

{rokbox title=|Heatmap representing normalized transcript abundance (transcript per million reads) of selected genes from bathypelagic prokaryotic communities in the different treatments and the original community (A) :: Image:

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Abhishek Srivastava, Daniele De Corte, Juan A. L. Garcia, Brandon K. Swan, Ramunas Stepanauskas, Gerhard J. Herndl and **Eva Sintes**, 2023. [Interplay between autotrophic and heterotrophic prokaryotic metabolism in the bathypelagic realm revealed by metatranscriptomic analyses.](https://doi.org/10.1186/s40168-023-01688-7)

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Abstract

Background

Heterotrophic microbes inhabiting the dark ocean largely depend on the settling of organic matter from the sunlit ocean. However, this sinking of organic materials is insufficient to cover their demand for energy and alternative sources such as chemoautotrophy have been proposed. Reduced sulfur compounds, such as thiosulfate, are a potential energy source for both auto- and heterotrophic marine prokaryotes.

Methods

Seawater samples were collected from Labrador Sea Water (LSW, ~2000 m depth) in the North Atlantic and incubated in the dark at in situ temperature unamended, amended with 1 μM thiosulfate, or with 1 μM thiosulfate plus 10 μM glucose and 10 μM acetate (thiosulfate plus dissolved organic matter, DOM). Inorganic carbon fixation was measured in the different treatments and samples for metatranscriptomic analyses were collected after 1 h and 72 h of incubation.

Results

Amendment of LSW with thiosulfate and thiosulfate plus DOM enhanced prokaryotic inorganic carbon fixation. The energy generated via chemoautotrophy and heterotrophy in the amended prokaryotic communities was used for the biosynthesis of glycogen and phospholipids as storage molecules. The addition of thiosulfate stimulated unclassified bacteria, sulfur-oxidizing Deltaproteobacteria (SAR324 cluster bacteria), Epsilonproteobacteria (*Sulfurimonas* sp.), and Gammaproteobacteria (SUP05 cluster bacteria), whereas, the amendment with thiosulfate plus DOM stimulated typically copiotrophic Gammaproteobacteria (closely related to *Vibrio* sp. and *Pseudoalteromonas* sp.).

Conclusions

The gene expression pattern of thiosulfate utilizing microbes specifically of genes involved in energy production via sulfur oxidation and coupled to CO₂ fixation pathways coincided with the change in the transcriptional profile of the heterotrophic prokaryotic community (genes involved in promoting energy storage), suggesting a fine-tuned metabolic interplay between chemoautotrophic and heterotrophic microbes in the dark ocean.

Keywords: Metatranscriptome, Gene expression, Bathypelagic, Labrador Sea Water, Thiosulfate, Dissolved organic matter (DOM), Dissolved inorganic carbon (DIC) fixation, Chemoautotrophy, Heterotrophy.