Review. Regulatory mechanisms involved in cold acclimation response

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Abstract

Freezing temperatures are one of the environmental stresses with more impact in plant development in temperate regions. By means of cold acclimation, many plant species are able to increase their freezing tolerance in response to low-nonfreezing temperatures. In the last years, an important effort has been made to characterize the molecular mechanisms that control this adaptive process. Transcriptome analyses indicate that cold acclimation is mainly regulated by low temperatures through changes in gene expression. In this regard, it has been reported that 3.4% of Arabidopsis genes are regulated by low temperature, including 95 genes annotated as transcription factors. The control of cold-inducible gene expression is very complex and involves many different signaling pathways that, in some cases, seem to share common intermediates. Interestingly, recent reports have shown that RNA processing and export, as well as post-translational modifications, including ubiquitylation and SUMOylation, also play important roles in regulating cold acclimation. Furthermore, histone modifications seem to be relevant in this regulation. In fact, histone acetylation and deacetylation are needed for correct activation of gene expression in response to low temperatures. All these data reveal that post-transcriptional mechanisms should be taken into consideration when analyzing the control of cold acclimation. Following, is a brief overview of the current understanding on the regulatory mechanisms that ensures the accurate development of this adaptive response.

Additional key words: abiotic stress, Arabidopsis, freezing tolerance, low temperature.

Resumen

Revisión. Mecanismos reguladores implicados en la respuesta de aclimatación al frío

Las temperaturas de congelación son uno de los estreses ambientales con mayor impacto en el desarrollo de las plantas en las regiones templadas. Por medio de la respuesta de aclimatación, muchas especies son capaces de incrementar su tolerancia a la congelación en respuesta a temperaturas bajas propiamente dichas. En los últimos años, se ha realizado un gran esfuerzo en la caracterización de los mecanismos moleculares que controlan este proceso adaptativo. Análisis transcriptómicos indican que la aclimatación al frío es regulada principalmente por cambios en la expresión génica. En este sentido, se ha descrito que la expresión de un 3,4% de los genes de Arabidopsis está regulada por las temperaturas bajas, incluyendo 95 genes anotados como factores de transcripción. El control de la expresión génica inducible por frío es muy complejo e implica diferentes rutas de señalización de la señal que, en algunos casos, parecen compartir intermediarios comunes. Trabajos recientes han mostrado que el procesamiento y movilización de RNA, y algunas modificaciones post-traduccionales de proteínas como la ubiquitinación y la SUMOilización también juegan un papel importante en la regulación del proceso de aclimatación a las temperaturas bajas. Más aún, la modificación de histonas parece ser también relevante en esta regulación. De hecho, la acetilación y deacetilación de histonas es necesaria para una correcta activación de la expresión génica en respuesta a las temperaturas bajas. Todos estos datos ponen de manifiesto que a la hora de estudiar el control de proceso de aclimatación se han de tener en cuenta los mecanismos de regulación post-transcripcional. A continuación, repasaremos los conocimientos actuales sobre los mecanismos que aseguran el correcto desarrollo de esta respuesta adaptativa.

Palabras clave adicionales: Arabidopsis, estrés abiótico, temperaturas bajas, tolerancia a la congelación.
Introduction

Plant development is severely limited by environmental conditions, particularly in temperate regions where important temperature changes occur between winter and summer seasons. Taken into consideration that plants are sessile organisms and cannot control their own temperature, survival to these changes is an important challenge. Many species have evolved an adaptive response that allows them to endure freezing temperatures. By means of this process, named cold acclimation (Levitt, 1980), they increase their freezing tolerance after a period of exposition to low-nonfreezing temperatures. Cold acclimation constitutes a representative example of plant interaction with the environment and how this interaction has conditioned the evolution of some species. Understanding the molecular mechanisms that control this adaptive process is not only interesting from a basic point of view but also has a high biotechnological potential. During the last years, many investigations have revealed that plant responses to low temperature and other abiotic stresses, such as high salt and drought, share several components (Salinas, 2002). The study of cold acclimation should provide essential information about how plants coordinately integrate responses to different adverse environmental conditions.

