

**GENETIC VARIATION and GENE FLOW of  
*COPTOTERMES FORMOSANUS* (ISOPTERA:  
RHINOTERMITIDAE) in ATLANTA, GEORGIA**

**Tracie M. Jenkins<sup>1</sup>, Daniel R. Suiter, and Brian T. Forschler<sup>2</sup>**

<sup>1</sup>The University of Georgia, Department of Entomology, Griffin Campus, 1109 Experiment St.  
Griffin, GA 30223-1797

<sup>2</sup>The University of Georgia, Department of Entomology, BioSciences Building, Athens, GA 30602

The purpose of this research was to evaluate the genetic variation and gene flow of *Coptotermes formosanus* (Isoptera: Rhinotermitidae) in the Atlanta, Georgia, metropolitan area using multi-locus DNA markers. Previous research from this lab using maternally inherited mitochondrial DNA sequence markers revealed that only one matrilineal line, which was linked to New Orleans, Louisiana, was represented from four, well-spaced metropolitan Atlanta sites. This surprising lack of maternal variation in the *C. formosanus* in Atlanta could be the result of a maternal kin-biased peripheral group within a New Orleans meta-colony being splintered off and transported to Atlanta. Overall genetic variation in termites, however, is a function of two parents, and gene flow can be more accurately evaluated using diploid markers. DNA fingerprints of individual *C. formosanus* workers from Atlanta sites over time were, therefore, collected and overall genetic variation and gene flow determined. These results are discussed in light of the implications for Formosan termite growth and adaptation to the Atlanta area.