Abstract

Prokaryotic environmental adaptations occur at different levels within cells to ensure the preservation of genome integrity, proper protein folding and function. Since amino-acid composition is principally determined by the structural and functional requirements of a given protein, one might expect it to correlate with a variety of factors. Conditions such as temperature, salt concentration, pH, and pressure within an organisms environmental niche are surely among the most important factors that cause selective pressure on the proteins evolving in different niches. Not all conditions are equally acceptable to all species: life is possible from -15C to 113C, up to 5.1 M NaCl, pH from 0 to 13. In this context, extreme conditions of life are those that exceed conditions for growth and reproduction that are optimal for the majority of organisms. Organisms that thrive in or even require extreme conditions are termed extremophiles. There are many different classes of extremophiles, corresponding to the way the environmental niche differs from that of the majority of mesophile organisms. Regardless of the environmental niche, however, adaptation and maintenance of protein integrity and function seems to be fundamental to survival of entire organisms. [13]

Therefore, in this project work it is aimed to do a computational analysis to find out differences in proteome sequences of prokaryotes such as thermophiles, mesophiles and psychrophiles those differ with respect to the optimal growth temperatures.Also to have a better insight towards the functional significance of di-nucleotides in thermal adaptation, the Relative Dinucleotide Frequency(RDF) in the non-coding regions in bacterial genomes is studied.

Keywords: Proteome, Genetic code, Extremophiles, Relative Dinucleotide Frequency.