

Review

Physiological and Molecular Mechanism Involved in Cold Stress Tolerance in Plants

Faujiah Nurhasanah Ritonga and Su Chen * 

State Key Laboratory of Tree Genetics and Breeding, Northeast Forestry University, Harbin 150040, China; ritongafaujiah@gmail.com

* Correspondence: chensu@nefu.edu.cn

Received: 18 March 2020; Accepted: 21 April 2020; Published: 28 April 2020



Abstract: Previous studies have reported that low temperature (LT) constrains plant growth and restricts productivity in temperate regions. However, the underlying mechanisms are complex and not well understood. Over the past ten years, research on the process of adaptation and tolerance of plants during cold stress has been carried out. In molecular terms, researchers prioritize research into the field of the ICE-CBF-COR signaling pathway which is believed to be the important key to the cold acclimation process. Inducer of CBF Expression (*ICE*) is a pioneer of cold acclimation and plays a central role in C-repeat binding (CBF) cold induction. *CBFs* activate the expression of *COR* genes via binding to cis-elements in the promoter of *COR* genes. An ICE-CBF-COR signaling pathway activates the appropriate expression of downstream genes, which encodes osmoregulation substances. In this review, we summarize the recent progress of cold stress tolerance in plants from molecular and physiological perspectives and other factors, such as hormones, light, and circadian clock. Understanding the process of cold stress tolerance and the genes involved in the signaling network for cold stress is essential for improving plants, especially crops.

Keywords: chilling; cold acclimation; freezing; low temperature; ICE-CBF-COR; tolerance

1. Introduction

Drought, salinity, and low temperature (LT) are the main abiotic stress factors that have strong impacts on plant growth and development [1]. In addition to drought stress, LT is one of the most harmful environmental stresses encountered by higher plants [2,3]. LT stress is divided into chilling stress (<20 °C) and freezing stress (<0 °C) according to the environmental temperature. In addition to affecting the growth and development of the plant, LT stress significantly restrains the geographical distribution of plants [4–7].

Tropical and subtropical plants are sensitive to chilling stress and lack the capacity of cold acclimation. However, temperate plants have the ability to tolerate freezing temperatures following a period of exposure to non-freezing temperatures, which is termed as cold acclimation [8]. Temperate plants are tolerant to seasonal changes in temperature and can tolerate cold stress during early spring and winter. Many important crops, such as rice, corn, soybean, potato, cotton, and tomato, are chilling sensitive and incapable of cold acclimation. In contrast, some crops, such as oats, are chilling tolerant but freezing sensitive. On the other hand, barley, wheat, and rye are well adapted in freezing temperatures [9]. However, some plants such as *Arabidopsis*, winter wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) are not able to tolerate nonfreezing temperatures without cold acclimation [10]. Similarly, *Santalum album* and *Betula utilis* (Himalayan Birch), as dominant vegetations in cold environments (Eastern Nepal), are also sensitive to cold during the growing season [11,12].

Each plant has different enrichment pathways in different periods of cold stress, such as the amino sugar and nucleotide sugar metabolism pathway, alanine and protein export, and the aspartate

and glutamate metabolism are highly enriched during the latter stages of cold stress periods in tea plants. In contrast, cellular components, biological processes, and the molecular function category are highly enriched in the early periods of cold stress in tea plants. The same result was found using transcriptome analysis in which flavonoid biosynthesis, phagosome, plant hormone signal transduction, and fructose were highly enriched at the beginning of cold stress [13]. In tomato, even though the expression of ethylene signaling genes decreased after cold stress, none of the protein genes decreased. This shows the different regulation of gene and protein levels [14]. In addition, abscisic acid (ABA) signaling pathway gene expression improved the cold hardiness in grapevine buds only during the cold acclimation period [15]. Furthermore, the overexpression of *GLR1.2* or *GLR1.3* enhanced cold tolerance by increasing endogenous jasmonate levels under cold stress. However, they could not interact with each other directly, indicating they interact indirectly to achieve cold tolerance [16]. In banana and *Zoysia japonica*, *MaPIPI2.7* and *ZjICE1* improved multilevel stresses, such as cold, salt, and drought stress [17]. These results show that every gene has a different mechanism in different plants to achieve abiotic or biotic stress tolerance. Due to these differences of signal transduction pathways and metabolisms, the mechanisms related to cold stress are complex [18].

