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17. *Tomicus* and *Anoplophora* Genetics: Important Research Needs

Robert A. Haack[1], Therese M. Poland[1], Jian Wu[2], and Hui Ye[3]

Tomicus piniperda (L.) (Scolytidae) and *Anoplophora glabripennis* (Motschulsky) (Cerambycidae) are two of the more recent exotic forest insects to become established in the United States. The native range of *T. piniperda,* the pine shoot beetle, includes much of the pine (*Pinus*) growing regions of Europe, Asia, and North Africa (Wood and Bright 1992). *Tomicus piniperda* was discovered in the United States near Cleveland, Ohio, in 1992 (Haack and Kucera 1993). It is primarily a pest of pine, but on occasion *T. piniperda* can reproduce and shoot-feed in other conifers such as trees in the genera *Abies*, *Larix*, *Picea*, and *Pseudotsuga* (Haack and others unpublished data, Lawrence and Haack 1995, Wood and Bright 1992). As for *A. glabripennis*, established populations were first discovered on Long Island, New York, in August 1996 (Haack and others 1997a) and then in Chicago, Illinois, in July 1998. *Anoplophora glabripennis* attacks hardwood trees, primarily maple (*Acer*), poplar (*Populus*), and willow (*Salix*). In this paper, we will briefly describe studies that address the genetics of *T. piniperda* and *A. glabripennis*, as well as other *Tomicus* and *Anoplophora* species.

Genetic Relatedness of North American Populations of *Tomicus piniperda*

In less than two months after the 1992 discovery of *T. piniperda* in Ohio, additional infestations were found in five nearby states: Illinois, Indiana, Michigan, New York, and Pennsylvania (Haack 1997, Haack and others 1997b). By the end of 1992, *T. piniperda* had been found in 43 counties in the above six US states. In spring 1993, Carter and others (1996) collected *T. piniperda* at eight locations among the original 43 infested counties (fig. 1). Subsequent tests of genetic relatedness, using random amplified polymorphic DNA (RAPD) methods for polymerase chain reaction (PCR) amplification, suggested that there had been two separate introductions, one in Illinois or Indiana at the southern tip of Lake Michigan, and a second in Ohio along southern Lake Erie.

Since 1992, *T. piniperda* has been found in only three additional U.S. states: Maryland and West Virginia in 1995 and Wisconsin in 1997. In Canada, *T. piniperda* was first discovered in Ontario in 1993, at which time seven infested counties were found. As of January 1999[4], *T. piniperda* was known to occur in 243 counties in 9 US states and in 22 counties in Ontario, Canada (fig. 1).

Given that the geographic range of *T. piniperda* has increased substantially from 1992 to 1998, it would be of interest to revisit the question of genetic relatedness. That is, would RAPD-PCR analysis of *T. piniperda* populations conducted in the near future provide evidence of additional new introductions? Or during the past several years could the North American *T. piniperda* populations have been sufficiently mixed (owing to natural spread and movement of infested pine

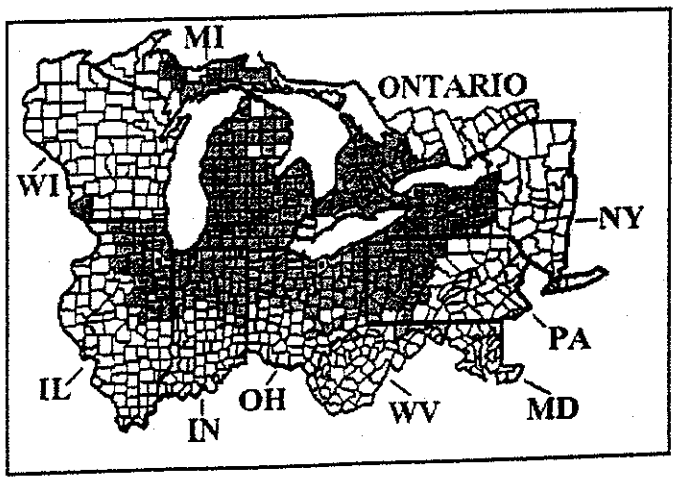

Figure 1—North American range of *Tomicus piniperda* as of January 1999. The seven infested counties with black rectangles represent the locations where *T. piniperda* was collected in 1993 for the *T. piniperda* genetics study reported in Carter and others (1996). There was one collection made in Illinois (IL), 2 in Indiana (IN), 2 in Michigan (MI), 1 in Ohio (OH), and 2 in New York (NY).

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[4] A few additional occurrences have been added between presentation and publication of this proceedings.

products) so that any differences between the founding populations will now be obscured?

