Genetic and Molecular Analyses of Natural Variation Indicate CBF2 as a Candidate Gene for Underlying a Freezing Tolerance Quantitative Trait Locus in Arabidopsis

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Natural variation for freezing tolerance is a major component of adaptation and geographic distribution of plant species. However, little is known about the genes and molecular mechanisms that determine its naturally occurring diversity. We have analyzed the intraspecific freezing tolerance variation existent between two geographically distant accessions of Arabidopsis (Arabidopsis thaliana), Cape Verde Islands (Cvi) and Landsberg erecta (Ler). They differed in their freezing tolerance before and after cold acclimation, as well as in the cold acclimation response in relation to photoperiod conditions. Using a quantitative genetic approach, we found that freezing tolerance differences after cold acclimation were determined by seven quantitative trait loci (QTL), named FREEZING TOLERANCE QTL 1 (FTQ1) to FTQ7. FTQ4 was the QTL with the largest effect detected in two photoperiod conditions, while five other FTQ loci behaved as photoperiod dependent. FTQ4 colocalized with the tandem repeated genes C-REPEAT BINDING FACTOR 1 (CBF1), CBF2, and CBF3, which encode transcriptional activators involved in the cold acclimation response. The low freezing tolerance of FTQ4-Cvi alleles was associated with a deletion of the promoter region of Cvi CBF2, and with low RNA expression of CBF2 and of several CBF target genes. Genetic complementation of FTQ4-Cvi plants with a CBF2-Ler transgene suggests that such CBF2 allelic variation is the cause of CBF2 misexpression and the molecular basis of FTQ4.

Plants are continuously exposed to a wide range of adverse environmental conditions that fluctuate along their life cycles. To survive, they have developed different tolerance strategies that protect them against abiotic stresses. Among such stress conditions, freezing temperature is one of the most relevant factors limiting the distribution of plant species (Weiser, 1970; Levitt, 1980). Due to its basic and applied interest, freezing tolerance has been studied in all sorts of plants, from annual to woody species. Freezing tolerance is acquired as a result of a complex stress response involving multiple physiological, biochemical, and molecular changes (Weiser, 1970; Levitt, 1980). This response is triggered or increased by environmental factors that anticipate the freezing temperature, thus regulating the proper timing of freezing tolerance acquisition. Most plant species from temperate regions increase freezing tolerance in response to low nonfreezing temperatures, a process called cold acclimation. Additionally, short-day (SD) photoperiods enhance the tolerance of many species from temperate regions (Fowler et al., 2001; Welling et al., 2002; Karlson et al., 2003).

Our understanding of the molecular mechanisms of cold acclimation has dramatically improved in the past years, mainly due to the study of the model plant Arabidopsis (Arabidopsis thaliana; Thomashow, 1999; Salinas, 2002). It has been found that most physiological changes during cold acclimation are associated with changes in gene expression (Thomashow, 1999; Maruyama et al., 2004). Numerous cold-induced genes have been identified that encode proteins involved either in the molecular mechanisms of tolerance or in signal transduction and regulation (Maruyama et al., 2004). Furthermore, a small gene family of AP2-domain transcriptional regulators, known as C-repeat.
(CRT)-binding factor/dehydration-responsive element (DRE)-binding factor (CBF/DREB1; Stockinger et al., 1997; Liu et al., 1998), was identified by its binding capacity to the CRT or DRE regulatory sequences (Thomashow, 1999). Expression of the CBF1/DREB1 genes (CBF1/DREB1B, CBF3/DREB1A, and CBF2/DREB1C; hereafter referred to by their CBF names; Gilmour et al., 1998) is transiently induced by low temperature and precedes the expression of the CBF target genes whose promoters contain the CRT/DRE element (Stockinger et al., 1997; Gilmour et al., 1998; Liu et al., 1998; Medina et al., 1999; Maruyama et al., 2004). Thus, a transcriptional cascade leads to the expression of the CTR/DRE class of genes, which act in concert to increase freezing tolerance. Overexpression of CBF1, CBF2, and CBF3 increases freezing tolerance in acclimated and nonacclimated plants, suggesting that they are sufficient to trigger the cold acclimation response (Jaglo-Ottosen et al., 1998; Liu et al., 1998; Gilmour et al., 2004). On the other hand, an insertion mutant of the CBF2 gene shows higher freezing tolerance and overexpression of CBF1 and CBF3 (Novillo et al., 2004), indicating that CBF2 negatively regulates CBF1 and CBF3 expression.

