UNRAVELING STRESS RESPONSIVE PATHWAYS IN THE METABOLIC VERSATILE *Rhodopseudomonas palustris*

Shaneka S. Simmons, Tamara Medley, Andreas Mbah and Raphael D. Isokpehi

*Center for Bioinformatics & Computational Biology, Department of Biology, Jackson State University, Jackson Mississippi 39217, USA*

**Abstract:** Microbial stress has been defined as (1) Any deviation from suboptimal growth conditions (physical/chemical conditions, temperature, salinity, flow, pressure or resources-nutrients, energy sources, and space) that results in reduced growth rate or microbial survival (2) an environmental situation resulting in damage of cellular components, and decreased cell viability, in the absence of a cellular response or (3) Any situation that stimulates expression of stress-responsive genes. The photosynthetic and metabolic pathways of microbes allow for the the ability to survive and colonize the most hostile environments including marine environments with high pressures (110 Mpa), extremely acidic (pH 0) or alkaline (pH 12.8) environments, high heavy metal concentrations, hydrothermal vents at 113 °C, frozen sea water at −20 °C, and deep freezing at 140°C. Sudden changes of environmental conditions elicit stress response in exposed microbial communities that is characterized by a distinct change in their gene expression pattern. Distinct adaptive stress responses enable organisms to protect vital processes through the induction of batteries of genes or stimulons encoding protein products well suited for changes to an environment. Microbial fuel production is often limited by the growth inhibiting toxicity of biofuels, therefore, functional traits that aid adaptive responses to stress have been of interest to the Department of Energy. To gain deeper insight into microbial multigenic systems, there is a need to overcome biological barriers for rapid design and optimization of microbial traits engineered for biofuel production. *Rhodopseudomonas palustris* has been extensively studied for its photosynthetic metabolism in energy conversion reactions. However, knowledge of stress responsive pathways is limited. *Rhodopseudomonas* has a genetic makeup that allows genes to be easily transferred, making them model microbes for functional and comparative genomics for understanding stress survival during hydrogen biofuel production. We are investigating the protein sequences of the universal stress proteins encoded in 7 publicly available genome sequences of *R. palustris*. Some of the key observations include (i) strain-specific universal stress protein for solute transport; (ii) phylogenetic clustering of USP sequences with size ranging from 274 aa to 293 aa; (iii) domain architecture and ligand binding residues; and (iv) chromosomal context. All together, these research findings are unraveling functional insights into the most likely role of *R. palustris* proteins containing the universal stress proteins.

**Acknowledgements:** RCMI-Center for Environmental Health, Jackson State University; National Institutes of Health (NIH-NCRR G12RR13459; NIH-NIGMS T36GM095335; NIH-NIMHD 1P20MD002725-01; NIH-NCRR-P20RR016476; NIH-NCRR-P20RR016460); National Science Foundation (EPS-0903787; NSF-DBI-0958179; DBI-1062057); and US Department of Homeland Security Science and Technology Directorate (2007-ST-104-000007; 2009- ST-062-000014; 2009-ST-104-000021). **Disclaimer:** The views and conclusions contained in this document are those of the authors and should not be interpreted as necessarily representing the official policies, either expressed or implied, of the funding agencies.