

Bark Beetle Genetics—an Overview¹

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Our understanding of bark beetle genetics is fairly rudimentary. A few studies have used enzyme variation to document population structure of *Ips* and *Dendroctonus* species in relation to geographic separation (Anderson and others 1979, 1983, Namkoong and others 1979), host trees (Langor and Spence 1991, Sturgeon and Milton 1986), dispersal (Florence and others 1982), and phenology (Gast 1987). Electrophoretic data have also been used to look at distance relationships of *Ips* species (Cane and others 1990b). Preliminary studies have investigated genetics of morphological (Linton and others 1984) and pheromonal (Piston and Lanier 1974) traits.

The three main priority areas that we see in need of particular attention (not necessarily in this order) are areas that, until recently, have not received attention:

1. Heritable variation in traits affecting bark beetle-natural enemy interactions, in particular, the use of bark beetle pheromones by predators and parasitoids in prey location and how it affects heritable qualities of bark beetle populations as well as population size. The basis for this research need is reports by Raffa and Klepzig (1989) and Herms and others (1991) show-

ing that the pheromone systems of *Ips pini* is significantly altered by predator eavesdropping. An understanding of the genetic control of pheromone production and response is essential to understanding these reciprocal predator-prey adaptations.

2. Heritable variation in host selection traits of bark beetles and how it can influence population dynamics through interactive selection between host trees and beetles under varying population densities. The groundwork in this area was laid by Raffa and Berryman (1987). The genetic component involved in interactions both among and within trophic levels has generally not been considered in bark beetle population biology.

3. The use of DNA techniques, particularly sequencing, in phylogenetic reconstruction. With an unparalleled array of mating systems, the family Scolytidae begs to become a model for the study of the evolution of mating systems as well as the evolution of host selection (i.e., which beetle taxa feed on which tree taxa). This can be done only in a phylogenetic context, and DNA sequences yield the most robust phylogenies.

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