

Transformation of *Brassica napus* via *Agrobacterium* Vector : Plant Regeneration and Progeny Analysis

KIM, Kyung Min* · SOHN, Jae Keun · CHUNG, Jae Dong¹

Department of Agronomy, College of Agriculture, Kyungpook National University, Taegu 702-701, Korea:

¹Department of Horticulture, College of Agriculture, Kyungpook National University, Taegu 702-701, Korea. *Corresponding author.

Agrobacterium 운반체를 이용한 유체의 형질전환: 식물체재분화와 후대검정

김경민* · 손재근 · 정재동¹
경북대학교 농학과, ¹원예학과

Cotyledonary petioles of *Brassica napus* cocultivated with *Agrobacterium* vectors for 72 h were transferred to MS medium with 0.5 mg/L NAA, 2.0 mg/L BA, 30 mg/L kanamycin, 100 mg/L cefotaxime, 30 g/L sucrose, 3 mg/L AgNO₃ and 2 g/L Gelrite. The cotyledonary petioles with green shoots were selected at a frequency of 17.5% in a selection medium and then rooted. Southern blot analysis confirmed the *rolC* and *NPT II* genes were incorporated into the regenerated plants. The stable inheritance of *rolC* gene was confirmed in progeny test of transgenic plants.

Key words: *Brassica napus*, *Agrobacterium*, transgenic plant.

Recently several reports concerning the transformation of plants using foreign gene have been made. In this field, the *Cruciferae* including some *Brassica* spp. are excellent host plants for bacterial vector systems (De Block et al., 1989). Transformation methods of the genus *Brassica* include cocultivation of *B. napus* with *Agrobacterium* vector (Charest et al., 1988), microinjection of DNA into cell (Neuhaus et al., 1987), and the electroporation performed in plant protoplasts (Chapel and Glimelius, 1990). In the transformation study of a plant which uses *Agrobacterium* vector, it is important that the frequency of plant regeneration is enhanced by explants co-cultivated with *Agrobacterium*. A variety of tissues such as stem explants (Pua et al., 1987), hypocotyl (De Block et al., 1989), and cotyledons (Moloney et al., 1989) of *B. napus*, have been used to improve the transformation efficiency. As a result, the use of *B. napus* as a model plant for transformation studies has not been efficiently improved.

The present paper reports an appropriate methodology for in vitro culture of *B. napus* and the development of an efficient procedure for genetic transformation via co-cultivation

of cotyledons with *Agrobacterium* vector of *rolC* which was associated with dwarfism of plant (Oono et al., 1990). Analysis of transformants, T₁ and T₂ plants was performed through biochemical assay for the *rolC* gene activity (NPT II), cotyledon culture on selective medium, and Southern blot analysis.

MATERIALS AND METHODS

Plant Materials and *Agrobacterium* Vector

Seeds of *Brassica napus* cv. Naehanyuche were kindly supplied by National Yeongnam Agriculture Experiment Station, Korea. Seeds were treated for 12 h at 4°C, and then sterilized in 70% ethanol for 30 sec, and 1% sodium hypochlorite for 30 min. They were washed in sterile distilled water three times and inoculated at a density of 25 seeds per plate(5×12cm) on 20 mL Murashige-Skoog (MS, 1962) medium with 3% sucrose and 0.2% Gelrite. The pH was

adjusted to 5.8 before autoclaving. Seeds were germinated at 26°C in a 16 h light/8 h dark photoperiod at light intensity of 60~80 $\mu\text{Em}^{-2}\text{s}^{-1}$. *Agrobacterium tumefaciens* strain LBA4404 (Hoekema et al., 1983) containing a binary vector was used. The binary vector, pGA 643-*rolC* (Figure 1) carries the neomycin phosphotransferase II gene (*npt II*). *Agrobacterium* was grown overnight at 28°C in the darkness at 120 rpm in LB medium (1% Bacto-peptone, 0.5% Bacto-yeast extract, 1% NaCl) supplemented with kanamycin (km, 50 mg/L) and carbenicillin (25 mg/L).

