

Trematominae and Artedidraconinae: contrasted mitogenome evolution for two Antarctic radiations

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Cellular respiration has been widely studied in Antarctic teleost fishes because of their peculiar adaptations to an extreme environment. In parallel mitochondrial sequence markers have become highly popular for molecular systematics. However, there are few whole mitochondrial genome sequences published, and none available for some of the subfamilies. Here, we present two large mitogenome datasets including most species and multiple sequences for many species of two subfamilies, Trematominae and Artedidraconinae (Duhamel et al. 2014). These include two highly diverse but very different adaptative radiations, with contrasting divergence dates, morphological polymorphism, and habitat dominance. The sampling is based on a well identified, extensive collection resulting from the 2008 CEAMARC survey and the subsequent REVOLTA surveys in Terre Adélie (IPEV), already DNA barcoded and sequenced in previous studies. The mitogenome sequences for these two subfamilies differ in composition, gene order, and relative divergence of mitochondrial markers, with strong, taxon-specific biases like very high C contents in some regions. The gene order change provides a synapomorphy for the subfamily Trematominae and an interesting development in teleost mitogenomes. The complete Artedidraconinae mitogenomes provide a much higher amount of variable sites (approx*30), while previous sequence datasets were plagued by low informativeness (Lecointre et al. 2011). As already established on single mitochondrial genes, intraspecific variability is lower than interspecific variability within each subfamily, however interspecific variability in Artedidraconinae is lower or similar to intraspecific variability in Trematominae. This expanded dataset confirms the unusual evolution of the mitochondrial coded sequences involved in the cellular respiration in Antarctic Nototheniidae, as well as the usefulness of complete mitochondrial genomes for their systematics. The two level multiplexing (Timmermans et al. 2010) and next generation sequencing of long PCR amplicons (following Hinsinger et al. 2015) is efficient to obtain large mitogenomic datasets representative of both inter- and intraspecific variability, key to the understanding of mitochondrial evolution and a step closer to resolving the relationships among these taxa.

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