ICE1: a regulator of cold-induced transcriptome and freezing tolerance in Arabidopsis

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Cold temperatures trigger the expression of the CBF family of transcription factors, which in turn activate many downstream genes that confer chilling and freezing tolerance to plants. We report here the identification of ICE1 (inducer of CBF expression 1), an upstream transcription factor that regulates the transcription of CBF genes in the cold. An Arabidopsis ice1 mutant was isolated in a screen for mutations that impair cold-induced transcription of a CBF3 promoter-luciferase reporter gene. The ice1 mutation blocks the expression of CBF3 and decreases the expression of many genes downstream of CBFs, which leads to a significant reduction in plant chilling and freezing tolerance. ICE1 encodes a MYC-like bHLH transcriptional activator. ICE1 binds specifically to the MYC recognition sequences in the CBF3 promoter. ICE1 is expressed constitutively, and its overexpression in wild-type plants enhances the expression of the CBF regulon in the cold and improves freezing tolerance of the transgenic plants.

Keywords: Cold signaling; freezing tolerance; bHLH protein; CBF regulation; transcriptome

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Cold is an environmental factor that limits the geographical distribution and growing season of many plant species, and it often adversely affects crop quality and productivity [Thomashow 1999]. Most temperate plants can acquire tolerance to freezing temperatures by a prior exposure to low nonfreezing temperatures, a process known as cold acclimation [Guy 1990; Hughes and Dunn 1996; Browse and Xin 2001]. Plants of tropical and subtropical origins are sensitive to chilling temperatures (0°C–10°C) and are incapable of cold acclimation. Many studies have suggested that cold-regulated gene expression is critical in plants for both chilling tolerance [Gong et al. 2002; Hsieh et al. 2002] and cold acclimation [Knight et al. 1999; Thomashow 1999; Tahtiharju and Palva 2001]. Cold-responsive genes encode a diverse array of proteins such as enzymes involved in respiration and metabolism of carbohydrates, lipids, phenylpropanoids and antioxidants; molecular chaperones, antifreeze proteins, and others with a presumed function in tolerance to the dehydration caused by freezing [Guy 1990; Thomashow 1999; Mohapatra et al. 1989].

Many of the cold and dehydration responsive genes have in their promoters one or several copies of the DRE/CRT cis-element, which has the core sequence, CCGAC [Yamaguchi-Shinozaki and Shinozaki 1994; Stockinger et al. 1997]. A family of transcription factors known as CBFs or DREB1s binds to this element and activates transcription of the downstream cold and dehydration-responsive genes [Stockinger et al. 1997; Liu et al. 1998]. Interestingly, the CBF/DREB1 genes are themselves induced by low temperatures. This induction is transient and precedes that of the downstream genes with the DRE/CRT cis-element [Thomashow 1999]. Therefore, there is a transcriptional cascade leading to the expression of the DRE/CRT class of genes under cold stress. Ectopic expression of CBFs/DREB1s in plants turns on downstream cold-responsive genes even at warm temperatures and confers improved freezing tolerance [Jaglo-Ottosen et al. 1998; Liu et al. 1998].

Since CBF transcripts begin accumulating within 15 min of plants’ exposure to cold, Gilmour et al. [1998] proposed that there is a transcription factor already present in the cell at normal growth temperature that recognizes the CBF promoters and induces CBF expression upon exposure to cold stress. Gilmour et al. [1998] named the unknown activator[s] “ICE” (inducer of CBF expression) protein[s] and hypothesized that upon exposing a plant to cold, modification of either ICE or an associated protein would allow ICE to bind to CBF promoters and activate CBF transcription.

Genetic analysis in Arabidopsis plants expressing the
firefly luciferase reporter gene driven by the CRT/DRE element-containing RD29A promoter (Ishitani et al. 1997) has identified several mutants with deregulated cold-responsive gene expression. The hos1 [high expression of osmotically responsive genes] mutant shows an enhanced cold-induction of CBFs and their downstream cold responsive genes (Ishitani et al. 1998). HOS1 encodes a RING finger protein that is present in the cytoplasm at normal growth temperatures, but accumulates in the nucleus upon cold treatment. Since many RING-finger proteins are known to serve as ubiquitin E3 ligases, HOS1 has been proposed to function by targeting certain positive regulator(s) of CBFs for ubiquitination and degradation (Lee et al. 2001). The transcription of CBF genes is also under feedback repression by its own gene product or its downstream target gene products. This was revealed by studies on the los1 mutant that is defective in the translational elongation factor 2 gene (Guo et al. 2002). The los1 mutation blocks cold induction of genes with the CRT/DRE element, but causes superinduction of the CBF genes. It was shown that protein synthesis in los1 mutant plants is disrupted specifically in the cold. Therefore, cold-induced CBF transcripts cannot be translated to downstream gene products, and feedback repression cannot occur, leading to superinduction of CBF transcripts (Guo et al. 2002).

