts. Since young trees die rapidly after infection and new uninfected germinants are added yearly, disease incidence remained low in the young cohorts. The cost of infection is lower for the older larger trees, thus the infected individuals can persist and accumulate over time and therefore the incidence of rust infection in the older cohorts was greater. The model confirmed that a low incidence of rust infection in live young cohorts can be consistent with high infection in the young cohorts and does not necessitate the interpretation that the young cohorts are 'escaping' infection relative to the older cohorts (Field and others, submitted). The model suggests that infection and subsequent mortality, and therefore natural selection for resistance, efficiently occurs in the young age classes. Therefore stimulating regeneration to promote selection may be a viable management option to accelerate natural selection and increase the frequency of rust resistance in a population (Schoettle and Snieszko 2007). Further application of the model to examine the selection process and the accumulation of resistance in the population and each age class over time is underway.

Understanding these interactions will facilitate evaluation of the ecological efficacy of management options to sustain high elevation pines over multiple generations and help inform proactive or restoration planning. This research is one aspect of an interdisciplinary project. It will be integrated with epidemiology, social preferences, non-market valuation and economic theory into a dynamic economic model to examine the economic trade-offs of different WPBR management options in high elevation pine ecosystems (see Bond and others this proceedings; Meldrum and others this proceedings; Jacobi and others this proceedings; Nelson and others this proceedings).

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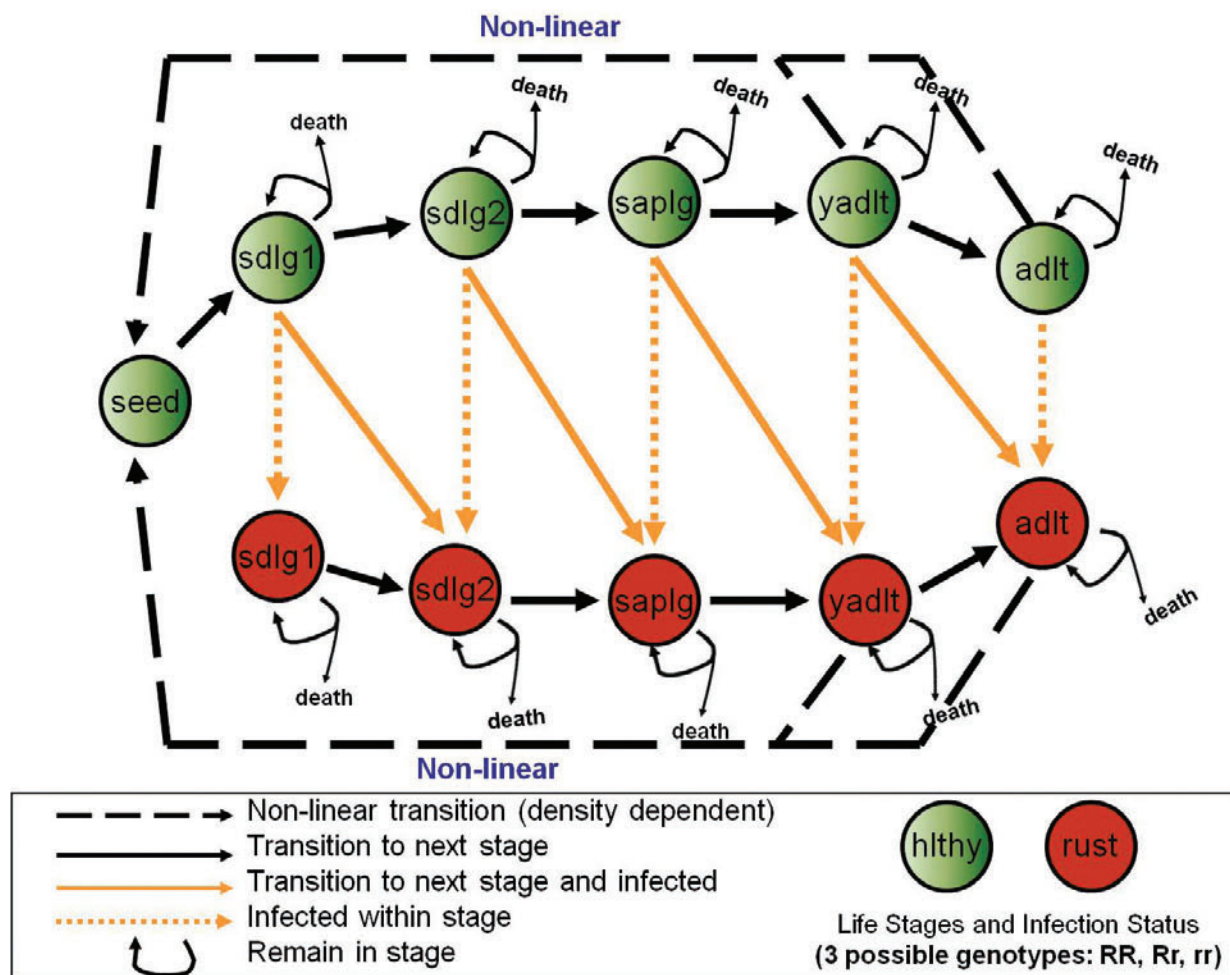


Figure 1. Schematic of the six age class population genetic model (adapted from Field and others, submitted). The six age classes (cohorts) are seeds, primary seedlings (sdlg1), secondary seedlings (sdlg2), saplings (saplg), young adults (yadlt) and mature adults (adlt). All age classes, except seeds, can become infected and transition into an infected class. Resistance is modeled for a simply inherited single dominant gene (R). The healthy cohorts (green) can be any of 3 genotypes (RR, Rr, rr) while only the susceptible genotype (rr) can be in the infected age classes (red).

that highlighted the interdisciplinary project to develop a dynamic economic model to evaluate efficient management of WPBR in high elevation ecosystems. Partial funding for this project was provided by USDA Economic Research Service Program of Research on the Economics of Invasive Species Management (PREISM; Award No. 58-7000-8-0096) and USDA Forest Service Rocky Mountain Research Station (Award No. 07-RJVA-11221616-252). We thank the PREISM Project team: Craig Bond, Patty Champ, Bill Jacobi, Cara Nelson and Richard Sniezko as well as Simon Taverer for helpful suggestions and discussions.

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