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Breeding for improved oil quality in high yielding soybean lines using molecular markers for selecting *FAD3A* and *FAD3C* mutant alleles

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Soybean [*Glycine max* (L.) Merr.] oil is a major commodity in the US with practical uses for both food and industrial products. Normal quantities of linolenic fatty acid in soybean oil causes rapid rancidity. To accommodate the need for a more stable oil, soybean breeders have identified alleles *FAD3A*, and *FAD3C*, which regulate linolenic acid (18:3). Improved oil necessitates a decrease in linolenic acid to < 3%. Using single nucleotide polymorphism's (SNP's) and gas chromatography to identify low linolenic (LL) soybean lines, soybean breeders can produce soybeans with more stable soybean oil. In 2016 we performed a multi-location yield study comparing four genotypic classes of F_7 near isogenic lines with parents and high yielding checks. The four genotypic classes assessed as lines were as follows; mutant/mutant (ffgg), mutant/wild-type (ffGG), wild-type/mutant (FFgg) and wild-type/wild-type (FFGG). This study was conducted with two replications of two row plots in a randomized complete block design (RBD) at East Tennessee Research and Education Center and Highland Rim Research and Education Center. We found that no yield drag was associated with any of the LL lines assessed when compared to checks and parents. The mean linolenic acid of the mutant line ffgg genotypic class was 2.6%. The results of this study indicate that through SNP analysis we can identify that low linolenic soybean lines with less than 3% linolenic acid.