

Integrated North Sea zooplankton identification: a combination of morphology, DNA and proteome analyses towards a cost and time-effective application

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In the course of taking stock of the Southern North Sea zooplankton diversity, traditional morphological and recent molecular techniques were combined and applied for species identifications. DNA sequence analyses were based on mitochondrial cytochrome c oxidase subunit I (COI) and nuclear ribosomal 18S sequences. Reliably identified specimens were used to test proteomic fingerprinting by applying the technology of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) as alternative method for valid, rapid and cost-effective species identification. For calanoid copepods, hydromedusae and scyphomedusae morphological and DNA-based species identifications showed congruent results for most of the species. Incongruent results were found in one copepod and one hydromedusae species caused by the occurrence of sibling species from American Atlantic waters not recorded in the North Sea before. For some groups like calanoid copepods proteomic fingerprinting with MALDI-TOF MS technology revealed the same species clusters like the DNA sequence analysis of the two marker genes. In order to establish MALDI-TOF MS as reliable technique for rapid and low cost metazoan species identification, different zooplankton organisms including different life-history stages are tested for valid species discrimination. Once established, a reliable reference library is a promising basis for analyzing high numbers of samples in order to provide a higher coverage and resolution by including early stages in the context of e.g. estimation of species abundances.

Keywords: Species identification, DNA analysis, proteomic fingerprinting, Southern North Sea, sibling species

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