

Understanding the biodiversity and evolutionary history of the amphipod genus *Eusirus* in the Southern Ocean

Frédérich Bruno¹, Lepoint Gilles², Verheye Marie³, Schön Isa^{3,4} and Salabao Louraine^{4,1}

¹ Laboratory of Functional and Evolutionary Morphology, Allée du 6 Août, 15, Liege (Sart-Tilman), Université de Liège, 4000 Liège, Belgium
E-mail: bruno.frederich@uliege.be

² Laboratory of Oceanology, MARE Centre, Allée du 6 Août, 15, Liege (Sart-Tilman), Université de Liège, 4000 Liège, Belgium

³ Royal Belgian Institute of Natural Sciences, OD Nature, Freshwater Biology, Vautierstraat 29, 1000 Brussels, Belgium

⁴ Centre for Environmental Sciences, Zoology, Toxicology and Biodiversity, Campus Diepenbeek, Agoralaan Gebouw D, 3590 Diepenbeek, Belgium

The diversity of the Antarctic marine fauna has been shaped by various evolutionary processes (dispersals, diversifications, extinctions), which were greatly influenced by the geological and climatic history of the region. Some Antarctic lineages are descendants of Gondwanan ancestors and arose by vicariance during the progressive breakup of Gondwana, which ultimately led to the complete geographical isolation of the Antarctic continent. The Plio-Pleistocene glacial cycles have been inferred to act as a “diversity pump” on the Antarctic continental shelf. Allopatric speciation of less dispersive organisms could have resulted from the isolation of populations in ice-free refugia during the glacial advances. These glacial cycles were often suggested to have influenced the diversification of numerous complexes of closely related and morphologically very similar Antarctic species. The continuous discovery of such (pseudo-) cryptic species in the Southern Ocean suggests that its biodiversity is currently greatly underestimated. Such species complexes have been found in the amphipod genus *Eusirus*. In a preliminary phylogeny (COI and 28S) of the whole genus, some Antarctic nominal *Eusirus* species are composed of genetically distant clades, suggesting putative new species. In this study, we will sequence complete mitochondrial genomes, using a combination of skim sequencing and long-range PCRs of different *Eusirus* species, to which sequence data from nuclear (28S, ITS2) will be added. By greatly increasing character sampling as well as taxon sampling (including Antarctic and non-Antarctic species) compared to preliminary studies, we intend to reconstruct a robust phylogeny of the genus. Based on this DNA dataset and the phylogeny, we aim to (1) provide a better estimate of the actual diversity within the genus, using various DNA-based species delimitation methods (GMYC, PTP, 4 theta rule and ABDG) and; (2) provide a better understanding of their evolutionary history: where does the Antarctic clade come from? Did *Eusirus* species disperse in and/or out of the Antarctic shelf at any time of their evolutionary history? Were there periods of increased diversification during their evolution on the shelf and how do these relate to the geological/glacial history of the region?

Keywords: Evolutionary history; Biodiversity; Southern Ocean; Amphipoda; *Eusirus*