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Title
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Assessment of Nitrogen utilization in Desulfovibrio vulgaris using phenotype microarray

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*nif* genes, found primarily in bacteria, encode the nitrogenase complex and other enzymes involved in nitrogen fixation. Though found in aerobic bacteria, nitrogen fixation occurs optimally in anaerobic conditions and *nif* genes are present in many obligate and facultative anaerobic bacteria as well as some archaea. The consensus sequences in these genes are highly conserved across nitrogen fixing bacteria, but variability exists in their regulation. In the anaerobic sulfate reducing soil bacterium *Desulfovibrio vulgaris* Hildenborough the *nif* genes are encoded on a 200kb megaplasmid which harbors approximately 5% of all of the genes in *D. vulgaris*. The function of the megaplasmid in the growth and survival of *D. vulgaris* is not well understood and the megaplasmid is documented to be lost in growth conditions that do not require nitrogen fixation (such as excess ammonium salts). In order determine the growth conditions that play a role in nitrogen utilization a wild type *D. vulgaris* strain containing the megaplasmid was compared with a *D. vulgaris* strain lacking the megaplasmid (MP(-)). Nitrogen source utilization is evaluated by direct growth response using Omnilog Phenotype Microarray assays. The selected nitrogen utilization phenotype microarray consists of a single 96-well plate loaded with 95 different nitrogen containing compounds. These assays, were used to track and compare the nitrogen utilization profiles and assess specific metabolic pathways for nitrogen assimilation. Activated megaplasmid *nif* gene function is seen with the growth of *D. vulgaris* on N₂ in the absence of added inorganic nitrogen compounds. For the megaplasmid containing wild type strain, growth on N₂ alone yields three-fold longer generation times which is not observed with the MP(-) strain. Genes on the megaplasmid may also confer resistance to toxic ions as *D. vulgaris* growth with NO₂ and NO₃ reaches higher final yields than the MP(-) strain. Here we demonstrate how phenotypic mapping of the two strains reveal some of the functions of the *D. vulgaris* megaplasmid.