

Use of DNA Barcoding as an Auxiliary Investigative Tool Reveals High Hidden Diversity in the Genus *Hypomasticus* (Characiformes, Anostomidae)

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INTRODUCTION & AIM

Characiformes represent the largest order of Neotropical fishes. Among the most diverse families within the group is Anostomidae, which includes 151 species across 17 genera, including *Hypomasticus*, a recently revalidated and poorly studied genus comprising 17 valid species.

This study aimed to investigate the species composition of the genus using DNA barcoding.

METHOD

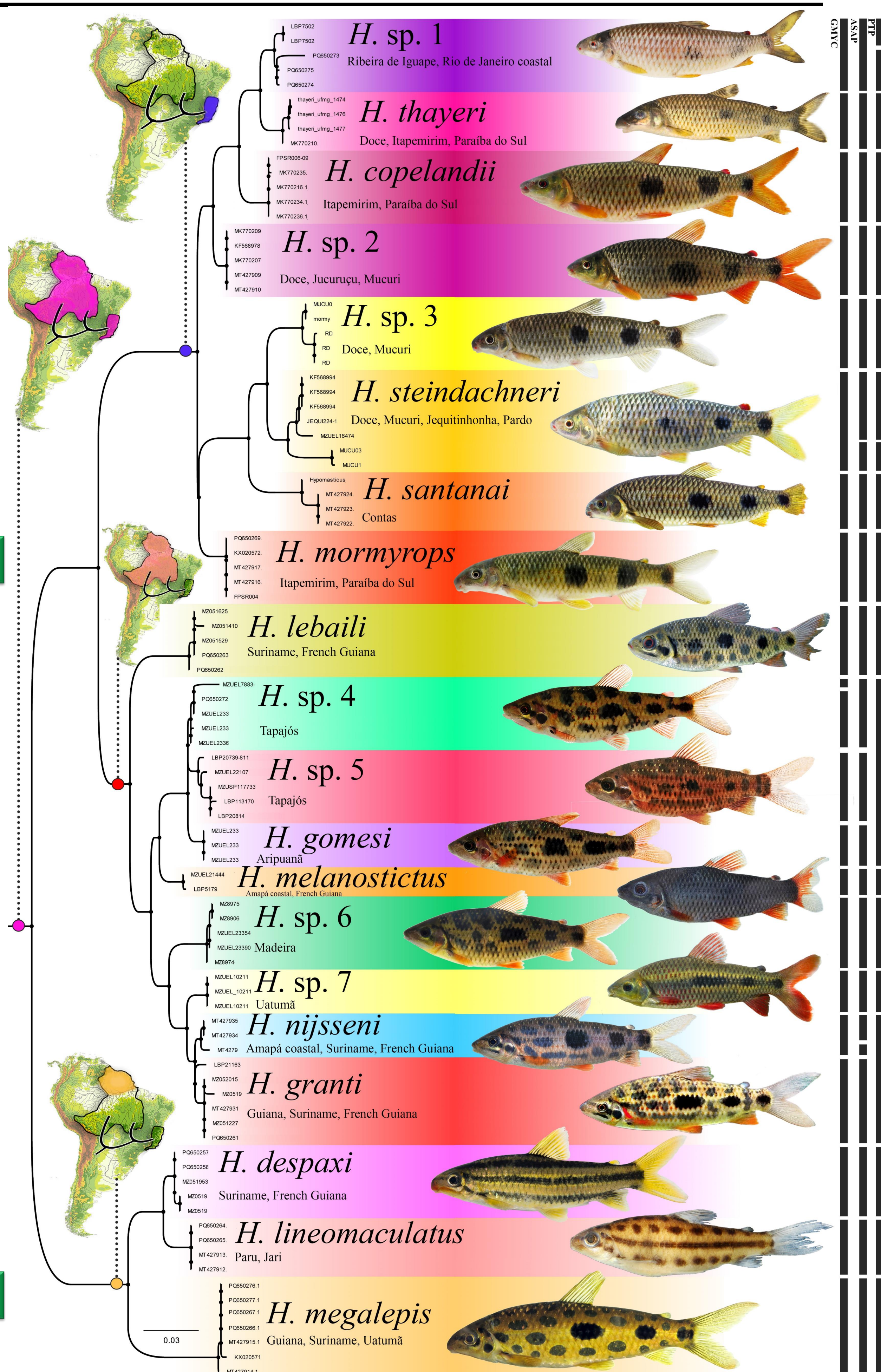
Tissue samples were collected from various river basins across South America, ranging from coastal drainages of the Guiana Shield and rivers of the Amazonian Shield, to Brazilian coastal drainages.

A ~640 bp fragment of the mitochondrial gene Cytochrome c Oxidase I (COI) was amplified and sequenced for molecular analyses. All available sequences from online repositories were also included.

The data were used to construct a phylogenetic tree to visualize species relationships and apply species delimitation analyses. Species delimitation was performed using three mitochondrial DNA-based approaches: ASAP, GMYC, and PTP.

RESULTS & DISCUSSION

The use of DNA barcoding as a taxonomic investigative tool revealed the existence of seven undescribed species, four from Amazonian basins and three from Brazilian coastal drainages, representing a 41.18% increase in species richness for the genus.



CONCLUSION

This study highlights the great utility of DNA barcoding as an investigative tool in Anostomidae, particularly within *Hypomasticus*, and demonstrates how the genus's hidden diversity underscores the need for a more comprehensive taxonomic revision.