Goldschmidt 2024 Abstract
https://doi.org/10.46427/gold2024.24695

Perturbations in the Proteome of *Shewanella oneidenis* Exudates in Response to the Presence of Se(IV) During Cell Growth and Exudate Production

LEAH C SULLIVAN AND JEREMY FEIN

University of Notre Dame

Presenting Author: l.sullivan2011@gmail.com

Through both metal complexation and metal reduction reactions, bacterial exudates can exert a strong influence on the aqueous speciation and behavior of a range of metals of environmental and geologic interest. The growth condition of bacterial cells can affect the ability of exudate molecules to promote redox reactions. For example, although exudates from some bacteria can reduce selenite when the cells are grown in the absence of Se(IV), *Shewanella oneidensis* exudates reduce selenite only when Se(IV) is present during cell growth and the production of the exudates, strongly suggesting that selenite reduction by *S. oneidensis* exudates is controlled by proteins associated with metal reduction that are up-regulated in response to the presence of Se(IV).

The use of comparative proteomics provides a powerful tool for determining the molecular-scale mechanisms responsible for protein-controlled reactions both for cells as a whole and for exuded molecules specifically. Here, we use comparative proteomics to measure the secretome of exudate molecules from *S. oneidensis* biomass grown either with or without the presence of aqueous Se(IV) in order to determine whether the change in Se(IV) reduction capability between these two exudate solutions is due to changes in the proteins that were up-regulated during cell growth. Selenite reduction by *S. oneidensis* exudates is inducible by exposure of the cells to Se(IV) during growth and exudate production, but can be stopped when exudate sulfhydryl sites are blocked. Therefore, determining the redox-active proteins that are up-regulated under these conditions and that contain sulfhydryl active binding sites constrains which proteins are responsible for the selenite reduction. 978 proteins were identified within the exudates, of which 375 proteins were differentially expressed in response to selenite exposure (178 up-regulated, 197 down-regulated). We identify six of the 178 up-regulated proteins that are known to possess redox activity against selenite and also contain a sulfhydryl active binding site: ahpF, ccoP, trxA, lpdA, sye4, and gor. The results of this study not only elucidate the proteomic response of cells to heavy metal exposure during growth, but also could be used to engineer and optimize selenite removal strategies for contaminated waters using bioremediation approaches.