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Calcium-Mediated Signaling in Plants: Calmodulin and Ca²⁺/Calmodulin-Dependent Protein Kinase

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Plants contain multiple genes that code for calmodulin (Zielinski *et al.*, 1990; Perera and Zielinski, 1992; Reddy *et al.*, 1991; Poovaiah *et al.*, 1992; Bottella and Arteca, 1994; Takezawa *et al.*, 1995). The role of these multiple genes in Ca²⁺/calmodulin-mediated signal transduction is not clearly understood. The amino acid comparison of different calmodulin genes from potato, *Arabidopsis*, barley and chick are shown in Fig. 1. Studies have shown that several cal-

modulin and calmodulin-related genes are responsive to signals. Various physical and chemical signals have been shown to induce mRNAs corresponding to calmodulin and camodulin-related genes. Using a potato calmodulin cDNA as a probe, we have (Jena *et al.*, 1989) investigated the effect of auxin and light on calmodulin gene expression. For example, exposure of dark grown Merit corn root tips to light increased the calmodulin mRNA level (Jena *et al.*, 1989). Takezawa *et al.* (1995) tested the effect of touch stimulation. Lee *et al.* (1995) have isolated a calmodulin isoform from soybean that activates calmodulin-dependent enzymes in a differential manner. In *Arabidopsis*, Braam and Davis (1990) have shown that rapid (10-30 min) induction of mRNAs corresponding to four cDNAs (*TCH 1*, *TCH 2*, *TCH 3* and *TCH 4*) in response to a variety of stimuli such as touch, wind, rain and wounding. Of these four genes, *TCH 1* was identified as a calmodulin and *TCH 2* and *TCH 3* were identified as calmodulin-related genes.



Fig. 1. Amino acid sequence comparisons of different calmodulin genes (PCM1, 5, 6 and 8) from potato with *Arabidopsis* CaM-2 (Ling *et al.*, 1991), barley CaM-1 (Ling and Zielinski, 1989), and chick calmodulin (Putkey *et al.*, 1983). The sequences in the fourth Ca²⁺-binding region toward the C-terminus are shown. Asterisks indicate the position of amino acids involved in Ca²⁺-binding (from Poovaiah *et al.*, J. Plant Physiol., 149: 553-558, 1996).

MANIPULATION OF CALMODULIN LEVELS IN TRANSGENIC PLANTS

The role of calmodulin in plant growth and development can be studied by overexpressing or blocking the expression of calmodulin. Transient overproduction of calmodulin levels in transformed mouse cells accelerated cell proliferation. Furthermore, decreased calmodulin levels by antisense RNA resulted in arrest of the cell cycle (Rasmussen and Means, 1989). To study the consequences of altered levels of calmodulin on plant growth and development, we produced independent transgenic potato plants carrying potato calmodulin cDNA (PCM-1) in sense or antisense orientation driven by the CaMV 35S and patatin promoters. These transgenic plants exhibited

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striking differences in growth and development including tuberization and their responsiveness to environmental signals (Poovaiah *et al.*, 1996). To study the regulation of PCM-1, transgenic potato plants carrying the PCM-1 promoter fused to the β -glucuronidase (GUS) reporter gene were produced. GUS expression was found to be developmentally regulated and touch responsive, indicating a correlation between the expression of PCM1 and GUS mRNAs (Takezawa *et al.*, 1985). Roberts *et al.* (1992) addressed the functional significance of calmodulin methylation by generating transgenic plants expressing normal (VU-1) and the methylation mutant (VU-3) calmodulins. VU-1 and VU-3 are identical except that VU-3 cannot be methylated. Introduction of these foreign calmodulins resulted in a two-fold increase in the calmodulin level, and the amount of foreign calmodulin was found to be equivalent to that of endogenous calmodulin. Transgenic plants expressing calmodulin the methylation mutant (VU-3) showed decreased stem internode, reduced seed and pollen viability, and reduced seed production. However, the transformants expressing VU-1 were found to be indistinguishable from control plants. The phenotypic differences in the transgenic plants containing VU-3 were attributed to mutant calmodulin.

