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Comparative Genomics of Sunflower MYB Transcription Factors and their Role in Drought Stress

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Abstract

Sunflower is the 3rd most important oil seed crop in the world. In Pakistan, sunflower is mainly cultivated in spring season and is badly affected by drought due to scarcity of irrigation water. Epicuticular wax act as a first line of defense to protect the plants from drought stress by sealing the areal parts of land plants to prevent them from non-stomatal water loss. The myeloblastosis (MYB) transcription factor (TFs) proteins are involved in various biotic and abiotic stresses. A comprehensive analysis of the sunflower and Arabidopsis *MYB* gene family was carried out to uncover the functions, gene structure, evolutionary history and expression pattern of these genes in sunflower. As the genome of sunflower has recently been sequenced and no such study was conducted in this crop. A blast search was used to find the relevant genes in sunflower. Physiochemical properties indicated that these MYB genes were present throughout the genome however, subcellular localization indicated that most of these genes were located in nucleus. Phylogenetic analysis showed that MYB proteins were divided in four clades.

Key Words: Sunflower, MYB, Transcription Factors, Drought, Wax biosynthesis

