Global Analysis of *Shewanella oneidensis* Strain MR-1 Proteome Using Accurate Mass Tags

Mary S. Lipton, Margaret F. Romine, Yuri A Gorby, and Richard D. Smith (PI)

Environmental Molecular Sciences Laboratory,
Pacific Northwest National Laboratory, Richland, Washington

Bacterial strains such as *Shewanella oneidensis* strain MR-1 are key organisms in the bioremediation of metals, due to their ability to enzymatically reduce and precipitate a diverse range of heavy metals and radionuclides. Important in these processes is the need to develop improved enzymatic pathways in these organisms. As a first step, the proteome of the organism—defined as the entire protein complement of the cell expressed under a given set of conditions—must be completely characterized. A single genome can exhibit many different proteomes, depending on stage in cell cycle, cell differentiation, response to environmental conditions (nutrients, temperature, stress, etc.), or the manifestation of disease states. Therefore, the study of proteomes under well-defined conditions can provide a better understanding of complex biological processes, which requires faster and more sensitive capabilities for the characterization of cellular constituents.

We have utilized a new technology, based on the combination of global tryptic digestion, high-resolution liquid chromatography, and tandem mass spectrometry and high field FTICR mass spectrometry, to define a proteome of an organism. One approach for protein identification is based on global approaches for protein digestion and accurate mass analysis; this approach resulted in the generation of an "accurate mass tags" (AMTs) database for *S. oneidensis*. Combined with analysis of intact proteins, we can identify post-translational modifications of these proteins. Additionally, we have extended the use of this AMT database based on stable-isotope labeling to quantitatively determine the changes in protein abundance from cells grown aerobically and anaerobically.