Abstract

The in-silico approach was utilised for prediction of structure, function and sub-cellular localization of the hypothetical proteins in Agrobacterium fabrum str. C58 plasmid At. In Agrobacterium fabrum str. C58 plasmid At out of 209 genes screened for hypothetical proteins, structures, functions and sub-cellular localization were predicted for 84 hypothetical protein. The Bioinformatics web tools like CDD-BLAST, INTERPROSCAN and PFAM were used for the functional annotations of hypothetical proteins; Cello v 2. 5 was used to determine the sub-cellular localization of annotated hypothetical proteins whereas, PS2 Server-Protein Structure Prediction server was used for generating 3-D structures of the identified proteins by searching
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protein databases for the presence of conserved domains and templates. This In silico study revealed much helpful information regarding the understanding of functional characteristics of hypothetical proteins in Agrobacterium fabrum str. C58 plasmid At as well as their role in the life cycle of the bacterium.

References


Index Terms

Computer Science
Applied Sciences

Keywords
Unknown proteins; Bioinformatics web tools protein databases tertiary structures functional characteristics.