

COMPREHENSIVE ANALYSIS OF THE COBRA GENE FAMILY IN SOYBEAN: GENOMIC ORGANIZATION, GENE STRUCTURE, PHYLOGENETIC RELATIONSHIPS AND EXPRESSION PROFILE

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COBRA gene family is co-expressed with a complex of genes related to cellulose synthesis. COBRA mutants result in reduced levels of cellulose and a disordered deposition of microfibrils causing defects in the cell wall. Some studies have correlated COBRA genes with the regulation of cell expansion and cell wall biosynthesis, but their specific function is still unknown in plants like soybean. To identify the COBRA genes in the soybean genome we carried out a genomic survey using COBRA genes of Arabidopsis thaliana as reference. We found 32 transcripts and 23 orthologs genes in soybean. Genes are composed of two to six exons with size ranged from 537 to 2,016 bp and proteins of 178 to 671 aminoacids residues. The identified genes had their protein sequences checked on the Pfam website to confirm the presence of the COBRA domain. The confirmation of N-terminal signal peptide and potential C-terminal GPI modification sites (ω -sites) on the COBRA proteins were performed on SignalP and big-PI websites. In order to demonstrate the phylogenetic relationships of the COBRA family a phylogenetic tree was constructed based on the alignment of 72 sequences of the COBRA domain: 23 of Glycine max, 12 of Arabidopsis thaliana, 10 of Vitis vinifera, 13 of Medicago truncatula and 14 of Phaseolus vulgaris. Phylogenetic analysis revealed that the soybean COBRA proteins are grouped in five clusters. The smallest cluster contains 11 members and the largest one 22 members of COBRA genes with eight from soybean and three from Arabidopsis, which suggests that this later group expanded after the speciation of soybean and Arabidopsis. To better understand the duplication and expansion of the COBRA family in soybean, the 32 COBRA sequences were mapped on the 20 soybean chromosomes. The distribution of COBRA genes on chromosomes reflected the occurrence of duplication events and also tandem duplication. The expression profile of COBRA family in sovbean was analyzed on Phytomine. The COBRA genes expression was highly variable, with some genes expressed only in flower, whereas other genes were expressed in all the tissues. Together, these data could increase the knowledge of COBRA family role in soybean.

Key words: Cobra family, Cell wall, Soybean. Supported by: CNPq, CAPES e FAPERJ.







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