STUDY OF THE STACHYOSE SYNTHASE GENE IN *GLYCINE MAX* L. MERRIL SEEDS

Fialho, L.S.[1], Barros, E.G.[2], Guimarães, V.M.[1], Rezende, S.T.[1]
[1]Departamento de Bioquímica; [2]Departamento de Biologia, BIOAGRO, UFV, MG, Brazil.

The galactooligosaccharides (GO) are present in leguminous and are source of energy during the germination of the seeds. In soybean, stachyose is biosynthesized by the enzyme stachyose synthase (STS), and is the main responsible for gastrointestinal disturbances in humans. There is interest in study the *sts* gene from soybean aiming genetic manipulations to reduce the stachyose content in seeds. The objectives of this study were to quantify the stachyose content and determine STS activity in soybean seeds, isolate a fragment of the *sts* gene and verify its patterns of expression during seeds development. The quantification of stachyose was done by HPLC. In mature soybean seeds, stachyose content was 4,1% and STS activity was 1,58 $\mu mol.mL^{-1}.h^{-1}$, using raffinose and galactinol as substrate. A fragment of the *sts* gene was isolated by PCR using seed cDNA in combination with degenerate *primers*. The analysis of the expression patterns, done by RT-PCR, showed that the *sts* gene is express in all development stages of the seed, besides leaves, stem and roots. The cloning of a 978 pb fragment in a vector pGEM-T Easy was confirmed by sequencing. The identity of the fragment, verified using tool BLAST, confirmed that the cloned sequence refers to the *sts* gene, until then not isolated in soybeans. Financial support: CAPES/FAPEMIG. Key words: soybeans, stachyose and stachyose synthase.