



Genetic variability and phylogenetic aspects in species of the genus *Macrobrachium*

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ABSTRACT. The genus *Macrobrachium* includes prawns, which are widely distributed in lakes, floodplains, and rivers in tropical and subtropical regions of South America. This genus presents nearly 210 known species with great ecological and economic importance. However, few studies are related to the biology of these crustaceans. In this study, we analyzed the genetic variability and phylogenetic relationship between *Macrobrachium amazonicum* and *Macrobrachium jelskii*, which are closely related species. Additionally, they are syntopics and their taxonomy poses problems because it is difficult to differentiate between the species. We used the mitochondrial gene sequences COI and 16S rRNA to assess the genetic structure of these species in 3 populations that were collected from Tiete hydrographic basin (São Paulo State, Brazil). The interspecific

comparison of samples that were collected at the same and different locations showed a low rate of genetic variability. This similarity was attributed to the recent introduction of these species in the regions that were sampled and the habitat conditions in which they inhabit. In addition, these results may be consistent with the hypothesis that they are a single species, interspecific hybrids, or metapopulation. The dendrogram analyses did not reveal the formation of clusters, confirming the disturbances in the genetic structure of the samples that were analyzed in this study. These data are pioneers to these crustaceans, and they confirm the ecological and evolutionary problems between these *Macrobrachium* species.

Key words: *Macrobrachium*; Crustacean; Genetic polymorphism; Genetic variability; COI; 16S rRNA