Naturally occurring variation for freezing tolerance has been found not only among species occupying different environments but also within species with broad geographic distribution (Sackville Hamilton et al., 2002; Andaya and Mackill, 2003; Karlson et al., 2003; Vágújfalvi et al., 2003; Tsarouhas et al., 2004). Intraspecific differences have often been associated with environmental parameters from the locations where the populations evolved, such as winter temperature and photoperiod (Sackville Hamilton et al., 2002; Karlson et al., 2003). Thus, intraspecific genetic variation is, presumably, a fundamental component determining adaptation to different environments. However, little is known about the molecular basis of the natural variation for freezing tolerance. Essentially, a number of studies have just initiated the genetic dissection of these differences in crop and forestry species, showing that it is a complex quantitative trait controlled by multiple quantitative trait loci (QTLs; Andaya and Mackill, 2003; Vágújfalvi et al., 2003; Francia et al., 2004; Tsarouhas et al., 2004).

To further understand the molecular basis of the naturally occurring variation for freezing tolerance, we have exploited the intraspecific differences existing for this trait in the model plant Arabidopsis, an annual wild species with a wide geographic distribution (Cook et al., 2004; Klotke et al., 2004; Koornneef et al., 2004; Rohde et al., 2004). We found that the Cape Verde Islands (Cvi) and Landsberg erecta (Ler) accessions differ in their freezing tolerance before and after cold acclimation and in their freezing tolerance response under different photoperiods. Using a QTL mapping approach, we have determined the genetic basis of this variation. Furthermore, we have pursued the molecular basis of the largest effect QTL, showing that allelic variation at the CBF2 gene might underlie this locus.

RESULTS

Ler and Cvi Differ in Freezing Tolerance

To identify Arabidopsis strains that differ in their natural freezing tolerance, we chose accessions Ler and Cvi because they originally came from very different geographic areas, Northern Europe and the subtropical Cape Verde Islands, respectively. Both accessions were grown under a long-day (LD) photoperiod, frozen at different temperatures, and the lethal temperature for 50% survival (LT50) estimated from fitted response curves (Fig. 1A). Cvi plants directly exposed to freezing temperatures showed a LT50 of −4.8°C, while Ler had a value of −6.3°C. In addition, we evaluated their freezing tolerance after cold acclimation, with Cvi and Ler plants displaying, respectively, LT50 values of −7°C and −9.2°C. Therefore, Cvi plants show a lower freezing tolerance than Ler, before and after cold acclimation. The Ler/Cvi freezing tolerance difference was maximal at a temperature of −8°C provided after cold acclimation, where 90% of Ler plants survived and about 90% of Cvi plants died (Fig. 1B). To determine the overall dominance of the trait, we evaluated the freezing tolerance of F1 (Ler × Cvi)
Natural Variation for Freezing Tolerance

To map the loci causing the freezing tolerance differences observed between Ler and Cvi after cold acclimation, we characterized a Ler/Cvi recombinant inbred line (RIL) population (Alonso-Blanco et al., 1998b). The freezing tolerance of 132 RILs was estimated under a LD photoperiod at the −8°C discriminatory temperature provided after cold acclimation. In addition, the freezing tolerance of a subset of 53 RILs was also evaluated in a similar assay performed under a SD photoperiod (Supplemental Fig. 1). Significant genotype (RIL) by environment (photoperiod) interaction was detected ($P < 0.001$), in agreement with the low correlation observed between tolerances under both photoperiods ($r = 0.28$). These data were used to map QTLs under LD and SD photoperiods (Fig. 2; Supplemental Table I), identifying five and four QTLs, respectively, whose total additive effects accounted for 46% and 58% of the phenotypic variance. A genome-wide search for two-way interactions did not detect any significant interaction among those QTLs or among any other pair of genomic regions ($P > 0.05$). Conservatively, we found a minimum number of seven different loci on chromosomes 1, 4, and 5, which we named as FREEZING TOLERANCE QTL 1 (FTQ1) to FTQ7. The relative effect of the FTQ loci varied from small (<5%) to very large (>15%). In all of them, the Ler allele increased freezing tolerance compared to Cvi, in agreement with the parental values. Only two QTLs, FTQ4 and FTQ6, were detected in both photoperiod conditions, suggesting that there is a limited common genetic component determining the variation in both photoperiods.

