

Assessing functional diversity of marine nematodes in the 21st century: moving away from the black box approach

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Nematodes are by far the most numerous and, at least at local scales, usually also the most species-rich metazoans in marine soft sediments. They affect ecosystem functions like nutrient cycling, organic matter decomposition and even sediment stability through a variety of trophic and non-trophic interactions with sediment microbiota. However, little is known on whether and how such functional roles depend on species composition and diversity. Assessments of nematode functional diversity still heavily rely on a black-box approach which assigns nematodes – usually at family level – to a limited number of feeding types, life-history groups, size groups or other guilds. Such guilds are of limited use for our understanding of nematode functional diversity because (a) categorically distributed descriptors of function are inherently inferior to continuous descriptors (e.g., a real size measure outperforms an assignment to size groups), (b) phylogenetic relatedness does not necessarily match functional relatedness (hence family-level approaches may be biased), and (c) functional diversity is often assessed from traits which bear little relationship with the ecosystem function at stake. We use stable isotope signatures to demonstrate differences in resource use and even in trophic level between confamiliar species. A metagenetic study of the microbiomes of individual nematodes even demonstrates differences in diet between cryptic species. These findings largely invalidate the traditional assignment of nematodes to family-level feeding guilds. We also discuss some of the latest methodological developments to unravel nematode resource utilization at the species and individual level. We then present an assessment of nematode functional diversity in relation to microbially driven ecosystem processes such as organic matter decomposition and nitrogen cycling based on relevant continuous descriptors approximating, among other factors, grazing rate and microbioturbation potential.

Keywords: functional diversity, nematodes, functional guilds, continuous descriptors of function