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Publication Date

2007-01-10

Comparison of *Desulfovibrio vulgaris* Hildenborough response to microaerobic and aerobic exposure

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Abstract

Though considered obligate anaerobes for many years after their discovery, sulfate reducing bacteria like *Desulfovibrio vulgaris* Hildenborough (DvH) are found in environments with very low sulfate and in many environments that are regularly exposed to oxygen or are normally aerobic. The best growth condition for DvH, measured as increase in biomass, remains a completely anaerobic environment. However, DvH is clearly able to tolerate sub-aerobic environments and can survive exposure to air for up to 20 days. Controlled experiments were conducted to expose DvH to aerobic and microaerobic conditions (0.1% O₂). Cell-wide responses were monitored via transcriptomics and proteomics measurements. Microaerobic conditions caused an overall decrease in growth without affecting the viability of the bacterium. Cellular responses to microaerobic conditions were mild and primarily included up-regulation of the putative PerR regulon, but other known oxidative stress response candidates remained unchanged. Other transcripts that show an expression profile similar to the PerR regulon genes included the *cydA/B* operon, encoding putative oxidative phosphorylation proteins. However, comparison with data from prior DvH functional genomics studies suggested that many of these changes could be part of a general stress response in DvH. In contrast, exposure to air produced drastic changes at both the transcriptome and proteome levels and had a detrimental effect on both growth and viability of DvH. During aerobic stress, increases in proteases and chaperones signified air exposure to be a very harsh stress in DvH. However, quantitative proteomics also indicated an accumulation of superoxide-dismutase, catalase as well as ferritins and thioredoxins, and these candidates may be critical for the survival of the small fraction of cells which survive air exposure. Our results indicated that DvH has very different responses towards microaerobic vs. aerobic exposure. Growth of DvH strains under these different O₂ exposures and the data from our integrated genomics experiment are presented and have been used to improve the model for O₂ stress response in DvH.

Presenter

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Funding Source

Environmental Stress Pathway Project (ESPP)

Keywords

Comparative Genomics, Functional Genomics, Metabolomics, Stress Response, Sulfate Reducers, Transcriptomics