

O09.8**Combining metagenomics with morphology-based approaches to understand microbiome –meiobenthos interactions**

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Abstract

Sediment microbiome has an essential role in regulating ecosystem functions, not only regulating primary productivity and nutrient cycling but also shaping trophic interactions with higher trophic levels. While the importance of microbiome in terrestrial soil systems is highly recognized, its role in marine aquatic environments remains much less studied. Microbiome can be highly affected by bottom up (abiotic factors) and top down (predation by meiofauna) effects. Understanding the interaction effect between abiotic and biotic factors on microbiome communities will be an essential step for future predictions of ecosystem stability. To address this knowledge gap we studied the interactions among microbiome diversity and nematode communities in highly heterogeneous Sado Estuary, SW Portugal. The samples were taken from three contrasting sites with varying sediment characteristics and human impact degrees. From each site, three replicate samples for sediment characterization (total organic matter, granulometry, total C and N), microbiome (*sensu lato*) and nematode community were taken. Total DNA from sediment was extracted using DNeasy Power Soil kit® (MOBIO, Qiagen) and processed for Illumina MiSeq platform sequencing targeting the V3-V4 region of 16S rRNA gene. Sediment characterization indicated heterogeneity between sites with distinct levels of contamination, which resulted in contrasting microbial communities. All sites showed a high α -biodiversity with predominance of Proteobacteria phylum, particularly Woeseiaceae, Desulfobacteraceae and Rhodobacteraceae families. Beside this heterogeneity in microbiome community, β -diversity was demonstrated to be very high, greatly discriminating among all three sites. Nematode composition and abundance followed a similar pattern as microbiome highlighting influential role of sediment characteristics. Combining abiotic sediment characteristics with metagenomics and morphological identification of higher trophic level communities might certainly contribute to the understanding of complex benthic interactions in marine ecosystems.

Keywords

Sado estuary (Portugal), Microbiome, benthic Nematodes, Metagenomics