

Deoxygenation effects on dissolved organic matter cycling and microbial metabolisms in a seasonally anoxic basin

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Oxygen minimum zones (OMZs) in the oceans are expanding with potentially far-reaching effects on marine element cycles. OMZs contain higher concentrations of dissolved organic matter (DOM), including carbon and sulfur (DOS), than oxygenated waters. Microbial metabolisms play a key role in the production and degradation of marine DOM, but there is no consensus on their contribution to DOM accumulation in OMZs. Recent advances in analytical chemistry enable the molecular characterization of DOM in unprecedented detail, revealing new insights into its source and history. Ultrahigh-resolution Fourier transform ion-cyclotron resonance mass spectrometry (FT-ICR-MS) has become an indispensable tool in this context. Current progress in sequencing technology can predict specific functions contributing to the molecular activity of microbial communities in environmental samples by metatranscriptomics, or to specific substrate assimilation by quantitative DNA stable isotope probing (qSIP). In this study, we investigated the interaction between microbes and DOM in the water column of the seasonally anoxic Mariager Fjord (Denmark, North Sea). We sampled waters from oxic-to-hypoxic conditions (99, 65 and 4% O₂, respectively). Natural environmental samples were combined with several incubations targeting (a) abiotic and biotic interactions in function of oxygen concentration; and (b) organosulfur cycling by active uncultivated microbes assimilating labeled DOS substrates. Samples were analysed for FT-ICR-MS, qSIP and metatranscriptomics. Our results showed that allochthonous terrigenous DOM input in the fjord dominated the DOM properties more than oxygen variations. However, distinct changes in microbial community composition and gene expression were directly related to the oxygen content. The surface oxic waters were dominated by Planctomycetes and Actinobacteria, while the hypoxic nitrite-rich waters were dominated by Gammaproteobacteria and Bacteroidota. Gene expression diversity was highest in the hypoxic waters, with reverse dissimilatory sulfate reduction and sulfur oxidation genes detected in the metatranscriptomes, despite the absence of sulfidic conditions. Regarding organosulfur cycling, methionine

was mainly utilized in oxic layers by Gammaproteobacteria, Alphaproteobacteria and Actinobacteria, while taurine was assimilated only in hypoxic waters mainly by Bacteroidota. Overall, our study includes novel implementation of state-of-art methods to elucidate new links between the microbial biosphere with the chemical diversity of DOM in the context of a changing, deoxygenated ocean.