

Signal transduction during cold stress in plants

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ABSTRACT

Cold stress signal transduction is a complex process. Many physiological changes like tissue break down and senescence occur due to cold stress. Low temperature is initially perceived by plasma membrane either due to change in membrane fluidity or with the help of sensors like Ca²⁺ permeable channels, histidine kinases, receptor kinases and phospholipases. Subsequently, cytoskeleton reorganization and cytosolic Ca²⁺ influx takes place. Increase in cytosolic Ca²⁺ is sensed by CDPKs, phoshatase and MAPKs, which transduce the signals to switch on transcriptional cascades. Photosynthetic apparatus have also been thought to be responsible for low temperature perception and signal transduction. Many cold induced pathways are activated to protect plants from deleterious effects of cold stress, but till date, most studied pathway is ICE-CBF-COR signaling pathway. However, the importance of CBF independent pathways in cold acclimation is supported by few *Arabidopsis* mutants' studies. Cold stress signaling has certain pathways common with other abiotic and biotic stress signaling which suggest cross-talks among these. Most of the economically important crops are sensitive to low temperature, but very few studies are available on cold susceptible crop plants. Therefore, it is necessary to understand signal transducing components from model plants and utilize that knowledge to improve survival of cold sensitive crop plants at low temperature. [Physiol. Mol. Biol. Plants 2008; 14(1&2): 69-79] *E-mail: arun@genomeindia.org*

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Nature nurtures all living beings by providing suitable resources like air, light, water, temperature and soil. Optimum level of these factors helps the organisms to grow in healthy condition. Adversities in these environmental conditions compel the organisms to change their habitats. How do sessile plants manage during adverse conditions? As a consequence of their sessile nature, plants have developed ability to adapt to external, often unfavorable environmental conditions. Cold is one of the most common environmental factors that limit the geographical distribution and growing season of many plant species (Guy, 1990). On the basis of survival ability in cold stress, plants can be divided into tolerant and susceptible. The plants growing in tropical or subtropical regions are susceptible to low temperature whereas plants growing in temperate region have ability to survive even at -30 °C, through the process of cold acclimation. By definition cold acclimation is the process, by which plants are able to adjust their metabolism to cold and increase freezing tolerance in response to low non-freezing temperature. The objective of this review is to understand the signal transduction process from cold

tolerant plants, mostly Arabidopsis and compare various features of this plant with cold-susceptible plants. Most of the economically important crop plants like rice, maize, tomato, soybean, cotton and fruit crops like banana, papaya, mango, grapes and orange are "chilling sensitive" often adversely affecting their quality and productivity. Understanding the importance of different signal transducing components will help to manipulate signaling pathway in susceptible plants to make them survive at low temperature. Therefore, it is necessary to understand it step by step, from stimulus to perception and from perception to early signal transduction which further eventually leads to dramatic alteration like change in plasma membrane fluidity, actin cytoskeleton rearrangement, cytosolic Ca²⁺ influx, protein phosphorylation, alteration in gene activity, increase in new protective gene products formation and secondary metabolism.

Physiological changes due to low temperature

The effect of cold stress depends on the degree of severity and the time of exposure. The seedling stage of plants is most sensitive to chilling. The potential chilling symptoms are: surface lesion, a water-soaked appearance

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of the tissue, discoloration, desiccation, tissue break down, accelerated senescence, ethylene production, shortened shelf life and faster decay due to leakage of plant metabolites (Sharma et al., 2005). Exposure of plants to temperature ranging from 0 °C to 10 °C causes chilling stress whereas exposure to temperature below 0 °C causes freezing stress. Chilling stress decreases the membrane fluidity due to fatty acid unsaturation in membrane lipids, changes composition and ratios of lipids to proteins in cell membrane (Wang et al., 2006). Low non-freezing temperature also causes dehydration, mainly due to reduction in water uptake by roots and an impediment to close stomata. At freezing temperature, membrane damage is caused by severe cellular dehydration, associated with ice formation. The accumulation of ice in the intracellular spaces causes the physical disruption of cells and tissues. Depending on the freezing temperature and the degree of cellular dehydration, different forms of membrane damages can occur, including expansion-induced lysis, lamellar-tohexagonal-II phase transition and fracture jump lesion. Freezing temperature also causes protein denaturation and precipitation of solutes as a result of freezing induced dehydration (Uemura et al., 1995; Salinas, 2002). Both low and freezing temperatures result in the oxidative stress due to generation of reactive oxygen species (ROS). These ROS disequilibrate the electron transfer reactions and disturb accompanying biochemical reactions. Thus generation of ROS leads to cellular injury, which ultimately leads to death of plant due to damage of photosystem II reaction centre and membrane lipids (Prasad et al., 1994; Suzuki and Mittler, 2006). Plants exposed to low or freezing temperatures confront a plethora of dangerous circumstances. Susceptible plants are unable to survive in such deleterious condition; however the tolerant plants are able to counter this deadly situation by triggering cold acclimation response, which is switched on by a systematic intracellular signaling cascade.

