

Carbon assimilating fungi from surface ocean to subseafloor revealed by coupled phylogenetic and stable isotope analysis

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Fungi are critical to the functioning of the terrestrial carbon cycle, but their roles in the marine carbon cycle are poorly understood. Over the last decade, fungi have been discovered to be ubiquitous in the ocean leading to the hypothesis that they play an important role in the marine carbon cycle as heterotrophic microbes alongside bacteria and archaea. To test this hypothesis, we used ¹³C DNA stable isotope probing coupled with phylogenetic analyses to directly link carbon assimilation by diverse of planktonic and benthic fungi in the Benguela Upwelling System (Namibia) [1]. Across the redox stratified water column and in the underlying sediments, assimilation of ¹³C-labeled carbon from diatom extracellular polymeric substances (¹³C-dEPS) by fungi correlated with the expression of fungal genes encoding carbohydrate-active enzymes. Phylogenetic analysis of genes from ¹³C-labeled metagenomes revealed saprotrophic lineages related to the facultative yeast *Malassezia* were the main fungal foragers of pelagic dEPS. In contrast, fungi living in the underlying sulfidic sediments assimilated more ¹³C-labeled carbon from chemosynthetic bacteria compared to dEPS. This coincided with a unique seafloor fungal community and dissolved organic matter composition compared to the water column, and a 100-fold increased fungal abundance within the subseafloor sulfide-nitrate transition zone. The subseafloor fungi feeding on ¹³C-labeled chemolithoautotrophs under anoxic conditions were affiliated with Chytridiomycota and Mucoromycota that encode cellulolytic and proteolytic enzymes, revealing polysaccharide and protein-degrading fungi that can anaerobically decompose chemosynthetic necromass. These subseafloor fungi, therefore, appear to be specialized in organic matter that is produced in the sediments. Our findings reveal that the phylogenetic diversity of fungi across redox stratified marine ecosystems translates into functionally relevant mechanisms helping to structure carbon flow from primary producers in marine microbiomes from the surface ocean to the subseafloor.

[1] Orsi, W.D., Vuillemin, A., Coskun, Ö.K. *et al.* Carbon