

Bark Beetle Genetics¹

Wyatt W. Anderson and C. Wayne Berisford²

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.

²Professor of Genetics, Dept. of Genetics, 101B Life Sciences Bldg., University of Georgia, Athens, GA 30602 and Professor of Forest Protection, University of Georgia, Athens, GA 30602