Cellular changes during low temperature stress

The very first step in cold signaling cascade is the perception of the low temperature. It was demonstrated that a very brief exposure to low temperature results in the onset of a cold signaling pathway and a continuous exposure of low temperature is not necessary (Henriksson and Trewavas, 2003). Temperature sensing in plants is dependent on the cooling rate, dT/dt, which means stepwise decrease in temperature rather than absolute temperature T. In *Arabidopsis*, roots were found to be sensitive to cooling rates of less than 0.01 °C/s dT/

dt (Minorsky and Spanswick, 1989; Plieth *et al.*, 1999). Various changes brought about by low temperature are described in following sections.

Changes in membrane fluidity: Membrane fluidity changes instantly as a result of low temperature. It undergoes qualitative as well as quantitative modification in its lipid composition under cold stress (Wang et al., 2006). The degree of fatty acid unsaturation and the content of phospholipids increases during cold acclimation. Therefore it is thought that membrane rigidification might play a major role in cold perception. This change in membrane rigidity is perceived by membrane proteins and they act as primary sensors or regulators (Mikami and Murata, 2003; Los and Murata, 2004). Many experimental evidences proved that membrane is the primary site of cold perception. Mutation in a gene encoding fatty acid desaturase, in a strain of Synechocystis exhibited plasma membrane rigidification even at room temperature and increased expression of number of cold inducible genes (Inaba et al., 2003). In alfalfa cell suspension culture, benzyl alcohol (BA), a membrane fluidizer, prevented the expression of cold induced genes and the Ca²⁺ influx at 4 °C, but these events were induced at 25 °C, when dimethylsulfoxide was used as membrane rigidifier (Orvar et al., 2000; Sangwan et al., 2002). Cold activation of Brassica napus BN115 promoter was strongly inhibited by BA, and induced at 25 °C by dimethylsulfoxide (Sangwan et al., 2001). Voultier et al. (2006) also suggested the role of membrane rigidification in cold perception and signal transduction process. They analyzed diacylglycerol kinase (DAGK) activation, which is very early event occurring within seconds of cold exposure.

Cytoskeletal reorganization: Rearrangement of the actin cytoskeleton occurs downstream of the changes in membrane fluidity but up-stream of Ca²⁺ influx (Orvar et al., 2000; Sangwan et al., 2002). In alfalfa cell suspension culture, the induction of cold acclimation specific gene (cas30) and Ca²⁺ influx at 4 °C were prevented by jasplakinolide (JK), an actin microfilament stabilizer, but induced at 25 °C by the actin microfilament destabilizer cytochalasin D (CD). This suggests the role of actin cytoskeleton reorganization in cold signaling (Orvar et al., 2000). It was also emphasized that the cytoskeleton may be a platform for several other physiological functions involved in cold acclimation, such as protein trafficking and modulation of activities of protein kinases/phosphatases that may or may not be dependent on Ca²⁺ influx (Orvar et al., 2000).



Cold sensors

Very little is known about cold sensors in plants. There are some potential low temperature sensors suggested by different researchers, but as yet there is no direct proof for either of them. Many authors emphasized the role of membrane based proteins as the sensors for detection of conformational changes in microdomain of membrane. Thus membrane located proteins sense the transition of the physical phase from the liquid-crystalline to gel state (Murata and Los, 1997; Los and Murata, 2004). Some putative sensors of cold are described here:

