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Molecular Phylogenetics and Mitochondrial Evolution

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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*, *rnl*, 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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Special Issue



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Message from the Editor-in-Chief

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