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Investigating genetic differentiation of the populations of the freshwater fish *Hoplias microlepis* from western Ecuador

Abstract

The ecology and evolution of the fauna in western Ecuador remains poorly understood. The area has been under severe anthromorphic pressure and most of the communities that have evolved are unique to the region; they occur nowhere else on Earth. In this study, we employed amplified fragment length polymorphism (AFLP) analysis as a neutral nuclear marker to analyze genetic differentiation of a species of freshwater fish in western Ecuador, the tahira *Hoplias microlepis*. We compare previous results obtained from sequencing a fragment of the mitochondrial loop with the samples of 32 specimens collected at four different sites (Quevedo River, Babahoyo River, Daule-Peripa Reservoir, Chongon Reservoir) in western Ecuador. By studying how populations in those sites vary, we hope to gain a better understanding of the evolutionary history of the neotropical fish fauna in the region. Furthermore, this study will improve our knowledge of how species respond to environmental stress, as the fauna in western Ecuador has been impacted by natural geological events and human development, including the creation of large artificial reservoirs.