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Funded by: Life Sciences Undergraduate Research Opportunity Program

Construction of a *tatA Desulfovibrio vulgaris Hildenborough*

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tatA Desulfovibrio vulgaris Hildenborough is a member of the obligately anaerobic bacteria growing by sulfate respiration and involved in environmental biocorrosion of ferrous metals. It also shows potential for bioremediation of toxic metals. Because these important metabolic activities of *D. vulgaris* are directly linked to electron flow, a better understanding of energy generation is needed. A model for augmenting respiratory energy production through hydrogen cycling has been proposed. This controversial model requires a periplasmic hydrogenase. The genome sequence of *D. vulgaris* reveals genes for four different periplasmic hydrogenases, the roles of which are currently unclear. There are two primary systems of transport of proteins such as hydrogenases to the periplasm or outer cell membrane. Both the Sec and Tat protein export systems translocate proteins across the cytoplasmic membrane. The Sec pathway exports short unfolded proteins, while the Tat system (Twin Arginine Translocation) translocates longer prefolded proteins. The latter generally contain redox cofactors and share a consensus motif (S/T)-R-R-x-F-L-K recognized for export. The Tat system is found in most prokaryotic plasma membranes. The Tat protein export system is encoded by four genes *in E. coli, tatA, tatB, tatC, and tatE*. However, only three of these genes, *tatA, tatB,* and *tatC*, have been putatively identified in *D. vulgaris*. Removal of one or more tat genes from *E. coli* causes deficiency in the transport of proteins by the Tat system. We propose to test the hydrogen cycling model for energy generation by creating a tatA deletion mutant in *D. vulgaris* that should block the production of all periplasmic hydrogenases. An examination of the deletion mutant should reveal the contribution of the hydrogen cycle to the energy economy of *D. vulgaris*.