The process of acclimation is very complex and involves many biochemical and physiological changes, mainly controlled at the gene expression level (Salinas, 2002; Kaplan et al., 2004; Zhu et al., 2007). While some of these changes are implicated in the stability of subcellular structures, essentially membranes (Nishida and Murata, 1996) and cytoskeleton (Mita and Shibaoka, 1984), others are directed to control the synthesis of pigments to protect from photoxidative stress (Schoner and Krause, 1990; Christie et al., 1994; Król et al., 1999), enzymes to reduce oxidative stress (Schoner and Krause, 1990; Prasad, 1997; Llorente et al., 2002), and compatible solutes to protect from osmotic changes (Ristic and Ashworth, 1993; Sauter et al., 1996; Xin and Browse, 1998; Wanner and Juntila, 1999; Gilmour et al., 2000; Garg et al., 2002). In addition, during cold acclimation the expression of genes encoding cryoprotective proteins, known as LEA, and antifreezing proteins (AFPs), is induced (Thomashow, 1999; Smallwood and Bowles, 2002).

Recent reports have revealed that the process of cold acclimation is subjected to a complex regulation, which involves several pathways. The implication of transcriptional regulation as well as RNA mobility and processing in controlling low temperature response will be revised. Furthermore, the role post-translational protein modifications play in cold-acclimation signaling will be discussed.

Transcriptional regulation of cold inducible gene expression

Microarray analysis have shown that 939 Arabidopsis genes are regulated by low temperature (Fowler and Thomashow, 2002; Kreps et al., 2002; Seki et al., 2002; Lee et al., 2005; Vogel et al., 2005). Among these genes, one third is down regulated, with only one encoding a transcription factor, which indicates that cold acclimation is mainly regulated by transcriptional activation (Lee et al., 2005). In addition, many early cold-induced genes encode transcription factors or proteins involved in transcription. Thus 113 genes have been annotated to function in transcription, 95 of them coding for transcription factors (Lee et al., 2005). These data indicates that different pathways are involved in cold-responsive gene regulation.

The small family of transcription factors named CBFs/DREB1s (Fowler and Thomashow, 2002) is the most characterized component mediating cold-inducible gene expression in Arabidopsis. It is composed by three members (CBF1-3) and regulates the expression of around 12% of the cold-inducible genes in Arabidopsis. CBFs have an AP2 DNA-biding domain, an acidic C-terminal region, that acts as a transcriptional activator motif, and bind to the CRT/DRE cis-element (CCGAC) (Stockinger et al., 1997). The expression of the CBF genes seems to be specifically induced by cold in a fast, transient, and specific way. In fact, CBF genes

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1 Abbreviations used: ABA (abscisic acid), ABF (ABRE binding factor), ABRE (abscisic acid-responsive element), AFP (antifreezing protein), bHLH (basic helix-loop-helix), CBF (CRT binding factor), CRT/DRE (C-repeat/dehydration responsive element), FRY (fiery), GR-RBP (glycine-rich RNA-binding protein), HAT (histone acetyltransferase), HDAC (histone deacetylase), HOS (high expression of osmotically responsive gene), ICE (inducer of CBF expression), LEA (late embryogenic abundant), LOS (low expression of osmotically responsive gene), LOV (light-oxygen-voltage), PP2A (protein phosphatase 2A), SCOF (soybean cold-inducible factor), STA (stabilized), SUS (sucrose synthase).
are not induced by cold-related stresses such as dehydration or high salt (Gilmour et al., 1998; Liu et al., 1998; Medina et al., 1999). Constitutive overexpression of CBFs in Arabidopsis induces the accumulation of mRNAs from genes that contain the CRT/DRE box in their promoters as well as an increase in freezing tolerance (Fowler and Thomashow, 2002). Among the genes induced by CBFs, there are some encoding transcription factors (i.e., RAP2.1 and RAP2.6), indicating that the CBF-regulon is constituted by several subregulons (Fowler and Thomashow, 2002). Furthermore, overexpression of CBF3 has been shown to induce different metabolic changes associated with cold acclimation (i.e. increase in proline and soluble sugars levels), some of them correlating with the expression levels of related genes, as is the case of AtP5CS2 (Gilmour et al., 2000). At the morphological level, Arabidopsis transgenic plants constitutively overexpressing individual CBFs show dwarf phenotypes, delayed flowering and low number of seeds (Gilmour et al., 2000), which indicates that CBFs are highly detrimental for plant development when present in nonphysiological levels, and suggests that their expression must be tightly regulated.

