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*Genetic differentiation in populations of *Nasutitermes corniger* (Isoptera) from Brazil*

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Termites are abundant and responsible for soil aeration, drainage and nutrient recycling in tropical and subtropical ecosystems and the genus *Nasutitermes* (Termitidae: Nasutitermitinae) is dominant in the Neotropical primary forests. Thus, the aim this work was to elucidate, using the mitochondrial gene 16S rRNA, the relationship between some populations of *Nasutitermes corniger* from north (upper Rio Madeira, RN), northeast (João Pessoa, PB), central (Corumbá, MS and Cáceres, MT), southeast (Jaboticabal, SP) and south (Castro, PR) Brazil, and compare them with samples from Ecuador, Suriname, Mexico and Central America, whose respective sequences were obtained from the Genbank. The results showed high genetic diversity in studied populations, a shown by the significant number of distinct haplotypes found (20 haplotypes to 62 sequences), plus an haplotypic diversity (Hd) of 0,897. Although shared haplotypes were found between populations from southeast and northeast Brazil and also between the central Brazil populations, broadly speaking, the species is genetically structured. Furthermore, population expansion events were detected in *N. corniger* samples from north Brazil, and also indication of stability through time, detected the bimodal curve Mismatch Distribution found in central Brazil samples and sequences from Genbank. Neighbor joining analysis found two groups: one composed by populations of north, central and south Brazil, and another group composed of the samples from southeast and northeast Brazil, Ecuador, Suriname, Central America and Mexico. In a phylogeographic analysis, restricted gene flow with isolation by distance was detected in the total cladogram analysis. These last results suggest that there are two dispersion corridors for *N. corniger*, mostly evidenced by the small genetic distances between the studied groups, together with the reduced haplotype sharing among their populations.