The CBF Cluster as a Candidate for FTQ4

Since FTQ4 was the strongest effect QTL detected under both photoperiods, we pursued its molecular characterization by a candidate gene approach. Analysis of the chromosome 4 genomic sequence (Arabidopsis Genome Initiative, 2000) detected the cluster of CBF1, CBF3, and CBF2 genes within the FTQ4 support interval. Location of these genes in the middle of the FTQ4 interval was confirmed by mapping of a CBF2 PCR marker in a subset of 33 Ler/Cvi RILs, including those with recombination events in the FTQ4 confidence interval (Fig. 2). To explore whether the CBF genes might underlie FTQ4, we analyzed their cold-induced expression in both parental lines and in the commonly used Columbia (Col) laboratory strain, which shows an overall freezing tolerance similar to Ler (Rohde et al., 2004; Fig. 3A). RNA expression analysis of CBF genes confirmed their cold induction in the three accessions, but there were considerable quantitative differences among accessions for the amount and timing of expression. Col plants displayed maximal expression of the three CBF genes after 2 h at 4°C and their expression was reduced following 4 h of cold treatment. In contrast, Ler plants showed a higher expression of CBF2 and CBF3 than Col after 1 h of cold treatment, indicating a faster induction. In addition, abundant expression was still detected after 4 h at 4°C, suggesting a slower reduction of expression in Ler than Col. The Cvi expression pattern of the CBF genes was distinct, with two main differences being detected with respect to Ler. First, the expression of CBF2 was greatly reduced in Cvi, showing a very limited maximal induction after 1 h at 4°C. Second, Cvi plants exhibit a slightly higher expression of CBF1 and CBF3 after 1 or 2 h of exposure to cold.

We also analyzed the expression of cold-induced genes that are activated by the CBF transcription regulators (Fig. 3B). The CBF target genes LTI78, COR47, and KIN1 exhibited much lower cold-induced expression in Cvi than in Ler, suggesting that gene expression regulated by the CBF genes was reduced in Cvi compared to Ler. Therefore, the FTQ4 freezing tolerance effect correlated with the expression of the CBF2 and CBF target genes, supporting a causal relationship between FTQ4 and the CBF cluster.

To find DNA polymorphisms in the CBF genes that could underlie FTQ4, we sequenced the Cvi genomic region containing the CBF cluster and compared it to available Ler and Col sequences (Fig. 4). A total of 83 polymorphisms were found among the three accessions in the 8.7-kb sequence. Ler and Cvi differed in 62 polymorphisms, while Ler and Col differed only in 33. Two relevant aspects were found when analyzing the 62 Ler-Cvi polymorphisms. First, Cvi carried a deletion of 1,630 bp in the promoter region of the CBF2 gene, located 160 bp upstream from the predicted transcription start. This polymorphism reduces the size of the CBF3-CBF2 intergenic region to 378 bp and determines a minimum CBF2 promoter. Second, the remaining 61 polymorphisms were not evenly distributed among the three CBF genes, CBF3 showing much more DNA allelic variation than CBF1 and CBF2. This was especially evident when comparing the promoter regions, since the first kilobase located 5‘ from the CBF3 start codon contains 23 polymorphisms, while the equivalent regions of the CBF1 and CBF2 genes carry only seven and three polymorphisms, respectively (Fig. 4). In addition, the CBF3 coding sequence contains more synonymous and replacement polymorphisms than the coding sequences of CBF1 and CBF2. Ler and Cvi differ in three-, two-, and three-amino acid substitutions for CBF1, CBF2, and CBF3, respectively. The Pro49 to Thr49 CBF2 change affects the first amino acid of the AP2 domain, whereas the remaining replacements
do not lead to meaningful changes in potential nuclear localization signals, phosphorylation sites, or protein acidic regions. Interestingly, the Cvi allele of CBF3 is Cvi specific, since no CBF3 polymorphism was found between Ler and Col.

