STRAIN-SPECIFIC OVERREPRESENTATION OF TRANSPOSASE AND INACTIVATED DERIVATIVES IN *RHODOPSEUDOMONAS PALUSTRIS*

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**Abstract:** Gene loss or acquisition is a major mechanism of bacterial adaptive evolution to local conditions in heterogeneous environments that contain a range of ecologically distinct habitats. Transposase and inactivated derivatives function to activate and move transposons, or mobile sequences of DNA. When transposons are moved, they can cause mutations in DNA and affect the organism's phenotype. A functional annotation approach called Cluster of Orthologus Groups (COGs) of proteins groups' genes that are similar to each other in function but are present in different organisms. The functions for Transposase and Inactivated Derivatives are part of the COG category Recombination, Replication and Repair. The objective of the present study is to analyze the presence of transposase and inactivated derivatives in the bacteria genus *Rhodopseudomonas palustris*. *Rhodopseudomonas* are one of the most metabolically versatile bacteria, exhibiting abilities such as converting carbon dioxide into cell material, nitrogen gas into ammonia, produces hydrogen gas and contributes tremendously to biofuel production. The COG Transposase profiles of six strains of *Rhodopseudomonas palustris* (BisA53, BisB18, BisB5, CGA009, HaA2, and TIE-1) were analyzed. Strain BisA53 was found to have the highest number of annotated transposase genes, with a total of 46. The profile generated also revealed COGs for transposase and inactivated derivatives that were exclusive to particular strains: BisA53 (COG 3335: 3 genes), HaA2 (COG 3677: 1 gene), and TIE-1 (COG 3293: 2 genes). We are currently studying the gene composition of the chromosomal location and potential adaptive fitness of strain-specific transposase in *Rhodopsuedomonas* strains.

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