The methods plants use to deal with adverse environmental stress, including stress avoidance and stress tolerance, have been examined in the literature [19,20]. Recent studies of LT stress and cold acclimation based on the model plant *Arabidopsis* contribute substantially to understanding the molecular mechanisms of cold acclimation [6]. In addition, numerous studies have been carried out in other plant species to reveal the molecular mechanism and gene regulatory networks. In this review, we aim to give a comprehensive overview of the current knowledge about plant under LT stress.

2. Genetical Changes during Cold Stress

Investigation of transcriptional alterations of plants during cold acclimation is crucial for understanding the underlying molecular mechanism under LT stress. Until now, a significant number of cold responsive genes have been identified and several gene regulated networks have been reported. Among these, ICE-CBF-COR is one of the most widely reported pathways. In most plant species, the ICE-CBF-COR pathway is induced by LT stress and then activates the appropriate expression of downstream genes, which encode osmoregulation substances [9]. Inducer of CBF Expression (*ICE*) is a pioneer of cold acclimation, an MYC-type basic helix-loop-helix family transcription factor (TF) [8,21,22]. It is reported that *ICE1* plays a central role in C-repeat binding factor 3 (*CBF3*) cold induction. When plants encounter LT stress, *ICE1* could be released from JAZs bound by DELLAs and induce the expression of *CBF3*. *CBF3* activates the expression of *GA2ox7* to reduce the bioactive gibberellic acid (GA) level, which promotes the accumulation of DELLAs. Therefore, DELLAs can regulate the cold induction of *CBF3* through *ICE1* via JAZs.

C-repeat binding factors (*CBFs*), also known as dehydration-responsive element-binding proteins (*DREBs*), act as a regulating gene that has an important role in cold acclimation [23]. *CBF* is a member of the APETALA2/ETHYLENE RESPONSE FACTOR (*AP2/ERF*) family and regulates the expression of the cold-responsive (*COR*) gene [24]. The *AP2/ERF* family is one of the largest TF families in plants and is characterized by having a minimum of one *AP2* DNA-binding domain [25]. *CBFs* activate the expression of *COR* genes via binding to cis-element in the promoter of *COR* genes (CRT: TGGCCCGAC) (Figure 1) [23,26]. In addition to LT stress, *CBFs* also play important roles in other abiotic stresses [7,26,27]. Some of the cold-responsive genes have an ABA responsive element and dehydration responsive element in their promoter regions [28]. *EgDREB1* from oil palm might also have a similar regulatory element located in a sequence promoter and are responsive to cold signaling [29]. It was also found in *DREB* [30] and *FtbHLH2* that the transgenic plant promoter was induced by cold and that many cis-elements of the *FtbHLH2* promoter collaborate in cold stress conditions [31].

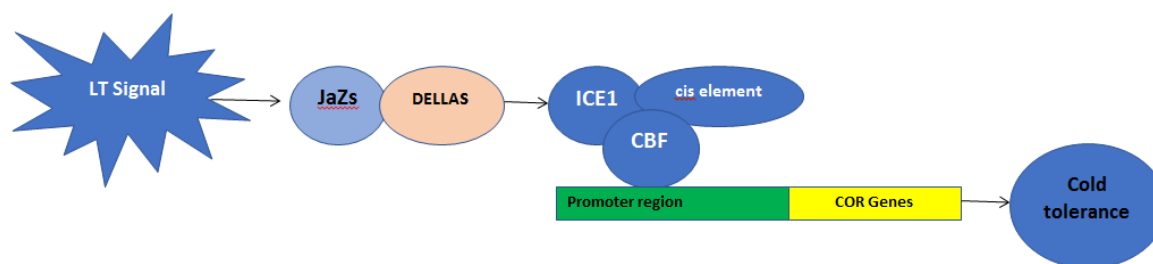


Figure 1. ICE-CBF-COR pathways in plants tolerance to cold stress. The expression of *CBFs* is mainly mediated by DELLA signaling and induced by *ICE1*. DELLAs contribute to the cold induction of *CBF* genes through interaction with JaZs signaling. *CBFs* activate the expression of *COR* genes via binding to cis-elements in the promoter of *COR* genes and result in the enhancement of cold tolerance in plants.

