

04-1-53

Agrobacterium-mediated Transformation of *Cucumis melo* L. using Polygalacturonase Genes

Do-Sun Kim^{1*}, Kwang-Ho Chung¹, ChangKyun Kim², Yun-Chan Huh¹, Jong-Gyu Woo¹, and Il Gin Mok¹

¹*Horticultural Biotechnology Division, Nat. Hort. Res. Inst., RDA, Korea*

²*Center for Fungi and Plant Genome Research, FnP Corp., Korea*

Objectives

To introduce polygalacturonase genes into *Cucumis melo*. L by Agrobacterium-mediated transformation, and to study the effect of the gene on fruit ripening process.

Materials and Methods

1. Materials

- Cultivar: Charentais, Busan #914, Busan #920
- Agrobacterium strain: LBA4404/pMPG1, pMPG2, and pMPG3 RNAi

2. Methods:

- Explant source: Cotyledon explant of 4 day-old seedlings
- Media used for selection and regeneration of transformants: LS + BA 1 uM + 2iP 1 uM + cefotaxime 500 mg/L + kanamycin 100 mg/L + sucrose 3% + agar 0.8%

Results and Discussion

Melon (*Cucumis melo*. L) is an important horticultural crop in tropical and subtropical regions. The texture of the melon fruit is controlled by changes of cell wall structure and composition. Some cell wall degradation enzymes include polygalacturonase (PG), expansin, and β -galactosidase. RNAi technology has been used to study these genes and promises to be a useful tool in attempts to produce fruit attenuated softening. Decreasing levels of PG by transgenic tomato altered traits such as cracking and viscosity, but had little effect on fruit firmness. To determine PG genes of Melon (MPG) were transformed by Agrobacterium tumefaciens LBA4404 harboring pCAMBIA2300 RNAi vector for MPG1, MPG2 and MPG3 genes of melon. Adventitious shoots were observed along the cut edges as early as 2 weeks after onset of culture. After 3 months, putative transgenic plants were regenerated on the selection medium containing kanamycin 100 mg/L. The plantlets were confirmed for gene insertion by PCR analysis with specific primer for MPG2 genes and by Southern blot analysis.