Mitochondrial genomes of ostracods from the Southern Ocean

Schön Isa[1], Martens Koen[1], Nunes Brandao Simone[2] and Agnès Duettai[3]

[1] Royal Belgian Institute of Natural Sciences, OD Nature, Aquatic and Terrestrial Ecology, Freshwater Biology, Vautierstraat 29, B-1000 Brussels, Belgium
E-mail: isa.schoen@naturalsciences.be
[2] Universidade Federal do Rio Grande do Norte, Departamento de Geologia (UFRN), Campus Universitário Lagoa Nova CEP 59072-970 Natal, RN, Brasil
[3] Département Systématique & Evolution,Muséum National d'Histoire Naturelle, 57 rue Cuvier, 75231 PARIS cedex 05, France

Ostracods are small, bivalved crustaceans occurring in all aquatic habitats. They also form an important component of marine microbenthos. Phylogenetic research on Macroscaphidae from the Southern Ocean (Nunes Brandao et al. 2010) showed that species from this family with circum-antarctic distribution are in fact a species complex with different morphological and cryptic species and limited geographic distribution. Further molecular studies on this taxonomic group have been hampered by the lack of suitable markers. The small size of ostracods and low amount of DNA makes it also still impossible to apply next-generation sequencing methods (NGS) like RAD seq.

An alternative are mitochondrial genomes, which are currently easy to amplify and sequence at low cost (Hinsinger et al. 2015). Because of their length of thousands of nucleotides, mitogenomes can improve the unravelling of phylogeographic relationships and dating of evolutionary events (see, for example, Keis et al. 2013) and, through comparisons with non-Antarctic taxa, allow to detect cold adaptations as for example in amphipods from Lake Baikal (Naumenko et al. 2017) and Antarctic nototheniids (Mark et al. 2012). Up to now, only few mitogenomes are available for ostracods. Ogoh & Ohmiya (2004, 2007) sequenced mitogenomse of the Japanese, bioluminescent myodocopid ostracod *Vargula hilgendorffi* from several populations, and an incomplete, unpublished mitogenome is available in Genbank from the non-marine ostracod *Cypridopsis vidua* (Genbank accession number KP063117.1). Both species are only very distantly related to ostracods from the Southern Ocean. Here, we will present our first results on the mitogenomes of Macroscaphidae from the Southern Ocean and compare these with mitogenomes of non-marine ostracods from cold Lake Baikal, tropical Lake Tanganyika and the putative ancient asexual ostracod *Darwinula stevensoni* with a General Purpose Genotype (Van Doninck et al. 2002).

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