Lawrence Berkeley National Laboratory

Recent Work

Title

A Powerful Integrated Approach to the Systems-Level Response of Bacteria to Environmental Stress

Permalink

https://escholarship.org/uc/item/1h88r6b6

Authors

Alm, E. Arkin, A. Hazen, T. et al.

Publication Date

2004-12-14

A Powerful Integrated Approach to the Systems-Level Response of Bacteria to Environmental Stress

E. Alm1, A. Arkin1, T. Hazen1, J. Keasling1, M. Keller2, A. Mukhopadhyay1, A. Singh3, D. Stahl4, D. Thompson5, J. Wall6, M. Fields, J. Zhou5;

1Lawrence Berkeley National Lab, Berkeley, CA, 2Diversa Corporation, San Diego, CA, 3Lawrence Livermore National Lab, Livermore, CA, 4University of Washington, Seattle, WA, 5Oak Ridge National Lab, Oak Ridge, TN, 6University of Missouri, Columbia, MO.

Background: The Virtual Institute for Microbial Stress and Survival (VIMSS) has developed an integrated pipeline to study the response of bacteria to common environmental stressors such as exposure to nitrate or oxygen, and salt shock.

Methods: The VIMSS stress response pipeline begins with cell growth experiments to determine the minimum inhibitory concentration at which a stressor affects cell growth. Within this region of concentrations, microarray experiments are used establish the timecourse over which the cell adapts to each stress, and to monitor the regulatory response of the cell at the transcriptional level. Proteomics experiments are then performed to probe regulation at the post-transcriptional level. In parallel, quantitative assays for lipid content and other metabolites are employed. Finally, computational methods are used to integrate data from all of these sources.

Results: The VIMSS integrated pipeline has been applied to study the effect of nitrate and oxygen exposure and salt shock in the sulfate-reducing bacterium Desulfovibrio vulgaris. In addition to factors that are known to be involved in these pathways in other organisms, this systems-level approach reveals how these stressors affect the unique energy production machinery that characterizes sulfate-reducing bacteria. In addition, integration of data from different experimental approaches highlights biological mechanisms that might not be apparent from any single technique alone, as well as drawing to light the particular strengths and biases of each approach.

Conclusions: The VIMSS systems-level approach to bacterial stress response yields new insight into Desulfovibrio vulgaris physiology.