

Engineering *Camelina sativa* for Improved Seed and Oil Yields via Manipulating Triacylglycerol Synthesis Pathway and the Associated Molecular and Biochemical Consequences

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Since the crude oil production is subjected to decrease worldwide, and as consequences for the limited production of crude oil, the current prices of the crude oil and its derivatives are rapidly rising. The less availability and the growing demand for the oils have crucially increased the demand for vegetable oils as alternative renewable resources for food, biofuel, biodiesel, and many other oil-based products. Among the seed oil-producing crops, *Camelina sativa* has attracted much interest in the last few decades as an emerging oilseed crop dedicated for biofuel and biodiesel applications as well as a source for edible oils. Its unique seed and oil qualities attract the researchers to engineer new varieties exhibiting improved oil quantity and quality. The overexpression of enzymes that catalyze the synthesis of the glycerol backbone and the sequential conjugation of fatty acids into this backbone appear to be far more promising targets for increasing the triacylglycerols (TAG, the main lipids in seeds). In our previous study, we combined the overexpression of two genes involved in TAG metabolism under the control of seed-specific promoters. The transgenic plants exhibited a higher percentage seed oil content, a greater seed mass, and overall improved seed and oil yields, on a per plant basis, than either the non-transgenic wildtype (WT) or manipulation of each gene individually. However, in order to further increase seed oil content in *Camelina*, we utilize metabolites profiling, in conjugation with transcriptome profiling during seed development in order to reveal the rate-limiting step(s) in the production of building blocks for TAG biosynthesis. The whole seed-specific transcriptome of transgenic lines revealed the identification of approximately 1,566 and 2,102 transcripts were differentially regulated (fold change ≥ 1.5 or ≤ -1.5 , p-value ≤ 0.05) in *Camelina transgenics*. Many of these transcripts were found to be involved in various functional categories, with many of them controlling alternative metabolic routes in fatty acid synthesis, TAG assembly, and TAG degradation. Further, we quantified the relative contents of over 240 metabolites by using GC/MS and LC/MS/MS platforms. The results indicate major metabolic switches in transgenic seeds, which are associated with significant changes in the levels of glycerolipids, phospholipids, most amino acids, sugars and organic acids, especially the ones involved in TCA cycle and glycolysis. Collectively, the integration of transcriptome and metabolome can be highly useful to understanding the regulation of TAG biosynthesis and identifying the bottlenecks in TAG pathways, providing a precise selection of candidate genes for generating *Camelina* varieties with improved seed and oil yields.

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