

Characterization of *Shewanella oneidensis* MR-1 *etrA* mutant using functional genomic approach

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The wide distribution and prevalence of *Shewanella* species in various natural environments can be attributed to the unique metabolic properties of these bacteria. The range of electron acceptors utilized by *S. oneidensis* MR-1 include organic compounds, such as fumarate, glycine, trimethylamine N-oxide and dimethyl sulfoxide, as well as inorganic acceptors such as Fe(III), Mn(IV), nitrate, nitrite, thiosulfate, sulfite and elemental sulfur. Despite the significant amount of data collected on the physiology of *S. oneidensis* respiration, little is known about the genes regulating the expression of the different electron-transport chain components. So far a single regulatory gene of *S. oneidensis* MR-1, *etrA*, responsible for the switch from aerobic to anaerobic growth has been identified. It was shown previously that EtrA exhibits 73.6% identity to the Fnr regulator of *Escherichia coli*. To further investigate the function of the *etrA* gene, we generated an insertional mutation in this gene. Phenotype analysis of the resulting EtrA⁻ strain revealed no detectable differences in the utilization of all the electron acceptors compared to the wild-type, MR-1. For more detailed analysis the expression profiles of the wild-type and EtrA⁻ strains grown under different conditions were studied using 2-dimensional (2D) gel electrophoresis and partial DNA microarrays. The wild-type and the mutant were grown under aerobic, fumarate-, nitrate- and iron-reducing conditions. Our preliminary results indicated differences in the 2D gel expression patterns of the wild-type and EtrA⁻ mutant. Microarray studies are underway to determine the identities and changes in expression levels of the affected genes.

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