A Ler CBF2 Transgene Complements the FTQ4-Cvi Allele

To further evaluate the CBF genes as candidates for FTQ4, we tested whether expression of a CBF2 gene from Ler complements the low freezing tolerance of lines carrying FTQ4-Cvi alleles. To this end, we isolated a binary cosmid clone carrying a Ler genomic insert that contains the complete coding sequence of CBF2 with 275 bp of its 5′ sequence from the start codon, and six other predicted open reading frames located 3′ downstream to CBF2 (see “Materials and Methods”). This genomic clone was used to generate transgenic plants in three different homozygous FTQ4-Cvi genetic backgrounds, Cvi, RIL42, and RIL44, as well as in the Ler parental background. These RILs were selected as carrying Cvi alleles at FTQ4 and Ler alleles at FTQ6 and FTQ7, which were the next largest effect QTLs detected under a LD photoperiod. RIL42 also carries Ler alleles at FTQ3.

To be able to test phenotypic complementation with this clone, we first determined the pattern of expression of the CBF2-Ler transgene. Several transgenic lines were analyzed by RNA hybridization of a CBF2 probe, before and after 2 h of cold treatment at 4°C (Fig. 5A). Unexpectedly, all tested transgenic lines showed considerably higher CBF2 expression before the cold treatment, which indicated that the CBF2-Ler transgene was over-expressed. However, a similar, strong cold-induced increment of CBF2 expression was also observed in these lines, indicating that the CBF2-Ler transgene responded to cold despite its small promoter region. The

Figure 2. QTL likelihood maps for freezing tolerance in the Ler-Cvi RIL population grown under two photoperiod conditions. Genetic maps of the Arabidopsis linkage groups are shown in the abscissa and LOD scores in the ordinate. Chromosome numbers are indicated in the top right corner of each image. The LOD threshold used for QTL detection is shown as a hatched horizontal gray line and the 2-LOD support intervals of the detected QTL are depicted as thick lines on the genetic maps. Continuous or hatched LOD profiles and 2-LOD intervals correspond to QTL mapping under LD or SD photoperiods, respectively. For each QTL, its name, the percentage of phenotypic variance explained, and its allele additive effect are shown. Allele effects are given in survival percentage units, positive values indicating that Ler genotypes show higher freezing tolerance than Cvi.

Figure 3. Expression of cold-induced genes in Ler, Cvi, and Col. A, RNA-blot hybridizations of CBF1, CBF2, and CBF3 in plants exposed to 4°C for 0, 1, 2, or 4 h. Ethidium bromide staining of the ribosomal RNA (rRNA) is shown as a loading control. B, RNA-blot hybridizations of CBF target genes in Ler and Cvi control plants (0 h) and plants exposed to 4°C for 24 h. Hybridization of a RBP4 probe is shown as a loading control.
molecular cause of the higher basal expression and increased cold response of this \textit{CBF2-Ler} transgene remains unknown, but since this behavior is independent of the genetic background, it seems mostly determined by the construct and not by the transgene positional effects. This higher basal expression of the \textit{CBF2-Ler} transgene could result from the lack of upstream promoter elements (Zarka et al., 2003) that could negatively regulate \textit{CBF2}. In addition, due to the short promoter region, the expression of the \textit{CBF2-Ler} transgene might be enhanced by the cauliflower mosaic virus 35S promoter that activates the \textit{nptII} reporter gene located 5' to \textit{CBF2} or by other sequences present in the cosmid vector.

