F206 BCTV Recombinants Show New Phenotypes in Arabidopsis

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Recombinant genomes derived from the BCTV Logan and CFH strains of the geminivirus BCTV have been analyzed for pathogenicity on *Arabidopsis thaliana*. Infectivity assays indicated that the latent period on Arabidopsis was primarily determined by a DNA fragment bearing the leftward open reading frames (ORFs) L1, L2, L3 and L4. Recombinants bearing leftward ORFs from the CFH strain were characterized as having a short latent period, while the reciprocal recombinants bearing leftward ORFs from the Logan strain had latent periods defined as long. Infectivity assays on Arabidopsis indicated that certain recombinant BCTV genomes exhibited novel pathogenic properties not common to either wild type strain, indicating the loss of systemic movement and replication competency, or asymptomatic systemic infection of Arabidopsis. The results indicate that Arabidopsis is more permissive and sensitive host than *Nicotiana benthamiana* with respect to heterologous combinations of BCTV genes, and that pathogenicity and virulence of BCTV in Arabidopsis requires the interaction of certain viral gene products and/or cis-elements that have coevolved in the same strain.

F207 Isolation and Characterization of cDNA Clones Encoding Asparagine Synthetase, Chitinase and Polyubiquitin from Root Nodule of *Elaeagnus umbellata*

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To identify genes specifically expressed during actinorhizal nodule development., a cDNA library made from poly $(A)^+$ RNA from root nodules of *E umbellata* was screened differentially with nodule cDNA probe and an excess of total RNA from root and leaf. Fom about 100 putative positive clones, three clones showing homology with asparagine synthetase, chitinase, polyubiquitin were selected and characterized. Asparagine synthetase clone (pEuNAS-1) encoding 585 amino acid residues was specifically exressed in the root nodule. *in situ* hybridization data showed that asparagine synthetase transcripts were detected in the infected cells of nitrogen-fixation zone. Chitinase clone (pEuNCHIT-1) encoding 335 amino acid residues showed high homology with that of class I chitinase. The expression of chitinase gene was markedly enhanced in nodules compared to root and leaf. *in situ* hybridization data showed that chitinase transcripts were detected in the meristem zone of nodule. Polyubiquitin clone (PEuNPUB-1) encoding 458 amino acid residues has 6 repeat structure of ubiquitin monomer consisted of 76 amino acid residues. The expression of polyubiquitin gene was highly enhanced in nodule compared to root and leaf.