

Abstract No: 141

Life Sciences

CALMODULIN-BINDING TRANSCRIPTION ACTIVATOR (CAMTA) GENES IN SOYBEAN AND THEIR EXPRESSION ANALYSIS

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Calmodulin Binding Transcription Activator (CAMTA) genes encode a special class of transcription factors (TFs) in eukaryotes, mainly in plants and animals. CAMTA TFs have been reported to mediate transcriptional regulation of plant stress response genes. However, the functions of CAMTA genes are yet to be well characterized in crop plants such as soybeans. Soybean is the world's fourth-largest commercial crop, which provides primary protein and oil sources. However, yield loss due to various stresses is a rising burden to farmers. It is crucial to employ various strategies to address this problem, including incorporating CAMTA genes into breeding programs. Therefore, it is necessary to characterize these genes in soybeans. However, gene redundancies in soybeans due to recent genome duplications pose a challenge in identifying gene functions. Therefore, finding the recently duplicated CAMTA is imperative to expedite the functional characterization. This study employed phylogenetic and expression analysis to investigate the evolutionary relationship and function of identified soybean CAMTA genes. The evolution of these genes compared to CAMTA genes of closely related species were analyzed. Furthermore, the study explored the expression patterns of these genes in different plant parts. The soybean CAMTA TFs were grouped into six major groups (with bootstrap support 100%), each containing two TFs. Genes in these clusters share a common evolutionary ancestor with *Glycine soja* but form a separate clade with other legumes (with bootstrap values above 60%), indicating they originated from a gene duplication event. Furthermore, two members of the four duplicated gene groups showed no statistically significant difference in expression levels in different parts. This suggests that the duplicated CAMTA gene retained the same expression patterns thus likely retained the same function. The expression data can be used in future studies to identify candidate genes to enhance soybean resistance to different diseases.

Keywords: Evolutionary relationship, Expression analysis, Phylogenetic analysis, Stress Response, Transcription factors