The freezing tolerance of three to four independent transgenic lines homozygous for the transgenes was tested in a similar assay to that performed for QTL mapping under LD photoperiod conditions (Fig. 5B). All \textit{FTQ4-Cvi} transgenic lines showed a very significant increase of freezing tolerance, on average exhibiting 49% higher survival to the \(-8^\circ\text{C}\) freezing temperature than the untransformed controls. The observed increase was rather similar in the three \textit{FTQ4-Cvi} genetic backgrounds. In contrast, a much smaller and not significant increase was obtained in the transgenic lines in the \textit{Ler} genetic background. Thus, the observed freezing tolerance effect, which is presumably produced by the \textit{CBF2-Ler} transgene, partly depends

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Figure 4. DNA sequence comparison of the genomic regions containing \textit{CBF1}, \textit{CBF2}, and \textit{CBF3} genes from \textit{Ler}, \textit{Cvi}, and \textit{Col}. Genomic organization of the \textit{CBF} cluster is shown in the top part. Single-nucleotide substitutions are depicted as vertical bars, different colors denoting allele compositions (indicated in the bottom left box). Indels are depicted as vertical arrows with similar color codes. Thirteen indels affect single nucleotides, one involves two nucleotides, and another five nucleotides. A large \textit{Ler-Cvi} deletion (Del) is represented as a yellow color box. Asterisks (*) indicate amino acid changes. A summary of the number of polymorphisms is presented in the bottom left box. \textit{Ler-Col} polymorphisms in the 1.6-kb genomic deletion of \textit{Cvi} are not considered and are depicted in black. Numbers in the top part correspond to the \textit{Ler-Cvi} polymorphisms in the 0.6-kb coding regions of the \textit{CBF} genes and in the first kilobase 5' upstream from the start codons. GenBank accession numbers of \textit{Cvi}, \textit{Ler}, and \textit{Col} sequences are AY667247, AF076155, and AL022197, respectively.

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Figure 5. Expression of a \textit{CBF2} transgene and freezing tolerance of transgenic lines. A, Expression of \textit{CBF2} in \textit{Cvi}, \textit{RIL44}, and \textit{Ler} untransformed plants and in transgenic lines containing the \textit{Ler CBF2} transgene. Expression was analyzed in control plants not exposed to cold (0) and in plants of the same line exposed to 4°C during 2 h (2). The ribosomal RNA (rRNA) stained with ethidium bromide is shown as a loading control. B, Freezing tolerance after cold acclimation under a LD photoperiod of transgenic lines overexpressing a \textit{Ler CBF2} gene. Dark gray color bars depict transgenic lines, and light gray bars represent untransformed controls. Bars correspond to mean ± se of each transgenic line derived from four replicates. Numbers in the top part of the images show the mean ± se of the various transgenic lines analyzed for each background. T2 Cvi, T2 RIL42, T2 RIL44, and T2 Ler denote different independent T2 transgenic homozygous lines in the corresponding genetic backgrounds.
on the genetic background. However, Ler alleles at other QTLs than FTQ4 seem unnecessary for this 
CBF2-mediated tolerance. We concluded that the highly expressed CBF2-Ler transgene complemented 
the low freezing tolerance of FTQ4-Cvi alleles. These results suggest that Cvi is not defective in any trans-
regulator necessary for the cold induction of CBF2 expression or in any essential downstream element 
mediating CBF2 freezing tolerance.

DISCUSSION

We have performed a genetic and molecular analysis of natural variation for freezing tolerance in two Arabi-
dopsis accessions, Ler and Cvi, originating from very 
different geographic areas. Both accessions differ con-
siderably in their basal freezing tolerance and in their 
aquired freezing tolerance after cold acclimation. In 
addition, Ler and Cvi differ in the cold acclimation re-
sponse in relation to photoperiod conditions. Using a 
QTL mapping approach, we have shown that the 
variation in freezing tolerance after cold acclimation is 
a multigenic trait determined by at least seven FTQ loci. 
Comparison of the QTLs identified in plants grown 
under LD and SD photoperiods reveals that photope-
riod is an important environmental factor affecting 
freezing tolerance in Arabidopsis. Different photope-
riods seem to affect the phenotypic expression of 
different QTLs, since three FTQ loci were detected 
only under LD while two others were only found under 
SD. Testing the adaptive relevance of these differential 
freezing tolerances and photoperiod responses awaits 
a detailed study of the genetic variation present in large 
collections of Arabidopsis wild accessions.

