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High-resolution community analysis of deep-sea copepods using MALDI-TOF protein fingerprinting

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Abstract

Knowledge of zooplankton community structure is essential to understand ecosystem functioning. Therefore, accurate species identification is a crucial step in plankton studies. Yet, with the current array of methodologies, species richness is still largely underestimated and high-resolution distribution patterns remain unknown. A novel, cost-effective and rapid alternative to morphological or genetic approaches is the identification of species by proteomic fingerprinting based on matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). The present study aims to demonstrate the applicability of proteomic fingerprinting for large-scale identification and quantification of the pelagic copepod family Spinocalanidae Therefore, MALDI-TOF MS was applied to discriminate, identify and quantify adult and juvenile planktonic copepods of the ecologically important deep-sea copepod family Spinocalanidae from stratified depth samples (0-