

Senior Biochemistry

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Funding Source: BioInformatics in Plant Sciences (BIPS)

## Molecular Resources to Improve Breeding of Food Grade Soybeans

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Soybean is a critical crop for most of the world. Yellow hilum soybeans, sometimes referred to as clear hilum soybeans, are especially prized for human consumption. Despite the many pages of research generated each year in soybean genetics and genomics, little is known about the mechanisms that control seed coat color and hilum color in soybean. These mechanisms were explored using GWAS (Genome Wide Association Studies) comparing different phenotypes of soybeans to find the most highly-associated SNPs, or single-nucleotide polymorphisms, linked to a change in the hilum color. The objective is to find a proxy SNP or SNPs that can be used to identify yellow hilum in soybean with a high accuracy rate without cloning. GWAS was run comparing all accessions with 50k data and the phenotype yellow hilum to accessions with 50k data and the phenotype black or brown hilum. Similar GWAS were run comparing yellow hilum to black or brown seed coat, black hilum to gray hilum, and black hilum to green hilum. From these GWAS, the top-associated SNPs identified were ss715602777, ss715602754, ss715602756. More experimentation must be performed to determine if these SNPs, together or separately, can predict the yellow hilum phenotype in soybeans.