

GENE NETWORKS ENCODING UNIVERSAL STRESS PROTEINS IN *BRUCELLA* GENOMES

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Abstract: The Universal Stress Protein (USP) superfamily in which members contains the USP domain (PF00582) are known to provide plants with the ability to adapt to and survive extreme environmental conditions would be fatal to most organisms. Bacteria such as *Mycobacterium tuberculosis*, *Pseudomonas aeruginosa*, and *Escherichia coli* are a few in which has undergone characterization of USPs. *Brucella* is a Gram-negative, intracellular coccobacillus, which causes brucellosis in humans and various animal species. The intracellular lifestyle of *Brucella* species makes it necessary for survival in adverse conditions. A gene family known to help bacteria respond to unfavorable conditions such as limited nutrients is the universal stress proteins. Preliminary visual analytics of functional annotation data of 165 USP genes from 42 *Brucella* genomes revealed the presence of 3 to 4 USP genes with protein sequence length ranging from 101 aa to 281 aa. The purpose of the reported investigation was to determine distinctive sequence features and genome context of universal stress proteins of *Brucella*. Gene neighborhood analysis in addition to visual analytics views enabled us to identify knowledge building insights from functional annotation data on *Brucella* universal stress proteins. For the 10 *Brucella abortus* genomes, protein sequence lengths observed were 148, 149, 162, 179 and 291 with the USP of sequence length 162 aa found only in *Brucella abortus* bv 1,9-941. Homologs of this USP were found in three additional genomes: *Brucella melitensis* bv. 1 Abortus 2308, *Brucella microti* CCM 4915, *Brucella* sp. BO1 and *Brucella suis* bv 1,1330. Genomic context analysis identified that some USPs of *Brucella* were part of transcriptional units with enzymes such as tryptophanyl-tRNA synthetase and PII uridylyl-transferase (glnD) which play a role in response to nitrogen stress. The 179 aa USP in *Brucella abortus* is adjacent to a gene for an enzyme, tryptophanyl-tRNA synthetase, located within its transcription unit. Understanding the function of tryptophanyl-tRNA synthetase would be crucial to gaining insights on the function of the 179 aa USP.

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