Another Arabidopsis mutation, los2, also impairs cold induction of CRT/DRE element-containing genes (Lee et al. 2002). LOS2 encodes a bifunctional enolase that can bind to the promoter of ZAT10, a zinc finger transcriptional repressor. ZAT10 expression is rapidly and transiently induced by cold in the wild type, and this induction is stronger and more sustained in the los2 mutant. Therefore, LOS2 may control the expression of delayed cold response genes via transcriptional repression of ZAT10 (Lee et al. 2002). The Arabidopsis LOS4 locus is involved in the accumulation of CBF transcripts under cold treatment (Gong et al. 2002). los4-1 mutant plants are sensitive to chilling stress, and the chilling sensitivity can be rescued by ectopic expression of CBF3 (Gong et al. 2002). LOS4 encodes a DEAD-box RNA helicase, suggesting that RNA metabolism may be involved in cold responses.

We carried out a genetic screen (Chinnusamy et al. 2002) to identify cold signaling components upstream of the CBF proteins. A cold-responsive bioluminescent Arabidopsis plant was engineered by expressing the firefly luciferase (LUC) coding sequence under the control of the CBF3 promoter. Homozygous CBF3–LUC plants were chemically mutagenized and mutants with altered cold-induced CBF3–LUC expression were isolated by luminescence imaging. Here we report on the ice1 mutant, which is impaired in the cold-induction of CBF3–LUC and is defective in cold acclimation. ICE1 encodes a MYC-like bHLH transcriptional activator that binds to the CBF3 promoter. Thus, ICE1 plays a key role in regulating cold-responsive gene expression and cold tolerance in Arabidopsis.

**Results**

**Identification of the ICE1 locus**

As noted above, Arabidopsis plants containing the CBF3–LUC transgene emitted bioluminescence in re-

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**Figure 1.** The ice1 mutation blocks the cold-induction of CBF3 and affects the expression of other cold-responsive genes. (A) Morphology (left) and CBF3–LUC luminescence images (right) of wild-type and ice1 seedlings. Luminescence images of the plants were collected after 12 h of cold (0°C) treatment. (B) Quantitation of the luminescence intensities of wild-type [solid circles] and ice1 [open circles] seedlings in response to different durations of cold treatment. (C) Transcript levels of CBFs and their downstream target genes in wild-type and ice1 plants in response to cold treatment. Seedlings were either not treated (0 h) or treated with cold (0°C) for the indicated durations [h]. The tubulin gene was used as a loading control. WT, wild type.
response to cold stress (Fig. 1A,B). The homozygous CBF3–LUC plants [herein referred to as wild type] were mutagenized by ethylmethane sulfoxonate, and the resulting M2 population was screened for mutants with aberrant bioluminescence responses under cold stress using a low light imaging system (Chinnusamy et al. 2002). Several mutants showing abnormal cold regulation of CBF3–LUC expression were recovered. One of these mutant lines, designated as ice1, is virtually blocked in CBF3–LUC expression in the cold [Fig. 1A,B]. In response to treatment at 0°C, wild-type plants showed strong luminescence, while the ice1 mutant showed very little induction of luminescence throughout the duration of cold treatment [Fig. 1A,B]. After 12 h of cold treatment, ice1 plants showed nearly 10 times less luminescence than that of wild-type plants, and are obviously defective in the cold regulation of CBF3–LUC expression [Fig. 1B].

The ice1 mutant plant was crossed with CBF3–LUC wild-type plants and the resulting F1 plants were examined for CBF3–LUC expression after 12 h of cold treatment at 0°C. As determined by luminescence imaging, all F1 plants showed reduced cold-induced CBF3–LUC expression similar to that of ice1. An F2 population from the selfed F1 segregated in an ~3:1 ratio between mutant and wild type (data not shown). These results show that ice1 is a dominant mutation in a single nuclear gene.

ice1 mutant plants are defective in cold-regulated gene expression

RNA blot analysis was carried out to analyze the effect of ice1 mutation on the transcript levels of endogenous CBFs and their target cold stress-responsive genes. Consistent with the imaging results, cold induction of the endogenous CBF3 gene was greatly impaired (almost abolished) in ice1 mutant plants [Fig. 1C]. Wild-type plants showed CBF3 induction after 1 h of cold stress and the expression peaked at 6 h. In contrast, CBF3 induction was almost abolished in ice1 plants [Fig. 1C]. While the CBF1 induction level in the ice1 mutant was lower than that of wild type at 1 and 3 h of cold stress, its induction level at 6 and 12 h was similar to that in the wild type. The CBF2 induction level was slightly lower in ice1 at 1 h of cold treatment, whereas at 6 and 12 h, the induction level was higher in the mutant [Fig. 1C]. We also examined the cold induction of the downstream target genes of CBFs. The expression levels of RD29A, COR15A, and COR47A under cold stress were lower in ice1 than in the

