Phospholipid Fatty Acid Analysis as Phenotypic Indicators of Common Stress Response Pathways in *Desulfovibrio vulgaris* and *Shewenella oneidensis*

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Metal-reducing bacteria are often exposed to stressors in the environment which will affect their viability as well as their ability to reduce metal species of interest in bioremediation processes. Although genomic expression and proteomic analysis can provide great insight into microbial stress response, fundamentally it is interesting to understand how these stressors directly effect cell growth. Both *Desulfovibrio vulgaris* and *Shewanella oneidensis* were grown in batch culture and exposed a variety of stressors, including cold, heat, pH, salt, nitrate, and oxygen. The phospholipid fatty acids were extracted from the cultures at different time points to determine how the cell membrane responded to stress and to determine if specific fatty acid patterns can be used as an indicator of phenotypic response to stress analysis. It has been shown that during salt stress, *D. vulgaris* increases its amount of lipid per cell, and at the same time increases its proportion of saturated lipids. During oxygen stress of *D. vulgaris*, no growth occurs in the cells, but no significant death occurs and there is little or no change in the lipid patterns or total amount of lipids in the culture. For *S. oneidensis*, many genes that are involved in production of saturated and/or branched-chain fatty acids are affected by both temperature and salinity. Our hypothesis is that these changes reflect the molecular mechanism by which the cells adapt their membrane fluidity to external conditions. These lipidomic results are also being linked to transcriptomic, metabolomic, and proteomic results for the same stressors to provide and high throughput evaluation and models of stress response pathways.