

GENETIC STRUCTURE of NATIVE and INTRODUCED POPULATIONS of the FORMOSAN SUBTERRANEAN TERMITE (ISOPTERA: RHINOTERMITIDAE)

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The Formosan subterranean termite, *Coptotermes formosanus*, is a severe invasive urban pest species. Presumably native to China, this termite has been introduced to many areas of the world including Japan, Hawaii, and the U.S. mainland. Improved regulatory and remedial control of this pest species requires knowledge about its invasion biology, such as origins of introductions and possible effects of introduction events on population genetic structure and colony social organization.

We compared the population structure and social organization of native and introduced populations of *C. formosanus* to address the following questions:

Do introduced populations show a lack of genetic diversity (genetic bottlenecks)?

Can individuals be assigned to source populations according to their genotypes?

Is there a difference in colony social organization between native and introduced populations?

To answer these questions we employed microsatellite markers and examined the genotypic distribution of up to 20 colonies from native populations in China, and from several introduced populations in the USA (Hawaii and Louisiana) and Japan. The genotype of one individual per colony at 12 different loci was used to investigate the genetic diversity and degree of inbreeding of populations by calculating *F*-statistics. To measure coefficients of inbreeding and relatedness of colonies within a population, we determined the genotypes for up to 24 workers at 5 to 12 loci per colony. To determine the number of active reproductives for each colony, we tested worker genotypes for deviations from the genotypic distribution expected for colonies headed by single pairs.

First results of this ongoing study show that (1) Introduced populations of *C. formosanus* have lower genetic variability than native populations. This variability can be explained by genetic bottlenecks we exclusively detected in introduced populations. (2) Genetic differentiation between populations is sufficient to allow classification of individuals to source populations with high confidence. This makes it possible to track origins of infestation on a local and global scale. (3) Colony social organization shows differences between native and introduced populations. We found that in introduced populations a lower percentage of the colonies are headed by multiple reproductives (36-65%) than are native populations (up to 100%). A wide range in degrees of intracolony relatedness and inbreeding indicates variable social organization in *C. formosanus* populations. Comparisons of genetic patterns of native and introduced populations will allow us to shed light on the invasion biology and history of *C. formosanus*.