A Survey of Protein Post-Translational Modifications Found in the Sulfate-Reducing Bacterium *Desulfovibrio vulgaris* Hildenborough: Search for Stress Response Mediators

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Post-translational modifications (PTM) play an important role in regulating protein structure (e.g. lipid anchors, disulfide bonds) and function (e.g. phosphorylation, glycosylation). Still others arise through cellular damage such as irreversible oxidation events. Information about these modifications cannot be obtained at the genome level, and so must be characterized at the protein level. We are currently focused on determining the PTM used by the sulfate reducing bacterium, *Desulfovibrio vulgaris* Hildenborough (DvH).

Sulfate reducing bacteria, found widely in nature, have both economic and ecological importance. A goal of the Environmental Stress Pathway Project 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 to determine the types of protein modifications that arise in DvH and how these modifications affect its ability to survive or adapt to its environment.

We are using both targeted proteomics and data mining to identify modifications of interest. We are investigating cysteine redox states in DvH proteins using a combination of cysteine labeling chemistries (N-ethylmaleimide and the Applied Biosystems cleavable isotope coded affinity tag) in conjunction with LC/MS/MS. This method allows us to target cysteine residues that undergo reversible oxidation and thus may be candidates for redox mediated activity. To obtain a global survey of PTMs in DvH, we are mining numerous proteomic LC/MS/MS data sets for evidence of modified peptides. Cell lysate for these LC/MS/MS experiments was generated from DvH cultures grown under a variety of stress conditions (nitrate, air, oxygen) as well as in co-culture. 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. Future work will focus on validation of these findings and determining which, if any, of these modifications play a regulatory role in DvH.