Transformation of *B. napus* via *Agrobacterium tumefaciens*

Cotyledons were excised at 5 d after seed germination that they included 2 mm petioles at the base. Care was taken to eliminate the apical meristem which sometimes adheres to the petioles. Individual excised cotyledons were taken from the plants described above and the cut surface of their petioles was immersed into this bacterial suspension for 2~4 s. They were immediately placed on the MS medium, 3% sucrose and 0.2% Gelrite enriched with 0.5 mg/L α -naphthalenacetic acid (NAA) and 0.2 mg/L 6-benzyladenine (BA). The cotyledons were co-cultivated with the *Agrobacterium* for 72 h. After co-cultivation, the cotyledons were transferred to regeneration medium including MS medium supplemented with 0.5 mg/L NAA, 2.0 mg/L BA, 100 mg/L cefotaxime, 30 mg/L kanamycin, 3 mg/L AgNO_3 . Each plate contained 10

explants. The explants were cultured on regeneration medium under light and temperature conditions specified above, for 30 d and then formations of root and shoot were investigated.

Southern Blot Analysis

Regenerated plantlets in MS medium with the appropriate antibiotics were transferred to 'rooting' medium containing MS medium, 3% sucrose, 0.5 mg/L 3-indoleacetic acid (IAA), and 0.2% Gelrite. As soon as a small root mass was obtained, the plantlets were transferred to potting mix supplemented with vermiculite:perlites:peatmoss(1:1:1). The plants were transferred to field.

Leaf tissue (approximately 1 g) from plants 1~2 weeks old was ground to a powder in liquid nitrogen and DNA was isolated according to the method described by Dellaporta et al. (1983). For Southern blot analysis, DNA was digested with *EcoRI*-*HpaI* and resolved by electrophoresis on a 0.8% agarose gel in a 0.5X TBE buffer (0.04417M Tris, 0.044M Boric acid, 1 μM EDTA). Resolved DNA was transferred to a nylon membrane (Hybond-N, Amersham) through standard methods as described by Southern (1975). The probes were randomly labelled with ^{32}P (an Amersham kit) to a specific activity 1×10^9 cpm/ μg . Hybridization to probes was performed in 0.5 M NaH_2PO_4 (pH 7.2), 1% BSA, 1 mM EDTA and 7% SDS at 65°C. The membranes were washed twice in 2X SSC, 0.1% SDS for 15 min at room temperature and then twice in 0.1X SSC, 0.1% SDS for 20 min at 42°C. Then filters were exposed to Kodak XAR-5 film using Dupont Cronex Quanta B intensifier screens at -80°C.

Genetic Analysis of Transgenic Progeny

Seeds from self-pollinated transformed plants and from a control plant were treated for 12 h at 4°C, and then were sterilized as described above. The seeds were inoculated at a density 30 seeds per plate (5×12 cm) on 20 mL MS medium supplemented with 3% sucrose, 30 mg/L kanamycin, and 0.2% Gelrite. Seeds were cultured at 26°C in 16 h light/8 h dark photoperiod light intensity of 60~80 $\mu\text{Em}^{-2}\text{s}^{-1}$. After 40 d, resistance or sensitivity was scored according to the presence/absence of normal roots and shoot growth. The Chi-square test was used for testing hypothesis concerning a different number of T-DNA insertions, and a different possible transmission of kanamycin resistance to the progeny.

