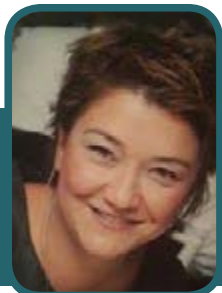


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Genome wide identification and characterization of various transcription factors in common bean (*Phaseolus vulgaris* L.) under abiotic stress conditions

Gene expression, especially at the level of transcription regulates many vital biological processes in a cell, tissue or organism, such as control of the cell cycle, metabolic and physiological balance, responses to the environment and differentiation. The fundamental aspect of development is based on the cellular capacity for differential gene expression, which is usually regulated at the transcriptional level and controlled by transcription factors (TFs) acting as switches of regulatory cascades. The TFs regulate transcription by binding to promoter sequences of a specific gene and play important roles in the growth and development of plants as well as all other organisms in nature. Up until now, approximately 30 families of TFs were identified that were classified according to their conserved motifs that code for the DNA-binding domains. Almost half of these families were recorded as plant-specific TFs such as AP2/ERF, WRKY, NAC, B3, SBP and DOF families. In recent years, genome-wide studies, bioinformatic approaches became common for the identification of new genes and proteins in plants. Although sub-disciplines of system biology

had the grave impact and manifested invaluable data on genomics, transcriptomics and metabolomics in plants, still not enough study has been conducted on genome-wide identification and expression analysis of transcription factor families in plant species such as common bean especially under stress conditions. The current presentation is mainly focused on to give and review the information obtained from our studies about identification and characterization of various transcription factors such as C2C2-YABBY, Growth Regulating Factors (GRFs), Hsp70 in common bean (*Phaseolus vulgaris* L.) under abiotic stress conditions. Various in silico approaches have been used for this purpose and also quantitative real-time PCR (qPCR) was performed for the identification of the putative genes. These studies revealed that TF genes might play an important role in abiotic stress response for common bean cultivars and variability between cultivars also suggests that these genes could be used as functional markers for various stress factors.

Biography

Sumer Aras is currently working in the Ankara university at Turkey as a senior Professor of Science. She also published her paper in various international journals.

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