In temperate plants of wheat and barley, *CBFs* are found in the Frost Resistance 2 (FR2) locus [4]. Winter barleys planted in early autumn need collaboration between Vernalization 1 (*VRN1*) and *CBF* genes to enhance cold acclimation. However, for spring barley, vernalization is not required. As a result, spring barley is not freezing tolerant. Similar to spring barley, 214 upregulated genes and 884 downregulated genes were found in grapevine cultivars after LT treatment [25], suggesting that cold stress induced the downregulated genes. This study found that *CBF1*, *CBF2*, and *CBF3* had no role in cold acclimation in grapevine leaves. This is due to the absence of *CBF1* and low levels of *CBF2* and *CBF3*. However, there were some exceptional cases in the mechanisms of the *CBF* gene family expression. A study found that *ICE1* mutation only had a small effect on the *CBF* transcript [21]. The expression of *CBF1* is also regulated by the *SVALKA*-*CBF1* cascade. *SVALKA* is a long non-coding RNA (lncRNA) that is transcribed by RNA polymerase II (RNAPII). Mutation in *SVALKA* affects expression of *CBF1* and plant freezing tolerance. The *SVALKA*-*CBF1* regulatory network has been found in species other than *Arabidopsis* [32].

The implementation of *CBF*-regulated genes is not only for cold stress but also for salt stress, hormone response, and even carbohydrate metabolism [33]. Previous research found that at 3 h or 24 h of cold treatment in *Arabidopsis cbfs* triple mutant, the number of up-regulated genes was 609 and 1375, respectively, and the number of down-regulated genes was 163 and 1349, respectively [33]. In addition, a total of 1394 cold-induced genes and 1113 cold-repressed genes were recognized in both the wild-type and *cbfs* triple mutant. This indicates that a large number of *COR* genes are not influenced in the *cbfs* triple mutant within cold stress.

In addition, numerous TFs that can regulate cold signaling and cold stress have been identified, such as *CBF1*, *CBF2*, *CBF3*, *ICE1*, *ICE2*, *CAMTA3*, *MYB15*, *ZAT12*, *COR15a*, and *COR15b* [34]. Some TF families found to be related to LT stress in *Pyrus ussuriensis* are DREB, WRKY, NAC, MYB, AP2/ERF, and bHLH [35]. Brassinosteroids are plant hormones that have an important role in plant growth and can also protect plants against abiotic stress such as cold stress. Two Brassinosteroids (BRs) TFs, namely, Brassinazole-resistance 1 (*BZR1*) and CESTA (*CES*), are direct regulators of *CBF* [36,37].

Several factors influence the binding affinities of TFs to specific sites, such as chromatin accessibility, DNA methylation, TF cooperativity, and TF interactions with non-binder cofactors and the transcription machinery [38]. A single TF regulates the expression of many downstream genes, so the utilization of TFs proffers many advantages in genetic engineering [39]. Some protein kinases (MEKK1-MKK1/2-MPK4) induce the expression of *CBFs*, especially *CBF2* [6,40]. Another gene that also plays a role in the cold acclimation process is Cold Induced Small Protein 1 (*CISP1*), which was found in the roots of the *Poaceae* plant (a case study on barley). Normally, *CISP1* is increased after 27 days of low-temperature treatment. Homologous adherents of *CISP1* (i.e., *CISP2* and *CISP3*) are also found in several *Poaceae*, and it also plays a role in the cold acclimation process [41].

Overexpression of *FtbHLH2* in the transgenic plant increases the expressional level of *CBF1-3* and enhances low temperature tolerance in plants [31]. Other studies suggested that ethylene response factors from *Vitis amurensis*, *VaERF080*, and *VaERF087* (AP2/ERF Family) regulate the expressional

levels of cold-related genes including *CBF1*, *CBF2*, *ICE1*, *ZAT12*, *KIN1*, *SIZ1*, *RD29A*, *COR15A* and *COR47* [42]. When treated by cold stress, *CBF1-8* of *Brachypodium distachyon*, a herbaceous grass species that can tolerate cold stress, was upregulated at a different time [43].

