

Diversity patterns of nematode microbiomes around a Pacific whale fall site (off-coast California)

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Nematodes are ubiquitous and numerically abundant in marine sediments, representing 85-96% of the total meiofauna community in the deep-sea. Yet, we still lack an overall understanding of the global patterns of biodiversity and biogeography for most sediment meiofauna. Even less well understood is the relationship between meiofaunal species and prokaryotic microbes, such as bacterial symbioses and predator-prey interactions. To address this knowledge deficit, we investigated nematode microbiomes at a Pacific whale fall site off the coast of California. Push core sediment samples were collected in June 2014 and immediately frozen at -80C upon collection. Individual nematodes were picked from processed sediment cores, washed in distilled water and transferred into lysis buffer to digest tissue and extract DNA. Nematode species and associated microbial taxa were identified using a combination of rRNA metabarcoding and whole-genome data, obtained via Illumina sequencing and downstream bioinformatic analysis. The goal of this work was to identify the diversity of bacterial/archaeal taxa associated with individual nematode worms at various distances from the whale fall site, including potentially chemosynthetic microbes acting as symbionts or food sources.