Genetic Adaptation to Salt Stress in Experimental Evolution of Desulfovibrio vulgaris Hildenborough

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INTRODUCTION

High salinity is one of the most common environmental stressors. In order to understand how environmental organisms adapt to salt environment, an experiment evolution with sulfate reducing bacteria Desulfovibrio vulgaris Hildenborough was conducted. Control lines and salt-stressed lines (6 lines each) grown in minimal medium LS4D or LS4D + 100 mM NaCl were transferred for 1200 generations. The salt tolerance was tested for LS4D supplemented with 250 mM NaCl. Statistical analysis of the growth data suggested that all lines adapted to their evolutionary environment. In addition, the control lines performed better than the ancestor with faster growth rate, higher biomass yield and shorter lag phase under salt environment they did not evolve in. However, the salt-adapted lines performed better than the control lines on measures of growth rate and yield under salt environment, suggesting that the salt-evolved lines acquired mutations specific to having extra salt in LS4D. Growth data and gene transcription data suggested that populations tended to improve till 1000 generations and active mutations tended to be fixed at the stage of 1000 generations. Point mutations and insertions/deletions were identified in isolated colonies from salt-adapted and control lines via whole genome sequencing. Glu, Gln and Ala appears to be the major osmoregulants in evolved salt-stressed line. Ongoing studies are now characterizing the contribution of specific mutations identified in the salt-evolved D. vulgaris.

MATERIALS AND METHODS

Bacteria strain: Single colony-based liquid culture was obtained from the original D. vulgaris Hildenborough stock. Six lines each were used for control and treatment respectively.

Medium and culture condition: LS4D was used as standard medium for the control. Medium for salt stress treatment was LS4D +100 mM NaCl. Cells were kept at 37°C and transferred every 48 hrs with one to one hundred dilution.

Handling of the samples: The glycerol stocks were archived for every 100 generations and a variety of molecular, physiological, and genomic analyzes were conducted to monitor their evolution/adaptation to environmental stresses.

Microarray analysis: 70mer oligonucleotide arrays for D. vulgaris Hildenborough that containing all ORFs (He et al., 2006) were used in this study. Total cellular RNA was isolated using TRIZol (Invitrogen) and RNeasy mini kit and labeled with Cy3 dye. Genomic DNA was isolated from D. vulgaris Hildenborough as described previously (Zhou et al., 1996) and labeled with Cy5 dye. The labeled CDNA and genomic DNA were co-hybridized to the array. Microarray data were processed as described before (Chhabra et al., 2006; Mukhopadhyay et al., 2006).

RESULTS

Growth of D. vulgaris is arrested by elevated salt in the medium

With 100 mM NaCl in the medium, the growth rate and final biomass were not affected except a few hours longer of lag phase;

With 250 mM NaCl in the medium, there was a very long lag phase and the final biomass was only half of the control.

The transcription profiling changes became stable at 1000g

DCA analysis of the all the gene expression data was shown. S: evolved stressed lines; C: evolved control lines; A: ancestor

The role of point mutation confirmed by complementation of knockout mutant

FW2013: knockout mutant of DVEU597; FW2013(c): complemented FW2013

A: Sulfite is necessary for the growth of JW2013. Complementation of JW2013 partially rescued the evolved phenotype became stable at about 1000 generations; adaptation;

B: With supplementation of sodium, salt tolerance of JW2013 was comparable to 89-11, salt resistance of complemented FW2013 was the same as wild type.

SUMMARY

- D. vulgaris cell lines long-term transferred in control or salt stress condition adapted to their evolution environment;
- The salt-adapted lines acquired specific mutations that enable better growth on salt;
- A decrease of fitness of in the absence of salt suggested a trade-off in salt adaptation;
- Growth data and gene expression profiling analysis suggested that the evolved phenotype became stable at about 1000 generations;
- Point mutations were identified in evolved control and treatment lines and most of the mutations were fixed or almost fixed;
- Point mutation in DVEU597 was a loss-of-function and the mutation contribute for the salt resistance.

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