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### EVOLUTION OF 5S rDNA IN FOUR ALOPATHIC POPULATIONS OF *Hypostomus ancistroides* (SILURIFORMES, LORICARIIDAE)

Dinaíza Abadia Rocha Reis<sup>1</sup>, Karina de Oliveira Brandão<sup>2</sup>, Lurdes Foresti de Almeida Toledo<sup>3</sup>, Rubens Pazza<sup>1</sup>, Karine Frehner Kavalco<sup>1</sup>

1. Institute of Biological and Health Sciences, Laboratory of Ecological and Evolutionary Genetics, Universidade Federal de Viçosa, Campus Rio Paranaíba, Rio Paranaíba – MG – Brazil; 2. Department of Anatomy and Embryology, Leiden University Medical Center, The Netherlands; 3. Institute of Biosciences, Universidade de São Paulo, São Paulo – SP – Brazil. \*Correspondence to dinaizabio@gmail.com

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Fish of the *Hypostomus* genus have wide geographic distribution, low vagility and high adaptive performance, which favors the formation of isolated populations. Partitioning a population can prevent gene flow among isolated subpopulations. This isolation alone does not represent the formation of new species, but these subpopulations will be evolving independently and different genes may be fixed in each of them. The objective of this work was to analyze four allopatric populations of *Hypostomus ancistroides* in the Tietê and Grande river basins, seeking to identify and understand possible evolutionary mechanisms for population markers. For this, the technique of Fluorescent in situ Hybridization (FISH) with 5S rDNA probes was used. All of the four populations had 68 chromosomes. FISH with rDNA 5S showed two terminal sites in all individuals. However, these sites exhibit localization polymorphism because they are on different chromosomes in the populations: metacentric in Araras/SP and Indaiatuba/SP and acrocentric specimens in Botucatu/SP and Terra Roxa/SP individuals, evidencing pericentric inversion. The existence of the two phenotypes in the two watersheds may reflect the dispersion of the species. An ancestral metapopulation would present the two observed phenotypes, which arose by pericentric inversion. With the increase of the level of the rivers in the interglacial eras, this metapopulation was dispersed by the basins. The rugged relief of the region with several mountain ranges, together with the decrease of the level of the waters in the ice ages, may have contributed to the isolation of the populations in the headwaters of the rivers. As only one 5S rDNA phenotype was observed in each population, there was probably founding effect or selective pressure. However, the two phenotypes are observed at nearby collection points, with no phenotype correspondence and geographical location. This shows evolution by dispersion, demonstrating that 5S rDNA may be a potential population marker.

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