Recently, Novillo et al. (2004) reported the molecular and functional characterization of a CBF2 null mutant. Interestingly, the absence of CBF2 increases Arabidopsis tolerance to freezing temperatures, before and after cold acclimation. This increase resulted to correlate with a higher accumulation of CBF1 and CBF3 transcripts, and, consequently, of CBF-target genes, under both control and low-temperature conditions (Novillo et al., 2004). These results indicate that CBF2 negatively modulates the expression of CBF1 and CBF3, ensuring the adequate expression of the CBF-regulon and, therefore, the proper response of Arabidopsis to cold stress (Novillo et al., 2004). In addition to CBF2, other transcription factors have been shown to control the expression of CBFs. A MYC-like bHLH transcription factor, ICE1, binds to the CBF3 promoter acting as a positive regulator of CBF3 gene expression (Chinnusamy et al., 2003). Unexpectedly, ICE1 expression is not induced in response to low temperature, suggesting it should be regulated at the post-transcriptional level (see below). ice1 mutant plants show low induction of CBF3 and the CBF-regulon in response to low temperatures, as well as impaired freezing tolerance (Chinnusamy et al., 2003). It has been reported that ICE1 controls the expression of around 40% of cold-regulated genes (Lee et al., 2005). However, it does not seem to control the expression of non-cold-inducible genes (Lee et al., 2005). The comparison of genes regulated by ICE1 with those regulated by CBFs and other transcription factors, revealed that ICE1 is more implicated in regulating CBFs-target genes, particularly CBF3-targets, consistently with its role as CBF3 activator (Lee et al., 2005). MYB15 is another transcription factor that binds to the promoters of CBFs, although in this case to repress their expression (Agarwal et al., 2006). myb15 null mutants are more tolerant to freezing stress than wild type plants, mainly due to an increase in cold-induction of the CBFs and target genes (Agarwal et al., 2006). MYB15 physically interact with ICE1, although the biological meaning of this interaction remains unknown (Agarwal et al., 2006). MYB15 is not the only transcription factor that negatively regulates CBFs expression. Vogel et al. (2005) reported that the overexpression of an Arabidopsis zinc finger, ZAT12, significantly dumped the induction of the CBFs in response to low temperatures. Strikingly, ZAT12 does not seem to affect CBF-targeted gene expression, which suggests a complex role for this protein in the regulation of cold-inducible gene expression and cold acclimation (Vogel et al., 2005). In fact, overexpression of ZAT12 increases the induction of several cold-inducible genes, some of them CBF targets. Furthermore, ZAT12 overexpression enhances the constitutive freezing tolerance of Arabidopsis but does not have any effect on cold acclimation (Vogel et al., 2005). All these results confirm the high complexity to which the regulation of CBF expression is subjected, and prompted the importance of an accurate control of this expression for the correct development of the cold acclimation process.

