Pepper defensin (*CADEF1*) clone was isolated from cDNA library constructed from pepper leaves infected with avirulent strain Bv5-4a of *Xanthomonas campestris* pv. *vesicatoria*. The deduced amino acid sequence of *CADEF1* is 82-64% identical to that of other plant defensins. Putative protein encoded by *CADEF1* gene consists of 78 amino acids and 8 conserved cysteine residues to form four structure-stabilizing disulfide bridges. Transcription of the *CADEF1* gene was earlier and stronger induced by *X. campestris* pv. *vesicatoria* infection in the incompatible than in the compatible interaction. *CADEF1* mRNA was constitutively expressed in stem, root and green fruit of pepper. Transcripts of *CADEF1* gene drastically accumulated in pepper leaf tissues treated with salicylic acid (SA), methyl jasmonate (MeJA), abscisic acid (ABA), hydrogen peroxide (H_2O_2), benzothiadiazole (BTH) and DL-β-amino-*n*-butyric acid (BABA). *In situ* hybridization results revealed that *CADEF1* mRNA was localized in the phloem areas of vascular bundles in leaf tissues treated with exogenous SA, MeJA and ABA. Strong accumulation of *CADEF1* mRNA occurred in pepper leaves in response to wounding, high salinity and drought stress. These results suggest that bacterial pathogen infection, abiotic elicitors and some environmental stresses may play a significant role in signal transduction pathway for *CADEF1* gene expression.

1-31. *Agrobacterium*-mediated transformation of *Lycopersicon esculentum* (cv. MicroTom) with two pathogen-induced hot pepper transcription factors

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Two pathogen-induced hot pepper transcription factors (CaNAC1 and CaPIf1) were introduced into 'MicroTom' tomato by *Agrobacterium tumefaciens*-mediated transformation. We used to *npt*II containing kanamycin resistance gene as a selection marker. Both transformed and non-transformed plants were transferred to pot after rooting test *in vitro*. To approximate the levels of *Ca*NAC1 transcript in leaves of wild-type and transgenic plants, RNA blots were hybridized with double-stranded full-length *Ca*NAC1 probe at moderate stringency. Although the relative signal strength for hybridization fluctuated among the samples on different blots, transgenic plant lines N-1, N-2 and N-3 consistently displayed increased levels of *Ca*NAC1 transcript relative to other transgenic lines and wild-type plants. Of all the transgenic lines examined, line N-7 had the least amount of *Ca*NAC1 transcript. Role of these transcription factors in pathogen defense will be examined by overexpression in tomato.

1-32. Isolation and Characterization of Pathogen-Inducible Putative Zinc Finger DNA Binding Protein from Hot Pepper *Capsicum annuum* L.

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To better understand plant defense responses against pathogen attack, we identified the transcription factor-encoding genes in the hot pepper *Capsicum annuum* that show altered expression patterns during the hypersensitive response raised by challenge with bacterial pathogens. One of these genes, *Ca1244*, was characterized further. This gene encodes a plant-specific Type IIIA - zinc finger protein that contains two Cys_2His_2 zinc fingers. *Ca1244* expression is rapidly and specifically induced when pepper plants are challenged with bacterial pathogens to which they are resistant. In contrast, challenge with a pathogen to which the plants are susceptible only generates weak *Ca1244* expression. *Ca1244* expression is also strongly induced in pepper leaves by the exogenous application of ethephon, an ethylene releasing compound. Whereas, salicylic acid and methyl jasmonate had moderate effects. Pepper protoplasts expressing a Ca1244-smGFP fusion protein showed Ca1244 localizes in the nucleus. Transgenic tobacco plants overexpressing *Ca1244* driven by the CaMV 35S promoter show increased resistance to challenge with a tobacco-specific bacterial pathogen. These plants also showed constitutive upregulation of the expression of multiple defense-related genes. These observations provide the first evidence that an Type IIIA - zinc finger protein, Ca1244, plays a crucial role in the activation of the pathogen defense response in plants.

1-33. Functional analysis of genes involved in rice disease resistance

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Several plant and microbial genes that could confer disease resistance in transgenic rice plants are being cloned and characterized. We are currently constructing transgenic rice lines that overexpress the gene products, such as a galactinol synthase, a defensin, and a bacterial ACC deaminase. Subtractive hybridization of a rice cDNA library constructed from the *Xanthomonas oryzae*-infected rice leaves resulted in isolation of many inducible cDNA clones including a elongation factor EF2, a oryzain alpha, a catalase, a aldehyde dehydrogenase, a S-adenosylmethionine synthetase, a caffeic acid O-methyltransferase, a glyceraldehyde-3-phosphate dehydrogenase, a light-regulated protein, WRKY transcription factors, and a nucleotide diphosphate kinase. Some genes among those may be useful genetic sources for construction of disease resistant transgenic rice. Full lengths of the rice *OsFIERG* and a rice oryzain genomic clones were cloned, and serial deletion fragments of the promoter regions of these genes were fused with GUS reporter gene in pCAMBIA1201, respectively. Promoter activities of these constructs will be examined upon various stresses and pathogen infections to obtain the pathogen specific inducible-promoter. This work was supported by a grant from BioGreen 21 Program, Rural Development Administration, Republic of Korea.

1-34. Hot Pepper Functional Genomics : Monitoring of Global Gene Expression Profiles During Non-Host Resistance Reactions in Hot Pepper Plant (*Capsicum annuum*).

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