

CHARACTERIZATION OF RAFFINOSE SYNTHASE GENES IN SOYBEAN

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ABSTRACT

As the use of soy products in foods and feeds increases, it is ever more important to consider the nutritional value of each component of the seed. The carbohydrate component is largely composed of sucrose, raffinose, and stachyose, which represent ~10% of the meal. Both raffinose and stachyose are considered anti-nutritional units; sucrose is considered nutritionally useful. Monogastric animals, including humans, lack the alpha-galactosidase enzyme required for the metabolism of raffinose and stachyose. However, microbes in the gut are able to utilize these carbohydrates causing flatulence and diarrhea; in livestock these complications ultimately reduce market value.

The objective of this project is to resolve the undesirable effects of raffinose and stachyose in soybean seeds by elevating the metabolizable energy, sucrose, at the expense of raffinose and stachyose. This change in seed composition has the potential to increase the available metabolizable energy for non-ruminant animals as well as reduce the adverse side effects caused by microbes in the gut. Raffinose is formed by a galactosyl transfer from galactinol to sucrose, mediated by the enzyme raffinose synthase. To date, candidate raffinose synthase genes have been identified and characterized in Williams 82 and a low raffinose line, PI 200508. The genotype of one candidate gene has been completely associated with the low raffinose and stachyose phenotype through the use of a segregating population and confirmed by an independently characterized EMS induced mutation. Perfect molecular marker assays have been developed and can be utilized for more efficient breeding.