Origin of the North American Populations of *Tomicus piniperda*

We do not know the country or countries of origin for the North American populations of *T. piniperda*. Identifying the origin(s) of the North American founder populations would be useful to help (1) predict the future limits of *T. piniperda*'s geographic range in North America, and (2) target foreign exploration for biological control agents (Carter and others 1996). Considering the native range of *T. piniperda*, there are certainly many candidate countries that could have served as the source of the North American populations (Haack and Cavey 1997). If recent interception records are a good indication of the potential origin of *T. piniperda*, then the most likely sources include France, United Kingdom, Spain, and Italy (table 1). A worldwide collection of *T. piniperda* populations with subsequent genetic testing, using molecular methods such as RAPD-PCR, could aid in pinpointing the likely origin(s) of the *T. piniperda* populations now present in North America.

Table 1. Number of *Tomicus piniperda* interceptions on wood products at US ports of entry during 1985-1998 by country of origin. (Source: USDA APHIS)

Number of interceptions	Country
28	France
19	United Kingdom
15	Spain
15	Italy
8	Belgium
8	Europe*
8	Germany
3	Netherlands
3	Russia
2	Japan
2	Unknown
1	China
1	Finland
1	Greece
1	Hong Kong
1	Portugal
1	Sweden
1	Switzerland

*Cargo originated in Europe, but no individual country was listed.

Genetic Variation Between Outbreak and Non-Outbreak Populations of *Tomicus piniperda* in China

In China, *T. piniperda* occurs throughout almost the entire country (fig. 2). However, based on the 1980 to 1998 annual forest pest reports from each province, *T. piniperda* was ranked as a major pest in only four provinces: Jiangsu, Jilin, Yunnan, and Zhejiang. In Yunnan, in southwestern China, *T. piniperda* outbreaks have occurred each year since the 1970s. Outbreaks are so severe in Yunnan that *T. piniperda* attacks and reproduces in live pine trees, resulting in significant tree mortality (Ye 1991, 1997). In Yunnan, the tree species that suffers the greatest mortality is Yunnan pine (*Pinus yunnanensis* Franch.). Yunnan pine is found primarily in Yunnan Province and in small portions of three neighboring provinces (Guangxi, Guizhou, and Sichuan) (Critchfield and Little 1966). Why has *T. piniperda* been so destructive in Yunnan? Are the *T. piniperda* populations in Yunnan more aggressive than in other parts of China? Or is the host tree, Yunnan pine, much more susceptible to stem-attack by *T. piniperda* than are other Chinese pines? One study that would address the

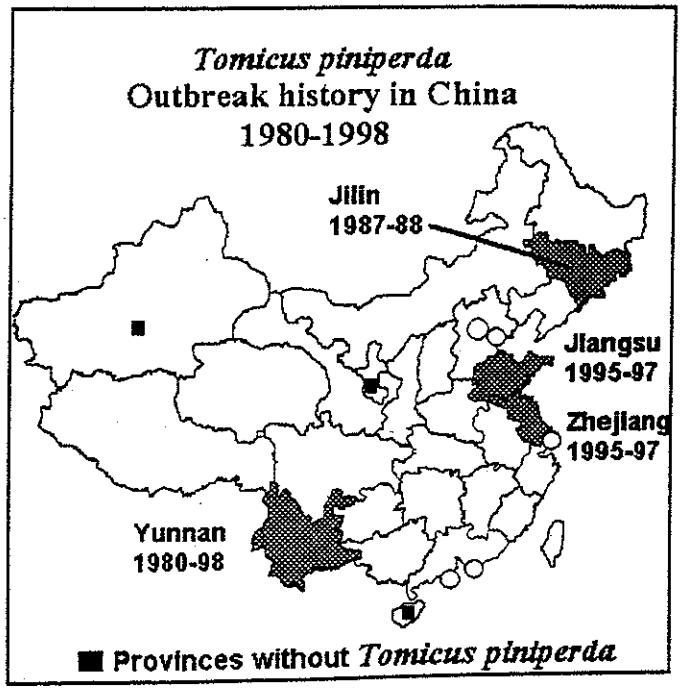

Figure 2—Map of China indicating the four provinces that reported *T. piniperda* as a major pest sometime during the period 1980 to 1998. *Tomicus piniperda* is not known to occur in the three "provinces" with black squares.

issue of *T. piniperda* aggressiveness would be to collect and compare the genetic relatedness of outbreak and non-outbreak populations within Yunnan as well as among *T. piniperda* populations from throughout China.

Genetic Relatedness Within the Genera *Tomicus* and *Anoplophora*

According to Wood and Bright (1992), six species of *Tomicus* occur worldwide. *Tomicus brevipilosus* (Eggers) occurs in China, India, Japan, and Korea. *Tomicus destruens* (Wollaston) occurs primarily in France, Italy, Portugal, Spain, Cyprus, Israel, and Turkey. *Tomicus minor* (Hartig) occurs throughout much of Eurasia; from Spain to Japan, and from Finland to southern China. *Tomicus pilifer* (Spessivtsev) occurs in China and eastern Russia. *Tomicus piniperda* has a range similar to that of *T. minor* but also includes parts of northern Africa such as Algeria and now North America. *Tomicus puellus* (Reitter) occurs mostly in eastern Russia. Each of these six *Tomicus* species uses *Pinus* as a host tree; however, on occasion some *Tomicus* species will use *Abies, Larix,* and *Picea.* It would be of interest to compare the genetic relatedness of these six *Tomicus* species and thereby reveal their evolutionary relatedness as well as provide evidence for the validity of each species.