HOS9 and HOS10 are homeodomain and R2R3-type MYB transcription factors, respectively, that have also been involved in regulating gene expression during cold acclimation (Zhu et al., 2004, 2005). hos9 mutant plants display reduced freezing tolerance, both before and after cold acclimation (Zhu et al., 2004). Intriguingly, while the cold-induction of CBFs in hos9 is as in the wild type, the cold-induction of some CBF-target genes is higher. Similarly, hos10-1 mutant also shows high sensitivity to freezing temperatures and is impaired in cold acclimation (Zhu et al., 2005). Moreover, although the cold induction of CBFs is not altered in hos10, the induction of several CBF targets by low temperature is faster in the mutant than in the wild type. Therefore, HOS9 and HOS10 seem to control cold-acclimation response by ensuring a proper cold-
inducible gene expression through CBF-independent pathways (Zhu et al., 2005). LOV1 is another transcription factor that has been implicated in regulating the expression of CBF-targets in a CBF-independent way (Yoo et al., 2007). lov1-4 null mutant is hypersensitive to freezing temperatures and has reduced acclimation capability, indicating a positive role for LOV1 during cold acclimation (Yoo et al., 2007). The cold-induction of CBF-target genes is significantly impaired in lov1-4 when compared to wild type plants, indicating that it acts as a positive regulator of this response. However, the cold-induction of CBFs is identical in lov1-4 and wild type plants, which demonstrates that LOV1 function is CBF-independent (Yoo et al., 2007). The ABA response element ABRE (PyACGTGCC, Guiltinan et al., 1990) is present in the promoters of numerous cold-inducible genes, including CBF targets (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994; Wang and Cutler, 1995) and could mediate CBF-independent gene expression in response to low temperature. Supporting this conception, a cold- and ABA-inducible gene from Arabidopsis has been described to encode a bZIP transcription factor (ABF1) that binds to the ABRE motif. ABF1 is able to activate gene expression through its interaction with the ABRE element in yeast, suggesting that it could mediate ABRE-dependent cold-induced gene expression (Choi et al., 2000). Another gene which expression is induced by cold and ABA, and encodes a transcription factor is SCOF1 from soybean (Agarwal et al., 2006). SCOF1 is a zinc finger protein whose overexpression in Arabidopsis originates constitutive expression of cold-inducible genes and increased tolerance to freezing temperatures (Kim et al., 2001). SCOF1 resulted to enhance the binding of SGB1, a bZIP transcription factor, to the ABRE motif (Kim et al., 2001), indicating that it is a positive regulator of cold-acclimation response through the ABRE-dependent pathway. From all these data, a picture can be drawn where gene expression is regulated by low temperature through a sophisticated network of signaling pathways to ensure the correct development of the cold-acclimation process (Fig. 1).

Post-transcriptional regulation of cold acclimation response

mRNA stability and translation yield also play important roles in the proper activation of the cold-acclimation response. In fact, the accumulation of some messengers during cold acclimation seems to be regulated at the post-transcriptional level (Hajela et al., 1990; Wolfram et al., 1993; Dunn et al., 1994). By using pharmacological experiments, Phillips et al. (1997) demonstrated that an unknown nuclear protein actively stabilizes transcripts corresponding to bli4.0, a cold-inducible barley gene. On the other hand, Xiong et al. (2002) identified an Arabidopsis gene, FRY2, which encodes a protein similar to animal and yeast factors involved in transcription regulation and pre-mRNA processing. Recessive mutations in FRY2 provoke the superinduction of CBF-target genes in response to cold, suggesting that FRY2 is a negative

Figure 1. CBFs constitute central intermediates in cold-acclimation signaling by inducing gene expression through CRT/DRE sequence. The induction of CBFs in response to low temperature is tightly regulated. ICE1 has been described to positively regulate CBF3 expression. Positive regulators of CBF1 and CBF2 have not been identified yet. ZAT12 and MYB15 negatively regulate CBF expression. In addition, CBF2 negatively regulates CBF1 and CBF3 expression. ICE1 has also been described to promote cold acclimation by inducing CBF-independent gene expression and to repress MYB15 expression. ABA activates cold acclimation through a CBF-independent pathway. ABA-dependent cold-induced gene expression is mediated by ABF1 via the ABRE cis-element. Although still is unknown how HOS9, HOS10 and LOV1 are activated in response to low temperatures they also activate cold-induced gene expression as well as cold acclimation through CBF-independent pathways.
regulator of the activation of gene expression by cold. In contrast, fry2 mutants are more sensitive to freezing temperatures than wild type. Taken in consideration the RNA binding domain of FRY2, Xiong et al. (2002) proposed that, as in animals, RNA structure could regulate the response of plants to stress and FRY2 could act as a RNA chaperone under low temperature conditions. The glycine-rich RNA-binding proteins (GR-RBPs) have also been proposed to act as RNA chaperones in plants. In this regard, it has been described that the expression of several GR-RBPs is induced by different abiotic stresses including cold (Sachetto-Martins et al., 2000). Functional characterization of one Arabidopsis GR-RBP, the atRZ1, provided interesting data about the role of these proteins in cold acclimation (Kim et al., 2005). atRZ1 mutants are more sensitive to low and freezing temperatures, whereas overexpressing plants are more tolerant to these stresses (Kim et al., 2005). On the basis of these results, Kim et al. (2005) concluded that atRZ1 might have an RNA chaperone activity leading to the destabilization of the over-stabilized secondary structures and, thereby, to facilitate an efficient translation at low temperature. Another Arabidopsis protein involved in pre-mRNA processing and cold signaling is STA1. STA1 is similar to the human U5 small ribonucleoprotein-associated 102-kD protein and to the yeast pre-mRNA splicing factors Prp1p and Prp6p, whose corresponding genes, as STAI, are induced by low temperature (Lee et al., 2006). Mutations in STAI increase Arabidopsis chilling sensitivity, although this mutant do not have any difference with wild type plants in their cold-inducible gene expression. Interestingly, the stability of some mRNAs and the splicing of the cold-induced gene COR15A are seriously affected in stai-1 mutant plants, suggesting that these processes are important in low temperature response (Lee et al., 2006).

