

Molecular characterization and phylogenetic relationships among species of the genus Brycon (Characiformes: Characidae) from four hydrographic basins in Brazil

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ABSTRACT. Brycon is one of the main genera of Neotropical freshwater fish. In Brazil, Brycon species have been found in many hydrographic basins, such as the Amazon, Paraná, Paraguay, and Araguaia-Tocantins basins. We examined the phylogenetic relationships among the species Brycon orbignyanus, B. hilarii, B. cf. pesu, B. cephalus, B. falcatus, and B. gouldingi, using mitochondrial and nuclear molecular markers. Specimens of B. orbignyanus were collected in the Paraná River. Specimens of B. hilarii were collected in the Manso River. Specimens of B. cephalus were obtained from a fish farm, and

specimens of B. cf. pesu, B. falcatus and B. gouldingi were sampled in the Araguaia-Tocantins basin. DNA extraction was carried out using the phenol/chloroform method. Molecular polymorphism studies of Brycon species were carried out with the inter-simple sequence repeat (ISSR) technique, using the total DNA of six specimens of each species. In DNA amplification of B. cf. pesu, eight specimens were used. The partial sequence of mitochondrial cytochrome b was amplified by PCR. The PCR products were used directly in sequencing reactions. Each ISSR primer produced from 7 to 14 scorable and reproducible bands. The (GGAC)₃A and (GGAC)₃C primers produced the greatest number of species-specific bands. A 264-bp fragment, corresponding to the partial region of mitochondrial DNA cytochrome b, was sequenced and used for analysis. According to the phylogenetic tree obtained from the data, these Brycon species can be divided into two clades: one comprised only B. cf. pesu, and the second comprised the remaining Brycon species. We conclude that ISSR primers can be used for the identification of species-specific bands in fish, such as Brycon spp.

Key words: *Brycon*; Phylogenetic relationships; mtDNA cytochrome b; Inter-simple sequence repeat