

عنوان مقاله:

Bioinformatically study of D1 and D2 proteins in two species of Chlorella

محل انتشار:

بیستمین کنگره ملی و هشتمین کنگره بین‌المللی زیست‌شناسی ایران (سال: 1397)

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خلاصه مقاله:

Green algae are the main group of algae that have the highest number of species with the highest global distribution. The genus of Chlorella has a thin and spherical with side or cupola chloroplast. In this work, the nucleotide sequences of Chlorella vulgaris and Chlorella sorokiniana and the protein sequences were obtained from NCBI and UniProt database. Then by using the Blast tool, PSIPRED, RaptorX and MEGA7 software programs, two different green algal species were examined. By using these software programs analysis such as similarities between different sequences, prediction of second and third structures of the protein and drawing phylogenetic tree were carried out. The Blast tool was used to determine similarities between the obtained sequences of these genes and the sequences of the same gene in NCBI gene bank as well as sequences itself. Nucleotide sequences of D1 and D2 in vulgaris and sorokiniana were obtained and the percentages of homology between D1-D1 and D2-D2 were 93% and 90% respectively. PROSITE software was used to evaluate the domain function. These proteins have one major domain and amino acid length in protein D1 in both species were 353 and in D2 were 352, molecular weight, isoelectric point and number of structural amino acids in D1 and D2 were obtained from isoelectric.ovh.org. The results showed a remarkable similarity in the nucleotide sequences, amino acids and number of alpha and beta structures and third structure of the protein in studied species. In order to study phylogenetic relationships between different green algal species, multiple alignment was performed using Clustalw software. Drawing phylogenetic tree was performed using the neighbor-joining method of MEGA7 software.

کلمات کلیدی:

Photosystem (II), Green alga, Protein, Bioinformatical study

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