

MOLECULAR PHYLOGENETIC RELATIONSHIP OF ASIAN *COPTOTERMES* SPECIES BASED ON MITOCHONDRIAL 16S SEQUENCES

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Abstract *Coptotermes* species subterranean termites are believed to have originated in Asia and have been transported around the world via infestations in the hulls of wooden boats and in lumber. Classification of *Coptotermes* species using morphological characters is difficult and complicated. This study reports the phylogenetic relationship of several Asian *Coptotermes* species: *C. curvignathus*, *C. gestroi*, *C. kalshoveni*, *C. frenchi*, *C. lacteus*, *C. acinaciformis*, and *C. formosanus*. Relationships are based on mitochondrial 16S sequences. Termite samples were first identified based on soldier mandibular and labral shapes and measurements. For molecular studies, DNA was extracted from the whole body of individual worker termites. A fragment of the mitochondrial gene, 16S was amplified with PCR and subjected to direct sequencing. DNA sequencing of the 16S ribosomal DNA amplicon revealed an average size of 428 bp. The average base frequencies were A = 0.43, C = 0.24, G = 0.12, and T = 0.21. Consensus sequences were obtained using the CAP sequence assembly machine and were aligned using CLUSTAL W. The multiple alignment results showed that several point mutations had occurred among different species, as well as within the same species from different colonies. Phylogenetic relationships were constructed using maximum parsimony, likelihood, and distance methods. The results suggested that: *C. formosanus*, *C. frenchii*, *C. acinaciformis*, and *C. lacteus* may be clustered under the same group; and, *C. acinaciformis* and *C. lacteus* are closely related species. This preliminary study demonstrated the use of molecular approach for accurate species identification in urban pest control. The molecular sequence data provide a practical means of resolving the weakly-defined morphospecies in this genus and will assist future efforts directed towards characterizing species and ecology.