The Ler/Cvi RIL population has been previously 
studied for flowering time in relation to the same 
environmental factors, with Ler and Cvi differing in 
the flowering response to photoperiod and cold treat-
ments (called vernalization; Alonso-Blanco et al., 
1998a). Allelic variation at the blue-light photoreceptor 
gene CRY2 accounted for the different flowering pho-
toperiod responses of these accessions (El-Assal et al., 
2001). However, although CRY2 is genetically linked to 
the photoperiod-dependent locus FTQ1, its map position 
suggests that CRY2 does not affect freezing toler-
ance. In addition, we cannot ignore that PhyA could 
mediate the photoperiodic regulation of freezing to-
erance in Arabidopsis, as shown for hybrid aspen 
(Welling et al., 2002). Supporting this hypothesis, PhyA 
is colocating with FTQ1, and this photoreceptor has 
been shown to regulate other Arabidopsis photope-
riod responses (Yanovsky and Kay, 2002). Furthermore, 
FTQ1 colocalizes with the ESPRESSO locus, which affects 
the circadian system and segregates in the Ler-Cvi RIL 
population (Swarup et al., 1999). Thus, FTQ1 might 
also be involved in the circadian regulation of CBF 
expression and/or freezing tolerance (Fowler et al., 
2005). Alternatively, FTQ1 colocalizes with the dehydrin 
genes COR47 and ERD10 as well (Maruyama et al., 
2004). Differential dehydrin expression has been cor-
related with natural variation for freezing tolerance in 
Arabidopsis (this work) and other species (Karlson et al., 
2003), and a dehydrin gene has been pointed to as 
the genetic cause of chilling tolerance variation in 
cowpea (Ismail et al., 1999). However, although these 
Arabidopsis genes are CBF targets (Maruyama et al., 
2004), further analyses will reveal the effect of their 
allelic variation on freezing tolerance.

Two out of three QTLs that affect the vernalization 
response of the Ler-Cvi population, FLG and FLH, 
overlapped with FTQ5 and FTQ7, suggesting that they 
might affect cold perception and transduction. A sim-
ilar role has been speculated for the Triticaceae VRN 
loci (Vágújfalvi et al., 2003; Francia et al., 2004) and 
indicated for the Arabidopsis HOS1 and FVE genes 
(Lee et al., 2001; Kim et al., 2004).

Finally, FTQ2 overlaps with a major QTL, explaining 
the low raffinose and stachyose seed content of Cvi 
compared to Ler (Bentsink et al., 2000). These sugars 
function as osmoprotectants (Taiji et al., 2002), and 
variation in raffinose content has been correlated with 
natural variation for freezing tolerance between Col 
and C24 accessions (Klotke et al., 2004). Thus, we hy-
pothesize that FTQ2 might be one of the genes en-
coding a raffinose synthase or a galactinol synthase 
that were previously mapped within the oligosaccha-ide QTL interval (Bentsink et al., 2000).

