



Genome-wide identification and expression analysis of the *CPP-like* gene family in soybean

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ABSTRACT. Cysteine-rich polycomb-like protein (*CPP-like*) genes are a group of transcription factors with highly conserved cysteine-rich domains and are widely distributed in animals and plants, but do not present in yeast. Previous studies have shown that members of this family play important roles in the development of reproductive tissue and in the control of cell division in plants. In this study, whole genome identification of soybean CPP transcription factors was performed using bioinformatic methods. The results showed that there were 20 CPP transcription factors in the soybean genome,

which encoded for 28 distinct CPP proteins. These transcription factors were distributed on 16 of 20 chromosomes. Phylogenetic relationship analysis showed that expression of CPP gene family members occurred before the differentiation of monocotyledons and dicotyledons. RNA-Seq analysis showed that 5 genes were highly expressed in all tissues, including Glyma10g39080, Glyma01g44670, Glyma101g66920, Glyma02g01540, and Glyma20g28740. One gene (Glyma14g14750) was specifically expressed in young leaves, while 2 genes (Glyma02g01540 and Glyma10g01580) were highly expressed in root nodules. Quantitative reverse transcriptase-polymerase chain reaction analysis revealed that the expression levels of most genes increased in the roots under high temperature stress. Our findings indicate that these genes are not only involved in growth and development, but also in the responses to high temperature stress in soybean roots.

Key words: CPP gene family; CXC domain; Expression analysis; Phylogenetic tree; Soybean