- a. Ca^{2+} permeable channels: Cold stress induces transient Ca^{2+} influx into the cytoplasm. Therefore, calcium permeable channels responsible for this Ca^{2+} influx are considered as sensors for low temperature (Monroy and Dindsa, 1995). The activation of calcium channels by cold is thought to be the result of physical alterations in cellular structure. Minorsky (1989) also proposed that the cold induced cytosolic Ca^{2+} response may be the sensor of cold.
- b. Histidine kinases: The two-component histidine kinases are the strongly advocated low temperature sensors in plants. The experimental evidence suggests that the cyanobacterium histidine kinase Hik33 and Hik19 (Suzuki et al., 2000) and the Bacillus subtilis histidine kinases DesK (Aguilar et al., 2001) are temperature sensors and regulate desaturase gene expression in response to low temperature. Several putative two-component histidine kinases are identified in Arabidopsis (Urao et al., 2000a, b) out of these AtHK1, has been found to be upregulated by low temperature, high salinity and dehydration. AtHK1 protein senses these stresses and transduces the signal to the nucleus through a phosphorylation cascade (Urao et al., 1999).
- c. Receptor kinases: Receptor like kinases (RLKs) are other putative low temperature sensors. They have membrane spanning domains, which function in transmitting extracellular signals into intracellular target molecules. In Arabidopsis, one member of this family, RPK1 was shown to induce its expression by cold, dehydration, high salt and ABA (Hong et al., 1997).
- d. Phospholipases: Changes in the membrane phospholipids metabolism are implicated in cold response signaling. Phospholipase C and D are accumulated as early as 15 seconds after cold treatment (Ruelland et al., 2002). It increases the production of phosphatidic acid (PtdOH) by hydrolyzing membrane phospholipids, which is proposed as membrane based secondary messenger molecule. Phospholipase D

- anchors the microtubules to "plasma membrane" so its activation can lead to conformational change in the cytoskeleton (Gardiner *et al.*, 2001; Dhonukshe *et al.*, 2003). It further leads to actin filaments rearrangement, thus probably activating stretch-induced Ca²⁺ channels.
- Photosynthetic apparatus: It is proposed that in low temperature, photosynthetic apparatus itself functions as a sensor for imbalance between the light energy absorbed through photochemistry versus the energy utilized through metabolism. Thus energy imbalance is sensed through alteration in the excitation pressure of photosystem II, which results into reduction in photosynthesis. It has been presumed that the redox signal, which is generated from the plastoquinone pool, regulates chloroplast and nuclear photosynthetic gene expression (Fey et al., 2005; Ensminger et al., 2006). Thus redox state of the photosynthetic apparatus can act as a low temperature sensor (Huner et al., 1998; Ensminger et al., 2006), which further interacts with other processes responsible for cold acclimation (Gray et al., 1997).

Cold signal transducers in plants

The elevation in cytosolic Ca²⁺ from extracellular spaces is an early event in the response to cold. This cytosolic Ca²⁺ is suggested as an important second messenger in low temperature signal transduction and developing cold acclimation. A positive correlation between cold-induced Ca²⁺ influx and accumulation of cold-induced transcripts has been shown for alfalfa (Monroy and Dhidsa, 1995; Reddy and Reddy, 2004) and Arabidopsis (Henriksson and Trewavas, 2003). Knight and coworkers used transgenic approach to demonstrate transient increase in cytosolic Ca²⁺ in response to cold. They developed transgenics of Arabidopsis and tobacco expressing the calcium-sensitive luminescent protein aequorin and demonstrated a rise in cytosolic Ca2+ concentration in response to low temperature (Knight et al., 1991). Different chelators and channel blockers were also used to show the cytosolic Ca²⁺ influx and its role as second messenger in response to cold in alfalfa (Monroy et al., 1993; Knight et al., 1996) and Arabidopsis (Tahtiharju et al., 1997). Along with cold, cytosolic Ca²⁺ influx also observed in other environmental stresses, which suggest that, there is a specific signature of the cytosolic Ca²⁺ for different stresses. Ca²⁺ signature can be described as the characteristics of the time course of changes in cytosolic Ca²⁺. Their sites of appearance in cells are used by the plant to identify the type and intensity of the stimulus (Evans et al., 2001; Plieth, 2005). Thus the precise kinetics, magnitude and cellular source of stimulusinduced cytosolic Ca²⁺ influx (calcium signature) have



been proposed to encode information regarding particular stimulus and to determine the specific end response (Lecourieux *et al.*, 2006). Various abiotic stress response use Ca²⁺ from different subcellular sources, including the extracellular compartment, vacuole and mitochondria (Knight *et al.*, 1996; Subbaiah *et al.*, 1998). It is also observed that effective Ca²⁺ signature is produced only in particular tissue or organs. During cold stress cytosolic Ca²⁺ influx occurs in whole plant, in contrast to drought, where it is present only in roots (Knight and Knight, 2000).

