## STRESS RESPONSE AND HYPOTHETICAL GENES IN *DESULFOVIBRIO VULGARIS* HILDENBOROUGH

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## **ABSTRACT**

The sulfate-reducing bacteria have a significant impact on the environment and the economy, necessitating further investigation of their physiology to harness their positive attributes and to minimize the damaging byproducts. Through the use of *in vitro* and *in silico* experiments, I have examined some of the metabolic pathways of *Desulfovibrio vulgaris* Hildenborough. The information obtained may contribute to an application of the SRB, *D. vulgaris* in particular, as an effective and economical means of bioremediation and also may play a role in controlling their activity in corrosion of metals and concrete.

During my work on this project, I have developed software tools to expedite the creation of targeted deletion mutants through marker exchange, protein tagging, and to identify the insertion sites of randomly integrated transposons. A substantial amount of microarray data from stressed cultures has been generated by our collaborators that I have analyzed for trends across the experimental conditions. My analysis has yielded new insights to the general and specific stress response systems of *D. vulgaris*. An interesting subset of data, the massive subset of hypothetical genes, offers many tantalizing opportunities for further study with the hints revealed by my analysis. Evidence for the translation of hypothetical genes, revised annotations of the functional descriptions, and clustering according to gene activation was compiled and used to assist in clarification of

the role of some of the hypothetical genes identified within the genome sequence.

Finally, physiological characterization of select deletion mutants that I constructed has also revealed interesting involvement of the specific gene products in the stress responses.

The tools that have been developed and the studies undertaken have yielded immediate results that have increased the knowledge base of the SRB. In addition, further questions became evident whose answers will hopefully lead to critical breakthroughs to reach the ultimate goal of a natural bioremediation tool.