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Dissecting the genetic loci accounting for seed oil content of Brassica napus with reciprocal introgression mapping populations

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Seed oil content of rapeseed is a very important economic trait for oil products. Dissection of important genetic loci or genes accounting for this trait would help the genetic improvement of oil yield. In our previous studies, a total of 33 quantitative trait loci accounting for seed oil content were detected across environments in BnaTNDH population of *B. napus* which derived from the cross between Europe cultivar "Tapidor" (T) and Chinese cultivar "Ningyou7" (N), eight of which has highest genetic effects each explaining more than 10% of phenotypic variance. In this study, we traced these QTL for fine mapping and further identified loci or alleles for seed oil content with the reciprocal introgression mapping population derived from backcrosses between the BnaTNDH population and its two parents. The N-BC4F2 population including ~800 lines with Ningyou7-introgression segments, and T-BC4F2 including ~300 lines with Tapidor-introgression segments, were genotyped through sequencing, and phenotyped for detecting seed oil content. More than 120,000 high quality SNP/Indel markers were scored based on the genome sequence of its own parents, Tapidor and Ningyou7, and were used to evaluate the introgression and background of the introgression population. Phenotyping and genotyping for seed oil content loci were traced to BC4F5, BC5F2 and BC6F1. The eight QTL regions were narrowed largely and will be further validated and narrowed with transcriptome analysis and genotyping. High density genetic maps with the BnaTNDH population, its reciprocal introgression populations and other three populations with T or N as common mapping parents were constructed, integrated and compared. The genomic footprints and recombination landscape from the founder parents of Tapidor and Ningyou 7 across the T, N and BnaTNDH population to the reciprocal introgression populations and other related populations were investigated and associated with the trait variation and improvement.