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Genome wide identification of microRNAs involved in fatty acid and lipid metabolism of *Brassica napus* by small RNA and degradome sequencing

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Abstract Rapeseed (*Brassica napus*) is an important cash crop consedered as the third largest oil crop worldwide. Rapeseed oil contains various saturation or unsaturation fatty acids, these fatty acids, whose could incorporation with TAG form into lipids stored in seeds play virous roles in the metabolic activity. The different fatty acids in *B.napus* seeds determine oil quality, define if the oil is edible or must be used as industrial material. miRNAs are kind of non-coding sRNAs that could regulate gene expressions through post-transcriptional modification to their target transcripts playing important roles in plant metabolic activities. We employed high-throughput sequencing to identify the miRNAs and their target transcripts involved in fatty acids and lipids metabolism in different development of *B.napus* seeds. As a result, we identified 826 miRNA sequences, including 523 conserved and 303 newly miRNAs. From the degradome sequencing, we found 589 mRNA could be targeted by 236 miRNAs, it include 49 novel miRNAs and 187 conserved miRNAs. The miRNA-target couple suggest that bna-5p-163957_18, bna-5p-396192_7, miR9563a-p3, miR9563b-p5 , miR838-p3, miR156e-p3, miR159c and miR1134 could target PDP, LACS9, MFPA, ADSL1, ACO32, C0401, GDL73, PlCD6, OLEO3 and WSD1. These target transcripts are involving in acetyl-CoA generate and carbon chain desaturase, regulating the levels of very long chain fatty acids, β-oxidation and lipids transport and metabolism process. At the same, we employed the q-PCR to valid the expression of miRNAs and their target transcripts that involv in fatty acid and lipid metabolism, the result suggested that the miRNA and their transcript expression are negative correlation, which in accord with the expression of miRNA and its target trascript. The study findings suggest that the identified miRNA may play important role in the fatty acids and lipids metabolism in seeds of *B.napus*.

Abbreviations: sRNA, small RNA; miRNA, micro RNA; ACSL, long-chain acyl-CoA synthetase; DAF, day after flowering; GO, gene ontology; KEGG, terms and Kyoto Encyclopedia of Genes and Genomes; ANOVA, Analysis of Variance; qRT-PCR, Quantitative Real time PCR; U, uridine; ARF, auxin response factor; SPL, SQUAMOSA promoter-binding protein-like; FATP, fatty acid transport protein; SPL, SQUAMOSA-PROMOTER BINDING PROTEIN LIKE; ACS, acyl-CoA synthetases; ACO, acyl-CoA oxidase; PDC, pyruvate dehydrogenase complex; TAG, triacylglycerol; RCA ribulose-bisphosphate carboxylase small chain

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