

DNA barcoding of hyperiid amphipods along the 2012 Atlantic Meridional Transect

Marloes Tump¹, Alice Burridge^{1,2}, Ronald Vonk^{1,2}, Erica Goetze³ and Katja T.C.A. Peijnenburg^{1,2}

¹ Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, The Netherlands

² Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, P.O. Box 94248, 1090 GE Amsterdam, The Netherlands

³ Department of Oceanography, University of Hawaii at Manoa, 1000 Pope Road, Honolulu, HI, 96822, USA

Hyperiid amphipods are a highly diverse marine macrozooplankton group that have successfully invaded a variety of open ocean ecosystems. Despite their worldwide distribution and numerous studies focused on their morphological characteristics, little is known about the genetic diversity of hyperiid amphipods. We examined genetic diversity based on DNA sequences of the mitochondrial cytochrome oxidase subunit I (COI) gene of hyperiids collected along a latitudinal transect in the Atlantic Ocean (AMT Cruise 22) to assess the validity of morphologically identified species. Hyperiids were collected at night from the upper ~300m at 21 locations from 34°N to 45°S. COI sequences were collected for 120 specimen representing 65 morphologically identified hyperiid species belonging to 35 genera. We extended our dataset with 51 GenBank sequences from near-shore environments of East-Japan, Hawaii (USA), Florida (USA), California (USA), Germany and the Weddel sea. Among the included specimens were three putative novel species in the genera *Lycaea*, *Brachyscelus* and *Parapronoe*, which resembled distinct clades in the mitochondrial gene tree. Although the COI barcode region showed too much variation to resolve higher level taxonomic arrangements, we found it a valuable marker for hyperiid species identification and discovery.

Keywords: Hyperiid amphipods, genetic diversity, Atlantic Meridional Transect, DNA barcoding

E-mail: m_tump@msn.com