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543

## Cold Shock Protein Genes of an Antarctic *Streptomyces* sp. AA8321

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Exposure to low temperature (cold shock) brings about the biosynthesis of specific sets of proteins, which include cold shock proteins (Csps). Csps constitute a family of small (~ 7.4 kDa) mostly acidic proteins. Csps are reported from various bacteria: nine Csp genes have been reported from *Escherichia coli* (CspA to I), and three from *Bacillus subtilis* (CspB, C, D). CspA homologs with identities of over 45% have also been found in a range of bacteria, including the mesophilic bacterium *Enterococcus faecalis*, the psychrotrophic bacteria, *Arthrobacter globiformis*, *Pseudomonas fragi*, *Pseudomonas putida*, and the psychrophilic bacterium *Shewanella violacea*. By contrast, some bacteria whose entire genomes have been sequenced lack Csp homologues.

Members of the Csp family have been implicated in various cellular processes, including adaptation to low temperatures, cellular growth, nutrient stress, stationary phase and endospore formation. They are regulated differently, but probably share the same general mode of action. The general mode of action is related to the binding of Csps to RNA or DNA, and this binding ability results from their protein structure suitable for binding, such as RNA-binding motifs, RNP1 and RNP2. Csp A of *E. coli* and Csps of *B. subtilis* are proposed to function as RNA chaperones, which bind to RNA and prevent the formation of secondary structures in RNA, presumably facilitating translation at low temperatures or function in coupling transcription and translation. By contrast, CspD of *E. coli* interacts with ssDNA and effectively inhibits DNA replication.

*Streptomyces* species are soil microorganisms that are exposed to various stresses including cold shock. *Streptomyces* species have been focused because they produce antibiotics and antifungal metabolites. Csp genes have been published from two *Streptomyces* species. In this study, four Csp genes were isolated from an Antarctic *Streptomyces* sp. strain AA8321. In addition, Csp amino acid sequences from various bacterial sources were compared in a phylogenetic analysis to examine their relationships of primary protein structures.