**Figure 2.** Morphology and freezing and chilling sensitivity of ice1 mutant plants. (A) Wild-type and ice1 seedlings in nutrient medium on agar under normal growth conditions. (B) Wild-type and ice1 plants in soil under normal growth conditions. (C) ice1 plants are defective in cold acclimation. Ten-day-old seedlings grown at 22°C were incubated for 4 d in light at 4°C before freezing treatment at −12°C. The picture was taken 3 d after the freezing treatment. (D) Comparison of survival rates after freezing treatments at the indicated temperatures. Open circles and open triangles represent wild-type and ice1 plants, respectively. (E) ice1 plants are sensitive to prolonged chilling treatment. After germination at 22°C, the plants were grown at 4°C for 6 wk. (F) Comparison of survival rates after 6 wk of chilling stress.
wild type, while the induction of KIN1 was lower in ice1 only after 48 h of cold stress (Fig. 1C).

Consistent with these RNA blot results, microarray analysis using Affymetrix near full genome genechips showed that out of 306 genes induced threefold or more in the wild type by a 6-h cold treatment, 217 are either not induced in the ice1 mutant or their induction is 50% or less of that in the wild type (Supplementary Tables 1A, 2). Thirty-two of these encode putative transcription factors, suggesting that ICE1 may control many cold-responsive regulons. For 87 of the 306 cold-induced genes, their induction levels in the wild type and ice1 differ by less than twofold (Supplementary Table 1B). Interestingly, two genes show higher levels of cold induction in the ice1 mutant (Supplementary Table 1C).

The ice1 mutation impairs chilling and freezing tolerance

At normal growth temperatures, ice1 and wild-type seedlings were similar in size (Fig. 2A). Although adult ice1 plants were smaller, they were not very different from the wild type in flowering time and fertility (Fig. 2B). Ten-day-old seedlings of ice1 and wild type grown on separate halves of the same agar plates were cold acclimated at 4°C for 4 d and then subjected to a freezing tolerance assay. The ice1 mutant was less freezing-tolerant than the wild type at all freezing temperatures [Fig. 2C,D]. Freezing at −10°C for 2 h killed about 50% of ice1 mutant plants, whereas <20% of wild-type plants were killed at this temperature [Fig. 2D]. When newly germinated (at 22°C) ice1 and wild-type seedlings were transferred to 4°C (with 30 ± 2 µmole quanta·m⁻²·s⁻¹ light), chilling injury became apparent in the mutant after 4 wk of cold treatment (Fig. 2E). After 6 wk of chilling stress, 100% of wild-type but only 20% of ice1 mutant plants survived (Fig. 2F).

Positional cloning of ICE1

To map the ice1 mutation, a homozygous ice1 mutant in the CBF3–LUC Columbia background was crossed to wild-type plants of the Ler ecotype. F1 plants from the cross were selfed to produce F2 seeds. Since the ice1 mutation is dominant, we selected from the segregating F2 population seedlings with the wild-type phenotype [based on plant size and morphology] for mapping. A total of 662 wild-type plants were selected and used for mapping with simple sequence length polymorphism and cleaved amplified polymorphic sequence markers [see Materials and Methods section for details], which initially placed ICE1 on the middle of chromosome 3, then narrowed its location to a 58-kb region on the MLJ15 and MDJ14 BAC clones. Candidate genes in this region were amplified from homozygous ice1 mutant plants and sequenced. The sequences were compared with the published sequence of Arabidopsis ecotype Columbia and a single G-to-A mutation in the hypothetical MLJ15.14 gene was found.

To confirm that MLJ15.14 is the ICE1 gene, the MLJ15.14 gene including 2583 bp upstream of the initiation codon and 615 bp downstream of the stop codon was cloned from ice1 mutant plants. This fragment was inserted into a binary vector and introduced into CBF3–LUC Columbia wild-type plants by Agrobacterium-mediated transformation. Transgenic plants were selected based on their hygromycin resistance, and cold-induced bioluminescence in the T2 lines was compared with that of the wild type. The MLJ15.14 gene from ice1 suppressed cold-induced luminescence from the wild-type plants [Fig. 3A,B] and reduced the plant height to that of ice1 mutant [data not shown], thus confirming that MLJ15.14 is ICE1.

