GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Identification of sequence-related amplified polymorphism and insertion-deletion markers linked to the male fertility restorer gene of *pol*-like CMS06J45 in heading Chinese cabbage (*Brassica rapa* subsp *pekinensis*)

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Genet. Mol. Res. 13 (4): 9606-9614 (2014)
Received September 30, 2013
Accepted September 10, 2014
Published November 14, 2014
DOI http://dx.doi.org/10.4238/2014.November.14.4

ABSTRACT. In order to map the restorer gene *BrRfp* of the *polima* (*pol*)-like cytoplasmic male sterility (CMS) 06J45 line in heading Chinese cabbage, an F_2 segregating population with 258 individuals of CMS06J45 and the restorer line 01S325 were tested by sequence-related amplified polymorphism (SRAP) and insertion-deletion (InDel) technologies combined with the bulked segregant analysis method. As a result, two SRAP markers, me3em3.366 and pm88bg5.263, that were linked with the *BrRfp* gene were identified from 463 SRAP primer pairs. By cloning, sequencing, and basic local alignment search tool analysis, the two markers were targeted to the BGIScaffold000053 of *Brassica rapa* in the *Brassica* database. Using the BGIScaffold000053 sequence, four InDel primer pairs were designed and identified to be linked with

the *BrRfp* gene in this population. Linkage analysis showed that these markers were distributed on both sides of the *BrRfp* gene, the linkage distances of two nearest markers InDel878.1125 and InDel920.713 were 0.82 and 0.46 cM, respectively, and the *BrRfp* gene was restricted to a 243-kb genomic region of *B. rapa*. These specific markers provided basic information for map-based cloning of the *BrRfp* gene and will be very valuable for the marker-assisted selection of a new restorer line in heading Chinese cabbage.

Key words: *BrRfp*; Heading Chinese cabbage; Insertion-deletion; Sequence-related amplified polymorphism; CMS06J4

