

Quantifying the Efficiency of Sulfide-oxidizing Metabolisms for the Remediation of Sour Reservoirs

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The production of Hydrogen Sulfide (H₂S) by microorganisms within oil and gas reservoirs is a serious problem for the petroleum industry. One solution to this problem could be bioengineering microbes to metabolize H₂S to harmless byproducts. However, a better understanding of how sulfide-oxidizing metabolisms operate in nature is still needed. The sulfide oxidation pathway (sox) consists of seven genes (*soxA*, B, C, D, X, Y, and Z) that encode four enzymes that metabolize H₂S to sulfate, possibly through intermediate compounds. The integrated approach that this study proposes will quantify the amount of H₂S that is metabolized when the genes for these enzymes are expressed in the lab by taking advantage of new metagenomics and proteomics techniques. My hypothesis is that natural variations in the DNA sequence of sulfide oxidizing genes result in changes in the enzyme structure that permit the enzymes to function optimally under different geochemical conditions. The most metabolically efficient enzyme will dominate in one set of geochemical conditions, while another enzyme will dominate under a different set of geochemical conditions. By identifying the most metabolically efficient sulfide oxidizing enzymes as they exist in nature and understanding the geochemical conditions at which they function most efficiently it will be possible to bioengineer robust, non-pathogenic, and metabolically versatile microbes so that they will express sulfide oxidation genes optimally, in whatever geochemical conditions are presented to them.