

Public Abstract

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Title:Improving Soybean Seed through Molecular Breeding for Raffinose Family Oligosaccharides, Lectin, and Trypsin Inhibitors

In 2011, soybeans were planted on 75 million acres in the US, and the total crop value exceeded \$35 billion.¹ After the oil is extracted from the soybean, the remaining high protein fraction is made into meal to be used in animal feed. Soybean meal requires processing to remove anti-nutritional compounds, including raffinose family oligosaccharides (RFOs), lectin, and trypsin inhibitors (TIs). These proteins all negatively impact the nutritional quality of soybean meal, requiring additional processing steps to remove their activity. With the recent release of the soybean genome², the DNA sequence of lines naturally containing reduced RFOs, TIs, and lectin can be investigated and molecular marker assays can be designed to screen for these favorable alleles, providing crucial tools to conventionally breed soybean lines for improved nutritional value. Molecular genetic investigations described in this work reveal the genetic basis of lines with the ultra-low RFO phenotype to be a variant allele of raffinose synthase 3 (rs3) and a molecular marker assay to screen for this allele, along with assays to screen for lines with reduced lectin and Kunitz TIs are reported. The environmental influence of nitrogen on TI activity 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 TIs in the 2012 growing season. Finally, the development of a nutritionally improved quadruple mutant line in a high protein background is described, which is currently being evaluated in animal feed trials. This work outlines the development of important soybean breeding tools having significant implications for the creation of nutritionally superior soybean lines for animal feed.

1. <http://www.soystats.com/2012/Default-frames.htm>

2. Schmutz, J., S. B. Cannon, J. Schlueter, J. Ma, T. Mitros, W. Nelson, D. L. Hyten, Q. Song, J. J. Thelen and J. Cheng (2010). "Genome sequence of the palaeopolyploid soybean." *Nature* 463(7278): 178-183.