Abstract

The Cyanophages are the phages infecting cyanobacteria. They are potential agents for the horizontal gene transfer. The complete genome of 10 known Cyanophages deciphered the presence of various gene sequences for hypothetical proteins whose functions are not yet understood. Our attempt is to predict the structure and function of these hypothetical proteins by the application of computational methods and Bioinformatics. The probable function prediction for the hypothetical proteins was done by using Bioinformatics web tools like CDD-BLAST, INTERPROSCAN, PFAM and COGs by searching protein databases for the presence of conserved domains. While tertiary structures were constructed using PS2 Server-Protein Structure Prediction server. This study revealed presences of functional domain in 258 uncharacterized proteins. These deciphered enzymatic data for hypothetical proteins can be used for the understanding of functional, structural and evolutionary development of cyanophages and its life cycle along with their role in host evolution.

References
Comparative Genomic Studies of hypothetical proteins in Cyanophages

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