

MALDI-TOF mass spectrometry as a novel tool for zooplankton biodiversity studies - Copepod distribution throughout the eastern Atlantic Ocean

Maya Bode^{1*}, Silke Laakmann², Patricia Kaiser¹, Wilhelm Hagen¹, Holger Auel¹, Astrid Cornils³

1 BreMarE - Bremen Marine Ecology, Marine Zoology, University of Bremen, P.O. Box 330440, 28334 Bremen, Germany

2 Senckenberg Research Institute, German Center for Marine Biodiversity Research (DZMB), Südstrand 44, 26382 Wilhelmshaven, Germany

3 Alfred Wegener Institute for Polar and Marine Research, Am Alten Hafen 26, 27568 Bremerhaven, Germany

*corresponding author email: mabode@uni-bremen.de

Keywords: COI, protein fingerprinting, species identification, copepod abundance

Abstract

Copepods dominate mesozooplankton communities in all marine regions. Their diversity is mainly regulated by environmental parameters and species-specific ecophysiological performances. Hence, distributional patterns of certain species may serve as environmental indicators for crucial changes in the marine habitat. We studied copepod distribution and diversity at six stations along a meridional transect in the eastern Atlantic Ocean (25°N to 21°S) via stratified sampling from the surface to a maximum depth of 2000 m. Community and trophic structures were analyzed with special focus on calanoid copepods. Below the euphotic zone, representatives of the family Spinocalanidae were particularly abundant and species identification of adult and juvenile stages based on morphological features was a real challenge. To elucidate diversity as well as species- and stage-specific vertical distribution patterns of Spinocalanidae we applied an integrated taxonomic approach combining morphology, DNA sequence analyses and proteomics using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). These three methodologies were performed on fractions of each copepod specimen. Species clusters were similar for DNA sequence analyses and MALDI-TOF MS, both resulting in higher amounts of species clusters than revealed by morphological identifications. Since MALDI-TOF MS is a rather time- and cost-efficient technology, we were able to identify large numbers of spinocalanid specimens. This yielded quantitative information with high species and stage-resolution on the diversity of adult and juvenile Spinocalanidae and their distributional patterns.