FUNCTIONAL ANNOTATION ANALYTICS OF UNIVERSAL STRESS PROTEINS ENCODED IN SHEWANELLA GENOMES

Baraka Williams, Hari H.P. Cohly, Wellington K. Ayensu and Raphael D. Isokpehi

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

Abstract: Shewanella bacteria are gram-negative, rod shaped, facultative anaerobes that can live on land, deep in the earth and in marine environments. Shewanellae are particularly distinguished by their ability to use toxic compounds and metals for growth and energy; thus, it is well suited for bioremediation potential. It has been determined that genes encoding the universal stress protein (USP) domain (PF00582) enables organisms to survive the impact of environmental stressors such as temperature changes, contaminated sediments, toxic metals, nutrient starvation, high and low pH levels and salinity. We hypothesize that comparison of abundance sequence length and chromosomal location of genes encoding universal stress protein domain in Shewanella genomes will reveal novel observations on survival of Shewanella species in extreme conditions. The objective of this study was to compare genomes in terms of clustering by functional protein profiles and identify genes that encode the USP domain in finished and draft genomes of Shewanella. We used clustering tools available on the Integrated Microbial Genome (IMG) database to generate hierarchical clusters and correlation matrices that summarize gene annotation in terms of four functional profiles: Clusters of Orthologous Groups of proteins (COG), Protein Families (PFAM), Enzymes and TIGRFAM. The Find Function Tool on the IMG database was used to identify genes encoding the Universal Stress Protein domain (PF00582) in Shewanella genomes. Our analysis revealed that S. benthica and S. woodyi have a hypothetical protein that is closely associated with tandem USPs (143 and 147). Interestingly, Shewanella frigidimarina NCIMB 400 contains a strain-specific universal stress protein fused to the hypothetical protein. Shewanella benthica KT99 and Shewanella frigidimarina NCIMB 400 warrant further investigation to understand the function of the fused and tandem genes.

Keywords: Comparative genomics, Shewanella, Universal Stress Proteins

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