The elevation in cytosolic Ca²⁺ transmits primary signal through Ca2+ regulated proteins called Ca2+ sensors and changes phosphorylation status of different proteins (Monroy et al., 1993). The major Ca²⁺ sensors in plants are calmodulin (CaM), CaM domain-containing protein kinases (CDPKs), calcineurin B-like proteins (CBLs) and CBL-interacting protein kinases (CIPKs). These Ca²⁺ sensors are categorized into "sensor relay" and "responders". Sensor relay bind to Ca²⁺ and undergo conformational changes that regulate the gene expression e.g., calmodulin (CaM) and calcineurin B-like proteins (CBLs). Responders, like protein kinase and phospholipase have effector domains through which they relay the message to their downstream targets (Reddy and Reddy, 2004; Klimecka and Muszynska, 2007). Thus elevation of cytosolic Ca²⁺ alone or in association with calmodulin could activate Ca2+ dependent protein kinases. Different Ca²⁺ signatures are distinguished by different Ca2+ binding proteins and protein kinases and decoding of these signals causes changes in gene expression leading to appropriate physiological responses (Yang and Poovaiah, 2003; Sathyanarayanan and Poovaiah, 2004). Some of the components of calcium signaling are described in the following sections.

a. CDPKs: Many CDPKs are found to be upregulated by cold in different plants. In alfalfa cell suspension culture, Monroy and coworkers utilized W7, an antagonist of CDPKs and CaM, which inhibited the capacity of the culture to cold acclimate (Monroy et al., 1993). In same study, H7, a protein kinase inhibitor, inhibited the capacity of cell cuture to cold acclimate upto 50%. Similar results were obtained by Tahtiharju et al. (1997) working with Arabidopsis. Kim et al. (2003) showed the role of CIPK3 in cold signaling via changes in expression pattern of RD29A (Responsive to desiccation 29A), KIN1 (cold-inducible1) and KIN2 (cold-inducible2) genes in Arabidopsis. They proposed that CIPK3 is located upstream of transcription factors and downstream of the Ca²⁺ signal. The over-expression

of OsCIPK03, OsCIPK12 and OsCIPK15 confers significantly improved tolerance to cold, drought and salt stress in rice (Xiang et al., 2007). In tobacco, a calmodulin gene NpCaM1 was found to be upregulated by cold (van der Luit et al., 1999). The comprehensive analysis of CDPKs in rice shows that OsCPK4, OsCPK5 and OsCPK13 (OsCDPK7) are unregulated in response to cold (Ray et al., 2007). The overexpression of OsCDPK7 in rice resulted in improvement of cold, salt and drought stress tolerance (Saijo et al, 2001). In another study, the overexpression of OsCDPK13 and calreticulin interacting protein (CRTintP1) conferred cold tolerance to rice (Komatsu et al., 2007). A direct involvement of protein kinase C dependent phosphorylation in cold stress in Brassica juncea was shown by Deswal et al. (2004).

Phosphatases: Protein phosphatases (PP2A and 2B) also act as Ca²⁺ sensor. Monroy et al. (1998) showed that low temperature provoked a rapid decrease in PP2A activity, and this inhibition was mediated by coldinduced Ca²⁺ influx and occurred at a post-transcriptional level. The cytoplasmic PP2A has been shown to inactivate MAP kinases, receptor protein kinases, and CDPKs in different systems (Salinas, 2002). They speculated that phosphatases acted either indirectly via inactivation of protein kinases or directly via regulating trans-acting factors. Thus, it can be concluded that when plants are exposed to low temperature, the signal is sensed and tranduced into an increase in cytosolic Ca²⁺, which in turn inhibits protein phosphates 2A (PP2A) activity and activates a series of phosphorylation switches involving CDPKs and low temperature regulated gene expression. The gene of CBL family, AtCBL1, was highly up-regulated by cold and drought in Arabidopsis (Kulda et al., 1999). Its over-expression led to enhanced tolerance to salt and drought stress but reduced tolerance to freezing stress, suggesting its role as a negative regulator of cold response in Arabidopsis (Cheong et al., 2003).

