

The chemistry and genetics of microbial thiosulfate disproportionation under haloalkaline conditions

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Soda lakes occur globally and are defined by their high salinity (0.6-4 M Na⁺) and stable alkaline pH conditions (pH 8-11), designating them as extreme haloalkaline environments. In contrast to other extreme environments, these haloalkaline lakes host a wide variety of microbes, which actively drive the extant biogeochemical nutrient cycles. The sulfur cycle is especially active in such habitats, enhanced by the chemical stability and low toxicity of sulfide, polysulfides and thiosulfate at these elevated pH conditions. Most notably, a variety of haloalkaliphilic anaerobes are able to extract metabolic energy from disproportionation of inorganic sulfur compounds. Hereby, the original sulfur compound is split into a more oxidized and more reduced sulfur species, thereby acting both as e⁻ donor and acceptor. However, the mechanisms and genes responsible for such disproportionation reactions remain largely unknown. In order to uncover the genetic mechanism of thiosulfate disproportionation, we cultivated the haloalkaliphile *Desulfonatospira thiodismutans* ASO3-1 anaerobically in thiosulfate-limited chemostats in 2 M Na⁺ medium at a pH of 10. Using a combination of analytical and molecular techniques we could analyze the transcriptome and substrate conversion by this haloalkaliphilic strain under steady state conditions. As the genome of strain ASO3-1 has been sequenced, we could identify genes involved in the reductive sulfur metabolism and couple them to gene expression levels in the laboratory cultures. These experiments bring us closer to the identification of key genes responsible for the poorly understood sulfur-dependent disproportionation metabolism.