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Genetic polymorphism, molecular characterization and relatedness of *Macrobrachium* species (Palaemonidae) based on RAPD-PCR

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ABSTRACT. The prawn genus *Macrobrachium* belongs to the family Palaemonidae. Its species are widely distributed in lakes, reservoirs, floodplains, and rivers in tropical and subtropical regions of South America. Globally, the genus *Macrobrachium* includes nearly 210 known species, many of which have economic and ecological importance. We analyzed three species of this genus (*M. jelskii*, *M. amazonicum* and *M. brasiliense*) using RAPD-PCR to assess their genetic variability, genetic structure and the phylogenetic relationship between them and to look for molecular markers that enable separation of *M. jelskii* and *M. amazonicum*, which are closely related syntopic species. Ten different random decamer primers were used for DNA amplification, yielding 182 fragments. Three of these fragments were monomorphic and exclusive to *M. amazonicum* or *M. jelskii* and can be used as specific molecular markers to identify and separate these two species. Similarity indices and a phylogenetic tree showed that *M. amazonicum* and *M. jelskii* are closest to each other, while *M. brasiliense* was the most differentiated species among them; this may be attributed to the different habitat conditions to which these species have been submitted. This information will be useful for further studies on these important crustacean species.

Key words: RAPD-PCR; *Macrobrachium*; Polymorphism; Prawn; Phylogenetic relathionship; Crustacean