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Genome-wide identification and characterization of acyl-CoA-binding protein (ACBP) gene family in soybean (*Glycine max* L.)

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Acyl-CoA-binding proteins (ACBP) are a class of stress-responsive proteins that may play a role in drought tolerance. ACBP family members are known to be involved in ABA-mediated reactive oxygen species (ROS) production in guard cells, thereby promoting stomatal closure, reducing water loss and enhancing drought tolerance. In this study, a genome-wide analysis identified 9 ACBP genes on nine different chromosomes of soybean (*Glycine max* L.). An overview of the soybean ACBP gene family is presented, including the chromosomal locations of the genes, gene structure, phylogeny, gene duplication, gene expression, and conserved promoter motifs. To understand ACBP evolution, a comparative analysis of soybean ACBP with orthologs from chickpea (*Cicer arietinum* L.), Medicago (*Medicago truncatula*), common bean (*Phaseolus vulgaris* L.), and Arabidopsis (*Arabidopsis thaliana*) was performed. Evaluation of available RNA-seq data obtained under biotic and abiotic stresses identified putative ACBPs involved in stress tolerance mechanisms in soybean. Haplotype analysis of ACBP genes based on whole genome re-sequencing (WGRS) data of 234 diverse soybean lines revealed structural variations among ACBP genes. SNP variations identified in re-sequenced lines can be used to develop markers to evaluate drought tolerant and sensitive lines. This genome sequence based analysis of soybean ACBPs sets the stage for further to better understand their role in soybean abiotic stress responses and their potential utility to improve soybean drought tolerance.