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Development of *Agrobacterium*-mediated transformation system and transgenic plant with ω-3 fatty acid synthesis gene in sesame

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Objectives

We have tried to develop the efficient transformation system using *Agrobacterium tumefaciens* and to produce the transgenic plants with perilla *fad*3 (ω-3 fatty acid desaturase) gene in sesame.

Materials and Methods

1. Material

Plant - Sesame (*Sesamum indicum*)

Agrobacterium strain - LBA4404/pCAMBIA2301 or pBINmGFP5-ER and EHA105/pMOG-CsIV

2. Methods:

Cotyledon or hypocotyls explants were precultured for 1 day on SIM and inoculated with *Agrobacterium*. After co-cultivation for 3 days on SIM with 100uM acetosyringone, the explants were washed and inoculated on selection medium. SIM was composed of MS salts, B5 vitamins, 5-10mg/L BA, 0.3-1.0mg/L IBA, 1.0mg/L ABA, 5.0-10mg/L $AgNO_3$ and 30g/L sucrose. Selection medium was SIM 500mg/L cefotaxime and 30mg/L kanamycin.

Results and Discussion

Sesame explants were transformed with *Agrobacterium tumefaciens* LBA4404/pCAMBIA2301, pBINmGFP5-ER, or EHA105/pMOG-CsIV which harbored genes for β-glucuronidase(GUS), GFP, or ω-3 fatty acid desaturase, respectively. Calli were formed around the cut edge of the transformed explants after 3 weeks in culture. Shoot regeneration was observed after 4-8 weeks in culture. The regenerated shoots were detached and cultured on shoot elongation medium. To determine the presence and expression of the transferred in the putative transgenic sesame, PCR analysis, GUS and GFP assay were performed. In GUS and GFP assay of transformed plant tissues, successful expression of the genes was observed. PCR analysis showed the expected bands of *npt*II and *fad3* gene. These results mean the stable incorporation and expression of the introduced genes in transgenic sesame.

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