We have used a candidate gene approach to identify 
the molecular basis of the largest effect QTL, FTQ4. 
This locus is closely linked to a complex locus con-
taining a tandem repeat of three highly similar CBF 
genes. Presumably, this cluster originated by two con-
secutive duplication events of an ancestral gene and 
subsequent divergence by single-nucleotide mutations 
(Medina et al., 1999). The CBF genes seem to play a 
central role in cold acclimation (Stockinger et al., 1997; 
Gilmour et al., 1998; Liu et al., 1998; Medina et al., 1999), 
and the observed allelic variation in all three genes 
might contribute to the FTQ4 effect. However, our data 
strongly suggest that allelic variation at CBF2 is un-
derlying FTQ4. The low freezing tolerance of Cvi 
and of the FTQ4-Cvi allele correlated with low cold-
induced expression of CBF2 and of several CBF target 
genes, in agreement with a comparison of Cvi and 
Wassilewskija-2 accessions (Cook et al., 2004). This 
suggested two main alternative genetic scenarios for 
FTQ4: Either the allelic variation at FTQ4 affected a 
trans-regulator of CBF2 expression located within the 
FTQ4 support interval, or FTQ4 actually corresponded 
to the structural CBF2 gene or its cis-regulatory se-
quences. Analysis of Cvi and FTQ4-Cvi transgenic lines 
carrying a highly expressed CBF2-Ler transgene sup-
ports that Cvi is not defective in any trans-regulator 
involved in the cold induction of CBF2, since these 
lines show strong cold-induced expression of CBF2. In 
addition, genetic complementation of the low freezing 
tolerance of FTQ4-Cvi genotypes with this transgene 
indicates that Cvi is not defective in any essential 
downstream regulatory element participating in the
CBF2-mediated freezing tolerance. Taken together, our results suggest that the 1.6-kb Cvi deletion is likely to be the functional polymorphism that affects CBF2 expression, an activation regulatory element being probably absent in Cvi. Thus, Cvi probably carries a CBF2 dysfunctional allele that strongly reduces its cold-induced expression, in agreement with the overall dominance of the higher Ler freezing tolerance. It has been previously shown that the CBF2 promoter contains two regulatory elements called induction of CBF expression region 1 (ICER1) and ICER2 (Zarka et al., 2003). Cvi lacks the ICER1 sequence located at position $-190$ bp in CBF2 promoter and probably other regulatory elements, which might be the cause of the low cold induction. Nevertheless, we cannot ignore that another closely linked gene might underlie FTQ4. Furthermore, it is also possible that the existing allelic variation at CBF1 and, especially, at CBF3, could contribute to the effects of FTQ4, as suggested by the large amount of CBF3 molecular polymorphisms found. This potential FTQ4 complexity is somehow supported by current molecular models on the function of the CBF cluster in cold acclimation, since the three CBF genes do not operate independently (Novillo et al., 2004).

Recently, an insect resistance QTL has been shown to involve a tandem repeat of two methylthioalkylmalate synthase genes (Kroymann et al., 2003). The analysis of genetic variation for the methylthioalkylmalate and CBF genes point to the complexity of the natural variation provided by clusters of gene families, 17% of the Arabidopsis genes belonging to this class (Arabidopsis Genome Initiative, 2000). First, several genes might contribute to a single QTL and significant genetic interactions among the various clustered genes might also be involved. Second, as elegantly shown by Kroymann et al. (2003), gene conversion between the various tandem repeated genes provides an additional mechanism to generate genetic variation. Detailed analysis of the molecular variation present in the CBF genes in other Arabidopsis wild accessions will help in understanding the relevance of these genes in intraspecific freezing tolerance variation and the evolutionary dynamics of this complex locus. The CBF-mediated pathway has also been found in Triticaceae and Brassica species, indicating a conserved CBF function in freezing tolerance among species (Jaglo et al., 2001). Such CBF-like genes have been proposed as candidates for freezing tolerance QTLs in barley and wheat (Vágújfalvi et al., 2003; Francia et al., 2004). Further molecular analyses of CBF genes in these and other species will reveal whether they have a conserved role across species as major genetic determinants of intraspecific variation for freezing tolerance.

**MATERIALS AND METHODS**

**Plant Materials**

Arabidopsis (Arabidopsis thaliana) accessions Col, Ler, and Cvi and 132 RILs derived from crosses between Ler and Cvi were analyzed (Alonso-Blanco et al., 1998a).

**Growth Conditions and Freezing Tolerance Assays**

Plants were grown in pots with soil and vermiculite at 3:1 proportion in 20°C growth chambers illuminated with cool-white fluorescent lamps. The LD photoperiod was 16 h light/8 h darkness, while the SD photoperiod was 10 h light/14 h darkness. Cold acclimation was supplied by growing 2-week-old plants at 4°C for 7 d under the appropriate photoperiod. Freezing treatments were provided in darkness by exposing 3-week-old plants to the corresponding freezing temperature during 6 h, after a temperature touch-down cycle consisting of 30 min at 4°C and a subsequent temperature lowering at a rate of 2°C h. Thereafter, temperature was increased at a similar rate to 4°C, and plants were thawed for 5 h in darkness before being returned to the original growth conditions.

