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Genetic characterization and fine mapping for multiple main inforescence in Brassica napus L.

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With the development of modern mechanized cultivation system in rapeseed production, to explore ideal plant architecture fitting with this system has become a key breeding objective. In comparison with the transplanting cultivation system, the mechanized cultivation system requires high plant density, resulting in the decrease in branches per plant and the increase in contribution to yield from the main inflorescence. Multiple main inflorescence (MMI) is one of the desirable traits for the genetic improvement of rapeseed to adapted the mechanized cultivation system. Previously, we obtained a stable mutant line with multiple main inflorescence derived from a cross between spring accession '506' and semi-winter accession 'SWU 01'. Genetic analysis showed that the penetrance of MMI trait is dominant over single main inflorescence (SMI). To understand the formation mechanism of the MMI trait, a doubled haploid (DH) population derived from a cross between SMI and MMI lines was investigated for the penetrance of MMI across three years and genotyped with 257 simple sequence repeat and sequence-related amplified polymorphism loci. After that, a major quantitative trait locus (QTL) for penetrance of MMI was mapped to a 9.31 Mb region on chromosome A05, explaining 45.81% of phenotypic variance on average. Subsequently, 13 SMI and 15 MMI DH lines were genotyped with the Brassica microarray, and the QTL interval of MMI was narrowed down to a 0.74 Mb region with 37 successive single nucleotide polymorphisms between SMI and MMI groups. Further, by screening 420 recessive F2 individuals with genome-specific markers, a 27.18 kb QTL interval was detected in the delimited region. BLAST result showed that this interval contained nine annotated genes. Of which, three genes were worth mentioning, since their protein analogs were reported to be associated with plant architecture. Next, we will validate the gene control the MMI trait by complementary test and illustrate the formation mechanism of the MMI. Our present results will be helpful for gene cloning and molecular breeding of multiple main inflorescence in rapeseed.