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Modification of Gerbera Transformation Protocol to Reduce the Level of Cell Death after *Agrobacterium*-infection

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Gerber(*Gerbera hybrida*) is a valuable ornamental species grown as a potted plant and cut flowers. However, genetic variability within the gerbera genus is very limited, So it is absolutely needed to introduce and widen genetic resources into gerbera lines by genetic transformation. For the purpose, 18 Korean gerbera lines were screened to establish *Agrobacterium*-mediated genetic transformation procedure. In an experiment to select Korean gerbera lines which are amenable to *Agrobacterium*-inoculation, 12 lines turned out to be positive to *Agrobacterium*-inoculation. After inoculation, more callus were produced from TDZ 0.5ppm, NAA 0.1ppm in callus induction medium for 4 weeks and then BA 1ppm, Zeatin 1ppm, IAA 0.1ppm in regeneration medium. In another experiment to find out optimal condition for highly efficient *Agrobacterium*-inoculation, petiole and leaf explants have been treated with four different pre-culture periods, two different co-culture periods and dipping treatment. As a result, high GUS expression has been showed from petiole and leaf explants treated in the condition such as without pre-culture period, 5 day co-culture period and dipping treatment. Strong *Agrobacterium*-infection causes some problem such as cell death. To avoid the problem low concentration dipping, 2 day co-culture, removal of vacuum and sonication treatment during co-culture were tried and confirmed high regeneration. These conditions improved the gerbera transformation efficiency with various genes introduced to gerbera.

Key words: Gerber(*Gerbera hybrida*) *Agrobacterium*

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Cloning and Characterization of *OgChitIV* and *OgChitIVa* Derived from Wild Rice(*Oryza grandiglumis*)

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Wild rice is an useful gene resource for rice improvement such as resistance to disease and insect, and tolerance to abiotic stresses. A set of subtracted library was constructed from *Oryza grandiglumis* (CCDD, 2n=48) through fungal elicitor and wound treatment. Plant chitinases are pathogenesis-related proteins believed to be involved in plant defense responses to pathogen infection. Genomic DNA for a class IV chitinase (*OgChitIV* and *OgChitIVa*) was cloned from wild rice (*Oryza grandiglumis*) leaves and sequenced. The deduced amino acid sequence shows 55 to 95% identity to chitinases from other plants. *OgChitIV* cDNA contains an open reading frame of 690 nucleotides encoding 229 amino acid residues with a predicted isoelectric point (pI) and molecular weight (Mw) of pI/Mw: 8.79/25278.49. *OgChitIVa* cDNA contains an open reading frame of 867 nucleotides encoding 288 amino acid residues with a predicted of pI/Mw: 8.48/30423.85. *OgChitIVa* include chitin-binding domain. Currently, gene expression patterns of are under investigation.

Key words: Chitinase, wild rice