Freezing tolerance was recorded as the percentage of plants that survive to the corresponding freezing temperature. For that, to 25 plants of each genotype were grown in an 80-ml pot and treated as described above. The number of surviving plants was visually scored 2 weeks after the freezing treatment. To evaluate the RIL population, two to four replicate pots per line were grown in a randomized incomplete block design, and the average tolerance per RIL was calculated. The various transgenic lines developed in this work were evaluated by growing four pots per genotype in a similar, randomized, incomplete block design.

**QTL and Other Statistical Analyses**

The mean RIL freezing tolerance was transformed by the angular transformation ($\arcsin\sqrt{y}$). These data were used to map QTLs on a set of 99 markers covering the Arabidopsis genetic map (Alonso-Blanco et al., 1998a). MapQTl 4.0 software (Van Ooijen, 2000; Kyazma B.V.) was used to apply interval mapping and multiple QTL model mapping methods as described in its reference manual (http://www.mapqtl.nl). A logarithm of the odds (LOD) threshold value of 2.6 corresponding to a genome-wide significance $\alpha = 0.05$ was used for QTL detection. This was estimated with the permutation test implemented in MapQTl, using 10,000 permutations. Two LOD support intervals were established as $\pm 95\%$ QTL confidence intervals (Van Ooijen, 1992). The additive allele effect, the percentage of variance explained by each QTL, and the total variance explained by all the QTLs were obtained from the multiple QTL model. The QTL additive allele effect corresponds to one-half the differences between the estimated means of the two RIL genotypic groups.

Two-way interactions were searched using EPISTAT (Chase et al., 1997) with log-likelihood ratio thresholds corresponding to a significance of $P < 0.0005$. Fifty thousand trials were used in Monte Carlo simulations performed with EPISTAT to establish the statistical significance. Results shown are based on transformed data, but a similar outcome was obtained when using the original percentage data. Other statistical comparisons were performed with the statistical package SPSS 12.

**Sequencing of the CBF Genomic Region and Isolation of a CBF2 Cosmid Clone**

A 7,066-bp genomic DNA fragment containing the CBF1, CBF2, and CBF3 genes from Cvi was sequenced. This sequence has been deposited in GenBank (accession no. AY567247).

To isolate a Ler clone containing the CBF genes, a 0.9-kb CBF2 probe was used to screen a genomic library of Ler DNA cloned in the binary cosmid vector pCLD 04541 (Soppe et al., 2000). Thus, cos10 was isolated, subjected to restriction analysis, and its insert borders sequenced. It was determined that cos10 carried a 20.4-kb insert corresponding to the CBF2 coding sequence and 275 bp 5’ from the start codon (and 126 bp from the predicted transcription start) as well as six other Arabidopsis open reading frames located 3’ downstream to CBF2 and annotated as At4g25450, At4g25440, At4g25435, At4g25434, At4g2533, and At4g2530 (Arabidopsis Genome Initiative, 2000; http://www.arabidopsis.org).

**Development of Transgenic Lines**

Plant transformation was performed by the floral-dip method (Clough and Bent, 1998). Transgenic plants were selected on medium supplemented with kanamycin. For each transformation assay, three or four independent transgenic plants carrying one single insertion were selected based on the antibiotic marker segregation. These were selfed to obtain the homozygous T2 lines and T3 plants analyzed.
Gene Expression Analysis

RNA expression was analyzed on 2-week-old plants by hybridization of blots containing 30 μg of total RNA. Specific probes for CBF1, CBF2, and CBF3 were derived from the 3' untranslated regions (Medina et al., 1999). Probes for LTI178, COR47, KN1, and RBP4 have been described elsewhere (Medina et al., 1999; Novillo et al., 2004). Plants for expression analyses were grown together under LD photoperiods, cold treated during the first hours of the light period, and harvested at the same time.

Sequence data from this article can be found in the GenBank/EMBL data libraries under accession number AY667247.

Received July 20, 2005; revised August 24, 2005; accepted September 9, 2005; published October 21, 2005.

LITERATURE CITED


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Plant Physiology Preview

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