Transcriptional Gene Expression Analysis of the Response to Acetone in *Desulfovibrio vulgaris* Using Whole-Genome Oligonucleotide Microarrays

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Desulfovibrio vulgaris has been studied extensively for its potential in the bioremediation of heavy metals and radionuclides. Hydrocarbons and solvents, as frequent environmental co-contaminants, have been reported to inhibit microbial activities and thereby posing a limitation on potential remediation efficiency. As a part of the Genomes to Life project to deduce the stress response pathways in metal/radionuclide reducing bacteria, we studied the responses of *D. vulgaris* to the presence of acetone, which belongs to the class of ketone solvents frequently found in contaminated DOE sites. Growth experiments indicated that *D. vulgaris* could maintain normal growth with 3%(v/v) acetone following a 1-h lag phase. With the presence of 5%(v/v) acetone, we observed a 2-h lag phase followed by a slower growth rate which was only 15% of the normal growth rate. At acetone concentration of 8%(v/v), no active growth was observed following 10 hours of incubation.

To assess the mechanism of solvent inhibition, genome-wide transcriptional profiles were studied on *D. vulgaris* cultures following 30-min acetone (5% v/v) treatment using whole-genome microarrays. Acetone shock (30 min) altered the expression of a large number of genes in the *D. vulgaris* genome, of which 309 were up-regulated by over 2 fold and 199 were down-regulated by over 2 fold. Transcripts highly up-regulated included genes encoding the flagella structural subunits, *flgB* (15 fold), *fliE* (11 fold), and *flgH* (10 fold). Chaperones comprised another group of genes highly induced in the presence of acetone, which included *dnaJ* (11 fold), *groES* (8 fold), and *hsp20* (8 fold). Down-regulated genes included two groups of genes, ribosomal proteins and amino acid transporters, suggesting a state of growth arrest upon acetone addition. These results suggested that *D. vulgaris* responds to elevated solvent levels by increased motility and maintenance of proper protein functions. Current work is focused on the analysis of regulatory pathways based on temporal transcriptional dynamics.