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Studying potential roles of acyl-CoA: diacylglycerol acyltransferases in soybean seed composition by trans-acting siRNA gene silencing

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Triacylglycerol's (TAGs) are the most common storage lipids in plant seeds, including soybean (*Glycine max*), and are synthesized through the Kennedy Pathway. The final step of the pathway is catalyzed by acyl-CoA: diacylglycerol acyltransferases (DGAT) enzymes that are considered to be the rate-limiting factors in TAG accumulations.

Among the three *DGAT* gene families identified in plant species, *DGAT1s* have been shown to play the most important role in TAG biosynthesis and accumulation in seeds.

To discover the potential roles of *DGAT* genes in soybean seed composition traits such as oil, protein, and fatty acid profiles, *DGAT1s* were down-regulated in soybean cv.

Jack, using trans-acting siRNA technology. The preliminary results from studying 18 transgenic lines, at T₀ and T₁, grown in a greenhouse environment showed significant (P<0.05) reduction in seed oil concentration with no effects on the fatty acid profiles, when compared to the control plants. The seed protein concentration were significantly (P<0.01) higher in transgenic lines than in control lines. The transgenic plants did not display apparent phenotypic changes when compared to the control plants, under controlled conditions in the greenhouse environment. We envision that the results of this study will provide soybean breeders and industries with a better understanding of the genetic control of soybean seed composition traits, which in turn can contribute to developing new cultivars with altered seed quality traits that will best fit industrial applications and end-user's needs.