1-03. Pathogenicity and localization of the tobacco mosaic virus 4.8 kDa protein(oral)

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In addition to the five well-characterized genes of *Tobacco mosaic virus* (TMV), this virus contains a sixth open reading frame (ORF6) that encodes a 4.8 kDa protein. TMV ORF6 overlaps the ORFs encoding the 30 kDa movement protein and the adjacent 17.5 kDa capsid protein. Although the 4.8 kDa protein could not be detected in vivo, alteration of the AUG codons of this ORF resulted in a mutant virus that attenuated the virulence of the mutated TMV in *Nicotiana benthamiana*, but not *N. tabacum* (tobacco). These sequence changes did not affect either the replication or movement of the mutated TMV. Expression of TMV ORF6 from the virus expression vector *Potato virus X* (PVX) intensified the virulence of this virus in *N. benthamiana*, but not tobacco, while expression of TMV ORF6 from the virus expression vector Tobacco rattle virus enhanced the pathogenicity observed in both *N. benthamiana* and tobacco. Thus, the TMV ORF6 is a host- and virus-specific virulence factor. However, two separate assays indicated that the TMV 4.8 kDa protein was not a suppression of RNA silencing. A fusion protein formed between the TMV 4.8 kDa protein and the green fluorescent protein was expressed from the PVX vector and localized to plasmodesmata. Possible roles of the 4.8 kDa protein in pathogenicity will be discussed

1-04. Development of transgenic disease-resistance root stock for growth of watermelon.(oral)

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To protect the plant against several soil-borne pathogens, we are currently constructing disease-resistant transgenic root stock for the growth of cucurbitaceae vegetable plants, watermelon and gourd. We made a watermelon cDNA library from *Cladosporium cucumerinum*-infected leaves for substractive hybridization and differential screening. We isolated the several pathogen inducible cDNA clones, such as caffeoyl-CoA-methyltransferase, IAA induced protein, receptor-like kinase homolog, hydroxyproline-rich glycoprotein, catalase, calmodulin binding protein, mitochondrial ATPase beta subunit, methyl tRNA synthetase and WRKY transcription factors. We previously obtained *CaMADS* in pepper and galactinol synthase (*CsGolS*) in cucumber that were confirmed to be related with disease-resistance. *CaMADS* and *CsGolS2* were transformed into the inbred line 'GO701-2' gourd, the inbred line '6-2-2' watermelon and the Kong-dye watermelon by *Agrobacterium tumerfaciens* LBA4404. Plant growth regulators (zeatin, BAP and IAA) were used for shoot regeneration and root induction for optimal condition. Putative transgenic plants were selected in medium containing 100mg/L kanamycin and integration of the *CaMADS* and *CsGolS2* into the genomic DNA were demonstrated by the PCR analysis. We isolated major soil-borne pathogens, such as *Monosporascus cannonballus*, *Didymella bryoniae*, *Cladosporium cucumerinum* from the cultivation area of watermelon or root stock, and successfully established artificial inoculation method for each pathogen. This work was supported by a grant from BioGreen 21 program, Rural Development Administration, Republic of Korea.