

Publication

The puzzling phylogeography of the haplochromine cichlid fish *Astatotilapia burtoni***JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**

ID 4492983

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Astatotilapia burtoni is a member of the "modern haplochromines," the most species-rich lineage within the family of cichlid fishes. Although the species has been in use as research model in various fields of research since almost seven decades, including developmental biology, neurobiology, genetics and genomics, and behavioral biology, little is known about its spatial distribution and phylogeography. Here, we examine the population structure and phylogeographic history of *A. burtoni* throughout its entire distribution range in the Lake Tanganyika basin. In addition, we include several *A. burtoni* laboratory strains to trace back their origin from wild populations. To this end, we reconstruct phylogenetic relationships based on sequences of the mitochondrial DNA (mtDNA) control region (d-loop) as well as thousands of genomewide single nucleotide polymorphisms (SNPs) derived from restriction-associated DNA sequencing. Our analyses reveal high population structure and deep divergence among several lineages, however, with discordant nuclear and mtDNA phylogenetic inferences. Whereas the SNP-based phylogenetic hypothesis uncovers an unexpectedly deep split in *A. burtoni*, separating the populations in the southern part of the Lake Tanganyika basin from those in the northern part, analyses of the mtDNA control region suggest deep divergence between populations from the southwestern shoreline and populations from the northern and southeastern shorelines of Lake Tanganyika. This phylogeographic pattern and mitochondrial haplotype sharing between populations from the very North and the very South of Lake Tanganyika can only partly be explained by introgression linked to lake-level fluctuations leading to past contact zones between otherwise isolated populations and large-scale migration events.

Publisher WILEY**ISSN/ISBN** 2045-7758**edoc-URL** <https://edoc.unibas.ch/67918/>**Full Text on edoc** No;**Digital Object Identifier DOI** 10.1002/ece3.4092**PubMed ID** <http://www.ncbi.nlm.nih.gov/pubmed/29938080>**ISI-Number** WOS:000435776600037**Document type (ISI)** Article