NADP-dependent D-sorbitol-6-phosphate dehydrogenase (*S6PDH*), anthocyanidin synthase (*ANS*), and phenylalanine ammonia-lyase (*PAL*) genes might play a vital role in the cold response of the loquat [44]. Studies reveals that the expression levels of *S6PDH*, *ANS*, and *PAL* are upregulated by cold treatment during the first 4 h but suppressed as the stress continues. A previous study shows that *SiDHN* found in *Saussurea involucreata* plays a pivotal role in low temperature and drought stress. After being grown under a low-temperature treatment for 24 h, the expression level of *SiDHN* is increased three-fold. This proved that *SiDHN* is responsive to cold stress [5]. Recently, *Arabidopsis* overexpressing RNA-DIRECTED DNA METHYLATION 4 (*RDM4*) showed the antagonist result with the *rdm4* mutant in facing cold stress. Overexpression of *RDM4* in plants increases the expression of *CBFs* and the downstream genes after chilling stress, subsequently improving the survival rate. However, while the *rdm4* mutant shows an increase of electrolyte leakage and H₂O₂ content, the survival rate decreased after chilling treatment [45]. In *Arabidopsis*, *RDM4* promotes the affinity of polymerase II (Pol II) to the promoter of *CBF* genes and, as a result, increases the cold tolerance of *Arabidopsis* [45].

In rice (*Oryza sativa*), during the recovery period from cold stress, transgenic lines overexpressing *OsGH3-2* exhibit enhanced cold tolerance compared to wild type plants. Even after 7 days of recovery, more than 80% of the transgenic plants remain vigorous, whereas almost all wild type plants died [46]. Another study shows that *OsMADS57* and *OsTB1* are directly targets of *OsWRKY94* and axillary bud regulated gene *D14* during cold adaptation in rice. This provides evidence that *OsMADS57* acts as a molecular linker between the developmental response and the tolerance to chilling stress in rice [47]. After the recovery process, *OsMADS57* could still preserve cell division during low temperatures [47]. Transgenic tobacco overexpressing *GhDREB1* showed improved tolerance to chilling stress compared to wild plants in early seedling and later seedling stages. *GhDREB1* was also detected as a transcriptional activator of *NtERD10B* and *NtERD10C* after cold stress treatment in transgenic tobacco [48]. A gene that is likely responsible for cold stress was also found in *Sorghum bicolor* [49]. The results were obtained through significant regions, proxies, or co-localization with single nucleotide polymorphisms (SNPs) and also on homology with photosynthesis and stress-responsive genes. The gene is a *GST* gene family, namely *SB08g007310* (Table 1). The gene function is also related to photosynthesis, and carbon and nitrogen metabolism [49]. Ectopic expression of a *CBF* pathway independent chilling tolerance gene (*AtGRXS17*) in tomato enhances chilling tolerance of tomato via collaboration with *CBFs* [50]. In recent years, transcriptome and bioinformatics has been increasingly used to address complex biological questions [51–55] and more cold stress related genes will be investigated. Moreover, a large number of mutant lines have been developed for the functional study of the genes in the plant genome, including those inserted by Transfer DNA (T-DNA) and RNA Interference (RNAi) [51,52]. In addition, Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/CRISPR-associated protein 9 (Cas9), also known as a genome editing tool, allow scientists to change the DNA of an organism. CRISPR/Cas9 has been widely used, since it can be successfully used to edit multiple genes in a plant [56–59]. However, the lack of sufficient genomic sequence information in many plants is a limitation of CRISPR/Cas9. In the future, it would be prudent to develop this technology's ability to elucidate multiple genes, TFs, and protein functions in plants that are yet to be identified and may have a role in cold stress.

Table 1. Cold stress-related genes in plants and their expression under different type of stress conditions.