In addition to mRNA processing, the control of mRNA export to the cytoplasm is also influential in plant response to low temperature. In this way, the implication of the Arabidopsis nucleoporin AtNUP160 in cold signaling has been described (Dong et al., 2006a). This protein seems to be involved in mRNA export since a null mutation in the corresponding gene causes mRNA accumulation in the nucleus (Dong et al., 2006a). The atnup160-1 mutant shows a reduced tolerance to chilling and freezing temperatures, probably due to a decrease in cold-induction of CBFs (Dong et al., 2006a). Moreover, transcriptome analysis revealed that the expression of other cold-inducible genes than the CBFs is affected in this mutant, which should contribute to its sensitive phenotypes (Dong et al., 2006a). LOS4, a DEAD-box RNA helicase, has also been implicated in cold acclimation (Gong et al., 2005). los4 mutants display improved cold-induction of CBF genes under low temperature conditions and are more sensitive to freezing than wild-type plants (Gong et al., 2005). As in the case of AtNUP160, in situ poly(A) hybridizations revealed that LOS4 is needed for a correct partition of mRNAs in the cell (Gong et al., 2005). Taken together, all these results provide a new scenario on the regulation of cold acclimation, where mRNA stability and processing, as well as mobilization, seems to be as important as transcriptional activation.

Translational and post-translational regulation of cold acclimation response

Protein synthesis has been described essential for adequate response to low temperature, indicating that cold acclimation is subjected to translational regulation. Consistently, the translation elongation factor 2-like protein, LOS1, has been shown to be a positive regulator of cold acclimation (Guo et al., 2002). The los1-1 mutation displays reduced cold-acclimation capability due to a reduced cold induction of the CBF-target genes (Guo et al., 2002). In contrast, the induction of the CBFs in response to low temperature is higher in los1-1 than in wild-type plants (Guo et al., 2002). Additionally, synthesis of new proteins under low temperature is severely impaired in los1-1, which could account for the reduction of cold-inducible gene expression (Guo et al., 2002). These results suggest that expression of CBFs is independent of new protein synthesis since they are overinduced in los1-1 mutant under cold conditions. The fact that CBF expression is overinduced in los1-1 indicates that it is subjected to feedback regulation (Guo et al., 2002).

Recent works have revealed that protein stability has important implications in the regulation of cold-acclimation response. In Arabidopsis, Ishitani et al. (1998) identified HOS1, a negative regulator of the CBF regulon that contains a RING finger domain characteristic of some plant E3 ubiquitin ligases. In agreement with its role as negative regulator, HOS1 expression is transiently inhibited in response to cold treatment (Ishitani et al., 1998). Although HOS1 negatively regulates cold-inducible gene expression, hos1-1 mutant is chilling and freezing sensitive when compared
to wild type, indicating that an accurate expression pattern of *HOS1* is essential for the correct response to low temperature (Ishitani et al., 1998). Subsequently, it has been demonstrated that, in fact, HOS1 has E3 ubiquitin ligase activity and polyubiquitilates ICE1 (see above) mediating its degradation and, therefore, inhibiting the cold-induction of *CBF3* and the CBF regulon (Dong et al., 2006b).