Ca²⁺/CALMODULIN-BINDING PROTEINS

Calmodulin, upon binding to Ca²⁺, interacts with a number of enzymes and other proteins called calmodulin-binding proteins that play a key role in plant growth and development (Poovaiah and Reddy, 1987, 1993; Roberts and Harmon, 1992). A number of calmodulin-binding proteins have been isolated, characterized, and identified in animals (Bachs and Carafoli, 1987; Bachs *et al.*, 1990; Colbran and Soderling, 1990; Klee, 1991; Soderling, 1994; Perrino *et al.*, 1995). This information has increased our understanding of how Ca²⁺ and calmodulin regulate the various biochemical and molecular processes that eventually lead to a physiological response. The calmodulin-binding proteins that have been identified in plants include NAD kinase, Ca²⁺ ATPase, nuclear NTPases, and protein kinases (Poovaiah Reddy, 1993). Reddy *et al.* (1993) isolated and characterized two calmodulin-binding proteins from corn root tips, one of which is signal responsive. Lu and Harrington (1994) have also cloned cDNAs that encode calmodulin-binding proteins in tobacco, the expression of which is reduced by heat shock treatment. Calmodulin-binding proteins with sequence similarity to the *E. coli* enzyme, glutamate de-

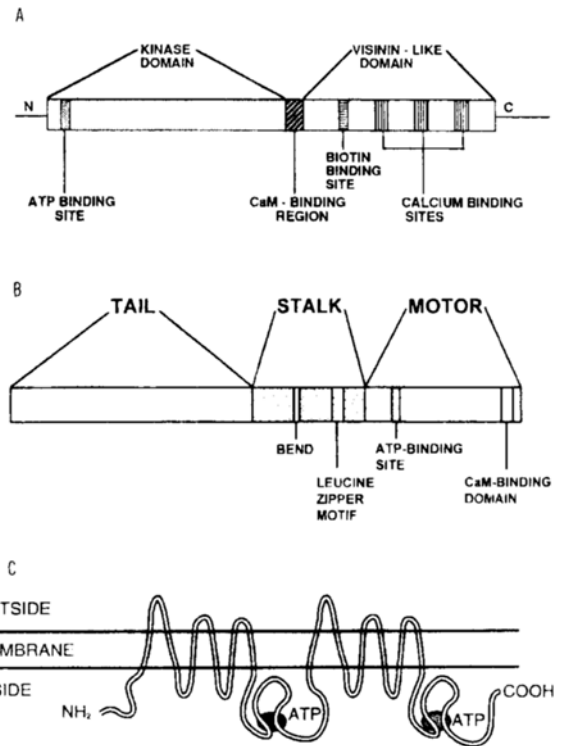


Fig. 2. Structural features of different calmodulin-binding proteins: calcium/calmodulin-dependent protein kinase (CCaMK) (A); calmodulin-binding kinesin-like protein (TCK1) (B); homolog of mammalian multidrug resistant P-glycoprotein (PMDR1) (C).

CCaMK	311	LIEPEVVSRLRSFNARRKLRAAAIASVLSS	340
CaMKII α	281	MHRQETVDCCLKKFNARRKLGAILTTMLAT	310

Fig. 3. Comparison of amino acid sequences surrounding the CaM-binding sites of CCaMK and the α -subunit of CaMKII.

carboxylase (GAD) which converts glutamate to γ -aminobutyric acid (GABA) have been reported (Baum *et al.*, 1993; Ling *et al.*, 1994). GAD levels are known to change in response to environmental stresses. Calmodulin-dependent protein kinases with homology to mammalian CaM KII have been reported in plants (Poovaiah *et al.*, 1992; Watillon *et al.*, 1993). Recently, a chimeric Ca²⁺/calmodulin-dependent protein kinase with a visinin-like Ca²⁺-binding domain was cloned and characterized in this laboratory (Patil *et al.*, 1995; Takezawa *et al.*, 1996a). The structural features of CCaMK are shown in Fig. 2A. A comparison of CCaMK and the α -subunit of CaMKII, is shown in Fig. 3. See the section on biochemical properties of CCaMK for addition details. Two other genes (*TCK1* and *PMDR1*) that encode for calmodu-

lin-binding proteins that are not kinases have also been cloned in our laboratory (Wang *et al.*, 1996a, b). The structural features of these three calmodulin-binding proteins are shown in Fig. 2.

