Identification of genes specifically required for the anaerobic metabolism of benzene in Geobacter metallireducens

Although the biochemical pathways for the anaerobic degradation of many of the hydrocarbon constituents in petroleum reservoirs have been elucidated, the mechanisms for anaerobic activation of benzene, a very stable molecule, are not known. Previous studies have demonstrated that Geobacter metallireducens can anaerobically oxidize benzene to carbon dioxide with Fe(III) as the sole electron acceptor and that phenol is an intermediate in benzene oxidation. In an attempt to identify enzymes that might be involved in the conversion of benzene to phenol, whole-genome gene transcript abundance was compared in cells metabolizing benzene and cells metabolizing phenol. Eleven genes had significantly higher transcript abundance in benzene-metabolizing cells. Five of these genes had annotations suggesting that they did not encode proteins that could be involved in benzene metabolism and were not further studied. Strains were constructed in which one of the remaining six genes was deleted. The strain in which the monocistronic gene Gmet 0232 was deleted metabolized phenol, but not benzene. Transcript abundance of the adjacent monocistronic gene, Gmet 0231, predicted to encode a zinc-containing oxidoreductase, was elevated in cells metabolizing benzene, although not at a statistically significant level. However, deleting Gmet 0231 also yielded a strain that could metabolize phenol, but not benzene. Although homologs of Gmet 0231 and Gmet 0232 are found in microorganisms not known to anaerobically metabolize benzene, the adjacent localization of these genes is unique to G. metallireducens. The discovery of genes that are specifically required for the metabolism of benzene, but not phenol in G. metallireducens is an important step in potentially identifying the mechanisms for anaerobic benzene activation.

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