The Proceedings reports the results of a workshop focusing on the topic of bark beetle genetics. The workshop evolved because of the growing interest in this relatively unexplored area of bark beetle research. Workshop participants submitted brief descriptions of their views of the current status of bark beetle genetic research and needs for the future. Contributions vary from broad overviews to detailed descriptions of specific projects. A common theme is the potential for rapid advances in this area of research given recent technological advances in the field of genetics. Also included is an extensive reference list.

Retrieval Terms: *Dendroctonus* species, *Ips* species, scolytid genetics, taxonomy

**Dedication**

We dedicate this report to the memory of Gerald Lanier, a valued colleague to all who share an interest in bark beetle research, and a dear friend of many of the workshop participants. It is particularly fitting that we pay tribute to Gerry for his pioneering efforts in bark beetle genetics and in recognition of his lasting contributions in the area of scolytid systematics.

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Preface

This report is the result of a workshop focusing on the topic of bark beetle genetics held May 17-18, 1992, in Berkeley, Calif. Bark beetles play a significant role in pine forest ecosystems throughout the world; this group of insects often causes severe economic damage and loss of wildlife habitat. In general, bark beetles threaten forest health in the short term. In the long term, however, they have served as natural agents to thin overcrowded stands in pine forests. Although bark beetles have been the focus of intensive research efforts, relatively little effort has been devoted to understanding bark beetle genetics. Our Workshop evolved because of (and reflects) the growing interest in this relatively unexplored area of bark beetle research. The objectives of this workshop were four-fold:

1. To promote interaction among researchers and exchange of ideas;
2. To foster collaboration;
3. To summarize the state of knowledge; and
4. To identify research needs for the future.

To accomplish the last two goals and to set the stage for discussions, participants were asked before the workshop to submit brief descriptions of their views of the current status of bark beetle genetics research and the needs for the future. How this assignment was fulfilled was as diverse as the participants' approaches to the topic. Contributions varied from broad overviews to detailed descriptions of specific projects. As a whole, these statements provide an insightful description of the state of knowledge in the area of bark beetle genetics.

Students of bark beetle biology will find this review and the combined reference list a valuable source of current information on this topic. Significant advances have been made in the available technology in the decade since the topic of bark beetle genetics was first reviewed (Mitton and Sturgeon 1982). Our knowledge of bark beetle biology has advanced slowly; however, as many contributors indicate, the potential for more rapid advances is imminent.

During the two-day workshop, participants gave brief presentations on the status of their ongoing research efforts. A general group discussion of research needs and goals followed. A topic of considerable concern to the group was the lack of recognition of the need and support for a continuous effort in the area of systematics. Declining support for systematics work has resulted in lack of training and career opportunities for the next generation of skilled systematists. Without a commitment by academic and funding institutions to support this fundamental research, we face a future without advances in this essential specialty area.

To structure our general discussions, priority research needs were identified by participants. The group recommended that research be initiated or continued on these 15 topics:

- understanding ancestry of scolytid species
- biosystematics of important species, including symbionts
- monitoring endemic vs. epidemic conditions, and understanding processes that trigger changes
- spatial statistical techniques for mapping geographic patterns of gene frequency (and changes in relation to population dynamics of bark beetles)
- interaction between phylogeography and population growth status
- genetics of variation in pheromone systems
- understanding individual variation in pheromone and other qualitative characteristics of individual beetles
- genetics of variation in interaction with natural enemies
- genetics of cold-hardiness
- understanding selection pressure (i.e., stage and mechanism)
- artificial rearing techniques for major species (especially Dendroctonus spp.)
- molecular population analyses that focus on phylogeography, gene flow, paternity
- gene expression (description of genome, protein and enzyme level, transcription) for key traits
- survey of polymorphisms identified from different analytical techniques
- applying information from other well-researched systems (e.g., Drosophila, Tribolium) to bark beetle genetics

Because items on this list were intentionally expressed in relatively broad terms and covered multiple levels of analysis (i.e., molecular to population to phylogenetic levels), we did not attempt to refine or prioritize this general list any further. Instead, we sought to identify more specific questions and technological advances necessary to address these questions. This discussion is summarized in table 1.

Through this report we seek to continue the productive efforts described at this workshop: to share information and ideas, and to encourage the pursuIts of others with interests in the challenges of research into genetics of bark beetles. All participants welcome further inquiries—addresses and telephone numbers are provided. We hope that this publication will aid those seeking to learn more about the topic, and we encourage efforts in studying new topics that are not mentioned here.

Jane L. Hayes
Jacqueline L. Robertson
Technical Coordinators
Table 1—Specific questions and technological advances necessary to address priority research needs.

