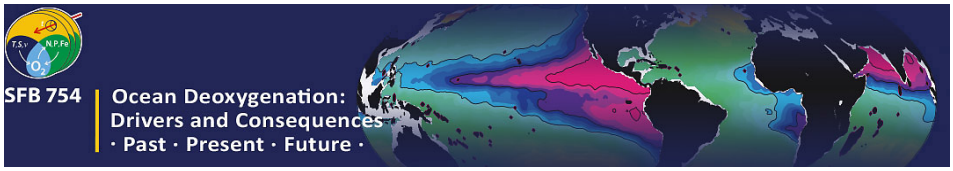

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A METATRANSCRIPTOMICS/METAGENOMICS APPROACH TO OBTAIN INSIGHTS INTO THE BIOGEOCHEMISTRY OF THE SUBOXIC ZONE OF THE BLACK SEA

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The Black Sea has a characteristic "suboxic" transition zone at the interface between the oxic and anoxic water layers that is known as an important site of element transformations. However, the interaction between the biogeochemical structure of the water column and the depth zonation of microbial activities is not yet understood. We used high-resolution chemical profiling together with an analysis of prokaryotic community structure (16S rRNA genes), heterotrophic and chemoautotrophic production, metagenomics analysis of dominant prokaryotes, and expressed genes (metatranscriptomics) to gain insights into the stratification of specific activities as well as the responsible prokaryotic key players. For unbiased gene expression profiles, an automated in situ fixation sampler was used. The dominant prokaryotes included several groups globally distributed in oxygen minimum zones, such as Thaumarchaeota, SUP05 cluster, Marinimicrobia, and Sulfurimonas, but also several taxa that seem to be characteristic for the Black Sea redoxcline. Quantitative analysis of expressed functional genes reflected a distinct vertical zonation of major biogeochemical transformations, including archaeal ammonia oxidation, anammox, and chemoautotrophic denitrification in conjunction with sulfur oxidation. However, for several transformations suggested by functional gene expression the underlying redox reactions remain unclear because the respective depths were devoid of known substrates for some of the processes (e.g., denitrification).

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