ICE1 encodes a constitutively expressed and nuclear-localized MYC-like bHLH transcription factor

The open reading frame of ICE1 was determined by sequencing cDNAs obtained by reverse transcriptase PCR (RT–PCR). ICE1 is predicted to encode a protein of 494 amino acids, with an estimated molecular mass of 53.5 kD. Database searches revealed that ICE1 contains a MYC-like bHLH domain at its C-terminal half [Fig. 4A,B]. Over the entire length of the protein, ICE1 shows...
amino acid sequence similarity to an unknown protein of Arabidopsis [At1g12860]. The ice1 mutation changes Arg236, conserved in these two Arabidopsis proteins, to His. The bHLH domain of ICE1 shows high amino acid similarity to that of known MYC-related bHLH transcription factors (Fig. 4B). All MYC binding promoter elements contain the CA nucleotides that are contacted by a conserved glutamic acid in the bHLH zipper domain [Grandori et al. 2000]. This glutamic acid residue (Glu 312) is also conserved in the basic DNA binding domain of ICE1 [Fig. 4B]. The bHLH family of transcription factors is characterized by an acidic domain near the N terminus and a conserved bHLH DNA binding and dimerization domain near the C terminus [Purugganan and Wessler 1994]. All these features are present in ICE1 protein [Fig. 4A].

To analyze the expression pattern of ICE1 in different tissues, T2 lines of transgenic Arabidopsis plants expressing an ICE1 promoter-GUS transgene were analyzed. GUS expression was detected in roots, leaves, stem, and floral parts. Semiquantitative RT–PCR analysis also showed that ICE1 was expressed constitutively and the expression was stronger in leaves and stems than in other tissues [Fig. 5A,B]. RNA blot analysis showed that the ICE1 transcript was slightly up-regulated by cold, NaCl, and ABA, but not by dehydration [Fig. 5C].

To examine the subcellular localization of the ICE1 protein, ICE1 was fused in-frame to the C-terminal side of the green fluorescent protein (GFP) and expressed under control of the CaMV 35S promoter. Confocal imaging of GFP fluorescence in T2 transgenic plants showed that the GFP-ICE1 fusion protein is present in the nucleus under either warm [Fig. 5D] or cold temperatures [data not shown].

ICE1 binds to MYC recognition sites in the CBF3 promoter

ICE1 has a bHLH domain and its amino acid sequence in the basic region is highly conserved with other bHLH proteins [Fig. 4B], and therefore may recognize promoter elements similar to the DNA binding sites for known bHLH proteins. These proteins recognize DNA with the consensus sequence CANNNTG [Meshi and Iwabuchi 1995]. In the promoter region of CBF3, there are five potential MYC-recognition elements within a 1-kb region upstream of the transcription initiation site [Shinwari et al. 1998]. These possible MYC-recognition sites, designated MYC-1 through MYC-5, fall into four groups because MYC-3 and MYC-5 share the same consensus sequence, CATTTC [Fig. 6A]. Thus, MYC-3 was used to represent both MYC-3 and MYC-5. To determine whether ICE1 binds to these MYC-recognition sites in
the CBF3 promoter, we expressed and purified His–ICE1 fusion protein from E. coli. Four DNA fragments encompassing each possible MYC-recognition site were used for interaction with His–ICE1 in an electrophoresis mobility shift assay (EMSA).

Several complexes were observed when ICE1 was incubated with any of the four DNA fragments {MYC-1 through MYC-4}, indicating that ICE1 is able to bind to these sequences [Fig. 6B]. The MYC-2 fragment formed one major complex with ICE1, while the other DNA fragments formed several complexes with ICE1. These complexes were abolished by the addition of increasing amounts of cold competitors with the same sequences, but not by P1 or P2, which contains a putative MYB-recognition site and a nonrelated sequence, respectively [Fig. 6B]. This specificity of competition strengthens the hypothesis that the interaction between DNA and ICE1 requires the MYC-recognition sequences. When the MYC-2 fragment was used as a probe, the complex was most efficiently competed off by the cold MYC-2 competitor, suggesting that ICE1 has a higher affinity for the MYC-2 site than for the other sites [Fig. 6C]. The complex formed by ICE1 and the MYC-2 fragment was less affected by a mutated competitor than by the wild-type competitor [Fig. 6D]. Together, these results show that ICE1 interacts specifically with the MYC-recognition sites in the CBF3 promoter. The ice1 mutation does not appear to affect ICE1 interaction with the CBF3 promoter, because the Arg 236 to His mutant form of ICE1 was also able to bind to the MYC-2 probe [Fig. 6E].

