

Revealing the genes responsible for sulfur respiration in *Thermovibrio ammonificans*

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Thermovibrio ammonificans, in the deep-branching family Desulfurobacteriaceae (phylum Aquificae), is a deep sea vent chemolithoautotrophic thermophile able to conserve energy from the oxidation of hydrogen and respiration of both nitrate and elemental sulfur. Comparison of growth under these two different electron-acceptor regimes was undertaken to elucidate the *T. ammonificans* pathway of sulfur respiration - as well as to gain insight into its core (original, and vertically acquired) versus its acquired (horizontally acquired) genes. A membrane and cytoplasmic hydrogenase, as well as two FAD-dependent pyridine nucleotide disulfide reductases (homologs to sulfide-quinone reductase (SQR) and to NADH-dependent sulfur reductase (NSR)), were highly over-expressed during sulfur respiration. Energy metabolism has co-evolved over billions of years alongside Earth's geology, from a purely anaerobic context to today's metabolic diversity. This diversity has been realized by an evolving network of electron-transfer enzymes. Sulfur, unlike oxygen or nitrate, would have been an electron acceptor available to life during the earliest steps of metabolic evolution. Enzymes dealing with its redox chemistry may be among the earliest relics of the oxidoreductase family. The core "sulfur-reducing" proteome of the deep-branching family Desulfurobacteriaceae (phylum Aquificae) can help better understand the early co-evolution of energy metabolism and geochemistry.