

Hydrogen oxidation coupled to sulfur reduction in deep-sea vent bacteria.

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Among deep-sea ecosystems, hydrothermal vents represent “relic” environments that resemble the early Earth. The genomes of modern vent microorganisms carry both ancestral and recently acquired genes providing excellent models to reconstruct how microbial metabolism co-evolved with our planet. Nautiliaceae (class Epsilonproteobacteria) and Desulfurobacteraceae (class Aquificae) are two key groups of bacteria in marine geothermal habitats. Although these bacteria are phylogenetically distant and colonize different temperature niches, they share key central metabolic characteristics: both fix CO₂ and obtain energy coupling the oxidation of H₂ to the reduction of elemental sulfur and/or nitrate. While nitrate reduction has been investigated, the sulfur reduction pathways have yet to be fully resolved. Focusing on the genomes of members of the Nautiliaceae, *Cetia pacifica*, *Nautilia profundicola* *Caminibacter mediatlanticus*, as well as the genomes of members of the Desulfurobacteraceae, *Thermovibrio ammonificans* strains HB-1 and HB-5, *Desulfurobacterium thermolithotrophum* and *Phorcysia thermohydrogeniphila*, we reported the distribution and phylogenetic reconstruction of four enzymes possibly involved in sulfur reduction. The genes encoding for polysulfide reductase and sulfide quinone oxidoreductase were identified in both the Nautiliaceae and the Desulfurobacteraceae, while the sulfhydrogenase II and the NAD/FAD-dependent reductase were identified in the Desulfurobacteraceae. Comparative genomic analyses were used to formulate hypotheses on how H₂ oxidation can be coupled with sulfur reduction. Experimental work to test these hypotheses will help to understand the interconnection between carbon fixation and respiratory pathways in this chemosynthetic-driven environment.