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Marker-assisted selection workflow and strategy to accelerate development of high-oleic and low-linolenic acid soybean varieties

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Soybean has arisen in agriculture as one of the most valuable protein and oil seed resources. Alteration of the fatty acid profiles in soybean oil is of particular interest to various food applications. Typical soybean oil is composed of palmitic, stearic, oleic, linoleic, and linolenic acids. High oleic and low linolenic acid contents in soybean seed are the key compositional traits that improve oxidative stability and increase oil functionality and shelf life. Development and deployment of high oleic and low linolenic soybean varieties will help eliminate the hydrogenation process and provide *trans* fat-free soybean oil to consumers. Genes that control the oleic acid (*FAD2*) and linolenic acid (*FAD3*) contents in soybean oil have been characterized. Tests results indicated that two *FAD2* mutant alleles and two *FAD3* mutant alleles can contribute to the lines with ~80% oleic acid and <3% linolenic acid content. To achieve this breeding goal and accelerate development of high oleic/low linolenic acid soybean varieties, we have developed a paralleling backcross and stacking workflow using seven functional SNP markers for the targeted fatty acids and run three backcrossing cycles per year in our Puerto Rican nursery. We have also established a seed chipping and high throughput genotyping platform to effectively identify the seed or plants homozygous for four genes. In the first cycle of 2017, over 13,000 individual plants were genotyped with various HOLL SNP markers for backcrossing and advancement. This workflow has successfully resulted in soybean lines with four genes homozygous for yield trials in three years.