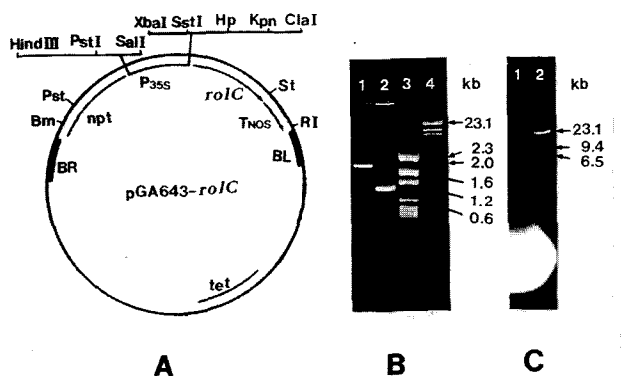


Figure 1. A: Structure of the expression vector. p35s, CaMV 35s promoter; *roIC*, coding region of the ORF 12 gene of *Agrobacterium rhizogenes*; Tnos, nopaline synthase terminator; BR, T-DNA right border; BL, T-DNA left border; *npt*, chimeric nos-*npt* (nopaline synthase-neomycin phosphotransferase) that serves as a selectable marker in plants; Tet, tetracycline resistance gene. B: *roIC* fragment from pGA 643-*rolC* vector. Lane 1: eluted *npt II*/BamHI-HindIII, Lane 2: eluted *roIC*/EcoRI-HpaI, Lane 3: pGEM size marker, Lane 4: λ digested with HindIII. C: Identification of pGA 643-*rolC*. Lane 1: intact pGA 643-*rolC*, Lane 2: λ digested with HindIII.

RESULTS AND DISCUSSION

The addition of AgNO_3 in the medium enhanced remarkably the shoot regeneration from the cotyledonary petioles. The maximum frequency of shoot regeneration (74.2%) was obtained from the cotyledonary petioles cultured on the medium with 3 mg/L AgNO_3 (Table 1). A comparison of different procedures for regeneration of *Brassica* spp. indicates wide variations in regeneration efficiency and measured by yield of differentiated shoots obtained. The regeneration efficiency varies between 67% for cotyledon and 42% for hypocotyl explants (Chi et al., 1990). The yield of regenerated plants obtained by this procedure was higher than in Chi et al. (1990).

Table 1. Effect of AgNO_3 on plant regeneration from cotyledonary petioles of *B. napus*

AgNO ₃ (mg/L)	No. of cotyledons		
	cultured	shooting (%)	rooting (%)
0	135	27(20.0)	65(48.1)
3	155	115(74.2)	132(85.2)

In transformation via co-cultivation of cotyledons with *Agrobacterium* vector of *rolC* gene, shoot regeneration frequencies for co-cultivation was 17.5% (Table 2). A comparison of different procedures for transformation of *B. napus* indicates wide variations in transformation efficiency as measured by yield of transformed shoots obtained. The transformation efficiency varies between 2% for epidermal explants (Charest et al., 1988), or 2.5% for hypocotyl explants (Radke et al., 1988) and 10% for stem explants (Pua et al., 1987). The yield of transformed plants obtained by this procedure was higher than in these three papers. But the transformation efficiency of this study was not higher than that of Molony et al. (1989). It may be attribute to different genotype of donor plants tested.

The green shoots regenerated on medium with antibiotics were recultured in the same medium with antibiotics (Figure

Table 2. Frequency of shoot regeneration from cotyledon of *B. napus* cocultivated with *Agrobacterium* vector

No. of cotyledons cultured	No. of cotyledons forming shoots(%)		
	total	green	white
120	54(45.0)	21(17.5)	33(27.5)

2). Southern blot showed in Figure 3. Genomic DNAs of transgenic plants (lanes 1~6) and control (lane 7) were digested with *EcoR*I-*Hpa*I restriction enzyme and probed with the *rolC* and *npt*II gene. In the results, questionable transformed plants were detected a 2.0kb band (*rolC* gene) in the lane 4. It is presumed that transformed plants were detected a 1.0 kb and a 2.0 kb band (*npt*II and *rolC*, respectively) in the lanes 2 and 6.

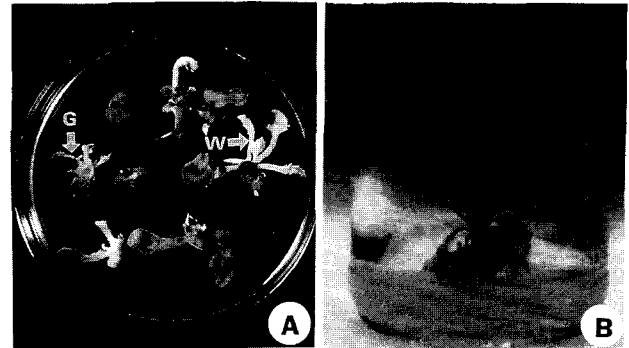


Figure 2. Shoot formation from cotyledonary petioles cocultivated with *Agrobacterium* vectors in *B. napus*. A: Shoot formation from cotyledonary petioles on selection medium (W: white. G: green). B: Normal green plant reselected from the medium with kanamycin.

