Desulfovibrio vulgaris Hildenborough responses to salt and H_2O_2 stresses

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The response of *Desulfovibrio vulgaris* Hildenborough to salt and H_2O_2 stresses were examined by physiological, global transcriptional, metabolite, and mutagenesis analyses. The growth of *D. vulgaris* was inhibited by 250 mM NaCl or 1 mM H_2O_2. Salt adaptation (long-term NaCl exposure) increased the expression of genes involved in amino acid biosynthesis and transport, electron transfer, hydrogen oxidation, and general stress responses (e.g., heat shock proteins, phage shock proteins, and oxidative stress response proteins). Genes involved in carbon metabolism, cell motility, and phage structures were decreased in expression. Comparison of transcriptomic profiles of *D. vulgaris* responses to salt adaptation with those of salt shock (short-term NaCl exposure) showed some similarity as well as a significant difference. Metabolite assays showed that glutamate and alanine accumulated under salt adaptation, suggesting that they may be used as osmoprotectants in *D. vulgaris*. Addition of amino acids (glutamate, alanine, tryptophan) or yeast extract to the growth medium relieved salt-related growth inhibition. A conceptual model is proposed to link the observed results to currently available knowledge for further understanding the mechanisms of *D. vulgaris* adaptation to elevated NaCl. Under H_2O_2 conditions, PerR regulon genes were significantly up-regulated, indicating the importance role of PerR in oxidative stress response. In addition, some Fur regulon genes were also strongly induced. Increased gene expression of thiol-peroxidase genes *ahpC* as well as thioredoxin reductase and thioredoxin genes indicated the involvement of thiol switch in the oxidative stress response. *rbr2* was the only significantly up-regulated H_2O_2 scavenging enzymes. The oxidative stress response of mutants Δ*perR* and Δ*fur* demonstrated that *ahpC* and *rbr2* were regulated by both Fur and PerR. The links between the up-regulated genes involved in H_2O_2 scavenging, protein fate, DNA metabolism and lipid metabolism and the down-regulated genes involved in sulfate reduction, energy production and translation were demonstrated by the gene co-expression network. The proteomics data provided further evidence at the translational

level and complemented the transcriptomics data. Taken together, diverse stress resistance mechanisms may be used in *D. vulgaris* for detoxification of H_2O_2 with the up-regulation of DNA repair systems and the down-regulation of energy metabolism and protein synthesis.