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

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Received July 26, 2010
Accepted September 17, 2010
Published November 30, 2010
DOI 10.4238/vol9-4gmr935

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 relationship; Crustacean