The toxicogenomic response of *Desulfovibrio vulgaris* Hildenborough to sub- and inhibiting concentrations of Hg(II)

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Mercury is a ubiquitous environmental toxicant that exists in multiple chemical forms. The optimal expression of central metabolic genes of an organism can strongly be influenced by genes or gene networks related to the resistance or/and tolerance to its toxicity. A lack of information exists regarding the toxicological effect of inorganic mercury (Hg(II)) to sulphate-reducing bacteria and the differences or similarities by which this chemical alters the physiology of the cell at the molecular level under different environmental conditions.

Here we report gene fitness analysis of *Desulfovibrio vulgaris* Hildenborough (DvH) pools of mutants following toxic exposures to inorganic Hg(II). A collection of unique 20 bp DNA barcoded transposon mutants in DvH were generated by conjugation and transposition of TagModule-marked pRL27 mini-Tn5 transposon delivery vector. For simultaneous competitive gene fitness assay in the presence of sub- and inhibitory concentrations of Hg(II), we used two pools of 3586 mutants each to minimize redundancy as there are less TagModules than insertion mutants. Thus, with 1249 mutants common to both pools, a total of 5923 unique insertion mutants were tested. These mutants accounted for 2704 of the 3417 annotated genes in the DvH genome. The negative or positive gene fitness scores calculated for each gene are indicative of genes whose mutation respectively results in lower or higher viability of the harboring strain relatively to the typical strain in the pools.

Bioinformatics analysis will be presented to determine if the gene fitness responses observed in DvH indicate that different biosynthetic pathways are possibly involved in transformation and bioavailability of Hg(II) at sub- and inhibitory concentrations under various physiological conditions.