<table>
<thead>
<tr>
<th>Levels of Analysis</th>
<th>Specific Questions</th>
<th>Techniques</th>
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<tbody>
<tr>
<td>1. Molecular genetics</td>
<td>a. Study patterns of expression for genes involved in semiochemical pathways, e.g., detoxification, pheromones. b. Study genetics of development, e.g., stage-specific gene (adult vs. juvenile, overwintered vs. pre-winter, etc.) c. Screen for specific patterns of expression associated with dispersal vs. feeding adults; cold hardiness; different seasonal cohorts; host-tree species. d. Development of molecular markers for ecological genetics. e. Studies of sex ratio anomalies (e.g., in Ips spp. etc.)</td>
<td>Determine more biochemical pathways. Develop DNA probes associated with key developmental events. Develop systems to describe transformation of trees or beetles. RAPDS, VNTR loci, mtDNA</td>
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<td>2. Quantitative genetics of ecologically important traits.</td>
<td>Once appropriate rearing techniques are established for controlling environmental and genetic background, focus on traits, establish role of genes and environment as influencing variations among individuals. a. Semiochemicals, correlations between them (production and response profiles) b. Cuticular hydrocarbons, e.g., changes during development and relationship with host compounds c. Cold-hardiness: examine patterns of expression in larvae d. Microbial interactions: involvement with overcoming host defenses, increased attack success, pheromone synthesis e. Morphological/physiological traits (e.g., elytra loadings, lipid contents) f. Genetics of host selection g. Trees: genetic and environmental determinants of susceptibility</td>
<td>Need rearing techniques for studying similarity within &quot;constant&quot; environment and for manipulation of environment. Artificial media vs. outdoor trees, logs. Explore Kermit Ritland's technique for h² estimation based on electrophoretic data. Fluctuating asymmetry analysis.</td>
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<tr>
<td>3. Selection and population dynamics</td>
<td>a. Stages and sources of selection in mortality during the life cycle due to host stress and predation and parasitism at various stages. b. Dynamics of beetle interactions (e.g., competition) as a function of population phase in the context of tree interactions. c. Do patterns of selection differ between population phase? (e.g., r-vs. k-type) d. Potential for selection experiments for key characterization (e.g., thick vs. thin phloem) (See level 4c and d).</td>
<td>Rearing techniques. Techniques for following cohorts of beetles below the bark (acoustics, radiography, infra-red detection)</td>
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continued
### Table 1, continued

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<th>Levels of Analysis</th>
<th>Specific Questions</th>
<th>Techniques</th>
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<tr>
<td>4. Population structure and phylodispersal</td>
<td>a. Calculate hierarchical F-statistics: between geographic regions, between populations, within populations (between host plants, pheromone &quot;groups&quot;, emergence groups, families) (See Level 5a) &lt;br&gt;b. Exploit existing data sets: <em>Dendroctonus</em> spp., <em>I. pini</em> (requires systematic sampling and coordination between groups). &lt;br&gt;c. Spatial analysis, interaction with GIS data now available. &lt;br&gt;d. Dependence of population structure on: &lt;br&gt; 1. local density &lt;br&gt; 2. stage of population growth (See Level 3d) &lt;br&gt; e. Direct analysis of dispersal, gene flow in relation to elemental labelling rare or unique alleles, mutants (beetles or symbionts) (See Level 3d)</td>
<td>Also relevant to Biosystematics &lt;br&gt;Spatial statistics development. &lt;br&gt;Elemental labelling (Mark-Release-Recapture).</td>
</tr>
<tr>
<td>5. Phylogenetic reconstruction and biosystematics.</td>
<td>a. Species taxonomy of bark beetles is relatively complete, but need phylogenetic reconstruction. &lt;br&gt;b. Focus on <em>Ips, Dendroctonus</em>, especially 1) species relationships within these groups, and 2) ancestral relationships between them. &lt;br&gt; 1. develop discrete characters for cladistic analysis, &lt;br&gt; 2. continue applying isozymes. &lt;br&gt;c. Based on phylogeny, consider evolution of following traits: &lt;br&gt; 1. pheromone production and composition (semiochemistry), &lt;br&gt; 2. behavior, including isolation mechanisms, &lt;br&gt; 3. aggregation response, and &lt;br&gt; 4. cuticular hydrocarbons</td>
<td>Develop discrete characters for: &lt;br&gt;1. morphometrics &lt;br&gt;2. mtDNA, nuclear markers &lt;br&gt;3. sequence data on rib. DNA (larger scale) &lt;br&gt;Apply new methods of phylogeny reconstruction and analysis.</td>
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