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Publication Date

2008-06-02



Global Transcriptional and Metabolite Analysis of *Desulfovibrio vulgaris* Hildenborough Responses to Long-Term Exposure to Elevated NaCl

Q-299

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Fig. 6 D. vulgaris cells grew at LS4D





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ABSTRACT

The mechanisms of Desulfovibrio vulgaris Hildenborough responses to long -term NaCl exposure were studied by global transcriptional and metabolite analyses. The growth of D. vulgaris was inhibited by high salinity, and salt inhibition could be relieved by an addition of amino acids (e.g., glutamate, alanine) or yeast extract. Salt shock (sudden increase in salt concentration) and salt adaptation (inoculating cells in the medium containing high concentrations of salt) showed a significant difference in respective transcriptomes. Salt adaptation induced expression of genes involved in amino acid biosynthesis and transportation, electron transfer, hydrogen oxidation, and general stress responses (e.g., heat shock proteins, phage shock proteins, and oxidative stress response proteins). Genes involved in energy metabolism, cell motility, and phage structures were repressed. Genes involved in Na+/H+ transport, K+ uptake and transportation, and proline biosynthesis and transportation were not significantly affected. Metabolite assays and external addition of amino acids into the growth medium of D. vulgaris suggest that amino acids, such as glutamate and alanine may accumulate as osmoprotectants in D. vulgaris. A conceptual model is proposed to link our observed results to currently available knowledge for further understanding the mechanisms of adaptation of D. vulgaris to sodium chloride.

MATERIALS AND METHODS

Cell culture and treatment: D. vulgaris cells were grown at the LS4D medium with or without yeast extract. To test the effects of amino acids on D. vulgaris growth, yeast extract was removed. NaCl was added into the LS4D medium to make desired concentrations when the LS4D medium was made.

D. vulgaris oligonucleotide array: 70mer oligonucleotide arrays that containing all ORFs were constructed as described (He et al., 2006).

Target preparation. labeling and array hybridization: Total cellular RNA was isolated and purified using TRIzolTM Reagent, and then labeled with Cy5 dye. Genomic DNA was isolated and purified from *D. vulgaris* as described previously (Zhou et al., 1996), and then labeled with Cy3 dye. The labeled RNA and genomic DNA were co-hybridized to the array at 45°C with 50% fornamide for 16 hrs in the dark. Image and data analysis were the same as described previously (Chhabra et al., 2006; Mukhopadhyay et al., 2006).

Metabolite determination: D. vulgaris cells were grown at the LS4D without added NaCl (the control), or with 250 mM additional NaCl (the treatment). A total of 150 ml of samples were collected for extraction of metabolites. Metabolite assays were conducted with capillary electrophoresis (CE) and mass spectrometric (MS) under optimal conditions.

RESULTS



Fig. 1 Effects of yeast extract on the growth of *D. vulgaris* under NaCl stress

- With yeast extract, *D. vulgaris* growth was inhibited ~15% by 250 mM NaCl (A); without yeast extract, its growth was inhibited ~50% by 250 mM NaCl (B).
- The results suggest that yeast extract significantly affected the growth of D. vulgaris in the presence of NaCl, which may be because certain substances in yeast extract help D. vulgaris cells adapt to high salinity environments.

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Flg. 4 Comparison of gene expression under short- and long-term NaCl exposure

metabolism, and regulatory processes.







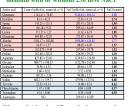
Table 2 Examples of up-regulated ORFs under long-term NaCl exposure but no significant changes under short-term NaCl exposure

Leen lag	Shart term NaCl exposure		Long tean HaCl expenses		
	Bad o	Zware	545 +	Dame	Annotati on
CANDELL	1.009400	1.11994	2,30583	3,65025	Challeu/The/fill dehydrogenese family protein
	1.527134	1.0364	1.41583	2.6865	sedium/alanine symperter family protein
		0.457774	1,00000	3,21825	trystophonese
		0.702945	2,70002		branched drain amino add ABC transporter, permeans protein
		1.050	1.50340	2.75832	amine soid AGC transposter, His/Glu/Sin/Arg/spine family
DV50740		0.850364	3.19217	5.90025	light affiliate for the state and a set of the company of the beginner.
DVV0742	8.906825	1,79501		2.0758	lighted interpretational and activities principle permanental
DAVISOR	-0.891971	-1.90429	LSTHE	2.07489	perplastic (Fe) hydrogenase, large subunit.
0455270	0.0300396	-612306	1.00004	2.5980	penplasnic (fe) hydrogenase, snall subunit
	0.0098716		1.6603	2.57935	hydropeniae expression/fermati in protein, public inc.
DAY 5341	8.182345		2,77189	4.15038	anti-sociali, AlgOTsafamily
	3.548254	1,6000	4.0000	7,41545	heat shock protein, Hig 28 family
	8.720896	1,40006	3,63066		heat shock protein, Hig 28 family
	1.000000	1.85726		4.47534	phage shock protein C
		-0.122503	1,34059	2.15832	heat-inductife transcripts on regresser Hrok.
	8.913000	0.495001	2.09412	2.00722	sigma-Skidependent transcripti anal regulator
DVUQ129	-0.309266	-67660	2.89297	3.09662	sensery box histi dine kinase/haponse regulator
DAY 0.289	8.15792	0.285075	1,90288	2.1907	transcripti ceal regulatur cit, putati ve
DAYOUR	2.80793	1.05000	2.40798	3.60329	transcripts coal regulator, putatt we
DAYORSE	1.992755	0.812048	1.41227	2.06046	ogna-58 dependent transmoti unal regulatur
DAVIDEDS.	1.688035	1,24993	2.00753	2.80837	transcraft lenal regulator, For family
	8.5KN12	0.648796	1.33884	2,47988	Englishen specific transport protein
		0.120201		4.00838	transcripts and regulators (split family)

Table 3 Examples of down-regulated ORFs under long-term NaCl exposure but no significant changes under short-term NaCl



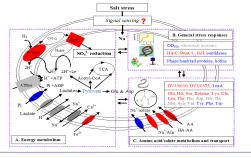
Table 4 D. vulgaris cells grew at LS4D medium with or without 250 mM NaCl



medium with or without 250 mM NaCl

- Glu and Ala significantly increased and intracellularly accumulated to ~9.2 and 2.0 µM, which may function as osmoprotectants.
- The results were consistent with microarray data and amino acid accumulation data (Table 3) in response to salt stress
- Growth was not affected for *D.*vulgaris cells without NaCl addition.
- Glu, Ala, Leu and Trp significantly relieved the NaCl inhibition of *D. vulgaris* cells.

Fig. 7 Conceptual model for D. vulgaris responses to long-term NaCl exposure



SUMMARY

- Glu and Ala may be used as potential osmotic protection solutes in DvH under salt stress conditions.
- Electron transport flows were induced while carbon metabolism was repressed under salt stress conditions.
- Gene expression had a similar trend but also showed differences under short- and long-term exposure of *D. vulgaris* to NaCl.
- Many function-unknown genes were identified to be associated with salt tolerance, indicting salt-tolerance mechanisms are largely

ACKNOWLEDGEMENT

ESPP2 (MDCASE) is part of the Virtual Institute for Microbial Stress and Survival (VIMSS) supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics:GTL Program through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.