

Colony and Population Genetic Structure of Formosan Subterranean Termites from Hawaii and Louisiana

by

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Colonies of the Formosan subterranean termite can vary in their social organization, ranging from simple (Mendelian) families headed by a single pair of reproductives to highly inbred families with numerous secondary reproductives. Colony structure can potentially be further complicated by budding, or by possible fusion of unrelated colonies. Thus, a given population may consist of a complex mixture of different types of colonies. Because control of *Coptotermes formosanus* focuses on colony elimination, knowledge of the composition of colonies and how they are organized is critical to successful management. The highly cryptic nature of the nesting and foraging habits of these pests makes it very difficult to determine many basic features of colony social organization through direct collections and observations. However, important aspects of colony social organization can be inferred from the use of genetic markers to quantify the patterns of genetic variation within and among colonies (Thorne *et al.* 1999, Husseneder *et al.* 2002).

We used microsatellite genetic markers (Vargo & Henderson 2000) to investigate the colony and population genetic structure of Formosan subterranean termites on Oahu, Hawaii, and in New Orleans, Louisiana. The results presented here are preliminary, and we expect to publish a more detailed report elsewhere.

To date, we have examined 20 workers from each of 20 colonies from Oahu. Each individual was genotyped at five microsatellite loci, which contained 3-5 alleles per locus. We determined the genotypes and their ratios for each colony, and we calculated coefficients of relatedness and various *F*-statistics for the population to infer the levels of inbreeding

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and the relative numbers of reproductives in colonies with more than a single king and queen (Thorne *et al.* 1999). Six colonies (30%) had genotypes in Mendelian ratios, indicating that they were simple families headed by a single pair of reproductives. Values of the relatedness coefficient and F -statistics suggest that the reproductives present in colonies are related to each other, leading to inbred colonies. The remaining 14 colonies (70%) had non-Mendelian ratios, consistent with the presence of multiple reproductives, although in every case the genotypes were consistent with the multiple reproductives within a colony being the descendants of a single pair of reproductives. The coefficient of relatedness and F -statistics suggest that these colonies contain on the order of dozens of secondary reproductives inbred for many generations. Thus, most of the colonies in this population appear to be headed by many highly inbred secondary reproductives that are derived from a single pair of reproductives that originally founded the colony. Analysis at the level of the population so far indicates no detectable structure among colonies from Oahu, suggesting that colonies spread through long-range mating flights and/or human-aided transport.

For the New Orleans population, 20 workers from each of 11 colonies were analyzed at 10 microsatellite loci. Of these, five (45%) had genotypes indicating simple families, whereas six (55%) had genotypes indicating the presence of multiple reproductives. A high coefficient of relatedness among workers in the simple families ($r = 0.71$), again suggests that the single king and queen heading colonies are related to each other. The non Mendelian families from New Orleans were less inbred than those from Hawaii, suggesting that the New Orleans colonies have fewer reproductives inbred for fewer generations. Possible reasons for the differences in colony genetic structure between the Hawaiian and New Orleans populations are currently under investigation. As in the Hawaiian population, no evidence of population structure was found, possibly due to long-range dispersal of founding alates or common spread through human activity.

Finally, we detected moderate a degree of genetic differentiation between the Hawaiian and New Orleans populations ($F_{ST} = 0.08$), demonstrating the sensitivity of microsatellites to detect genetic differences between populations. These results will be followed up in the future by a more detailed analysis of the genetic relationship of different introduced and native populations of *C. formosanus* to investigate possible routes of introduction and spread of this destructive pest.

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