

BioSyst.EU 2013
Global systematics!



universität
wien

NOBIS AUSTRIA
NETWORK OF BIOLOGICAL SYSTEMATICS

naturhistorisches
museum wien **nhm**



GfBS
Gesellschaft für
Biologische Systematik
Organismen Diversität Evolution



SWISS
SYSTEMATICS
SOCIETY



Svenska Systematikföreningen

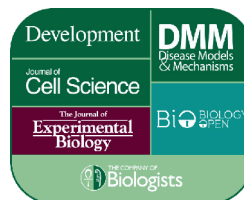
BioSyst.EU 2013 Global systematics! 18-22 February 2013

Abstract volume

Austrian
Official Carrier

Springer

Sponsored by



LGC Genomics

KBio science
Incorporating



We make it visible. **BRILL**

Evidences for several species within the cosmopolitan eurybathic deep-sea lysianassoid amphipod *Eurythenes gryllus* s.l. [Poster]

Charlotte Havermans

Royal Belgian Institute of Natural Sciences, Brussels, Belgium

Gontran Sonet

Royal Belgian Institute of Natural Sciences, Brussels, Belgium

Zoltan Nagy

Royal Belgian Institute of Natural Sciences, Brussels, Belgium

Torben Riehl

Centre for Marine Biodiversity Research, Senckenberg Research Institute, Hamburg, Germany

Saskia Brix

Centre for Marine Biodiversity Research, Senckenberg Research Institute, Hamburg, Germany

Patrick Martin (presenter)

Royal Belgian Institute of Natural Sciences, Brussels, Belgium; Patrick.Martin@naturalsciences.be

Christoph Held

Department of Functional Ecology, Alfred Wegener Institute for Polar and Marine Research, Bremerhaven, Germany

Cédric d'Udekem d'Acoz

Royal Belgian Institute of Natural Sciences, Brussels, Belgium

Eurythenes gryllus (Lichtenstein, 1822) is a presumed cosmopolitan eurybathic benthopelagic giant deep-sea amphipod. However, previous studies already highlighted genetically divergent lineages in the Atlantic and Pacific Oceans, which appeared to be vertically stratified, and minor morphological differences between populations were also recorded. With an aim to quantify the geographic and bathymetric patterns of genetic variations, the genetic diversity in *Eurythenes gryllus* was investigated at the global scale (Arctic, Atlantic, Pacific and Southern Oceans) using three different genes (COI, 16S rRNA, 28S rRNA). This genetic analysis was accompanied by a thorough morphological study. Phylogenetic and phylogeographic analyses revealed the existence of at least eight well-supported clades, two bathyal and six abyssal, which were separated by genetic distances at the level of usual interspecific divergences. A subsequent morphological analysis confirmed the genetic findings and revealed small but consistent differences between the different clades, which will be described as separate species. Furthermore, a clear genetic break was observed between specimens sampled above and below 3000 m. This bathymetric break below 3000 m has already been reported for several organisms and regions, suggesting its role as a ubiquitous phylogeographic barrier for barophysical tolerance. The *Eurythenes* clade, comprising specimens sampled at bathyal sites in the Arctic and Southern Oceans, is presumably the true *E. gryllus*. This represents, to our knowledge, the first molecular evidence for a bipolar distribution in a macro-benthic deep-sea organism. The present results clearly highlight the difficult nature of research on the systematics of deep-sea crustaceans and shows that the abyss is a more complex environment than previously assumed, likely to harbour an important hidden diversity.

SmartHerper Comoros, a free field guide to the herpetofauna of the Comoro archipelago as a mobile application [Software Bazar]

Oliver Hawlitschek

Zoologische Staatssammlung München, Münchhausenstr. 21, 81247 Munich, Germany; Zoologische Staatssammlung München, Münchhausenstr. 21, 81247 Munich, Germany; oliver.hawlitschek@gmx.de