

University of Zabol Faculty of Basic Science Department of Bioinformatics

A Thesis Submitted for the Degree of M.Sc. in Bioinformatics

Genomic and Phylogenetic Analysis of SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (SPL) gene family in *Carthamus tinctorius* L.

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Abstract

SPL gene family plays an important role in plant growth, development and stress responses. This study presents a comprehensive genomic and phylogenetic analysis of the SPL gene family in safflower, an economically important oilseed crop. Using the BLAST tool against the safflower genome, 44 sequences containing the second conserved SBP were identified, which shows the complexity and evolutionary importance of this gene family. Physicochemical analyzes showed a wide variation in molecular weight, isoelectric points and stability indices, indicating the diverse biological roles of these genes. Structural analysis reveals a complex structure of exons and introns, while mainly the localization of proteins in the plasma membrane points to their critical roles in cell signaling and membrane-related processes. Phylogenetic analysis revealed significant genetic diversity in SPL genes, reflecting adaptive responses to various environmental stresses. Promoter analysis also points to the existence of various regulatory elements, which indicates the precise control of gene expression in response to external stimuli. These results can be an important basis for genetic engineering and plant breeding programs with the aim of improving key characteristics in safflower, including increasing oil production, strengthening resistance to environmental stresses and improving agricultural performance.

Keywords: SPL gene family, phylogenetic analysis, safflower, comparative genomics, genomic analysis, promoter analysis, Carthamus tinctorius