TCK1: The *TCK1* cDNA encodes a protein with 1265 amino acid residues. Its structural features are very similar to those of known kinesin heavy chains and kinesin-like proteins from plants and animals, with one distinct exception. Unlike other known kinesin-like genes from plants and animals, TCK1 contains a novel calmodulin-binding domain which distinguishes it from all other known kinesin proteins (Wang *et al.*, 1996a). *E. coli*-expressed TCK1 binds calmodulin in a Ca^{2+} -dependent manner. In addition to the presence of a calmodulin-binding domain in the motor domain at the carboxyl-terminal, it also has a leucine zipper motif in the stalk region (Fig. 2B). The amino acid sequence at the carboxyl-terminal of TCK1 has striking homology with the mechanochemical motor domain of kinesins. The motor domain has ATPase activity that is stimulated by microtubules. Southern blot analysis revealed that *TCK1* is coded by a single gene. Expression studies indicated that *TCK1* is expressed in all of the tissues tested. Its expression was highest in the stigma and anther, especially during the early stages of anther development. Our results suggest that Ca^{2+} /calmodulin may an important role in the function of this microtubule-associated motor protein and may be involved in the regulation of microtubule-based intracellular transport.

PMDR1: A homology of the multidrug resistance (MDR) gene was obtained while screening a potato stolon tip cDNA expression library with ^{35}S -labeled calmodulin. The mammalian MDR gene codes for a membrane-bound P-glycoprotein (170-180 kDa) which imparts multidrug resistance to cancerous cells (Gottesman & Pastan, 1993). The potato cDNA (PMDR1) codes for a polypeptide of 1,313 amino acid residues (approximately 144 kDa) and its structural features are very similar to the MDR P-glycoprotein (Fig. 2C). The N-terminal half of the PMDR1 encoded protein shares striking homology with its C-terminal half, and each half contains a conserved ATP-binding site and six putative transmembrane domains (Wang *et al.*, 1996b). Southern blot analysis indicated that potato has one or two MDR-like genes. PMDR1 mRNA is constitutively expressed in all organs studies with higher expression in the stem and stolon tip.

Ca^{2+} AND Ca^{2+} /CALMODULIN-DEPENDENT PROTEIN PHOSPHORYLATION

Protein phosphorylation is one of the major mechanisms by which eukaryotic cells transduce extracellular signals to intracellular responses (Cohen, 1992). Ca^{2+} and Ca^{2+} /CaM-dependent protein kinases are involved in amplifying and diversifying the action of Ca^{2+} -mediated signal (Veluthambi and Poovaiah, 1984; Edelman *et al.*, 1987; Colbran and Soderling, 1990; Schulman, 1993). In animals, Ca^{2+} /CaM-dependent protein kinases are known to play a pivotal role in cellular regulation (Nairn *et al.*, 1985; Colbran and Soderling, 1990; Hanson and Schulman, 1992). Several types of CaM-dependent protein kinases (CaM kinases, phosphorylase kinase, and myosin light chain kinase) have been well characterized in mammalian systems (Fujisawa, 1990; Colbran and Soderling, 1990; Klee, 1991; Mochizuki *et al.*, 1993). Although very little is known about Ca^{2+} /CaM-dependent protein kinases in plants (Poovaiah *et al.*, 1992; Watillon *et al.*, 1992, 1993), Ca^{2+} -dependent, but CaM-independent protein kinases (CDPKs) have been well documented (Harmon *et al.*, 1987; Harper, *et al.*, 1991; Roberts and Harmon, 1992; Roberts, 1993; Stone and Walker, 1995). Extracellular signals, either directly or through second messengers, regulate the activity of protein kinases which in turn regulate the activity of their substrates by phosphorylation. Studies in animal systems indicate that CaM-dependent protein kinases are central to Ca^{2+} -mediated signal transduction pathways (Colbran and Soderling, 1990). Amplification and diversity in the action of some signals is achieved by phosphorylation and dephosphorylation of proteins (Cohen, 1985). Many key regulatory proteins undergo phosphorylation, resulting in conformational changes in these proteins eventually leading to altered biological properties.

