FUNCTIONAL RELATEDNESS OF ENERGY PRODUCING 
RHODOPSEUDOMONAS PALUSTRIS GENOMES

Shaneka S. Simmons, Raphael D. Isokpehi and Hari H.P. Cohly

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

Abstract: We have observed that 82% (538 of 624) completely sequenced prokaryotic genomes contain genes that encode proteins that have the universal stress protein domain (USP, Pfam00582). Furthermore, the following bacterial species: Geobacter metallireducens, Shewanella oneidensis MR-1, Rhodopseudomonas palustris, Desulfovibrio vulgaris, Deinococcus radiodurans R1, Nitrosomonas europaee, and Clostridium thermocellum, have been sequenced by the Department of Energy’s Joint Genome Institute and are relevant to research on sustainable bioenergy. Among these bacteria, only Rhodopsuedomonas had the highest number of sequenced genomes as well as highest number of genes encoding proteins with the USP domain. The universal stress proteins provide biological cells with the ability to respond to environmental stresses such as nutrient starvation, drought, high salinity, extreme temperatures and exposure to toxic chemicals. As of February 6, 2009, there were six finished sequenced genomes of R. palustris: BisA53, BisB5, BisB18, CGA009, HaA2 and TIE-1. We hypothesize that genomes with similar functional profiles will cluster together. The objective of this study was to determine the functional relatedness of finished genomes of R. palustris based on Cluster of Orthologous protein Groups. Hierarchical Clustering and Correlation Matrix were generated using tools on the Integrated Microbial Genome (IMG) Database. The genomes were clustered according COG, PFAM, Enzyme, and TIGRFAM. Two major clusters were obtained. Strains HaA2, CGA009 and BisH53 clustered together with HaA2 sharing the same node. Strains BisA53 and BisB18 shared the same node. The maximum and minimal correlation values between genomes were 0.84 and 0.95 respectively. We intend to compare the expression of genes encoding universal stress protein in various stress conditions. Such knowledge of how R. palustris responds and adapts to stress factors including pH, salt, toxic chemicals, and extreme temperatures can be useful for optimizing engineered strains of R. palustris capable of stress tolerance and enhanced biofuel production.

Keywords: Universal Stress Protein, Rhodopseudomonas palustris, bioenergy, Pfam, Ortholog

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