

Abstract:

The hadal zone marks the deepest part of the ocean and is primarily found in clusters of trench ecosystems along tectonic subduction zones. Recent studies indicated that the hadal zone harbors unique microbial communities, which are more active in the benthos and more abundant than in adjacent abyssal settings. However, the variability of microbial abundance and community structure along a trench axis, as well as the importance of viruses, remained scantily investigated. Here, we systematically quantified microbial and viral abundance from the ocean surface down to 40 centimeters into the sediment at several sampling sites along the Kermadec and Atacama trench axes and determined the benthic microbial community structures with amplicon sequencing. Microbial and viral abundances generally decreased with increasing oceanic depth and *in-situ* fixation experiments showed that these abundances were not affected by potential sampling artefacts associated with decompression and temporal heating during recovery. Combining our results with data from the Mariana and Japan trenches into a global compilation of abundance data revealed an unprecedented variability of virus-microbe ratios at great oceanic depths. In the benthos, microbial abundance followed site-specific fluctuating concentrations of organic carbon with increasing sediment depth. However, these bulk concentrations of organic carbon neither affected viral abundances along the trench axes nor benthic microbial community structure. In the case of viruses, this was most likely due to delayed response times of viral abundance to input of organic material during marine landslides. Microbial abundance in the sediment was mostly structured along a vertical redox gradient, and factors other than bulk organic carbon concentration caused the differences observed between the two trenches and between the individual trenches and their adjacent shallower settings. Phylum level changes with increasing sediment depth were driven by redox stratification. In particular, the intersection of the nitrogenous and ferruginous zones marked the recruitment of deep-biosphere taxa. Each redox zone had a distinct set of core-microbes that was present along individual trench axes and was to a large extent shared between trenches. *Scalindua* was part of this core-microbiome in the nitrogenous zone and contributed up to 91% and 67% of N_2 production in the Kermadec and Atacama trenches, respectively. As was the case for most other hadal microbes, *Scalindua* observed in hadal samples were phylogenetically similar to members of the same clade found in shallower environments. Ultimately, this study enhances our understanding of both top-down control by viral lysis and bottom-up control by biogeochemistry on benthic microbial communities in the hadal realm and beyond.