In addition to *Tomicus*, the genetic relatedness within the Asian cerambycid genus *Anoplophora* should be examined. About 44 species of *Anoplophora* are currently recognized in Asia. Molecular techniques could be employed to determine the genetic relatedness of the *A. glabripennis* populations now established in New York and Chicago, as well as to compare them with *A. glabripennis* populations from throughout China. In addition, molecular techniques could be used to aid in the revision of the genus *Anoplophora*.

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This proceedings contains contributions from each author or group of authors who presented their current research at the bark beetle genetics workshop held 17-18 July 1998 on the campus of the University of Wisconsin in Madison, Wisconsin, USA. This was the second meeting on this subject; the first was held in 1992. The subject of bark beetle genetics is of growing, international interest; researchers from Austria, Hungary, and Mexico, as well as from across the United States have contributed to this proceedings. The topics covered included molecular approaches to genetic analysis of bark beetles, genetic structure of bark beetle populations, variability in ecologically important traits: effects on beetle fitness, and systematics of bark beetles.

Keywords: Scolytidae, molecular genetics, genetic variation, behavior, pheromones, natural enemies, host selection, population dynamics, phylogeny, systematics.

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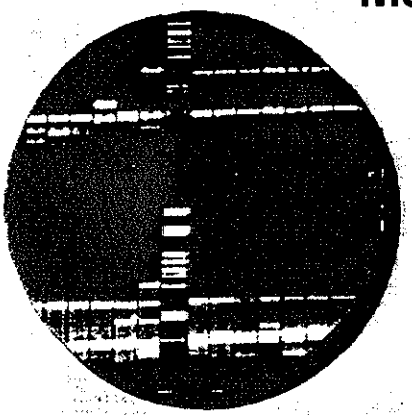

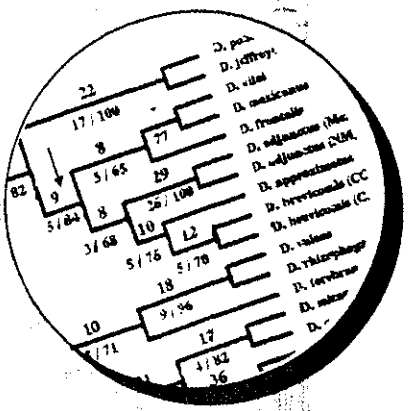

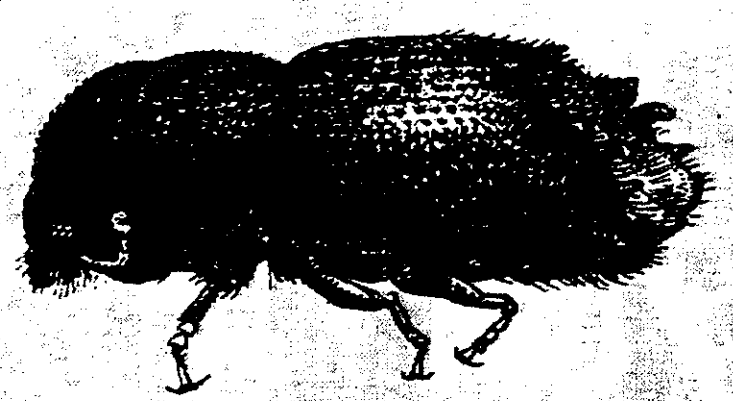

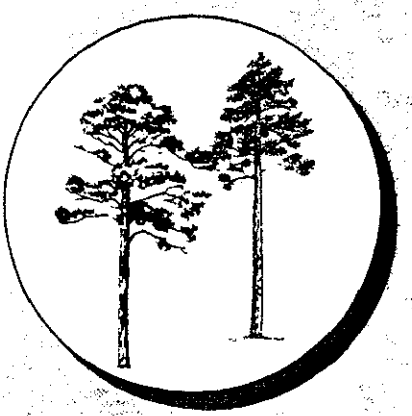

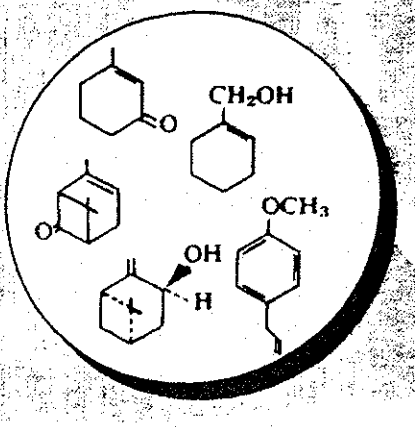

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