



AI-ASSISTED REVIEW OF THE SCIENTIFIC LITERATURE ON MITOCHONDRIAL HETEROPLASMY IN FISH

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Identifying mitochondrial heteroplasmy in fish has become increasingly relevant for studies involving eDNA analyses, species conservation, and genetic identification, especially for differentiating native and hybrid species. This study aimed to identify fish species previously reported to exhibit mitochondrial heteroplasmy. We used the GPT-4o-mini artificial intelligence model to screen articles on mitochondrial heteroplasmy based on titles, abstracts, and keywords from records retrieved from Scopus. FishBase was used to confirm the taxonomic identity and habitat classification of the species identified. A total of 58 fish species with reported mitochondrial heteroplasmy were identified in the literature. The main mitochondrial regions associated with heteroplasmy were the control region, with 41 records; protein-coding genes, with 14 records; and unidentified regions, with 18 records. Among specific locations, the control region was the most frequently reported, with 38 records, followed by the *ND6* gene, with 3 records, and the *COI* gene, with 2 records. Of the 58 species, 20 were freshwater species, 27 were marine species, and 11 were species that move between freshwater and marine environments. Among freshwater species, *Hypoptopoma incognitum* was highlighted. Our results indicate that mitochondrial heteroplasmy in fish is most frequently reported in the mtDNA control region, but it can also occur in protein-coding genes, including genes commonly used as eDNA markers. The relatively small number of species reported also suggests an important knowledge gap regarding the occurrence of mitochondrial heteroplasmy in fish. Finally, this study highlights the potential of AI tools to support the screening and organization of scientific data, contributing to studies on conservation, genetic identification, and eDNA-based analyses.

Keywords: *bioinformatics, Control region, FishBase, limnology, mtDNA.*