

Microbial interactions under carbon, sulfur, and nitrogen-cycling conditions in an anoxic bioreactor

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Microorganisms are main drivers of the sulfur, nitrogen and carbon biogeochemical cycles [1]. Given the spread of marine oxygen-deficient zones as a consequence of climate change [2], it is imperative to study microbial interactions that impact biogeochemical cycling under anoxia in order to understand and predict future changes. Here, we investigated a sulfur, nitrogen, and carbon-cycling microbial community in a laboratory-scale bioreactor model that closely mimicked anoxic estuary or brackish sediment conditions [3]. The bioreactor simultaneously consumed sulfide, methane and ammonium at the expense of nitrate. Anammox bacteria, *Ca. Methanoperedens* archaea, *Ca. Methyloirabilis* bacteria and two proteobacterial groups mostly accounted for such reactions. Interestingly, competition for nitrate did not lead to exclusion of one particular group.

Metagenomic analysis showed that the most abundant organism represented a new family within the *Nitrospirae* phylum, being distantly related to *Thermodesulfovibrio* sp. (87–89% 16S rRNA gene identity, 52–54% average amino acid identity). A high quality draft genome of the new species was recovered, and analysis showed high metabolic versatility. Related microbial groups are found in diverse environments where sulfur, nitrogen and methane cycling take place, indicating that these novel bacteria might contribute to biogeochemical cycling in natural habitats. Ongoing transcriptomic analyses and incubation experiments will further elucidate their metabolism.

[1] Falkowski *et al.* (2008) *Science* **320**, 1034–1039. [2] Diaz & Rosenberg (2008) *Science* **321**, 926–929. [3] Arshad *et al.* (2017) *Env. Microbiol.* **19**, 4965–4977.