SULFUR METABOLISM IN *GLYCINE MAX* [L.] MERR: CHARACTERIZATION OF SERINE ACETYLTRANSFERASE AND *O*-ACETYLSERINE (THIOL) LYASE

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ABSTRACT

Soybean (*Glycine max* [L.] Merr) is considered an excellent protein source for both humans and livestock. Further improvement of quantity and quality of soybean protein is vital for maintaining the utility of this versatile plant derived nutrient. Although high protein soybean lines are currently available, the cysteine and methionine content is still not adequate to meet the dietary needs of livestock and poultry. Currently, rations for these animals are supplemented with synthetic methionine, a procedure costing the animal industry millions of dollars annually. Efforts to enhance the sulfur amino acid content of soybean protein through genetic engineering and traditional breeding have met with limited success. Expression of exogenous high methionine proteins in soybeans has not substantially increased the overall sulfur amino acid content. A possible explanation is that the availability of sulfur amino acids in developing seeds may be limiting. Effectively increasing the accumulation of sulfur amino acids in soybean will require metabolic engineering of the sulfur assimilatory pathway. In an attempt to improve the nutritional quality of soybean seed proteins, molecular techniques are being employed to manipulate key enzymes involved in sulfur assimilation. The molecular cloning and characterization of serine acetyltransferase (SAT) and *O*-acetylserine (thiol) lyase (OAS-TL, cysteine synthase), key enzymes in cysteine biosynthesis, is presented here.