

Experimental elucidation of meiofaunal trophic interactions: From radioactive tracer techniques to next generation sequencing

Tom Moens¹, Nele De Meester¹, Katja Guilini¹, Anna-Maria Vafeiadou¹, Ann Vanreusel¹ & Sofie Derycke²

¹ *Ghent University, Biology Department, Marine Biology Lab, Krijgslaan 281/S8, 9000 Gent, Belgium*

² *Royal Belgian Institute of Natural Sciences, Operational Directory Taxonomy & Phylogeny, Vautierstraat 29, 1000 Brussels, Belgium*

tom.moens@ugent.be

nele.demeester@ugent.be

katja.guilini@ugent.be

annamaria.vafeiadou@ugent.be

ann.vanreusel@ugent.be

sofie.derycke@naturalsciences.be

Nematodes are by far the most numerous and often also the most species-rich metazoans in aquatic sediments. They affect various ecosystem functions through a variety of trophic and non-trophic interactions. However, our understanding of the importance of nematodes in benthic ecosystem processes remains limited because a) qualitative information on the mechanisms and diversity of trophic interactions involving meiofauna is still very incomplete, and b) most interactions and processes remain poorly quantified. In addition, assessments of the potential contribution of nematodes to carbon flows still heavily rely on a black-box approach, which assigns nematodes to a limited number of feeding guilds and assumes that the trophic interactions of all members of a particular guild are at least qualitatively similar.

Here, we present a brief overview of several decades of research on the roles and trophic positions of nematodes in benthic food webs, and of our continuing struggle with some fundamental qualitative and nearly all quantitative questions. We point at large discrepancies between studies highlighting a significant contribution of nematodes to benthic carbon processing and studies showing exactly the opposite. This discrepancy has remained despite methodological advances. We argue that in order to substantially advance our understanding of nematode feeding ecology, we have to move away from the mere use of morphology-based feeding guilds and shift our focus to a) species-specific and b) context-dependent approaches, where possible encompassing inter-individual variability in resource use. We use natural stable isotope ratios to demonstrate that confamilial species (belonging to the same feeding guild) can differ substantially in resource use and even trophic position in one and the same food web, and that the same genus in different food webs may exhibit differences in feeding

ecology. We then use next generation sequencing (NGS) to analyse the microbiomes of individual nematodes and demonstrate that even cryptic nematode species, belonging to the same morphospecies complex, display species-specific resource use, and that individuals of the same species can vary substantially in their resource use. In addition to NGS, we point at novel stable-isotope approaches (NanoSIMS) which allow analysis of trophic interactions at the level of individual meiofaunal organisms.