

## TITLE

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**The enigmatic SAR202 cluster up close: shedding light on a globally distributed dark ocean lineage involved in sulfur cycling**

The dark ocean microbiota represents the unknown majority in the global ocean waters. The SAR202 cluster belonging to the phylum Chloroflexi was the first microbial lineage discovered to specifically inhabit the aphotic realm, where they are abundant and globally distributed. The absence of SAR202 cultured representatives has been a significant bottleneck towards understanding their metabolic capacities and role in the marine environment. In this work, we use a combination of metagenome-assembled genomes from deep-sea datasets and publicly available single-cell genomes to construct a genomic perspective of SAR202 phylogeny, metabolism and biogeography. Our results suggest that SAR202 cluster members are medium sized, free-living cells with a heterotrophic lifestyle, broadly divided into two distinct clades. We present the first evidence of vertical stratification of these microbes along the meso- and bathypelagic ocean layers. Remarkably, two distinct species of SAR202 cluster were found to be highly abundant in nearly all deep bathypelagic metagenomic datasets available so far. Many SAR202 members appear to be sulfite-oxidizers and are predicted to play a major role in sulfur turnover in the dark water column and suggesting an unsuspected availability of these nutrient sources to allow for the high abundance of these microbes in the deep sea.