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Metabolic engineering to increase the corn seed storage lipid quantity and change its compositional quality**Ali Izadi-Darbandi**

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Given the limited global food supplies and the fact that the global population is expected to double by 2050, there is an urgent need for the development of high-calorie foods, including culinary oils. The seeds of oil crops contain high-energy density oil composed of Triacylglycerides (TAGs) at up to 80% by dry mass. However, maize (*Zea mays L.*) seeds are relatively poor in calorie and nutritional values. Therefore, in this report, we address this constraint via metabolic engineering to improve maize seed lipids including TAG and seed TAG nutritional values by overexpression of three major genes, including: (1) The *Arabidopsis thaliana* (L.) Heynh. Diacylglycerol Acyltransferase 1 (*AtDGAT1*), a gene that catalyzes the TAG biosynthesis final step prior to packaging of TAGs into oil bodies. (2) The transcription factor WRINKLED 1 (*WRI1*), which promotes the regulation of the expression of genes involved in fatty acid biosynthesis and the *A. thaliana* oleosin (*AtOleosin*) gene, a gene coding for a protein that protects TAGs from degradation. The overexpression of the above three genes and probably certain unintentional *in vitro* culture genetic variabilities resulted in 117% increase of seed TAGs and 25% increase in total oil contents when compared with the wild-type control corn seeds. In addition, the above genetic modifications led to major shifts in the fatty acid profiles in favor of human health.

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