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Effects of environmental stressors on signature lipid biomarkers in *Desulfovibrio vulgaris*

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Shifts in component patterns of signature lipid biomarkers (SLB) have been correlated to stress and growth of microorganisms in the environment, and can be used as an indicator of phenotypic response to stress. As part of ongoing work in rapid deduction of stress response pathways in *Desulfovibrio vulgaris*, we have been mapping SLBs (phospholipid fatty acids) that indicate stress. Our initial studies have focused on oxygen, zinc and synergistic effects with growth states and iron concentrations for this sulfate reducer. To investigate SLB response to oxygen stress, cells were grown anaerobically to log phase then treated with air-, N₂-, or no-sparging for 24, 48, and 72 h. SLB results indicate continued growth (measured as pmol phospholipid/g of sample) in the N₂ and no sparge conditions, and no significant changes in viable biomass after the start of aeration in the aerated samples. SLB patterns were similar between the three conditions. Cells were also inoculated into aerated fresh medium, followed by anaerobic incubation. Results from these oxygenated-medium growth experiments show different SLB patterns, specifically an increase in branched, unsaturated lipids and a decrease in branched, saturated lipids, as compared to those acclimated anaerobically prior to aeration. This may indicate that oxygen stress response is dependent on growth stage. PLFA and biomass changes were also assessed due to varying concentrations in Fe and Zn during anaerobic growth in defined lactate-sulfate medium. The data clearly show that exposure to elevated levels of Zn (>15 ppm) in the absence of Fe, was toxic to *D. vulgaris*. The consistent appearance of certain signature lipids (e.g. i17:1w9c, a17:w9c, 18:1w7c) for *D. vulgaris*, regardless of growth or stress condition, was also verified with convention techniques to screen for contamination during large scale biomass production. SLBs could be useful as a complement to traditional methods to routinely monitor both biomass and the purity of batch and chemostat cultures especially during our rapid deduction studies of stress response pathways.