ICE1 is a transcriptional activator that positively regulates CBF expression

Transient expression assays were carried out to determine whether ICE1 acts as a transcriptional activator or repressor. An effector plasmid was constructed by fusing ICE1 with the DNA binding domain of the yeast GAL4
transcriptional activator (GAL4–ICE1; Fig. 7A). When the wild-type GAL4–ICE1 and a GAL4-responsive reporter gene, GAL4–LUC, were delivered into Arabidopsis leaves by particle bombardment, the luciferase activity increased 20-fold relative to the control with or without an effector plasmid containing only the GAL4 DNA binding domain (Fig. 7B). The Arg 236 to His mutant form of GAL4–ICE1 also activated the GAL4-responsive transcription (Fig. 7B). These results suggest that ICE1 is a transcriptional activator, and that the ice1 mutation does not affect the function of the transcriptional activation domain.

A null allele of ice1 created by T-DNA insertion does not show any phenotypes of the dominant ice1 mutant [data not shown], suggesting that there is functional redundancy in the ICE1 gene family. We overexpressed ICE1 in wild-type Arabidopsis plants by using the strong constitutive super promoter. None of the overexpression
Lines showed any ice1 mutant phenotypes. RNA blot analysis showed that ICE1-overexpression did not activate CBF3 expression at warm temperatures. However, ICE1-overexpression enhanced the expression of the endogenous CBF3 gene as well as the CBF3–LUC reporter gene in the cold (Fig. 7C,D). Cold-induction of CBF2, RD29A, and COR15A was also enhanced in the Super-ICE1 transgenic plants (Fig. 7C). When the Super-ICE1 transgenic plants and wild-type control plants in the same agar plates were cold acclimated at 4°C for 5 d and then subjected to freezing treatment at −8°C for 4 h, the ICE1 overexpression transgenic seedlings showed a higher survival rate (75.9% ± 6.5%) than that of control plants (37.2% ± 12.6%; Fig. 7E). The ICE1 overexpression transgenic plants did not exhibit obvious growth or developmental abnormalities (data not shown). These results suggest that ICE1 is a positive regulator of CBF3, and that the dominant nature of ice1 is likely caused by a dominant negative effect of the mutation.

Discussion
Cold temperatures trigger the transcription of the CBF family of transcription factors, which in turn activate the transcription of genes containing the DRE/CRT promoter element [Thomashow 1999]. The CBF target genes presumably include some transcription factors [Fowler and Thomashow 2002]. Therefore, cold signaling for freezing tolerance requires a cascade of transcriptional regulations. In the present study, we have identified ICE1, a very upstream transcription factor of this cascade. Our results show that ICE1 is a positive regulator of CBF3 and has a critical role in cold acclimation. ICE1 encodes a MYC-like bHLH transcription factor. Five pu-

Figure 7. ICE1 is a transcriptional activator and its overexpression enhances the CBF regulon in the cold and improves freezing tolerance. (A) Schematic representation of the reporter and effector plasmids used in the transient expression assay. A GAL4-responsive reporter gene was used in this experiment. Nos, the terminator signal of the nopaline synthase gene; Ω, the translational enhancer of tobacco mosaic virus; GAL4 DB, the DNA-binding domain of the yeast transcription factor GAL4. (B) Relative luciferase activities after transfection with GAL4–LUC and 35S-GAL4–ICE1 or 35S-GAL4–ice1. To normalize values obtained after each transfection, a gene for luciferase from Renilla was used as an internal control. Luciferase activity is expressed in arbitrary units relative to the activity of Renilla luciferase [as described in Ohta et al. (2001)]. The values are averages of three bombardments, and error bars indicate standard deviations. (C) RNA blot analysis of ICE1 and cold-responsive gene expression in wild-type and ICE1 overexpressing transgenic (Super-ICE1) plants. Seedlings were either not treated (0 h) or treated with low temperature (0°C) for 3 or 6 h. Ethidium bromide stained RNA bands are shown as loading control. (D) CBF3–LUC expression (indicated as luminescence intensity) in wild-type and ICE1 overexpressing transgenic (Super-ICE1) plants. (E) Improved survival of ICE1 overexpressing transgenic (Super-ICE1) plants after a freezing treatment.
tative MYC recognition sequences are present in the CBF3 promoter, while CBF1 and CBF2 promoters each contain one such element [Shinwari et al. 1998]. This is consistent with the fact that CBF3 is more strongly affected by the ice1 mutation than are CBF1 or CBF2. DNA binding assays showed that ICE1 can specifically bind to the MYC recognition sequences on the CBF3 promoter but not to a putative MYB recognition sequence [Fig. 6]. The ice1 mutation abolishes CBF3 expression, and reduces the expression of CBF-target genes in the cold. Consistent with its role in cold-responsive gene regulation, ICE1 is important for chilling and freezing tolerance of Arabidopsis plants.

