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Analysis of mutant lines derived from T-DNA insertion in Chinese cabbage

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To apply insertional mutagenesis using T-DNA of *Agrobacterium* for functional genomics in Chinese cabbage, the study was carried out to produce a large number of transgenic plants which were obtained by inoculating the hypocotyls of *Brassica rapa* with *A. tumefaciens* containing the pRCV2 vector. Mutant screening was accomplished in T_0 transgenic plants and, firstly, two mutant lines which one had small size flower (M1) and the other had leaves with dark green and thick mesophyll (M2) were analyzed.

Because the *Agrobacterium*-mediated transformation was performed though tissue culture technique, especially regenerated shoots were induced through callus phase, this line should be analyzed at chromosome level before it was analyzed at gene level. As a result, M1 and M2 were normal chromosome numbers (2n=20). To obtain plant flanking DNA from mutant line, inverse PCR was performed after confirmation of integration pattern. Finally inverse PCR product containing plant flanking parts of T-DNA borders were obtained from these mutant lines. In M1, one flanking parts was homology with *Brassica rapa* subsp. napus SI13, SIk, Srk, CePP, SIAHI, AtPP, SIAHI, AtPP, SIAH2, and ClpP genes, the other part was *Brassica rapus* partial RT gene for reverse transcriptase from gypsylike retroelement 21G75-47. And in M2, one flanking parts was *Arabiodpsis thaliana* At3g07720/F17A17-6 mRNA, and the other part was *Arabidopsis thaliana* putative myrosinase binding protein (At2g33070) mRNA.

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