

PW034 Novel sulfate- and sulfur-reducing bacteria from the Black Sea: metagenomics, enrichment and isolation

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Background: Anoxic and euxinic marine waters are of importance to the biogeochemistry of modern-day ocean as well as the ancient Proterozoic ocean. In these environments, sulfate- and sulfur-reducing bacteria (SRB) play a key role through the reduction of oxidized sulfur compounds such as sulfate, thiosulfate and elemental sulfur to sulfide. In previous studies, these marine SRB were found to be comprised of both canonical *deltaproteobacterial* and non-canonical, mostly uncultured lineages.

Objectives: We aimed to test these findings, and to assess the diversity of SRB in the Black Sea, the largest euxinic basin on the planet and a well-studied model ecosystem.

Methods: To this end, we screened a cross-assembled metagenome and binned genomes for functional marker genes. In parallel, we set up duplicate anaerobic enrichments and dilution series selecting for the reduction of sulfate, thiosulfate or elemental sulfur with various electron donors. The enriched microorganisms were identified through 16S rRNA gene amplicon sequencing.

Results: From a cross-assembled metagenome, we retrieved 86 *dsrD* genes and genomes of seven *Deltaproteobacteria* and one *Thermodesulfovibrionia* with a complete dissimilatory sulfate reduction pathway. Moreover, we detected 46 genes encoding iron-sulfur molybdoenzymes related to the polysulfide/sulfur/thiosulfate reductase catalytic subunit, present in *Deltaproteobacteria*, *Planctomycetes* and *Marinimicrobia* binned genomes. Furthermore, we isolated and characterized a novel sulfate-reducing *Desulfobulbaceae* bacterium related to *Desulfotalea* and *Desulfopila* species, which potentially represents a novel genus. In conclusion, a combined metagenomics and anaerobic cultivation approach revealed novelty within canonical and non-canonical SRB lineages, and confirmed the sulfate- and sulfur-reducing metabolism of specific taxa.