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Spatial distribution patterns of microbiome and free-living benthic nematodes in response to sediment ecological conditions in Sado estuary, Portugal.

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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 [1]. While the importance of microbiome in terrestrial soil systems is being widely recognized, its role in marine aquatic environments remains much less studied [2]. Microbiome can be highly affected by bottom up (abiotic factors) and top down (predation by meiofauna) effects [3]. 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 spatial distribution patterns of microbiome communities and nematode assemblages 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, chlorophyll a and phaeopigments, contaminants: heavy metals and metalloids, organochlorine pesticides, PAH and PCBs), 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 and 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 Desulfobulbaceae families. Beside this heterogeneity in microbiome community, β -diversity of microbiome communities was demonstrated to be very high, greatly discriminating among all three sites. Instead, nematode assemblages did not yield clear distributional patterns suggesting that their response is rather driven by the within site specific factors, acting at the smaller spatial scales. Studying the relations between sediment ecological conditions and microbiome and meiobenthic communities greatly advance our understanding on benthic ecosystem functioning.

Keywords: Sediment microbiome - Benthic nematodes - Metagenomics - spatial distribution - Interactions.

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