

Phylogeography and cryptic diversity of *Charcotia* amphipods in the Southern Ocean

Aerts Dorien^{1,2}, Christiansen Henrik¹, Van De Putte Anton^{1,2,3}, Volckaert Filip¹ and Schön Isa^{2,4}

¹ Laboratory of Biodiversity and Evolutionary Genomics (LBEG), KU Leuven, Charles Deberiotstraat 32, Leuven, Belgium

E-mail: daerts@naturalsciences.be

² Royal Belgian Institute for Natural Sciences (RBINS), Vautierstraat 29, 1000 Brussel, Belgium

³ Marine Biology Laboratory, Université Libre de Bruxelles (ULB), Avenue F.D. Roosevelt 50, 1050 Brussel, Belgium

⁴ Zoology Research Group, University of Hasselt, Agoralaan gebouw D, 3590 Diepenbeek, Belgium

Polar ecosystems are among the fastest changing regions on earth, causing a shift in species distributions, changes in food web dynamics and decreasing productivity (Harley *et al.*, 2006). A long history of oceanographic isolation has led to **high levels of endemism in the Southern Ocean (SO)** resulting in a hotspot of biodiversity for many crustaceans (Malacostraca) (Crame, 2018). Furthermore, it is expected that **species inventories in the SO are underestimated** due to high levels of eurybathy as adaptation to the oscillating ice caps in the past (Arntz *et al.*, 1994; Brey *et al.*, 1996). Molecular studies revealed that numerous species are in fact (cryptic) species complexes of morphologically similar individuals. **Cryptic speciation** has been documented across **all ecological groups of amphipods** (Havermans, 2016; Katouzian *et al.*, 2016). Amphipods are ideal model organisms to link evolutionary processes, with local ecological dynamics since their **limited dispersal capabilities** represent natural replicates (Fišer *et al.*, 2018). In this study we investigate the species composition of two *Charcotia* amphipods from the SO. The genus is part of the superfamily Lysianassoidea which is one of the most dominant gammarid amphipod groups in the SO (De Broyer *et al.*, 2004). The genus, formerly known as *Waldeckia* (Chevreux, 1906), contains 16 morphospecies of which two live in Antarctic waters, i.e. ***Charcotia obesa* and *C. amundseni*** (D'Udekem D'Acoz *et al.*, 2018). Both species are **strictly benthic scavengers**, but differ in depth range, 0-200 m for *C. obesa* and 150-1000 m for *C. amundseni*. They play an important role in the Antarctic trophic food web as scavengers and prey of higher trophic levels (Linkowski *et al.*, 1983; Offredo & Ridoux, 1986). We used mitochondrial COI DNA sequencing data to investigate species boundaries, based on phylogeny and haplotype networks in combination with DNA-based methods. **Preliminary results indicate higher levels of biodiversity than previously thought.** Further population genetic research based on single nucleotide polymorphisms (SNP) should help in defining conclusive species boundaries in combination with taxonomic studies. This knowledge on speciation supports sound biodiversity management and conservation of the precious biota of the SO.

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