**Whole-Genome Expression Analysis of *Desulfovibrio vulgaris* Cells Throughout Exponential Phase into Stationary Phase Growth in a Defined Medium**

Matthew W. Fields[1], Melinda E. Clark[1], Zhili He[2], Qiang He[2], Liyou Wu[1], Judy D. Wall[3], Terry C. Hazen[4], Jizhong Zhou[2]

[1]Department of Microbiology, Miami University, Oxford, OH
[2]Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN
[3]Department of Biochemistry, University of Missouri, Columbia, MO
[4]Center for Environmental Biotechnology, Lawrence Berkeley National Lab, Berkeley, CA

*Desulfovibrio vulgaris* is a sulfate-reducing, δ-*Proteobacterium* with a genome size of 3.6 Mb and 3584 predicted ORFs, and whole-genome microarrays have been constructed with 70mer oligonucleotides. Three biological replicates were grown in a defined medium with lactate and sulfate as the electron donor and acceptor, respectively. Samples were removed over time for the analysis of protein, carbohydrate, lactate, acetate, sulfate, pH, and RNA. Four samples were removed during exponential growth (T1-T4), and a similar number of ORFs were up-expressed (>3-fold) at each respective time point (7 to 9% of the genome). At the same time points, approximately 5.5 to 6.0% of the ORFs were down-expressed (<3-fold). A majority of the predicted ORFs did not display significant changes in expression from early to late-exponential growth (10 to 25 h). For example, *D. vulgaris* has six annotated lactate permeases, and five of the six were expressed at consistent levels throughout exponential growth. However, the data suggested that approximately 1% of the genome had altered expression patterns during exponential phase growth (from early- to late-exponential). In relation to the ORFs with altered expression levels during exponential phase, very few of the ORFs abruptly changed expression levels but rather displayed a gradual shift over the sampled time. As the cells entered into early stationary phase, approximately 7% of the ORFs were up-expressed, whereas 3.5 to 4% of the genome was up-expressed as the cells experienced prolonged stationary-phase (approximately 35 h). Within the first hours of stationary-phase, up-expressed ORFs included proteases, chaperonins, permeases, hypothetical proteins, and an Archaeal membrane protein shared with *Desulfovibrio desulfuricans*. Interestingly, preliminary comparisons suggest that many of the ORFs that were up-expressed in early stationary phase also had altered expression levels in response to other cellular stresses (e.g., salt, nitrite, oxygen).