

Abstract

Soybean is considered as one of the best sources of protein for the nutrition of humans and mammals, and also is cultivated as an economic source of both vegetable oil and protein. Soybean like other Leguminosae, contains low levels of S-amino acids (methionine and cysteine). The purpose of this study is transferring *11 kDa delta-zein* and *EPSPS* genes to improve the methionine content and induce resistance to glyphosate herbicide. The presence of *11 kDa delta-zein* and *EPSPS* genes in T0 and T1 transgenic plants was confirmed by PCR. Shikimic acid and Chlorophyll content analysis also revealed that these two indexes in transgenic lines compared to wild type were significantly decrease and increase, respectively after glyphosate application. Also, in order to better understand the pathway of cysteine biosynthesis in legumes, we analyzed the sulfur amino acids and expression levels of genes involved in the biosynthesis of cysteine in developing seeds of the model plant (common bean). Metabolite profiling during seed development in total S-methylcysteine accumulation showed that γ -glutamyl-S-methylcysteine accounts for most of the total S-methylcysteine in mature seed. Correlation between the expression of *BSAS4;1* gene and the S-methylCys concentration in early developmental stage of seed indicated that *BSAS4;1* can be considered as a candidate gene for the synthesis of S-methylcysteine. Also, the expression of *hGS* may regulate the accumulation of γ -glutamyl-S-methylcysteine, through the provision of homoglutathione and S-methylhomoglutathione.

Key Words: Soybean, glyphosate, methionine S-methylcysteine, γ -Glu-S-metCys, *BSAS4;1*.



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