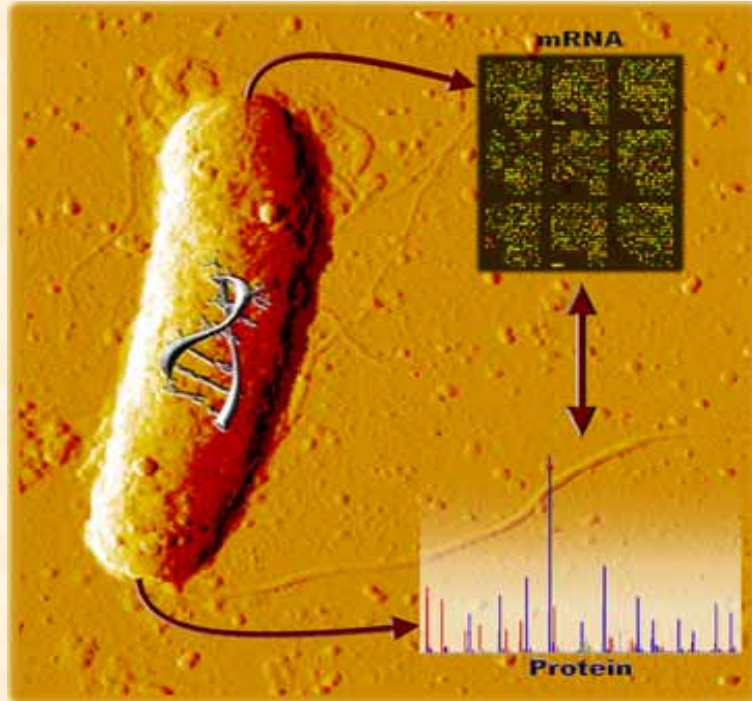


Molecular Dynamics of the *Shewanella oneidensis* Response to Chromate Stress

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- Hexavalent chromium [Cr(VI)] is a highly soluble and toxic heavy metal contaminant found at unacceptable levels at DOE waste sites and is considered a priority pollutant by the DOE for bioremediation.
- Effective bioremediation of Cr-contaminated sites requires knowledge of the molecular mechanisms and regulation of heavy metal resistance and biotransformation by dissimilatory metal-reducing bacteria.
- An integrated experimental approach focusing on temporal gene and protein expression measurements was used to understand the molecular basis of the *S. oneidensis* MR-1 cellular response to acute chromate exposure.
- The early response of MR-1 to chromate shock requires a complex combination of different regulatory networks that involve genes with annotated functions in oxidative and protein stress protection, detoxification, iron acquisition, and DNA repair mechanisms.
- This study also identified a potential heavy metal response regulator and revealed functional biomarkers that might serve as useful indicators of bacterial responses in metal-contaminated environments.

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Temporal genomic profiling and whole-cell proteomic analyses were performed to characterize the dynamic molecular response of the metal-reducing bacterium *Shewanella oneidensis* MR-1 to an acute chromate shock. The complex dynamics of cellular processes demand the integration of methodologies that describe biological systems at the levels of regulation, gene and protein expression, as well as metabolite production. Genomic microarray analysis of the transcriptome dynamics of mid-exponential-phase cells subjected to 1 mM potassium chromate (K_2CrO_4) at exposure time intervals of 5, 30, 60 and 90 min revealed 910 genes that were differentially expressed at one or more time points. Differential proteomics based on multidimensional high-performance liquid chromatography-tandem mass spectrometry (HPLC-MS/MS) was used to complement the transcriptome data, resulting in comparable induction and repression patterns for a subset of corresponding proteins. The initial response of *S. oneidensis* to chromate shock appears to require a combination of different regulatory networks that involve genes with annotated functions in oxidative stress protection, detoxification, protein stress protection, iron and sulfur acquisition, and SOS-controlled DNA repair mechanisms.

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