The ice1 mutation also affects the cold-induction of CBF1 and CBF2; their expression is slightly reduced early in the cold, but at later time points the expression is not reduced. Instead, the expression of CBF2 is actually enhanced in the ice1 mutant after 6 and 12 h of cold treatment. The expression of CBF genes is known to be repressed by their gene products or the products of their downstream target genes [Guo et al. 2002]. The correlation between the reduced CBF3 expression and enhanced CBF2 induction suggests that CBF3 may repress CBF2 expression. When the CBF2 gene is disrupted, CBF1 and CBF3 show more sustained induction in the cold [J. Salinas, pers. comm.], suggesting that CBF2 may repress the expression of CBF1 and CBF3. The potential negative regulation of each other among the CBF transcription factor genes may be important for ensuring that their expression is transient and tightly controlled.

The three CBF genes are generally presumed to be functionally redundant. Their individual contribution has not been examined by loss-of-function analysis. Even though the ice1 mutation only blocks the expression of CBF3, the downstream genes such as RD29A, COR15A, and COR47 are substantially affected. This suggests that CBF3 plays a critical role in the cold regulation of these genes. In comparison, the cold regulation of KIN1 is less affected by the ice1 mutation. Therefore, it is possible that the three CBF genes may each have their own set of preferred target genes.

ICE1 is expressed constitutively in all tissues [Fig. 5A,B], and is only slightly up-regulated by cold [Fig. 5C]. Consistent with what has been speculated for “ICE” proteins [Gilmour et al. 1998], cold-induced modification of the ICE1 protein or of a transcriptional cofactor appears to be necessary for ICE1 to activate the expression of CBFs. This is supported by our evidence because ICE1 is expressed constitutively and localized in the nucleus, but the CBF expression requires cold treatment; and transgenic lines constitutively overexpressing ICE1 do not show CBF3 expression at warm temperatures, but have a higher level of CBF3 expression at cold temperatures. The ability of transcription factors to activate gene transcription may be regulated by protein phosphorylation and dephosphorylation in the cytoplasm or in the nucleus [reviewed by Liu et al. 1999]. The ice1 mutation is very near potential serine phosphorylation residues [Ser 243 and Ser 245], and thus might affect the phosphorylation/dephosphorylation of ICE1.

It is known that MYC-related bHLH transcription factors require MYB cotranscription factors and/or WD-repeat containing factors for transcriptional activation of target genes [Spelt et al. 2000, Walker et al. 1999]. The promoters of CBFs contain MYC as well as potential MYB recognition sequences [Shinwari et al. 1998], suggesting that a MYB-related transcription factor may also be involved in the cold induction of CBFs. The ice1 mutation, which substitutes Arg 236 with His, may interfere with hetero-oligomer formation between ICE1 and an ICE1-like protein or a MYB-related cofactor. Alternatively, the putative dominant negative effect of ice1 could be a consequence of ice1 interference with potential ICE1 homo-oligomer formation, protein stability, nuclear localization, or cold-induced posttranslational modification of ICE1.

Materials and methods

Plant materials and mutant isolation

The CBF3 promoter, a region from 1126 to 100 bp upstream of the initiation codon, was obtained by PCR using the following primer pair: 5’-TCATGGATCCACCAATTGGTTAATGCATGATGG-3’ and 5’-GCTCAAGCTTTCTGTTCTAGTTCAGG3’. This promoter was placed in front of the firefly luciferase (LUC) coding sequence in a plant transformation vector [Ishitani et al. 1997]. Arabidopsis thaliana ecotype Columbia (with the glabrous1 mutation) was transformed with Agrobacterium tumefaciens containing this CBF3–LUC construct by the floral dipping method. Plants homozygous for the CBF3–LUC transgene were selected from the second generation after transformation. One such plant with a single copy of the CBF3–LUC transgene was chosen for subsequent experiments [hereafter referred to as wild type]. This wild-type plant did not show any bioluminescence when grown under normal growth conditions, but emitted bioluminescence when cold stress was imposed. The CBF3–LUC plant seeds were mutagenized with ethyl methanesulfonate (EMS). Seedlings of the M2 generation were used to screen for mutants defective in cold-regulated CBF3–LUC expression by luminescence imaging. Seven-day-old seedlings grown on 0.6% agar plates containing 3% sucrose and 1x Murashige and Skoog (MS) salts [RH Biosciences] were screened for deregulated luciferase expression in response to low temperature treatment at 0°C for 12 h, using a low-light video imaging system (Princeton Instruments). Luminescence intensities of individual seedlings were quantified with the WinView software provided by the camera manufacturer (Princeton Instruments; Chinnusamy et al. 2002).