c. MAPKs: Mitogen activated protein kinase cascade is also involved in cold stress signaling. MAPKs perform their function as a part of protein kinase modules, which is mainly composed of MAPKs, MAPKKs and MAPKKKs. Cold associated increase in mRNA levels of MAPKs has been observed in response to high salt, drought, wounding and pathogen attack (Widmann et al., 1999; Nakagami et al., 2005). It has been reported that AtPK6 and AtPK19 are upregulated in response to low temperature (Mizoguchi et al., 1995). Other two genes AtMPK3 (MAPK) and AtMPKK1 (MAPKKK) are also transcriptionally induced by cold (Mizoguchi et al., 1996).



In accordance with a role of AtMPK3 in cold acclimation, a closely related alfalfa homologue, MMK4, is also upregulated upon cold stress (Jonak et al., 1996). A stress activated MAP kinase (SAMK) was also upregulated in alfalfa in response to cold (Sangwan et al., 2002). The reactive oxygen species, which is integral part of cold stress, have been shown to activate a MAPK cascade in Arabidopsis. This cascade includes ANP1 (a MAPKKK), AtMPK3 and AtMPK6 and its positive regulator, nucleoside diphosphate kinase 2 (Kovtun et al., 2000; Moon et al., 2003). Homologue of ANP1 from tobacco, NPK1 functions in cold signal transduction cascade and influences the auxin signal transduction (Kovtun et al., 1998) and plant development (Jin et al., 2002). NPK1 acts as a positive regulator of cell death associated with plant immunity and disease (del Pozo et al., 2004). The overexpression of NPK1 also enhances freezing and drought tolerance in transgenic maize (Shou et al., 2004a, b). This suggests that stress tolerance not only involves cold-responsive mechanism but also the basic machinery of the plant.

d. Reactive Oxygen Species (ROS): Cold stress results into an oxidative burst due to the generation of active oxygen species like superoxide, hydrogen peroxide and hydroxyl radicals. These reactive oxygen species induce ROS scavengers and other protective mechanisms, as well as damaging agents contributing to injury in the plants (Prasad et al., 1994). The mechanism by which plants are able to sense the oxidative burst in response to cold is still unknown. But some reviews have elaborated the role of ROS in stress signal transduction (Mittler, 2002; Mittler et al., 2004; Suzuki and Mittler, 2006).

Transcriptional cascade

The low temperature signal is perceived by membrane and transduced by different transduction components results in stimulation of transcription of several genes. Numerous transcription factors that facilitate cold signaling and control expression of cold regulon have been identified in *Arabidopsis* (Shinozaki *et al.*, 2003; Gilmour *et al.*, 2004; Chinnusamy *et al.*, 2006; Yamaguchi-Shinozaki and Shinozaki, 2006, Zhu *et al.*, 2007) and homolog of these factors have been reported in other plants also (Jaglo *et al.*, 2001; Zhang *et al.*, 2004).

a. CBF pathway: The linking components between signal transduction and activation of transcription factors are yet to be revealed. But, present information support that ICE1 (Inducer of CBF Expression 1) a MYC-like transcription factor is the upstream component

