Improving Soybean Seed Composition Through Molecular Breeding for Raffinose Family Oligosaccharides, Lectin, and Trypsin Inhibitors

Katherine Hagely

Dr. Kristin Bilyeu, Dissertation Supervisor

Abstract

In 2011, soybeans were planted on 75 million acres in the US and the total crop value exceeded $35 billion. After the oil is extracted from the soybean, the remaining high protein fraction is made into meal to be used in animal feed, however first the meal must be processed in order to destroy the activity anti-nutritional proteins. This work reports on the development of molecular breeding methods to screen for soybean lines with improved seed composition containing ultra-low raffinose family oligosaccharides (RFOs), lectin null, and Kunitz trypsin inhibitor (TI) null alleles. A variant allele of RS3 (rs3SNP5) was found to perfectly associate with the ultra-low RFO phenotype, and molecular marker assays for this allele and lectin null and Kunitz TI null alleles are described. The environmental influence of nitrogen on TI phenotype was also investigated, and while adding nitrogen to growth chamber plants resulted in seed with reduced TIs, a field location experiment including two locations with potentially enhanced nitrogen availability did not have reduced TI activity in the 2012 growing season. Finally, the development of a quadruple mutant ultra-low RFO, lectin null, and Kunitz TI null soybean line in a high protein background is reported. This work outlines the development of important soybean breeding tools having significant implications for the creation of nutritionally superior soybean lines for use in animal feeds.