The structure of CCaMK and its regulation independently by Ca^{2+} and Ca^{2+} /CaM makes it distinct from other kinases. The catalytic and CaM-binding domains of CCaMK have high homology to corresponding domains of CaMKII, a well characterized Ca^{2+} /CaM-dependent protein kinase in animals. CaM-dependent protein kinases are known to be maintained in an inactive state by the interaction of the catalytic region with an autoinhibitory domain located on the same polypeptide (Colbran, 1993). Binding of Ca^{2+} /CaM releases the catalytic site of these kinases from the autoinhibitory domain. Removal of the autoinhibitory domain of rat brain CaMKII by deletion or truncation converts the enzyme to Ca^{2+} /CaM-independent form (Hagiwara *et al.*, 1991). This was further confirmed by creating a series of substitutions of CaMKII and measuring their Ca^{2+} /CaM-independent

activity (Cruzalegui *et al.*, 1992). CaMKII is known to autophosphorylate at Thr-286 upon binding Ca²⁺/CaM, which further disrupts the interaction of the autoinhibitory region with the catalytic site. After CaM dissociates from an autophosphorylated CaMKII, the subunits modified by autophosphorylation remain partially active. Site-directed mutagenesis showed that a mutant CaMKII which has Ala-286 does not exhibit Ca²⁺-independent activity after dissociation of CaM. Furthermore, replacement of Thr-286 with negatively charged amino acids mimics the effect of autophosphorylation (Fong *et al.*, 1989).

BIOCHEMICAL CHARACTERIZATION OF CCaMK

The biochemical characterization of this novel kinase (CCaMK) revealed that it is modulated by Ca²⁺ and Ca²⁺/calmodulin (Takezawa *et al.*, 1996). CCaMK contains all eleven major conserved subdomains of the catalytic domain of serine/threonine kinases. Sequence comparisons revealed that CCaMK has high similarity to mammalian Ca²⁺/CaM-dependent protein kinases, especially in the kinase and CaM-binding domains (amino acid residues 1-338). The CaM-binding region of CCaMK (FNARRKLRyAAAIAASVL, residues 323-338) is similar to the CaM-binding domain (FNARRKLGAILTTML, residues 293-309) of α -subunit of mammalian CaMKII. The sequence downstream of the CaM-binding region of CCaMK (amino acid residues 339-520) does not have significant similarity to known Ca²⁺/CaM-dependent protein kinases. Further analysis of this region revealed the presence of three Ca²⁺-binding EF-hand motifs that had high homology (52-54% similarity; 32-35% identity) to frequenin, neurocalcin, hippocalcin, and visinin-like neural Ca²⁺-binding proteins. These proteins are members of a family of Ca²⁺-sensitive regulators, each containing three Ca²⁺-binding EF-hand motifs. The structural features of CCaMK indicate that it is a chimeric Ca²⁺- and Ca²⁺/CaM-dependent protein kinase with two distinct regulatory domains; a CaM-binding domain and a visinin-like Ca²⁺-binding domain. Fig. 4A and 4B show Ca²⁺/calmodulin-dependent and independent activity of wildtype and mutant CCaMKs. We have observed a calmodulin isoform-specific effect on autophosphorylation and substrate phosphorylation (Liu *et al.*, unpublished data).