in cold transcription cascade (Chinnusamy et al., 2003). Zhu and coworkers suggested that in Arabidopsis, ICE1 get phosphorylated in response to cold treatment and therefore transcription cascades that are directed by ICE1 and ICE1-like bHLH proteins are probably activated by the cold sensing and signaling pathway via protein phosphorylation (Zhu et al., 2007). Recent advances suggest that the HOS1 (high expression of osmotically responsive genes), a RING-type ubiquitin E3 ligase negatively regulates the function of ICE1 at low temperature by ubiquitination-mediated degradation (Dong et al., 2006), but the SUMO E3 ligase SIZ1mediated sumoylation represses the polyubiquitination that leads to an increase in its stability at low temperature (Miura et al., 2007). Moreover, it was observed that at normal growth temperature, HOS1 resides in the cytoplasm, but it is shifted to nucleus upon cold treatment, suggesting its role in relay of cold signal to the nucleus (Lee et al., 2001). An R2R3-type MYB transcription factor, AtMYB15, was also found to be physically interact with ICE1 (Agarwal et al., 2006). Phosphorylation and SIZ1-mediated SUMO conjugation/ deconjugation of ICE1 are the key processes that finally activate ICE1 to bind to its target genes. Active ICE1 binds to MYC cis-elements (CANNTG) in the CBF3 (Crepeat Binding Factor) promoter to induce its expression (Chinnusamy et al., 2003). There are three CBF genes present in Arabidopsis genome in tandem and are induced by low temperature (Stockinger et al., 1997; Medina et al., 1999). These are the most characterized transcription factors which directly or through other transcription factor activate cold regulon (Liu et al., 1998; Thomashow, 1999; Yamaguchi-Shinozaki and Shinozaki, 2006). Protein products of these *CBF* genes bind to core CRT/DRE (C-repeat/Dehydration Responsive Element) cis-element (A/GCCGAC), that are present in promoters of target genes through their AP2/ERF DNA binding domains (Yamaguchi-Shinozaki and Shinozaki, 1993, 1994, 2005; Thomashow, 1999). Low temperature transiently induces the expression of all CBF transcription factors within minutes (Vogel et al., 2005). Overexpression of each CBF gene constitutively induces CBF regulon and enhances freezing tolerance in transgenic plants (Jaglo-Ottosen, 1998; Gilmour et al., 2000, 2004). A study using loss of function mutant cbf2, the gene encoding CBF2, suggests that CBF2 is the negative regulator of CBF1 and CBF3 (Novillo et al., 2004), where as Chinnusamy et al. (2003, 2006) suggested that CBF3 acts as negative regulator of CBF2. In recent years, many microarray experiments have been carried out for identifying genes that are present in CBF regulon (Gilmour et al., 2004; Vogel et al., 2005). The genes

assigned to this regulon encode proteins that fall into a wide range of functional categories like transcription factor, signal transduction pathway components, biosynthetic proteins, cryoprotectants and other stress related proteins as well as a huge number of genes encoding proteins of unknown function (Thomashow, 1998; Fowler and Thomashow, 2002; Maruyama et al., 2004; Vogal et al., 2005). Many proteins from this regulon have been previously shown to contribute to increased freezing tolerance. Cryoprotectant protein, COR15a, an enzyme involved in regulating proline levels (P5CS2) and galactinol synthase, the enzyme that catalyzes the first step in the synthesis of raffinose are few of such proteins (van Buskirk and Thomashow, 2006). Several genes from CBF regulon encode transcription factors such as RAP2.1, RAP2.6 and ZAT10. This suggests that in cold acclimated plant like Arabidopsis ICE1-CBF-COR pathway plays an important role.

CBF independent pathways: Apart from CBF, there are some other pathways which contribute to cold tolerance in Arabidopsis. ZAT12 is a transcription factor, regulon of which is well characterized and has been shown to be activated by ROS (Davletova et al., 2005; Vogel et al., 2005). Other transcription factors like HOS9, a putative homeodomain transcription factor (Zhu et al., 2004) and HOS10, a putative R2R3-type MYB transcription factor (Zhu et al., 2005) also confer cold acclimation to Arabidopsis, via CBF independent pathways. Recently identified gene for eskimo1 mutant, ESK1 also acts in a manner independent of CBF pathway and provides tolerance to Arabidopsis plants in cold stress via set of genes regulated by salt and osmotic stress and ABA treatment (Xin et al., 1998, 2007). This shows that along with ICE-CBF-COR pathway, other transcriptional networks are simultaneously activated for cold acclimation.

c. Transcriptional activators: In addition to the transcription factors, which directly bind to the ciselements in the promoter regions of the stress responsive genes, transcriptional activation also needs some additional cofactors. These cofactors play an important role in determining the levels of gene expression. In Arabidopsis, CBF1-mediated transcription requires the transcriptional adaptor ADA and the histone acetyltransferase GCN5 (Stockinger et al., 2001). The mutation in either of them can affect the low temperature regulation of COR genes. It has been proposed that mutation in Arabidopsis sfr6 may fall in this category, because in sfr6 mutants expression of some COR genes get affected without any change in expression pattern of CBF genes (Knight et al., 1999).