Chilling and freezing tolerance assays

Chilling sensitivity of ice1 and wild-type plants were tested by exposing the seedlings immediately after radicle emergence. After 2 d of stratification at 4°C, mutant and wild-type seeds were germinated at 22°C on MS nutrient medium with 3% sucrose and 1.2% agar. Chilling stress was imposed by incubating the seedlings at 4°C ± 1°C with 30 ± 2 µmole quanta m⁻² s⁻¹ light. Freezing tolerance was assayed as described [Xin and Browse 1998]. Briefly, wild-type and ice1 seeds were sown on agar (0.9%) plates with Gamborg basal salts and 1.5% sucrose. After 2 d of stratification at 4°C, the plates were kept at 22°C under 50 ± 2 µmole quanta m⁻² s⁻¹ continuous light. Ten-day-old seed-
lings were cold acclimated at 4°C ± 1°C and 30 ± 2 μmole quanta, m⁻² · s⁻¹ light for 4 d. These plants on petri dishes were placed on ice in a freezing chamber [Percival Scientific] set to -1°C ± 0.1°C for 16 h. Ice chips were sprinkled on these plants before the chamber was programmed to cool at 1°C h⁻¹. Petri dishes of plants were removed after being frozen at desired temperatures for 2 h unless indicated otherwise, thawed at 4°C for 12 h in the dark, and then transferred to 22°C under 50±2 μmole quanta, m⁻² · s⁻¹ continuous light. Survival of the seedlings was scored visually after 2 d.

Gene expression analysis

For RNA analysis, 10-day-old seedlings of wild-type and ice1 plants grown on separate halves of the same MS agar plates were used. Total RNA extracted from control and stressed plants was analyzed by RNA blotting as described by Liu and Zhu [1997]. The RD29A gene-specific probe was from the 3′ noncoding region [Liu and Zhu 1997]. COR15A and COR47 cDNAs [Gilmour et al. 1992; Lin and Thomashow 1992] were kindly provided by M.F. Thomashow (Michigan State University). The CBF2 and CBF3 gene-specific probes were generated by PCR with the following primer pairs: CBF2-forward primer, 5′-GGGATCCGAGGAACATGACAG-3′; CBF2-reverse primer, 5′-CAGCAATACAGAGCC-3′. The probe for KIN1 (Kurkela and Franck 1990) was a 0.4-kb EcoRI fragment of the Arabidopsis EST clone YAP368T7. The β-tubulin gene was used as a loading control and was amplified by PCR with the following primer pairs: forward primer: 5′-GGGAACATGACAG-3′; reverse primer 5′-CTGGATCCTCAGATCATACCAG-3′.

For Affymetrix GeneChip array analysis, 20 µg of total RNA from the wild-type and ice1 seedlings with or without cold treatment (6 h under light) were extracted using the RNeasy Plant Mini Kit [Qiagen] and used to make biotin-labeled cRNA targets. The Affymetrix Arabidopsis ATH1 genome array GeneChips, which contain >22,500 probe sets representing ~24,000 genes, were used and hybridization, washing, and staining were carried out as directed in the manufacturer's manual. Microarray data were extracted from scanned GeneChip images and analyzed using MicroArray Suite version 5.0.1 [Affymetrix].

Mapping and cloning of the ICE1 locus

Genetic analysis of F₂ and F₃ progenies of the ice1 cross with wild type showed that ice1 is a dominant mutation. Hence, to clone ICE1, a homozygous ice1 plant was crossed with the Arabidopsis Landsberg erecta [Ler] ecotype and the F₂ progeny from self-pollinated F₁ were used to select mapping samples with the wild-type phenotype. Genomic DNA extracted from these seedlings was used for PCR-based mapping with simple sequence polymorphism markers or cleaved amplified polymorphic sequence markers. New SSLP mapping markers on F16J4, MTC11, MLJ15, MDH14, K17E12, and T32N15 BAC clones were developed based on insertion/deletions identified from the Ceon Arabidopsis polymorphism and Ler sequence collection [http://www.arabidopsis.org]. Genomic DNA corresponding to candidate genes was amplified by PCR from ice1 mutant and wild-type plants and sequenced to identify the ice1 mutation.

For ice1 mutant complementation, the MLJ15.14 gene, including 2583 bp upstream of the initiation codon and 615 bp downstream of the stop codon, was PCR-amplified by LA Taq polymerase (Takara) using ice1 mutant genomic DNA as template. The PCR primers used were as follows: forward primer: 5′-AGGGATCCGGACCGACCGTCAATTACATCGTTAAGT AG-3′; reverse primer: 5′-CGAATTCGCGACGGCACTAAC TATGCTCCTCTCTATCTC-3′. The resulting 5035-bp fragment was T-A cloned into the pCR2.1 TOPO vector [Invitrogen] and then subcloned into pCAMBIA1200 between the BamHI and EcoRI sites. This and all other constructs described here were completely sequenced to ensure that they did not contain PCR or cloning errors. The binary construct was then introduced into Agrobacterium strain GV3101 and transformed into CBF3-LUC Columbia wild-type plants. Hygromycin-resistant transgenic plants were selected and their T2 progenies were tested for CBF3-LUC expression in response to cold stress.

