Elucidating the Genetic Architecture of Extremely Elevated Seed Stearic Acid in Soybean Using Genotyping-By-Sequencing

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Introduction

Stearic Acid (C18:0)

- Unsaturated fatty acids, such as linolenic (C18:3) and linoleic (C18:2), are oxidatively unstable, and tend to go rancid rapidly
- These fatty acids must be hydrogenated to increase stability (Figure 1)
- The hydrogenation process results in the formation of trans fatty acids, which are tightly linked with heart problems in humans and "not generally regarded as safe" by the USDA
- Stearic acid (C18:0) is a long chain fully hydrogenated fatty acid that has been shown to have no negative effect on LDL levels (unlike other saturated fatty acids)
- Soybean oil with elevated saturated fatty acid content is desirable for solid fat baking applications, and could potentially eliminate the need for expensive solid fats like cocoa butter and heart-unhealthy fats such as palm oil

Mutant lines: A6 and 194D

A6 is a mutant characterized by several large deletions, including 1/8 chromosome deletion on Gm14 predicted to encompass 30 genes from the Glyma 1.0 high confidence gene set, including SACPD-C (Figure 4)

A6 exhibits poor germination and severe field defects such as reduced height and yield

194D is an EMS-induced mutant with moderate levels of stearic acid (~12%) due to a point mutation (V211E) in the protein-desaturase gene, SACPD-C

Previous work by Zhang et al (2008) and first demonstrated that the elevated stearic acid trait in soybean is due to loss of function mutations affecting a stearyl-acyl carrier protein-desaturase gene, SACPD-C

Materials and Methods

GBS/QTL mapping

- Eliminating the need for expensive solid fats like cocoa butter and heart-unhealthy fats such as palm oil

Future Plans

- High stearic line A6 and selected high stearic (>20%, A6 x 194D) progeny have recently been resequenced to identify causative alleles
- Registration of A6 germplasm line of soybean
- 2016 Multi-location phenotype stability study just completed
- Support of soybean oil improvement.

GBS genotyping

- Singe nucleotide polymorphism (SNP) markers identified by GBS
- Performing an initial scan for G61 in high using GBS
- Performing a second scan with microsatellite markers in order to coarsely identify interactions between G61 and small-effect QTL
- Reference the final model and calculate association heritability

Phenotypic distribution in NIRS calibration data set

- NIRS model accurately predicts oil content with a correlation coefficient of 0.95

Fatty acid NIRS calibrations

- Gas chromatography analysis destructive assay yields correlations = 0.95
- Instrument: monochromator model FOSS 6500 using the transport quarter cup (dimension 97mm x 55mm)
- Software: UnScrambler® software 6.11

Correlation coefficients >0.9 for 4 soybean fatty acids

References

- Gillman D, Stacey MG, Cui Y, Berg H, Stacey G: Deletions of the SACPD-C locus elevate seed stearic acid levels but also result in fatty acid and morphological alterations in nitrogen fixing nodules. BMC Plant Biol 2014, 14:162

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