

## What do free-living nematodes tell us about the benthic ecosystem functioning? Insights from the northern Adriatic Sea

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Between July 2010 and July 2012, free-living nematodes were seasonally investigated at a time-series shallow site of the northern Adriatic Sea, synoptically to the estimates of several biological processes (e.g. microbial exoenzymatic activities, prokaryotic C production, primary production and benthic oxygen consumption) and the study of microphytobenthos (i.e. benthic diatoms). This effort allowed to insert nematodes within an overall evaluation of the benthic ecosystem functioning, as it is described in Franzo et al. (2016), in order to investigate the interactions between nematofauna and the other components of the ecosystem. Overall, 72 genera of free-living nematodes, belonging to 24 families, were identified indicating the presence of a well-structured assemblage both in terms of taxonomic composition and functional diversity (the latter synthetically expressed by the Maturity Index and Index of Trophic Diversity). Over the 2-year study, nematofauna showed significantly higher abundances in summer samplings. The concomitance of such peaks with those of microphytobenthos suggested a noticeable role exerted by benthic diatoms in supporting nematodes numbers. This link was additionally supported by the fact that nematodes' higher abundances during summer were mainly ascribable to epistrate feeders, i.e. nematodes that forage preferably on microalgae. The distance-based linear model (DISTLM) routine further confirmed the interactions between microphytobenthos and nematofauna since the outputs indicated Chl *a*, i.e. a proxy of microalgal abundance, as the only environmental variable that predicted the variation of nematode genera assemblage ( $F = 1.9624$ ,  $p < 0.001$ ).

Among epistrate-feeders that proliferated in summer samplings, *Ptycholaimellus* was the dominant genus. This result shed light on the interactions of nematofauna with the microbial heterotrophic component of the benthic ecosystem since *Ptycholaimellus*, an agglutinating nematode, builds complex networks of tubes that stimulate the interaction with heterotrophic microbes for the cleavage of polysaccharides with consequent repercussions for the overall degradation of the organic matter. An indication of the link between *Ptycholaimellus* and benthic prokaryotes was suggested by the significant relationship between the abundance of this genus and  $\beta$ -glucosidase rates, the latter ascribable to prokaryotic exoenzymes ( $r^2 = 0.715$ ;  $p < 0.01$ ).

Our results indicate that free-living nematodes interact with both the autotrophic and the heterotrophic microbial components of the benthic ecosystem, by exploiting microalgal proliferation during summer and by influencing prokaryotic degradation of the organic matter. Notwithstanding, since at the investigated time-series site nematofauna showed to be prone to inter-annual changes of challenging explanation, the study of this assemblage deserves to prosecute in a forthcoming time-series of data.

### Reference

Franzo, A., Cibic, T., Del Negro, P., 2016. Integrated approach for the assessment of the benthic ecosystem functioning at a coastal site in the northern Adriatic Sea. *Continental Shelf Research*, 121, 35-47.

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