

Genetic Architecture of Differences in Fitness Traits Among Geographically Separated *Dendroctonus ponderosae* Populations

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Introduction

The mountain pine beetle, *Dendroctonus ponderosae* Hopkins (Coleoptera: Curculionidae, Scolytinae) (MPB), is widely distributed across western North America spanning 25 degrees latitude and more than 2,500 m elevation. In a common garden experiment, Bentz and others (2001) observed that MPB populations from a southern location required significantly more time to develop than individuals from a population in the northern part of the range, although both populations exhibited univoltinism. Adults from the southern population were also significantly larger, even when reared in a common host and temperature. These results suggest that local selection plays a role in MPB adaptation to temperature, which can vary dramatically across the broad range of MPB. In a recent phylogeographic analyses of MPB, Mock and others (2007) found evidence of genetic structuring among populations that followed a broad isolation-by-distance pattern, confirming that genetic differences exist among geographically isolated populations. Little is known, however, about the underlying genetic architecture of important MPB life history traits, such as development time. To adequately forecast the effects of climate change on MPB population success and adaptability, a better understanding of the underlying environmental and genetic control of these traits, and variability across geographically separated populations, is needed. The main objective of our study was to examine the genetic architecture of differences among three geographically separated populations of MPB that differ in total development time and adult size. We used line cross experiments to analyze the relative influences of additive and nonadditive genetic effects on population differences in these traits.

General Approach

Adult MPB from three geographically isolated populations and infesting three host tree species were used in the study: 1) MPB from southern California infesting pinyon pine (*Pinus monophylla*), 2) MPB from central South Dakota infesting ponderosa pine (*P. ponderosa*), and 3) MPB from central Idaho infesting lodgepole pine (*P. contorta*). We quantified total development time

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and adult size of beetles from each population reared in the lab in a common host, lodgepole pine, at a range of temperatures (12.5 °C, 17.5 °C, 22.5 °C, 27.5 °C). Using beetles reared at 22.5 °C, reciprocal crosses were also made among the populations by mating males and females, respectively, from each population. Offspring from each population cross were also back-crossed to the original parent population. Fitness characteristics, total time to complete development, and adult size were measured and sex determined for all offspring by mating group and generation. Line-cross or generation means analysis was used to compare observed means with expected means derived from genetic models accounting for additive, dominance, epistatic, and maternal effects (Mather and Jinks 1982).

Results

In general, mean development time for all populations was slower and adults were larger at cold rearing temperatures when compared to warm temperatures. However, population response to temperature was not consistent across latitude, and a greater proportion of beetles from the southern population completed development at 17.5 °C compared to the northern populations. At this temperature, a large proportion of individuals from the northern populations did not pupate. These results suggest adaptation to local environments that could lead to geographically specific voltinism patterns under a global warming scenario. Results from line-cross analyses indicate that epistatic interactions are responsible for many of the genetic differences in adult size and total development time among the MPB populations sampled. We also observed sterility in F_2 males from the southern California population when mated with adults from the northern populations. Although infestation by differing strains of *Wolbachia* may cause F_2 breakdown, F_2 sterility may also be an indication of epistatically linked loci and is the first trait to evolve in incipient speciation. The shallow mtDNA lineage found by Mock and others (2007) suggests that if *Wolbachia* spp. are not the cause, it may be a very recent incipient speciation event for MPB.

References

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