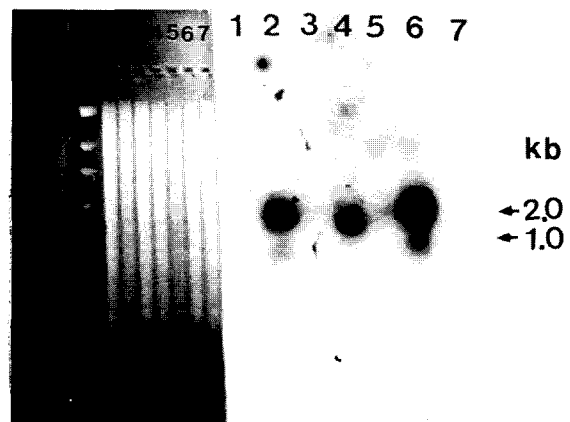


Figure 3. Southern blot analysis of *EcoR*I-*Hpa*I digests of genomic DNA isolated from putative transformed *B. napus*. Probe DNA: 1kb of *rolC* coding sequence and 2kb of *npt*II coding sequence. Lanes 1~6: samples, 7: control, 8: λ DNA (*Hind*III digested).

The seeds of individual transformed plants were germinated normally in selective conditions (30 mg/L kanamycin) while nontransformed progenies did not. The segregation ratio for *km* resistance of seedlings derived from self-fertilization of three independent transgenic plants were analyzed and results are reported in Table 3. The transformants were segregated

Table 3. Segregation ratio for kanamycin resistance of seedlings derived from self-fertilization of three independent transgenic plants (km^R =kanamycin resistance; km^S =km sensitivity).

T ₂ family	Segregation of		χ^2 values ($p=0.05$) 3:1
	km^R	km^S	
T ₂ -2	84	31	0.23
T ₂ -4	58	11	3.02
T ₂ -6	91	21	2.33
Control	0	114	-

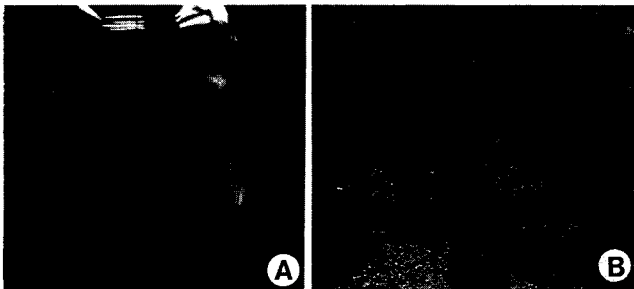


Figure 4. Transgenic *B. napus* cv. Naehanyuche. A: Plants from T₂ seeds on selection medium (R: resistance, S: sensitivity). B: Transformants grown in soil.

with ratio of 3 km resistance:1 km sensitivity.

Rotino et al. (1992) reported that 9 lines segregated according to the Mendelian Genetics from 11 lines of transformed *Solanum integrifolium* via *Agrobacterium tumefaciens* in km resistance examination. In this experiment, T-DNA of putative transformed plants with *rolC* gene was inherited in progeny.

적 요

유체의 자엽조직을 *rolC* 유전자를 가진 *Agrobacterium* 운반체와 공동배양하여 형질전환체를 얻고, 후대에 대한 유전 분석을 실시하였다. *Agrobacterium* 운반체와 공동배양된 유체의 자엽조직을 5 mg/L NAA, 2.0 mg/L BA, 30 mg/L kanamycin, 100 mg/L cefotaxime, 30 g/L sucrose, 3 mg/L AgNO₃ 및 2 g/L Gelrite가 첨가된 MS 배지에 배양하였을 때 형질전환된 식물체의 분화율이 17.5%로 나타났다. 형질전환체로 확인된 식물체를 자가수정시켜 얻어진 후대에 대한 유전 분석을 실시한 바 *rolC* 유전자가 후대로 유전됨을 확인 할 수 있었다.

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