Analysis of ICE1 expression

The promoter region [2589 bp upstream from the initiation codon] of the ICE1 gene was PCR-amplified with the following primer pair: forward primer, 5′-AGGGATCCGGACCGACCGTCAATTACATCGTTAAGT-3′; reverse primer, 5′-CGAATTCGCGACGGCACTAAC TATGCTCCTCTCTATCTC-3′. The resulting 5035-bp fragment was T-A cloned into the pCR2.1 TOPO vector [Invitrogen] and then subcloned into pCAMBIA1200 between the BamHI and EcoRI sites. This and all other constructs described here were completely sequenced to ensure that they did not contain PCR or cloning errors. The binary construct was then introduced into Agrobacterium strain GV3101 and transformed into CBF3-LUC Columbia wild-type plants. Hygromycin-resistant transgenic plants were selected and their T2 progenies were tested for CBF3-LUC expression in response to cold stress.

Overtexpression of ICE1

The ICE1 cDNA was amplified from Arabidopsis (ecotype Columbia) RNA by RT–PCR using the following primers: a forward primer: 5′-GGGATCCGGACCGACCGTCAATTACATCGTTAAGT-3′ and a reverse primer 5′-GGGAACATGACAG-3′. The PCR product was digested with XhoI and KpnI, and cloned into the pBIB vector under control of the superpromoter, which consists of three copies of the octopine synthase upstream-activating sequence in front of the mannopine synthase promoter [Li et al. 2001]. Agrobacterium tumefaciens strain GV3101 containing this binary construct was used to transform Arabidopsis plants. Transformants were selected on MS medium containing hygromycin (30 mg/L).

Expression and localization of GFP–ICE1 fusion protein

The full-length ICE1 cDNA was obtained from wild-type plants by RT–PCR using the following primers: forward primer, 5′-AGGAATTCGCGACCGACCGTCAATTACATCGTTAAGT-3′; reverse primer, 5′-CTGGATCCGACCGACCGTCAATTACATCGTTAAGT-3′. The resulting PCR fragment was digested with EcoRI and BamHI and cloned into the binary vector pEGAD downstream from the CaMV 35S promoter. This
GFP–ICE1 construct was introduced into Agrobacterium strain GV3101 and transformed into wild-type Arabidopsis. T2 transgenic lines resistant to Basta (glufosinate) were selected and analyzed for GFP expression. To visualize the nucleus, root tissues were stained with propidium iodide (1 µg/mL). Green fluorescence (GFP expression) and red fluorescence (propidium iodide staining) analyses of transgenic plants were performed with a confocal laser-scanning microscope.

DNA binding assay

The wild-type and mutant ICE1 cDNAs were amplified by RT-PCR and inserted into NdeI and BamHI sites in the expression vector pET14b [Novagen]. Wild-type and mutant His–ICE1 fusion proteins were prepared from E. coli cells [BL21 DE3] according to the instruction manual of His-Bind Buffer Kit [Novagen]. The electrophoresis mobility shift assay [EMSA] was carried out as described [Hao et al. 1998]. The following double-stranded oligonucleotides listed in Figure 6A [MYC-1, MYC-2, MYC-3, MYC-4, and MYC-5] were used as probes and competitors in EMSAs. Nucleotide sequences P1 [−949 to −930] and P2 [−909 to −890] were also used as competitors. P1 contains a putative MYB-recognition site. P2 does not contain any typical cis-elements. DNA probes were end-labeled with [γ-32P]dCTP using the Klenow fragment and purified through a Sephadex G-50 column. The labeled probes [ca 0.02 pmole] were incubated for 20 min at room temperature with 2.3 µg of purified His–ICE1 fusion protein in 1× binding buffer (Hao et al. 1998) supplemented with 20 pmole poly(dI-dC). The resulting DNA–protein complexes were resolved by electrophoresis on a 6% polyacrylamide gel in 0.5× TBE buffer and visualized by autoradiography. For competition experiments, unlabeled competitors were incubated with the His–ICE1 fusion protein on ice for 30 min prior to the addition of labeled probes.

Transient expression assay

The wild-type [ice1] cDNAs and mutant [ice1] cDNAs were amplified by RT-PCR, digested with SalI and inserted into SalI and SalI sites of the plant expression vector 35S-GAL4 DB [Ohta et al. 2000]. The plasmid DNA of the resulting effector, GAL4–ICE1, and a GAL4 responsive reporter, GALA–LUC [Ohta et al. 2000] were delivered into Arabidopsis leaves using particle bombardment [Ohta et al. 2001].

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