

## عنوان مقاله:

Coding sequences in Light-Harvesting Chlorophyll-a/b revealed by different plant species comparisons

## محل انتشار:

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## خلاصه مقاله:

Gene families often show degrees of differences in terms of exon-intron structures depending on their distinct evolutionary histories. Comparative analysis of gene structures is important for understanding their evolutionary and functional relationships within plant species. Here, we present a comparative genomics database NCBI for every plant, just coding Comparison and also evolution studies. Plants are always exposed to a wide range of environmental stresses, both biological and abiotic, that strongly affect their growth and production. Molecular and physiological mechanisms are involved in the tolerance of plants to environmental stresses, the identification of which can be an important step to deal with the destructive effects of these stresses. In this study, sensitive and resistant to cold stress physiological responses were studied and chlorophyll a and b, carotenoids and free amino acid proline were measured. Nucleotide fragments of stress-responsive genes were also examined by bioinformatics software. For this purpose, gene sequences were obtained from the NCBI and Graingenes websites. In order to classify EST sequences, determine ion-associated proteins (contigases and singletons), Functional grouping and statistical tests were performed using the Egassembler database, the NCBI website blast, the Max Planck Institute website, and the MEGA software, respectively. The database contains all the annotated genes extracted from plant genomes. These genes were classified based on nucleotide. Examined all regions, between the different genes (coding) For  $\Delta$  plants Around the Light-Harvesting Chlorophyll-a/b (LHC) genes, the gene structure evolution of orthologous gene groups was determined using the NCBI Blast, BioEdit and Mega v.5 software programs that can be accessed within the database. Blast part in NCBI and Mega software programs drawing schematic diagrams of gene structures. Also is a powerful tool for comparing gene sequences and provides valuable insights into the evolution of LHC gene structure in .plant genomes

## کلمات کلیدی:

Coding sequence, Sequence comparison, Gene families, LHC

## لینک ثابت مقاله در پایگاه سیویلیکا:

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