Genetic Mapping of Phytate Genes in Soybean. (C01-walker162245-Poster)

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Abstract:

Approximately 95% of the phosphorous (P) in soybean, Glycine max (L.) Merr., seed is stored as phytic acid (phytate), and is unavailable to nonruminant animals. This reduces the nutritional value of soybean meal and can cause environmental problems. Phytate is also a chelating agent that reduces the availability of iron, zinc, calcium and magnesium from soybean meal. Low phytic acid (LPA) soybean mutants have been developed that have reduced phytate levels and increased inorganic P contents. Our objective was to map the gene(s) responsible for the LPA phenotype. Bulked segregant analysis with simple sequence repeat markers in an F2 population derived from a cross between G99-G725 (a high phytate, backcross-derived line of 'Boggs' with glyphosate tolerance) and CX1834-1-2 (a low phytate line) was used to identify genomic regions associated with phenotypic variation for the trait. QTL mapping techniques were then used to map the genes. The results indicate that a gene with a recessive allele is located on soybean molecular linkage group N, but that another recessive allele at an independent locus also conditions reduced phytate content in CX1834-1-2.

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