

Bark Beetle Genetics¹

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1. Previous work

- A. Protein electrophoresis the basic technique for most work.
- B. Genetic variability has been characterized.
- C. Population differences demonstrated and analyzed.
- D. Genetic population structure assessed.
- E. Basic molecular systematics explored; phylogenetic trees developed.
- F. Attempts to link protein loci to phenotypic characters such as behavior.

2. Our work at University of Georgia

- A. Starch gel electrophoresis of *Dendroctonus* and *Ips* populations, in terms of genetic variability, population structure, and population differences.
- B. mtDNA studies, using restriction site analysis and DNA sequencing.
 - (1) Cloned part of mitochondrial DNA
 - (2) Completed restriction site analysis of SPB populations
 - (3) Begun sequencing of several mtDNA segments

3. Work to be done

- A. Long-term study to follow genetic variability and population structure in relation to population cycles of SPB. Electrophoresis and perhaps restriction mapping techniques of choice.
- B. Studies using mtDNA as molecular markers of population history in relation to geographic location—phylogeography. Restriction mapping and sequencing of PCR-amplified sequences techniques here.
- C. Molecular systematics of bark beetle taxa such as *Dendroctonus* species, using mtDNA and nuclear loci. Restriction mapping and sequencing of PCR-amplified sequences techniques here.

¹In lieu of a full narrative paper, the authors submitted this outline for publication. Any questions should be directed to the authors.

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