FUNCTIONAL COUPLING OF STRESS RESPONSE AND CATION TRANSPORT IN RHODOPSEUDOMONAS PALUSTRIS

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Abstract: Genes that encode the universal stress protein (USP) domain 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. *Rhodopseudomonas palustris* strains are metabolically versatile with the ability to convert atmospheric carbon dioxide into biomass, recycle aromatic polymers of lignin, produce hydrogen gas for energy production, and fix atmospheric nitrogen. Their ability to adapt and live under various environmental constraints as well as biodegrade pollution to be used as biofuel, make them a model system for research on renewable energy from biological sources. As of February 6, 2009, there were six finished genome sequences of *R. palustris* strains: BisA53, BisB5, BisB18, CGA009, HaA2 and TIE-1 available in the Joint Genome Institute's Integrated Microbial Genome (IMG) system. The gene count of these *R. palustris* strains ranged from 4492 to 5377. We report a study to determine USP genes of *R. palustris* strains that are functionally coupled with other genes. According to the National Microbial Pathogen Data Resource (http://www.nmpdr.org/), genes whose relative position is conserved in at least four other species are functionally coupled. Six USP genes from strains BisB18, CGA009 and HaA2 were analyzed using the GenomeViewer Tool at NMPDR. There was evidence the gene fig|316056.14.peg.3812 from BisB18 and its orthologs in strains CGA009 and HaA2 were functionally coupled with the upstream adjacent gene predicted to encode a cation-transporting ATPase (ctATPase). Bacteria use membrane-bound ctATPase to pump out toxic heavy metal ions. In conclusion, this study uncovered evidence for coupling of stress response and cation transport in three strains of *R. palustris*.

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