SUMOylation is another post-translational modification that can control protein stability and activity. SUMOylation, as ubiquitilation, requires the sequential action of three enzymes, E1, E2, and E3 (Kurepa et al., 2003; Colby et al., 2006). The Arabidopsis genome only includes one gene homolog to E3 sumo ligases, *SIZ1* (Miura et al., 2007). *SIZ1* expression is not induced by cold although mutations in *SIZ1* decrease Arabidopsis tolerance to freezing and chilling temperatures, indicating that SUMOylation also plays an important role in plant response to low temperature (Miura et al., 2007). *SIZ1* catalyzes the SUMOylation of ICE1 which in turn impedes the ubiquitilation of ICE1 (see above) and, thereby, the induction of *CBF3* (Miura et al., 2007). Furthermore, ICE1 SUMOylation inhibits the expression of MYB15, a negative regulator of *CBF* expression (see above) (Miura et al., 2007). Although it has not been reported how SUMOylation affects ICE1 stability, it has been proposed that most probably would induce its stabilization. A hypothetical model that would integrate HOS1, SIZ1 and ICE1 activities in the regulation of cold acclimation is presented in Figure 2. In this model, under control conditions, HOS1 would be targeting ICE1 for its degradation by the proteosome, maintaining the accumulation of the protein at low levels. Temperature decrease would activate, by still unknown pathways, SIZ1. This activation would induce the SUMOylation of ICE1 and, thereby, a decrease in its ubiquitilation levels. The increase in ICE1 accumulation would then induce the expression of the *CBFs*, directly by its interaction with their promoters and indirectly by the repression of *MYB15*, and, therefore, the CBF regulon and the cold-acclimation process.

*AtCHIP* also encodes an Arabidopsis E3 ubiquitin ligase which expression is cold induced (Yan et al., 2003). AtCHIP seems to be a negative regulator of freezing tolerance since overexpression of the corresponding gene increases Arabidopsis sensitivity to freezing temperatures (Yan et al., 2003). The A subunit of protein phosphatase 2A, PP2A, has been identified as one of the AtCHIP substrates (Luo et al., 2006).

**Figure 2.** Hypothetical model for post-transcriptional regulation in cold acclimation. Protein modification seems to have an important role in the transduction of the cold signal. Under control conditions, HOS1 ubiquitylates ICE1 leading to its degradation by the proteosome. Low temperature would activate, by still unknown mechanisms, SIZ1, which, in turn, would label ICE1 with SUMO to stabilize the protein. The stabilization of ICE1 would increase the expression of several genes, including *CBF3*. In addition, ICE1 SUMOylation seems to repress MYB15 expression, which is inhibiting *CBF3* expression. The synthesis of CBF3 depends on the activation of LOS1, a translation elongation factor 2-like protein. On the one hand, CBF3 binding to the CRT/DRE element to activate gene expression would be positively regulated by its interaction with different components of the HAT complex, such as ADA2 and GCN5. HAT activity would remove inhibitory chromatin structures by acetylating histones near to the CRT/DRE box. On the other hand, FVE, a component of the HDAC complex, would inhibit the activation of gene expression by CBF3 binding to the CRT/DRE box through the deacetylation of the same histones. HDAC inhibition of gene expression would be required to ensure an accurate expression pattern of the cold inducible genes, and the correct cold-acclimation response.
PP2A is a negative regulator of sucrose synthase (SUS), and therefore of sugar biosynthesis, that has an important role in tolerance to low temperatures, including freezing ones. AtCHIP-overexpressing plants show an increased PP2A activity under cold, which could account for the freezing sensitivity of these plants (Luo et al., 2006). AtCHIP seems to monoubiquitylate PP2A that would not lead to PP2A degradation (Luo et al., 2006). It has been proposed that PP2A monoubiquitylation could alter its interaction with another subunit of PP2A which would increase its phosphatase activity, provoking a decrease in freezing tolerance (Luo et al., 2006). F-box proteins are the degradation substrate receptor subunits of SCF-type E3 ligases (Jin et al., 2005). AtFBP7 encodes an F-box protein which expression is induced by low temperature (Calderón-Villalobos et al., 2007). fbp7 mutants have an impaired protein synthesis under low temperature conditions although they do not show any significant difference in growth and cell integrity compared to wild-type plants (Calderón-Villalobos et al., 2007). Therefore, it seems that, although AtFBP7 has a role in the regulation of protein synthesis under cold conditions, its function is not essential for plant tolerance to low temperature stress.

