H201 Constitutive Expression of Pepper CaGST cDNA in Tobacco and Its Role in Various Stress Conditions

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CaGST encoding glutathione S-transferase (GST) in hot pepper (*Capsicum annuum* L.) has a high homology with type II GST, carnations. Nucleotide sequence of *CaGST* has an open reading frame of 1,012 bp which encoded a polypeptide with a molecular weight about 24.5 kD. The protein has ability of protecting cells from dying in toxic substances. *CaGST* exists in the form of multiple copies in pepper genome. The environmental stresses increased the level of *CaGST* mRNA expression. Especially, NaCl, indoleacetic acid (IAA), and paraquat drove those results in a few hours, but cold stress had no effect of expression of *CaGST* mRNA until 3 days. In order to confirm the resistance of *CaGST*, we transformed it into tobacco (*Nicotiana xanthi*). We got thirty transgenic tobacco plants confirmed by northern blot analysis. We investigated the role of pepper *CaGST* in various stress conditions, such as low temperature (4℃), chilling (0℃), NaCl, IAA, and 2,4-D (2,4-dichlorophenoxy acetic acid), using the transgenic tobacco plants.

H202 Catalpol from Suspension Cells,Advantitious Roots,and Transformed Roots of Rehmannia glutinosa Libosch.

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Rehmannia glutinosa is a perenial herb distributed in the central China. The root mainly contains catalpol, rehmannin, and some alkaloids. It is a cardiac tonic and diuretic; these actions are probably effected by producing renal vasodilation. The production of catalpol was studied in suspension cultured cells, advantitious roots, and transformed roots of *R. glutinosa*. The highest catalpol content in hairy root cultures, 0.54% g^{-1} dry weight, was obtained in the WPM medium containing 4% sucrose, 0.1% fungal extracts, pH 5.8. Unlike that found in hairy roots, the content of catalpol in suspension cells and advantitious roots seemed to be clearly associated with plant growth regulators. The highest level of catalpol in advantitious root cultures was obtained from MS medium supplemented with 3% sucrose, 2 mgl^{-1} IAA, 3 mgl^{-1} IBA, pH 5.8. This was less than 39% of the catalpol produced by hairy root cultures.

H301 Study of NHEJ(Non-Homologous End-Joining) Mechanism on TAR Cloning

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The transformation-associated recombination (TAR) cloning technique allows selective and accurate isolation of chromosomal region and gene from complex genomes. The technique is based on in vivo recombination between genomic DNA and a linearized vector containing homologous sequence, or hooks, to the gene of interest. In spite of this usefulness of TAR cloning, the frequency of positive clones among total transformants. The ends of chromosomal DNA double-strand breaks(DSBs) can be accurately rejoined by at least two discrete pathways, homologous recombination and non-homologous end-joining(NHEJ). The NHEJ pathway is essential for repair of specific classes of DSB termini in cells of the budding yeast S. cerevisiae. To know the effects of the NHEJ in TAR cloning, several isogenic strains with defects in NHEJ pathway genes are examined.