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Seed oil content QTL mapping and gene cloning in rapeseed

Liang Guo¹

¹ Huazhong Agricultural University, Wuhan, China

Background:

Rapeseed is the third largest source of plant oil, and it produces approximately 15% of the edible oil globally. Seed oil content (SOC) is an important trait which has large phenotypic variation in rapeseed. However, the mechanisms regulating the SOC of rapeseed remains largely unknown.

Objective:

In this study, we attempted to elucidate the genes and networks regulating the SOC and provide QTL and gene information for improving SOC in rapeseed.

Methods:

We re-sequenced a natural population having 505 inbred lines of rapeseed and collected over 600 RNA-seq datasets of developing seed in two stages. Multi-omics analysis approaches including genome-wide association analysis studies (GWAS), transcriptome-wide association analysis studies (TWAS), mGWAS, eGWAS etc were used to comprehensively map the SOC-related QTLs, predict the candidate genes, and establish the gene networks.

Results:

GWAS identified 27 reliable loci controlling SOC in eight environments. TWAS identified 692 genes and four gene modules significantly associated with SOC. Furthermore, 2,172 metabolites in mature seeds were quantified by LC-MS/MS, in which 131 marker metabolites were identified to be correlated with SOC. These 131 metabolites were selected for further mGWAS analysis and a few mQTLs were identified to impact the SOC. Based on the results of multi-omics analysis, we selected a few candidate genes for further functional study. We generated both overexpression lines and CRISPR mutants of rapeseed for these candidate genes. Nine candidate genes were shown to significantly impact the SOC. We also dissected the molecular and biochemical mechanism of these validated SOC-controlling genes.

Conclusions:

We comprehensively dissected the genetic and molecular mechanisms of SOC in rapeseed by multi-omics analysis using genomic, transcriptomic and metabolomic data. These works provide important resources for breeding rapeseed cultivars with high SOC.

References:

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