

a community of those 5 species with a typical total abundance of 60 ind.cm⁻², the volume of sediment mixed per surface unit (1 m²) is 8.34x10³ cm³.d⁻¹. As a comparison, a population of *Heteromastus filiformis*, a polychaete inhabiting the same ecosystem as the studied foraminifera, can mix up to 1.44x10³ cm³.day⁻¹. These results unambiguously show that sediment reworking by benthic foraminifera is not to be neglected, and it stresses the need for further experimental work to furthering our understanding of the role of benthic foraminifera in bioturbation processes (*i.e.* particle reworking) but also the related biogeochemical fluxes at the water-sediment interface.

Keywords: Benthic foraminifera, bioturbation processes, experimental approach, species and community scales

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Genetic barcoding in marine nematodes - promises and pitfalls

Florian Scharhauser^{1,*}, Harald Gruber-Vodicka¹, Nikolaus Leisch¹, Gabriela Dang¹, Philipp Pröts¹ and Jörg Ott¹

¹ Department of Limnology and Bio-Oceanography, University of Vienna,

Althanstraße 14,UZA 1, 1090, Vienna, Austria

*f.scharhauser@gmx.at

Correct identification of marine meiofauna organism is crucial for ecological as well as for phylogenetic studies. Genetic barcoding and metabarcoding have become important and often used tools for fast and less time consuming identification of marine meiofauna. Here we compare classical PCR and metagenome barcoding approaches using members of the marine nematode order Desmodorida and highlight the importance of carefully curated and reliable databases using full length gene sequences. We compare the performance of two highly used marker gene sets (18S rRNA and COI) in correct taxonomic identification and phylogenetic studies. Depending on the marker gene and primer set classical PCR based approaches can be the source of many mistakes and therefore metagenome based tools are more reliable and less error prone with a high potential not only for one or two but a whole set of multiple marker genes or even genomes.

Keywords: Metagenome, genetic barcoding, marine nematodes, Desmodorida

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Inter-and intraspecific competition influence the resource utilization and niche width of closely related nematode species

Nele De Meester^{1,2}, Sofie Derycke^{3,1}, Annelien Rigaux^{1,2} and Tom Moens^{1,2,*}

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

² Ghent University, Centre for Molecular Phylogeny and Evolution (CeMoFe),
Ledeganckstraat 35, 9000 Gent, Belgium

³ Institute for Agricultural and Fisheries Research, Ankerstraat 1, 8400 Oostende, Belgium

*tom.moens@ugent.be

Nematode assemblages have high abundances and a high species diversity, where many species, including functionally very similar ones, coexist. This challenges competition theory, since competition should be most

severe between species with a high ecological equivalence. Species may alter their diet in response to competition, following either niche pre-emption or dominant plasticity. In the former, the superior competitor(s) can ‘monopolize’ a preferred food source, forcing weaker competitors to switch resource. In the latter, superior competitors exhibit resource plasticity and change niche width as a function of the competitive environment, be that inter- or intraspecific. Hence, competition can reduce the resource niche width of individuals, while at the same time increasing interindividual variation, thereby widening the niche width at the population level. A microbiome represents the collective genomic content of the microbiota of a host, including bacteria ingested as food. Here, we test whether intra- and interspecific competition influence the microbiome composition of two cryptic species of *Litoditis marina*. We know that when Pm I and Pm III are combined, the former can outcompete the latter. However, in the presence of Pm IV, both Pm I and Pm III are inferior competitors. We performed a monospecific experiment in which the starting densities of Pm I and Pm III were varied to assess intraspecific competition; and an interaction experiment combining Pm I with Pm III, in presence and absence of Pm IV, to evaluate interspecific competition. Nematodes were fed bacteria for two days, after which we analysed the microbiomes of 10 specimens per species using next generation sequencing of the 16S rRNA gene on an Illumina MiSeq. The microbiome of Pm III was mostly affected by interspecific competition, indicating the niche pre-emption theory. Differences in composition, diversity and biomarker taxa of the microbiome were found. The microbiome of Pm I mainly reflected a contracted individual niche width in the presence of both intra- and interspecific competition (dominant plasticity). This result indicates that individuals may mitigate the effects of competition by reducing niche overlap with both conspecific and heterospecific competitors.

Keywords: Competition, intraspecific, interspecific, nematodes, microbiomes, coexistence

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New multivariate approaches to access and predict metacommunity patterns

Gustavo Fonseca^{1,*}, Marco Brustolini², Danilo Candido Vieira¹, Fabio Cop Ferreira¹

¹Instituto do Mar – UNIFESP, R Carvalho de Mendonça 144, Santos/SP 11070-100, Brazil

²Institute of Marine Science, University of Auckland, P O Box 349, Warkworth 0941, New Zealand

*gfonseca.unifesp@gmail.com

Ecological communities are characterized by many coexisting species, which patterns are dictated by several structuring and interacting abiotic and biotic variables, which in turn rule over at multiple spatial and temporal scales. Metacommunity adds a new layer of analytical complexity, since deals with interconnected communities in space and time. Metacommunity is therefore one of the most challenging entity to be analyzed and predicted. Today analytical tools to explore a metacommunity can be separated in two groups depending whether includes or not the “a priori” categorical factors among the predictors. Till now the “a posteriori” approach lack significance tests. A posteriori tests are however particularly valuable when species distributions are discontinuous and were not considered in the sampling design. In order to explore whether there is a significant discontinuity in a data set, we introduce two methods: the kernel density estimation (KDE) and the segmented redundancy analysis (segRDA). The KDE is based on the principle of mapping the density probability function of a multivariate scatterplot and set the 95% interval as the threshold between communities. The segRDA was designed