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POPULATION STRUCTURING OF *CALANUS HELGOLANDICUS* S.L. IN EUROPEAN WATERS

L. Yebra ^{1*}, D. Bonnet ², R. P. Harris ³, P. K. Lindeque ³ and K. T. Peijnenburg ⁴

¹ Instituto Español de Oceanografía, Centro Oceanográfico de Málaga, Apdo. 285, 29640 Fuengirola, Málaga, Spain - lidia.yebra@ma.ieo.es

² Ecosystèmes lagunaires, Unité mixte de recherche CNRS-UMI 5119, Université Montpellier II, Place Eugène Bataillon, Case Courrier 093, 34095 Montpellier Cedex 5, France

³ Plymouth Marine Laboratory, Prospect Place, Plymouth, PL1 3DH, UK

⁴ Marine Biodiversity, Ecology and Evolution, UCD School of Biology and Environmental Science, Science and Education Research Centre (West), University College Dublin, Belfield, Dublin 4, Republic of Ireland

Abstract

Calanus helgolandicus s.l. genetic differences have been identified for the first time between and within European basins, as well as a decrease of prosome length with latitude. Our study explores the population structuring of this key species in relation to morphology, genetics and hydrography.

Keywords: *Copepoda*, *Biogeography*, *Hydrography*, *Genetics*

The marine copepod *Calanus helgolandicus* is of considerable importance in the marine food web. It plays a critical role in marine ecosystems as a grazer of microplankton and as a major food source for commercially important fish. The distribution of *C. helgolandicus* in European waters covers a wide range of habitats, from open ocean to coastal environments. Recent studies [1, 2] have shown that *C. helgolandicus* is sensitive to changes in climate. Its distribution range and abundance has increased as European waters have warmed over recent decades. Building on the network of laboratories created by Bonnet *et al.* for their review on *C. helgolandicus* (2005), we collected samples in 95% ethanol from 19 European sites (figure 1).

R. Diekman, A. Dos Santos, E. Gaard, S.H. Jonasdottir, L. Kamburska, D. Lucic, M.G. Mazzocchi, J.C. Nejtgaard, S. Poulet, A. Ramfos, P. Thor and V. Tirelli for supplying *Calanus helgolandicus* specimens. We thank P. Pickerill for his sequencing of the samples, D. Conway for his help in sorting and identifying *C. helgolandicus* from the various samples received, and L. Blanco-Bercial and A. Bucklin for their comments on the early manuscript. This work was undertaken while L.Yebra and D. Bonnet were at the Zooplankton Group at Plymouth Marine Laboratory (PML). This work is a contribution to the PML Core Strategic Programme.

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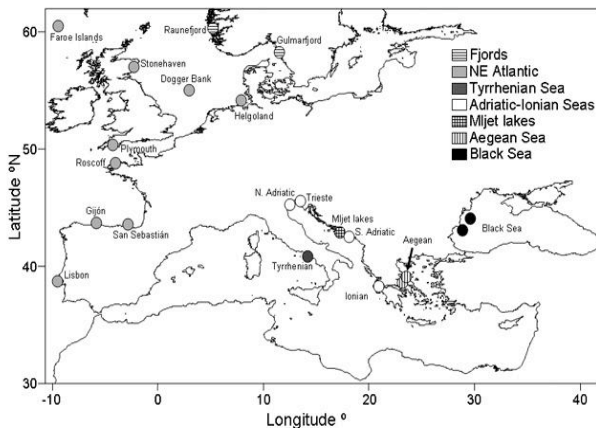


Fig. 1. Map of the stations. Different shades indicate different genetic regions: Fjords, NE Atlantic, Tyrrhenian Sea, Adriatic and Ionian Seas, Mljet lakes, Aegean Sea, Black Sea

To reveal barriers to dispersal within this species' distribution range (including the closely related *C. euxinus* from the Black Sea) we compared morphological (prosome and urosome length) and genetic (mitochondrial 16S rDNA gene) structuring of populations and linked these with sea surface temperature and other hydrographic features. *Calanus* populations showed high levels of genetic diversity and strong population genetic structuring with six major groupings: (1) NE Atlantic and Tyrrhenian Sea, including the subgroup (2) northern fjords, (3) Eastern Mediterranean, which contained subgroups (4) seawater lakes of Mljet island in the Adriatic Sea and (5) Aegean Sea, and (6) Black Sea. Morphological structuring is congruent with the genetic groupings within the E Mediterranean. However, groupings differed within the Atlantic, where latitude (i.e. temperature) appears to affect morphology more than gene flow. *Calanus* populations from the Mljet lakes, Aegean Sea and Black Sea are isolated at the genetic, morphological and hydrographical levels and might represent incipient species.

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