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Genome-wide analysis of soybean LATERAL ORGAN BOUNDARIES domain-containing genes: a functional investigation of GmLBD12

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Plant-specific *LBD* (*LATERAL ORGAN BOUNDARIES Domain*) genes play critical roles in various plant growth and development processes. However, the number and characteristics of *LBD* genes in soybean [*Glycine max* (L.) Merr.] remain unknown. Here, we identified 90 *LBD* homologous genes in the soybean genome that phylogenetically clustered into two classes (I and II). The majority of the *GmLBD* genes were evenly distributed across all 20 soybean chromosomes, and 77 (81.11%) of them were detected in segmental duplicated regions. Furthermore, the exon–intron organization and motif composition for each *GmLBD* were analyzed. A close phylogenetic relationship was identified between the soybean *LBD* genes and 41 previously reported genes of different plants in the same group, providing insights into their putative functions. Expression analysis indicated that more than half of the *LBD* genes were expressed, with the two gene classes showing differential tissue expression characteristics; in addition, they were differentially induced by biotic and abiotic stresses. To further explore the functions of *LBD* genes in soybean, *GmLBD12* was selected for functional characterization. GmLBD12 was mainly localized to the nucleus and showed high expression in root and seed tissues. Overexpressing *GmLBD12* in *Arabidopsis thaliana* (L.) Heynh resulted in increases in lateral root (LR) number and plant height. Quantitative real-time polymerase chain reaction (qRT-PCR) analysis demonstrated that *GmLBD12* was induced by drought, salt, cold, indole acetic acid (IAA), abscisic acid (ABA), and salicylic acid SA treatments. This study provides the first comprehensive analysis of the soybean *LBD* gene family and a valuable foundation for future functional studies of *GmLBD* genes.