DISTRIBUTION OF GENES ENCODING UNIVERSAL STRESS PROTEIN DOMAIN IN SALMONELLA GENOMES

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Abstract: The genus Salmonella consist of Gram-negative facultative rod-shaped bacteria that infect the intestinal tract of warm-blooded animals. Salmonella causes typhoid fever, paratyphoid fever, and foodborne illness. The repeated multistate outbreak of Salmonella infections from 2006-2010 in the United States has to the forefront the need to understand the intrinsic features that enable bacteria pathogens to survive a variety of food processing conditions. Genome sequences have revealed that genes are organized in gene families and that the gene count for families may vary. Furthermore, the knowledge of size variation or number of genes in a gene family particularly within a species is required to understand the observed difference between organisms in morphology, physiology and complexity. Genes encoding the universal stress protein (USP) domain (PF00582) are known to provide a variety of pathogenic bacteria with ability to adapt to changing growth and host conditions. The objective of this investigation was to determine predicted number of genes in Salmonella genomes encoding universal stress protein domain. We hypothesize that integrative analysis of the distribution of genes encoding the universal stress protein domain in Salmonella will reveal insights into complexity of the stress response modulated by USP genes. The Integrated Microbial Genome Database contains 39 annotated Salmonella genomes annotated with 236 genes encoding proteins with the universal stress protein domain. The USP gene count per genome ranged from 4 (enterica serovar: Typhi404ty) to 8 (enterica serovar: Typhi AG3). A total of 33 genomes had a gene count of 6. Further analyses are ongoing to define the common USP genes in Salmonella genus as well as uniquely present genes.

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