

community as a whole. Metabarcoding approaches are limited by the quality and extent of properly identified taxa in available databases. However, they have been proven useful for rapid assessment of these communities and therefore could serve as a highly beneficial tool in ecological monitoring and impact assessment research.

005 **What drives marine nematode species distribution across various spatial scales in Antarctic continental shelf sediments? Insights from community and population genetic analyses**

Freija Hauquier<sup>1</sup>, Sofie Derycke<sup>1,2</sup>, Annelien Rigaux<sup>1</sup>, Bjorn Tytgat<sup>3</sup>, Frederik Leliaert<sup>1</sup>, Elie Verleyen<sup>3</sup>, Ann Vanreusel<sup>1</sup>

<sup>1</sup>Ghent University, Biology Department, Marine Biology Research Group, Ghent, Belgium

<sup>2</sup>Royal Belgian Institute of Natural Sciences, Operational Directory Taxonomy & Phylogeny, Brussels, Belgium

<sup>3</sup>Protistology and Aquatic Ecology, Ghent University, Ghent, Belgium

Understanding the processes that explain organisms' distribution patterns across the globe is a major goal in community ecology, but at the same time forms the subject of much debate. Traditionally, many studies have focused on local species-environment interactions as drivers of community composition. But what if this direct effect of environment on local communities is overrated and we merely detect a correlation between an environmental and faunal matrix because they share the same underlying spatial structure? In other words, how important are more regional large-scale processes in explaining distribution of species? And how connected are populations over larger spatial scales? Especially in the marine environment, which presents few barriers for free dispersal of organisms, such questions remain difficult to answer. This study therefore assessed community composition and genetic differentiation of free-living endobenthic nematodes at shelf depths in the Antarctic Weddell Sea, at various spatial scales. Through a combination of i) the application of some general concepts in community ecology and ii) assessment of gene flow within and between species and populations of two genera, we investigated to what extent spatial scale and environment are able to explain differences in community composition and distribution of species. Results show that in spite of the endobenthic lifestyle and associated dispersal limitation in free-living nematodes, large-scale links (> 2000 km) are present for some species, while others exhibit strong spatial patterns and population genetic structure, even at smaller geographic distances. Furthermore, in addition to a strong horizontal divergence between communities at the eastern and western side of the Weddell Sea, there was a clear vertical segregation of species between surface and deeper sediment layers. Our findings suggest that surface communities are more prone to passive transportation by means of bottom currents and hydrodynamics, responding to local environmental cues and resulting in larger contribution of species-environment relationships. Alternatively, communities buried deeper in the sediment are more restricted in their dispersal and are thus mainly structured by large-scale spatial processes.