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Adaptation of *Desulfovibrio vulgaris* to Elevated NaCl Conditions

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Desulfovibrio vulgaris Hildenborough is a δ -*Proteobacterium* with a genome size of 3.6 MB and 3584 ORFs. It is well known for its metabolic versatility and wide distribution. Here we have examined the global gene expression changes when this bacterium grew at elevated NaCl conditions using the whole-genome microarrays. *D. vulgaris* growth was not significantly affected by 50 and 100 mM NaCl. However, cells grew slower with a longer lag and reduced biomass at 250 and 500 mM NaCl, and they could not grow in 1 M NaCl medium. Cells grew in the LS medium with 0, 100, 250, and 500 mM NaCl, and samples were taken at the mid-log phase for microarray analyses. Among up-regulated genes, some were common to salt stress, and some were specific to certain concentration of NaCl. Those commonly up-regulated genes included holin (DVU1505), major facilitator family transporter (DVU1895), Na⁺/H⁺ antiporter family protein (DVU2645), sensory box (DVU2679 and DVU0457). Although cell growth was not significantly affected under 100 mM NaCl condition, a set of genes were significantly up-regulated, and those genes included dissimilatory sulfite reductase B (DVU0404), cytochrome c family protein (DVU2791), sensory box protein (DVU1547), sigma-54 dependent transcriptional regulator/response regulator (DVU0110 and DVU0653). In the presence of 250 mM NaCl, a group of diverse genes significantly were up-regulated. For example, DVU1255 was 4-fold up-regulated. This gene is a member of *Sua5/YciO/RrdC/YwlC* family, which relates to gene regulation. Interestingly, *Sua5* is necessary for cell normal growth in yeast. Genes involved in DNA synthesis and repair genes (DVU0071 and DVU2463) and regulatory functions (DVU2281 and DVU2894) were up-regulated under high (500 mM) NaCl conditions. Further study may generate knockouts to characterize some regulators, such as DVU2281, DVU2894, DVU1547, DVU0110, DVU0653, DVU2679 and DVU0457, and elucidate gene regulatory networks.