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Genomic Identification, Characterization and Phylogenetic analysis of the AP2 Gene Family in Glycine Max

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Abstract

Genetic makeup of Glycine max is crucial for unraveling its traits, improving crop yield and quality, and developing sustainable agricultural practices. Glycine max harbors a large number of transcription factor families, including AP2/EREBP, MYB, WRKY, NAC, and bZIP which are involved in diverse developmental processes and stress responses. The AP2 gene is a member of the AP2/EREBP (APETALA2/Ethylene Responsive Element Binding Protein) transcription factor family, which is widely distributed in plants and involved in various physiological and developmental processes. To learn more about the evolution of the AP2 gene family in soybean, the gene structure, or the distribution pattern of introns and exons, of 50 AP2 genes, was identified. Using the NCBI webserver's basic local alignment search tool (BLASTP), the potential AP2 TFs were verified. Map Chart was used to create a chromosomal localization map of the non-redundant Glycine max AP2 genes. The neighbor-joining approach was used to create a phylogenetic tree using the generated alignment. The discovered genes were then checked to see if the proteins they encoded included any AP2-specific primary domains. The average peptide length of AP2 proteins was 211 amino acids, although the range from 2 to 420 amino acids. Two genes are scaffold genes which gives structural support and tissue development in soybean. Gene Structure analysis revealed that Soybean AP2 genes exhibited a diversity with respect to the number of introns e.g ranging from 1 to 9. The gene structure of Glyma.08G225200 was observed because of having maximum portion of exons and only two introns, while there is absence of non-coding region due to very short size of its genomic DNA sequence i.e 0.7 Kb. To identify conserved domains, MEME was applied to the peptide sequences of all AP2 TFs. According to NCBI, all of the genes exhibit duplication in conserved regions. Using the cercoletto tool, genomic areas from Glycine max (soybean) and Arabidopsis thaliana (as a model plant) were examined to learn more about the evolutionary link and functional conservation of the AP2 genes found in both species. These analyses will greatly aid in expediting the functional characterization of AP2 TF.

Key Words: *Glycine max, AP2 gene family, Arabidopsis, Characterization, Phylogenetic Analysis*

