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Ectopic expression of *Arabidopsis* aliphatic glucosinolate biosynthesis genes in *Brassica campestris*

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Objectives

Our aim is to study the effects of *Arabidospsis* aliphatic glucosinolate biosynthetic gene expression on the composition and content of glucosinolate in Chinese cabbages.

Materials and Methods

1. Material

Plant: *Brassica campestris* cv. Seoul

Agrobacterium strain: GV3101

2. Methods

Four *Arabidopsis* genes involved in aliphatic glucosinolate biosynthesis (MAM1, CYP79F1, CYP83A1, AOP2) were isolated by RT-PCR. Isolated cDNA clones were subcloned into pC21 (pCAMBIA2301-modified vector) and transformed into *Agrobacterium* strain GV3101. For transformation, the hypocotyls of 14-day Chinese cabbage seedlings were cut into 0.5~1 cm sections, which were kept in MS media. *Agrobacterium* cells were resuspended in 25 ml liquid infection media (MS+4.0 mg/l BA + 1.0 mg/l NAA + 10 mg/l acetosyringone). The explants were infected by immersing in *Agrobacterium* solutions for 15min and were placed onto co-cultivation media (MS + 4.0 mg/l BA + 1.0 mg/l NAA + 10 mg/l acetosyringone + 4.0 mg/l $AgNO_3$) for three days under the dark condition. After co-cultivation, they were placed in selection media (MS + 1.6% agar + 4.0 mg/l BA + 1.0 mg/l NAA + 200 mg/l cefotaxime + 5 mg/l hygromycin + 4.0 mg/l $AgNO_3$) and cultivated at 21℃ under the 70% humidity and 16 hr light/ 8 hr dark photoperiod. Co-cultivated explants were subcultured in the selection media every two weeks.

Results and Discussion

PCR analysis combined with GUS staining initially identified 14 independent putative transgenic Chinese cabbages. Nine of them was found to contain single copy transgenes as indicated by Southern blot hybridization. Glucosinolate variations between transgenic Chinese cabbages and wild-type Chinese cabbage were examined by HPLC analysis.

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