Special Issue

Molecular Phylogenetics and Mitochondrial Evolution

Message from the Guest Editors

Is mitochondrial phylogenetics trustworthy? In fact, mitochondrial genes are long-time phylogenetic markers: they are widely used to infer evolutionary trees across all eukaryotic realms, making *cox1*, *rrnL*, and their kin possibly the most popular genes in the world. They were initially chosen because of some key features that they were supposed to share universally. In recent years, an increasing body of knowledge has shown several exceptions, including evidence of recombination, noncanonical ways of mitochondrial inheritance, strong selective constraints on some mitochondrial regions, and complex interactions with the nuclear genome. Conversely, massive sequencing technologies brought phylogeny into the -omics era, and the use of ESTs and transcriptomes is now common in phylogenetics, often unveiling discrepancies between the signal massively retrieved from nuclear sources and the signal carried by weird organellar chromosomes. This Special Issue aims to unravel different topics on mitochondrial evolution, with special emphasis on their implications on phylogenetic reconstruction.

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Deadline for manuscript submissions

closed (10 June 2021)

Life

an Open Access Journal by MDPI

Impact Factor 3.4
CiteScore 6.0
Indexed in PubMed

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Life (ISSN 2075-1729) is an international, peer-reviewed open access journal that publishes scientific studies related to fundamental themes in life sciences. Some papers are published individually, while others are submitted for inclusion in special issues with guest editors. You are invited to contribute a research article, essay, or a review to be considered for publication.

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