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Rapid delineation of the potential candidate genes underlying fatty acid-associated loci via combining gene co-expression network analysis and QTL and GWAS in Brassica napus L.

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Global demand for vegetable oils is increasing at a dramatic rate, while our understanding of the regulation of oil biosynthesis in plants remains limited. Many QTLs and GWAS regions for seed oil content and fatty acid compositions have been identified. While genes involved in acyl-lipid metabolism have been explored in model plant, such as Arabidopsis thaliana. To gain insights into the mechanisms that govern oil synthesis and fatty acid metabolism in the early stage of seed development, a system-level approach combining genome-wide association study (GWAS) and co-expression network analysis was employed to explore genes related to seed oil content (SOC) and fatty acid compositions (FAs) in 157 rapeseed lines, since that the nutritional and economic value of SOC is determined by its FAs and its content. The gene co-expression network revealed that tight transcriptional coordination of fatty acid and lipid biosynthesis in the plastid with photosynthesis, carbon metabolism, hormone metabolism and defense response. It also revealed that light harvesting complex genes was the major genes most tightly connected to lipid biosynthesis genes in the network. In addition to the known transcription factor ABI3, a novel transcription factor, named EFR72, was at the core module of fatty acid and lipid biosynthesis, which maybe regulate lipid metabolism in rapeseed by simultaneously interacted with known TF and the hub genes. To confirm the effect of our analysis, we selected T-DNA mutations of 12 genes to test the SOC. Among of them, 9 mutations showed significant difference in SOC from wild-type lines. Our findings may pave the way for uncovering the regulation mechanism of seed oil accumulation in rapeseed.