A Survey of Protein Post-Translational Modifications Found in the Sulfate-Reducing Bacterium *Desulfovibrio vulgaris* Hildenborough

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Sulfate reducing bacteria (SRB), found widely in nature, use sulfate as the terminal electron acceptor in their respiratory cycle, leading to the production of hydrogen sulfide. These bacteria have both ecological and economic importance. SRB play a role in various biogeochemical cycles including the sulfur and carbon cycles. They have a negative economic impact on the oil industry, where their metabolism causes corrosion and clogging of machinery, and fouling of oil wells. However, they have also been shown to reduce and/or immobilize toxic water-soluble metals such as copper (II), chromium (IV) and uranium (VI), and thus are candidates for bioremediation applications.

Desulfovibrio vulgaris Hildenborough (DvH) is a member of the most well studied genus of SRBs. A goal of the Environmental Stress Pathway Project (ESPP) in the Virtual Institute for Microbial Stress and Survival (VIMSS) is to understand the regulatory networks in DvH for applications to bioremediation. One aspect of this is the elucidation of protein post-translational modifications (PTMs) in DvH.

PTMs play various roles in the cell. Some modifications play a role in protein structure, such as lipid anchors or some disulfide bonds. Others are directly involved in regulation of protein function such as phosphorylation and glycosylation. Still others arise through cellular damage such as irreversible oxidation events. Whatever the role these PTMs play, they must be characterized at the protein level because they are not directly coded for in the genome. Furthermore, DvH may be particularly likely to use PTMs as a regulatory mechanism: Evidence for this includes the observation that the DvH genome encodes an abnormal number of histidine kinases. Our goal is to determine the types of protein modifications that arise in DvH and how these modifications affect the ability of DvH to survive or adapt to its environment.

This work leverages the unique resources of the Virtual Institute for Microbial Stress and Survival: Quality controlled biomass produced at LBL (Hazen lab) is used for all proteomic LC/MS/MS measurements at LBL (Keasling lab). Our initial survey of PTMs in DvH was obtained by mining these numerous proteomic LC/MS/MS data sets acquired over the course of ESPP for evidence of modified peptides. Data mining for PTMs is performed at Sandia National Labs. The searched-for modifications were determined based on literature precedence and a genome search for the existence of relevant transferases. To date we have found preliminary evidence for cysteine oxidation, lysine acetylation, and methylation of lysine and arginine. Data mining for additional PTMs is ongoing. Future work will focus on validation of these findings and

determining which, if any, of these modifications play a regulatory role in DvH. Validation will require selective isolation of the proteins of interest for further characterization. Here, protein isolation is made possible through the work being performed at LBL and the University of Missouri to generate DvH mutants containing tagged versions of DvH proteins.