CaPF1 is also induced upon various abiotic stresses including ethephon, MeJA, cold stress, drought stress and salt stress treatments. To study the role of *CaPF1* in plant, transgenic *Arabidopsis* and tobacco plants which express higher level of pepper *CaPF1* were generated. Global gene expression analysis of transgenic *Arabidopsis* by cDNA microarray indicated that expression of *CaPF1* in transgenic plants affect the expression of quite a few GCC box and DRE/CRT box-containing genes. Furthermore, the transgenic *Arabidopsis* and tobacco plant, expressing *CaPF1* showed tolerance against freezing temperature and enhanced resistance to *Pseudomonas syrnigae* pv. *tabaci*. Taken together, these results indicated that *CaPF1* is a novel EREBP/AP2 transcription factor in hot pepper plant and it may has a significant role(s) in regulation of biotic and abiotic stresses in plant.

1-29. A pathogen-induced osmotin-like protein gene, *CAOSM1*, from pepper : Differential expression and in situ localization in pepper tissues during pathogen infection and abiotic stresses

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An osmotin-like protein (*CAOSM1*) gene was isolated from pepper leaves infected with the avirulent strain Bv5-4a of *Xanthomonas campestris* pv. *vesicatoria*. The cDNA encodes a polypeptide of 250 amino acids with a molecular mass of 27, 361 Da. Its amino acid sequence is highly homologous to various osmotin-like proteins from other plant species. The *CAOSM1* gene expression was organ- and tissue-specifically regulated in pepper plants. The *CAOSM1* mRNA was intensely localized in the endodermis area of root tissue and in the phloem cells of vascular bundles of red fruit tissue, but not in leaf, stem, and green fruit tissues of healthy pepper plants. Infection by *X. c.* pv. *vesicatoria*, *Colletotrichum coccodes*, or *Phytophthora capsici* iinduced *CAOSM1* transcription in the leaf or stem tissues. Expression of the *CAOSM1* gene was somewhat higher in the incompatible than the compatible interactions of pathogens with pepper. The *CAOSM1* mRNA was prevalently localized in the phloem cells of the vascular bundle of leaf tissues infected by *C. coccodes*. The CAOSM1 gene was activated in leaf tissues by treatment with ethylene, methyl jasmonate, high salinity, cold acclimation and mechanical wounding, but not by abscisic acid (ABA) and drought. These results indicate that the pepper CAOSM1 protein functions in response to pathogens and some abiotic stresses in pepper plants

1-30. Differential expression and *in situ* localization of a pepper defensin (*CADEF1*) gene in response to pathogen infection, abiotic elicitors and environmental stresses in *Capsicum annuum*

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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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