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*Molecular characterization of Nasutitermes similis and Nasutitermes guayanae using 16SrRNA*  
Rullian Ribeiro, Tiago Carrijo, Eliana Canello, **Adriana Correa e Castro**

The termite species *N. similis* and *N. guayanae* (Termitidae, Nasutitermitinae) are morphologically very similar, therefore requiring other means of taxonomic identification, like molecular markers. Thus, our aim in this study was to characterize, using the mitochondrial gene 16S rRNA, *N. guayanae* and *N. similis* samples collected in the upper Rio Madeira, in the Brazilian Amazon, and in French Guiana, together with *N. guayanae* samples from Trinidad and Tobago, obtained in Genbank. Six haplotypes were found in 38 sequences belonging to *N. guayanae*, and two haplotypes were found in 49 belonging to *N. similis*. The average genetic distance between the two species haplotypes was 0.017. The phylogenetic reconstruction using Bayesian evidence shown that the *N. guayanae* haplotypes from Brazil share a close relationship, as also the haplotypes from Trinidad and Tobago and French Guiana, pointing to a possible genetic structuration in the species. A similar genetic pattern was not found for *N. similis*, since the two haplotypes found by us belong to the same clade, showing a low genetic distance and a possible genetic homogeneity in the species. The relaxed molecular clock estimate time for the most recent common ancestor of the Brazilian samples of *N. guayanae* and *N. similis* is 1.86 my, a lesser time than the equivalent one found by us in the analysis of the clade formed by the *N. guayanae* samples from Trinidad and Tobago and French Guiana - 2,49 my. In conclusion: although morphologically very similar, *N. guayanae* and *N. similis* are very distinct genetically.