The mechanisms of CCaMK activation by calcium and calcium/calmodulin were investigated using various deletion mutants. The use of deletion mutants of CCaMK lacking either one, two, or all three calcium-

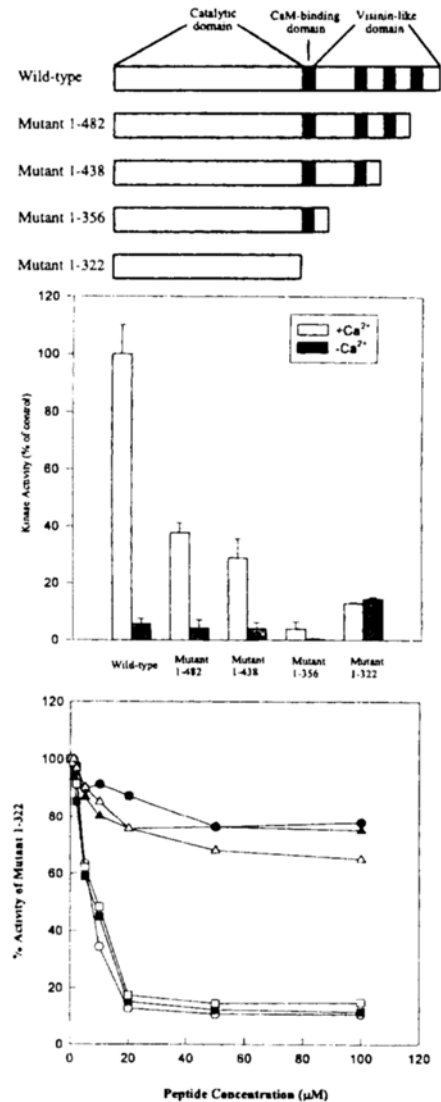


Fig. 4. A. Schematic diagrams of wildtype CCaMK and the deletion mutants. B. calcium/calmodulin-dependent and independent activity of wildtype and mutant CCaMKs. The kinase activity of CCaMK and its mutants were assayed in the presence of 0.5 mM CaCl₂ plus 1 µM calmodulin (open bars), or 2.5 mM EGTA (solid bars). The mean values and standard deviation were calculated from three independent experiments (from J. Biochem., Ramchandiran *et al.*, 121: 984-990, 1997). C. Effect of various synthetic autoinhibitory peptides on the activity of the constitutively active CCaMK mutant (1-322). Mutant CCaMK both the visinin-like domain and the calmodulin-binding domain (200 ng) was assayed in the presence of 0.5 mM calcium, 100 µM GS peptide and indicated concentrations of synthetic peptides corresponding to amino acids 328 to 340 (●) 322-340 (○), 317-340 (■) or 311-340 (□), 322-333 (▲) or 317-333 (△) for 2 min at 30°C under standard assay condition. The activity is represented as a percentage of control activity without the inhibitory peptides (from J. Biochem., Ramchandiran *et al.*, 121: 984-990, 1997).