Comparison of cold signaling in tolerant and susceptible plants

Although the mechanism of cold perception, signal transduction and activation of cold-responsive machinery is yet to be revealed completely, a lot is known in model plant like *Arabidopsis* (Zhu *et al.*, 2007) with reverse genetic tools developed by Ishitani and coworkers (1997) and available mutants. However, it is yet to be found out if this signaling cascade is similar in other cold tolerant and susceptible plant species. Different response of tolerant and susceptible plants to cold stress may be due to inactivation of some signaling molecules or transcription factors during long period of evolution, or may be due to loss of function of regulatory molecules acting downstream to signaling components. This could be possible due to mutation in genes or their promoter regions, or due to loss of some important genes responsible for cold acclimation. One study of Poaceae family by Sarhan et al. (1997) with cold tolerant species wheat and rye; and cold susceptible species rice and maize, has revealed that all cereals contain homologues of low temperature regulated wheat genes in their genomes. But gene expression in response to cold is found only in the tolerant cereals (Sarahan and Danyluk, 1998). This suggests changes in promoter activity of top ranking components of signal transduction or transcription factors in susceptible plants. In another study, the comparison of the CBF regulon in Arabidopsis and a cold susceptible tomato plants again supported this view (Zhang et al., 2004). As discuss earlier, in Arabidopsis, CBF pathway actively participates in cold acclimation, but unlike Arabidopsis, tomato cannot cold acclimate. It was shown that all three CBF genes are present in tomato in tandem like that of Arabidopsis, out of which only the expression of LeCBF1 gene gets up-regulated in response to cold in tomato. The constitutive overexpression of either LeCBF1 or AtCBF3 in transgenic tomato plants did not improve freezing tolerance. Gene expression study using microarray identified only four genes, which were induced 2.5 fold or more in the LeCBF1 or AtCBF3 over-expressing plants (Zhang et al., 2004), whereas there are more than 500 genes (Vogel et al., 2005) and 250 metabolites (Cook et al., 2004) in Arabidopsis CBF regulon. This indicate that CBF regulon changed in tomato in due period. But this conclusion is subject to change if complete set of cDNA data of tomato used for microarray experiment.

Cross-talk with other stresses

Many reviews are available on cross-talk among different abiotic stresses (Knight and Knight, 2001; Zhu, 2001; Xiong *et al.*, 2002; Chinnusamy *et al.*, 2004; Beck *et al.*,

2007; Vij and Tyagi, 2007). Dehydration is the common physiological disorder during cold, drought and salt stress (Beck *et al.*, 2007). Decrease in turgour pressure due to freezing is known to induce biosynthesis of plant stress hormone ABA. In cold stress, ABA dependent pathway plays very little but significant role (Gusta *et al.*, 2005). As discussed before, generation of reactive oxygen species occurs in almost all abiotic stresses. At every node of signaling, from Ca²⁺ influx, signal transducers (CDPKs and MAPKs) to transcription factors, cross-talk is possible (Knight and Knight, 2001). So it is necessary to consider cold signaling as a network, in which much more overlap between its branches is possible.

CONCLUSION AND PERSPECTIVES

Current review covered the recent advances in low temperature signal transduction and activation of molecular response in plants. On the basis of growth under cold stress, plants are divided into tolerant and susceptible types. Physiological changes in plants can be categoried into changes due to chilling and changes due to freezing. The very first organelle to perceive low temperature change is plasma membrane. Changes in plasma membrane are sensed by different sensor proteins and result in cytoskeleton reorganization, which finally leads to cytosolic Ca2+ influx. Calcium signal transduction further transduces these signals to nucleus by different kinases and phosphatases and switched on a complete transcriptional cascade. reprogramming of gene expression in response to low temperature results in the accumulation, not only of protective proteins but also of hundreds or more of metabolites, some of which are known to have protective response. To gain a better understanding of different signaling components, their functions and how these signals communicate with others, it is important to develop novel methods of analysis. A single effort of developing mutant population of Arabidopsis plants over-expressing *luciferase* gene under the control of cold and dehydration inducible CBF3 promoter throws light on cold tolerance mechanism. Development of mutants using transposon tagging and T-DNA insertion lines will help to analyze the function of identified genes. The availability of the complete genome sequence of cold acclimated plant Arabidopsis and cold susceptible plant like rice has enabled the use of strategies like genomewide expression profiling to identify genes associated with cold acclimation or genes responsible for hazardous effect in sensitive plants. Comparative analysis of coldtolerant to cold-susceptible species is now possible due

to the advances in sequencing information from several species. In summary, a complete understanding on how cold acclimation response is activated in tolerant plants, with the help of transgenic approach will help to manipulate susceptible crop plants and increase agricultural productivity.

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