

Abstract

Widespread Gene Reorganizations in Teleost Mitochondria Are Driven by Ecological Transitions [†]

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[†] Presented at the XI Iberian Congress of Ichthyology, Vila Real, Portugal, 23–27 June 2026.

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Abstract

The vertebrate mitochondrial genome (mitogenome) is a small, circular DNA molecule typically ~16–17 kb in length, encoding 37 genes that are essential for the electron transport chain, the mechanism that drives mostly all the ATP synthesis in cells. Owing to its central role in energy metabolism, its structure is highly conserved across vertebrate lineages in both the number and relative position of each gene in the genome. Nevertheless, different variations have been found in several teleost lineages, including antarctic fishes (Nototheniidae), gadiforms, hatchetfishes (Sternoptychidae), and Batrachoidiformes. The explanation for these phenomena remains unknown yet may reflect shifts in functional constraints and can provide insights into lineage-specific and/or coevolutionary processes. This raises the possibility that mitogenome structure is related to habitat selection, potentially reflecting environmental influences on energetic regulation. To further test this hypothesis, we studied more than 400 teleost species across all major teleost lineages. The mitogenome sequences were downloaded from NCBI and annotated using two independent algorithms (MITOZ and MITOS) and then compared with a reference (*Danio rerio*) to find any deviation from the standard structure. Similarly, ecological data was downloaded from FishBase using the R Package “rfishbase” 5.0.3. Two independent ancestral reconstruction analyses were carried out for both traits, “Mitogenome” and “Habitat”, using a reference evolutionary tree for teleosts to unravel both evolutionary histories. The possible association between mitogenome and habitat was then assessed using a suite of phylogenetic comparative methods, including Pagel’s correlation test (corHMM) to evaluate whether both traits evolved in a correlated fashion, branch-level co-transition analysis to identify lineages where structural changes and habitat shifts co-occurred, and node-by-node comparisons of ancestral state probabilities across the phylogeny. Preliminary results suggest a correlation between some deep-sea environments and a modified mitogenome structure, with structural deviations tending to cluster in lineages inhabiting greater depths. These exploratory findings raise the possibility that changes in mitogenome architecture may be linked to adaptations in energetic metabolism required for life in extreme low-energy environments. Further analyses are underway to clarify the functional significance of these genomic changes and their relationship to ecological and metabolic pressures in teleost evolution.

Keywords: mitogenome; ancestral state reconstruction; deep-sea



Academic Editor: Alberto Teodorico Correia

Published: 18 June 2026

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Author Contributions: Conceptualization, D.B.-G. and F.B., sampling and laboratory, F.B., software analysis, A.G.-d.-S., D.B.-G. and A.M.M., original draft preparation, D.B.-G., review and editing, A.G.-d.-S., A.M.M. and F.B., funding acquisition, F.B. All authors have read and agreed to the published version of the manuscript.

Funding: Fundaçao para a Ciencia e a Tecnologia (FCT) supported DBG (2020.04364.CEECIND/CP1599/CT0008 and DOI identifier <https://doi.org/10.54499/2020.04364.CEECIND/CP1599/CT0008>) and AGS (2023.07625.CEECIND/CP2848/CT0010 and DOI identifier <https://doi.org/10.54499/2023.07625.CEECIND/CP2848/CT0010>). FCT also provided funds within the scope of the Strategic Funding UIDB/04423/2020 (<https://doi.org/10.54499/UIDB/04423/2020>), UIDP/04423/2020 (<https://doi.org/10.54499/UIDP/04423/2020>), and LA/P/0101/2020 (<https://doi.org/10.54499/LA/P/0101/2020>).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Openly available data.

Conflicts of Interest: The authors declare no conflicts of interest.

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