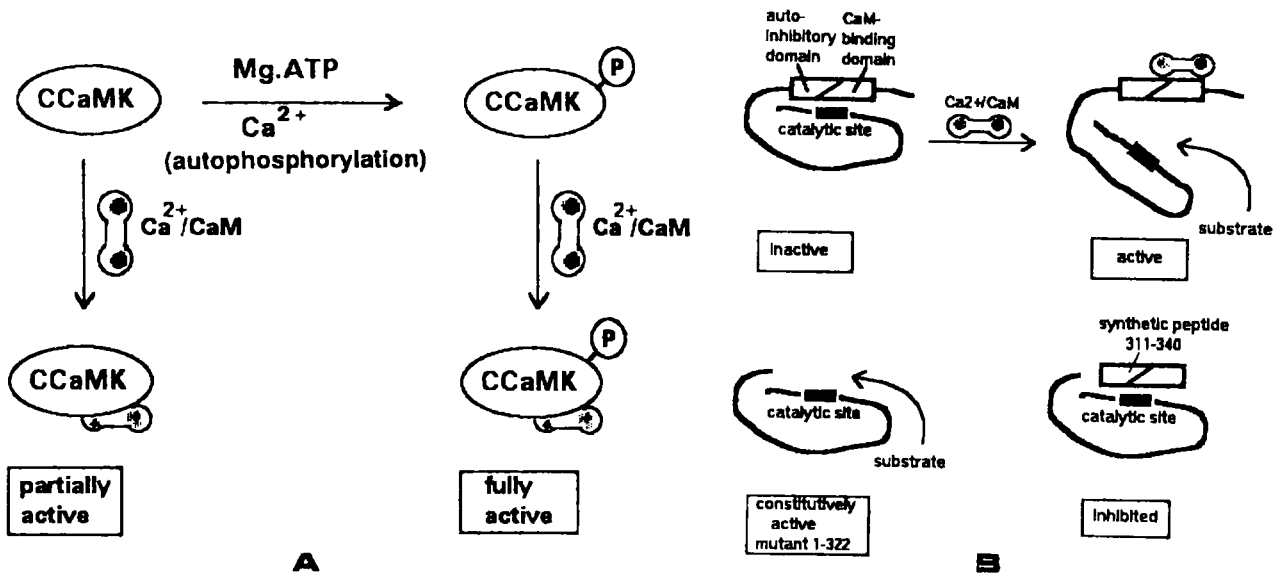


Fig. 5. Proposed model showing regulation of CCaMK by Ca^{2+} and $\text{Ca}^{2+}/\text{calmodulin}$ (A), and autoinhibitory domain (B).



Fig. 6. A. Homology model of the kinase domain and calmodulin binding domain of CCaMK. CCaMK has a bilobate structure and the C-terminal CaM binding regulatory element is displayed in green. The five antiparallel beta sheets constitute the catalytic site and includes the ATP-binding region. The model was drawn using MOLSCRIPT (Kraulis, 1991). B. Model of CaMK I from X-ray crystallography (Goldberg *et al.*, 1996). C. Homology model of the visinin-like domain of CCaMK based on the NMR structure of different calcium-binding proteins. The three EF hands are shown in orange.

binding EF-hands indicated that all three calcium-binding sites in the visinin-like domain were crucial for the full calcium/calmodulin-dependent kinase activity. As each calcium-binding EF hand was deleted, there was a gradual reduction in calcium/calmodulin-dependent kinase activity from 100% to 4%. Another mutant (amino acids 1-322) which lacks both the visinin-like domain containing three EF hands and the calmodulin-binding domain was constitutively active, indicating the presence of an autoinhibitory domain

around the calmodulin-binding domain. By using various synthetic peptides and the constitutively active mutant, we have shown that CCaMK contains an autoinhibitory domain within the residues 322-340 which overlaps its calmodulin-binding domain (Fig. 4C). Kinetic studies with both ATP and the GS peptide substrate suggest that the autoinhibitory domain of CCaMK interacts only with the peptide substrate binding motif of the catalytic domain, but not with the ATP-binding motif (Ramachandiran *et al.*, 1997). Pro-

posed models for the regulation of CCaMK by Ca²⁺ and Ca²⁺/calmodulin, and the autoinhibitory domain are shown in Fig. 5.

HOMOLOGY MODELING OF THE KINASE, CALMODULIN-BINDING, AND THE VISININ-LIKE DOMAINS OF CCaMK

The unique structural features and the structure/function relationships of CCaMK were studied by homology modeling. The homology model of the kinase and calmodulin-binding domain was built based on its homology with CaMK I. At the amino acid level CCaMK has 31% sequence identity and 68% similarity with CaMK I. Overall, the kinase domain and the calmodulin-binding domain of CCaMK are structurally similar to CaMK I (Fig. 6A-C). The initial results indicated that there was high conservation of these two kinases and the structure surrounding the catalytic core could be relatively plastic. The presence of the visinin-like domain with different structural features suggests a role as a calcium sensor element (antenna) in mediating kinase activity (Sathyanarayanan *et al.*, unpublished results).

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