

# Editorial: Evolution of Mitochondrial Genomes

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Animal mitochondria have their own genome (mtDNA), which is typically described as small (~16 kb), circular and maternally inherited with 37 genes, i.e. 13 for protein-coding genes involved in ATP production, and 22 for transfer RNAs and two for ribosomal RNAs. However, recent data show that the functional repertoire of the animal mtDNA has been underestimated, even in humans. Moreover, while several animal groups are relatively conservative in terms of their mt genome content and organization, recent studies revealed that some groups exhibit an astonishing diversity in mt chromosome form and number as well as coding content and organization.

One aim of this Research Topic was to better understand the evolutionary processes that underlie the structural and functional diversity of mt genomes (e.g. Nishimura et al. 2020; Roy Smith 2020), which content is paradoxically thought to be distilled to its core minimum (reviewed in Lane 2006). For example, one major difference in mitochondrial gene content between animals and plants + some unicellular eukaryotes resides in the occurrence in the latter two of cytochrome *c* maturation genes, or *ccm* genes. In their study, Nishimura et al. were interested in two evolutionarily distinct systems for cytochrome *c* maturation in mitochondria—Systems I and III—the former involves a set of mitochondrion-encoded proteins whereas the latter is operated exclusively by nucleus-encoded proteins. Specifically, the authors tested the previous hypothesis that cytochrome *c* maturation switched from System I to III in the early evolution of Cryptista, one of the major taxonomic clades of eukaryotes, by sequencing two new mtDNAs from two key cryptist members. The two newly sequenced mtDNAs revealed a patchy distribution of the two evolutionarily distinct systems and prompted the authors to revise previously proposed scenarios for the evolution of cytochrome *c* maturation in this group. In another study, Smith (2020) focused on the proliferation of a repeat element that is common to the mt and plastid (pt) genomes in chlamydomonadalean green algae. In this singular model, mt and pt genomes share a large proportion of identical sequences, an observation that is quite remarkable owing to its rarity. The evolutionary origin of this phenomenon, which is however little understood, could be due to horizontal gene transfer.

Another aim of this Research Topic was to disentangle the evolutionary history of some animal groups at a wide scale (from micro- to macro-evolutionary scales), using characters of mt genomes or complete mtDNA sequences. Indeed, some characters, such

as atypical secondary structures of transfer RNAs, which have been consistently found in nematodes, insects, spiders, mites and ticks, have potential value to decipher the phylogeny and evolution of animals at a higher level (class, order or family). For example, Du et al. (2020) used whole mt genomes at the population scale to infer processes of genetic diversity as well as population divergence and differentiation. Kern et al. (2020), reviewing the use of mt genomes in nematode phylogenies, have shown that complete mtDNA sequences (1) have higher resolutions than partial gene sequences (2) suggest alternative topologies compared to nuclear markers, and (3), perhaps most importantly, that gene order offers an informative character for studying nematode evolution. Overall, this Research Topic aimed at elucidating the genetic, life history, and ecological factors that contribute to the evolutionary dynamics of mt genomes in animals.

## References

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