Histone acetylation mediated by histone acetyltransferases (HATs) and histone deacetylases (HDACs) is another post-translational mechanism that has been related to cold acclimation. Several reports have involved HATs in transcriptional regulation by remodeling repressive chromatin structures (Sterner and Berger, 2000; Roth et al., 2001). In Arabidopsis, different components of the HATs complex have been identified (ADA2a, ADA2b and GCN5) which interact in vitro with CBF1 and seems to be needed for CBF1 function (Stockinger et al., 2001). Functional characterization of ADA2b and GCN5 showed that these proteins control cold-inducible gene expression (Vlachonasios et al., 2003). ada2b and gcn5 mutant plants display wild-type CBF expression, although the cold induction of their targets seems to be reduced (Vlachonasios et al., 2003). Interestingly, only the induction of the CBF-regulon is affected in ada2b and gcn5 mutants, suggesting that the activity of the HATs complex in response to cold is highly specific (Vlachonasios et al., 2003). Reversibility of histone acetylation seems also to have a role in regulating cold-inducible gene expression. Thus, Kim et al. (2004) identified the Arabidopsis mutant acg1 as a negative regulator of the CBF-regulon. The acg1 mutant has similar constitutive freezing tolerance as the wild type but increased cold-acclimation capability, which correlates with a higher cold induction of CBFs and their target genes (Kim et al., 2004). ACG1 resulted to encode FVE, a component of the HDAC complex in Arabidopsis homolog to the mammalian retinoblastoma associated protein (Kim et al., 2004). Components of the HDAC complex in Arabidopsis (i.e. FVE) participate at this regulating level. Once gene expression is activated, mRNA mobility, stability and structure would be the subsequent level of regulation, involving FR Y2, GR-RBPs and atRZ proteins as RNA-chaperones, and STA1 and LOS4 in RNA mobilization. Finally, at the fifth level, activation of protein synthesis at low temperature by proteins such as LOS1, would be essential for the induction of gene expression response to low temperatures. A third level of regulation involves histone modifications, which are also necessary for the activation of gene expression. Components of the HATs (i.e. ADA2a, ADA2b and GCN5) and HDACs (i.e. FVE) participate at this regulating level. Once gene expression is activated, mRNA mobility, stability and structure would be the subsequent level of regulation, involving FR Y2, GR-RBPs and atRZ proteins as RNA-chaperones, and STA1 and LOS4 in RNA mobilization. Finally, at the fifth level, activation of protein synthesis at low temperature by proteins such as LOS1 would be essential for the induction of gene expression and the cold-acclimation response. Besides, new protein synthesis would negatively regulate cold-inducible gene expression. This regulatory level would also be controlled by protein stability mechanisms as it has been demonstrated in atfbp7 mutants.
al., 2004). All these results indicate that histone acetylation is important for the interaction of CBFs with the CRT/DRE element, and the subsequent activation of gene expression under low temperatures, in all likelihood to avoid inhibitory chromatin structures.

**Future directions**

In this review, recent results that have contributed to extend our knowledge on how the cold-acclimation response is regulated have been summarized (Fig. 3). It has been shown that regulation of gene expression during cold acclimation involves different pathways. At this point, a raising question that needs to be answered is how plants precisely coordinate these signaling pathways and whether they share common components. Regarding the post-transcriptional regulation, the data reported so far evidence the essential role of this kind of regulation for the correct development of cold acclimation. The identification of intermediates in the regulation of mRNA transport and stability will be essential in order to have a complete scenario on how plant response to low temperatures is controlled. Finally, protein stability plays also a role in low temperatures response, involving, at least, ubiquitylation and SUMOylation. The identification and characterization of new ubiquitin and SUMO E3 ligases involved in the regulation of the cold-acclimation process should constitute an important challenge for the future.

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