In silico analysis of chalcone synthase 1 protein sequences from different plant species

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ABSTRACT : Chalcone synthase 1 protein in flowering plants has diverse providing floral pigments like anthocyanin, antibiotics, UV protectants and insect repellents. A total of 16 full lengths of chalcone synthase 1 protein sequences from different plant species available in uniport were evaluated by using bioinformatics tools to investigate physico-chemical properties such as pI, EC, AI, GRAVY and II, secondary structure prediction, putative phosphorylation sites, conserved motif search and phylogenetic tree construction. The secondary structure of the protein sequences contains alpha helix was predominant, followed by random coil, extended strand and least beta turn. The most abundant phosphorylation site is serine residues in chalcone synthase 1 protein sequences. Conserved protein motifs subjected to MEME to obtain the best possible matches. The phylogenetic tree represented three major clusters and chalcone synthase 1 protein sequences of plant species belongs to same family clustered together. The obtained results could be used for further *in silico* analysis and homology modeling studies.

Key Words : Chalcone synthase 1 protein, polyketide synthase, *in silico*, homology modeling and bioinformatics.