Gene Name	Family	Species	Type of Stress Condition	References
<i>FtbHLH2</i>	bHLH	<i>Fagopyrum tataricum</i>	Cold stress	[31]
<i>BpUVR8</i>	UVR	<i>Betula platyphylla</i>	ABA response and cold stress	[60]
<i>FDA2-3</i>	FDA	<i>Gossypium hirsutum</i>	Cold stress	[30]
<i>FDA2-4</i>				
<i>FDA8</i>		<i>Arabidopsis thaliana</i>	Cold stress	[30]
<i>Sb08g007310</i>	GST	<i>Sorghum bicolor</i>	Cold stress	[49]
<i>Sb06g018220</i>	ZEP	<i>Sorghum bicolor</i>	Epoxidation of zeaxanthin in the xanthophyll cycle	[49]
<i>AtGRXS17</i>	Trx	<i>Solanum lycopersicum</i>	Chilling stress	[50]
<i>AtCBF3</i>	AP2/ERF	<i>Arabidopsis</i>	Cold Stress	[50]
<i>VaERF080</i>	AP2/ERF	<i>Vitis amurensis</i>	Cold stress	[31]
<i>VaERF087</i>				
<i>SiDHN</i>	DHN	<i>Saussurea involucreta</i>	Freezing stress and drought stress	[5]
<i>OsGH3-2</i>	GH3	<i>Oryza sativa</i>	Drought and cold stress	[46]
<i>MYBS3</i>	MYB	<i>Oryza sativa</i>	Cold stress	[4]
<i>RDM4</i>		<i>Arabidopsis</i>	Cold stress and freezing stress	[45]
<i>OsMADS57</i>		<i>Oryza sativa</i>	Chilling stress	[47]
<i>GHDREB1</i>	DREB	<i>Gossypium hirsutum</i>	Chilling stress	[48]
<i>AtHAP5A,</i> <i>AtXTH21</i>		<i>Arabidopsis thaliana</i>	Freezing stress	[61]
<i>PUB25/26</i>		<i>Arabidopsis thaliana</i>	Freezing stress	[62]
<i>MaPIP2-7</i>	AQP	<i>Musa acuminata</i>	Drought, cold and salt stress	
<i>MaPIP2-7</i>	AQP	<i>Musa acuminata</i>	Drought, cold and salt stress	[17]
<i>CsCPKs</i>	CPK	<i>Camellia sinensis</i>	Cold tolerance	[63]
<i>COR413</i>	COR	<i>Saussurea involucreta</i>	Cold and drought tolerance	[64]
<i>SET, JmjC</i>		<i>Brassica rapa</i>	Heat and cold stress	[65]
<i>TaTPS11</i>		<i>Triticum aestivum</i>	Cold stress	[66]
<i>TaSMT1, TaSMT2</i>		<i>Triticum aestivum</i>	Cold stress	[67]
<i>14-3-3ε, 14-3-3ω</i>		<i>Arabidopsis thaliana</i>	Cold and oxidative stress	[68]
<i>CsLEA</i>	LEA	<i>Camellia sinensis</i>	Cold and dehydration stress	[69]
<i>MdMYB108L</i>	MYB	<i>Malus domestica</i>	Cold stress	[70]
<i>MdHY5</i>	bZIP	<i>Malus domestica</i>	Cold stress	[70]
<i>DIICE1</i>	bHLH	<i>Dimocarpus longan</i>	Cold stress	[71]
<i>ZjICE1</i>	bHLH	<i>Zoysia japonica</i>	Cold, dehydration and salt stress	[72]
<i>VvCBF</i>	DREB	<i>Vitis vinifera</i>	Cold stress	[15]
<i>AtGLR1.2AtGLR1.3</i>		<i>Arabidopsis thaliana</i>	Cold stress	[16]
<i>STCH4</i>		<i>Arabidopsis thaliana</i>	Cold stress	[73]

3. Physiological Changes during Cold Stress

A large number of plant species display physiological or cellular perturbations when encountering LT stress. Under LT stress, plants need to maintain cell behavior and activity, and, in particular, the stability of the cell membrane and structure of the protein with biological activity, for survival in adverse environments [47]. The exposure of plants to subzero temperature leads to ice formation in plant tissues [74]. Higher concentrations of active ice nucleators in the apoplastic solution of plants leads to a higher freezing point. As a result, ice crystals first form in the extracellular space of plant cells. Ice formation outside cells reduces the water potential of the apoplastic solution, which leads to water flowing from the cells. Therefore, freezing stress at the cellular level is often followed by dehydration stress. Ice crystals will lead to an increase in electrolyte leakage and membrane lipid phase changes. As the freezing continues, osmotic forces produce cellular dehydration, which facilitates the formation of intracellular ice crystals. At the extreme, ice crystals can puncture plant cells and lead to cytosol outflow, and ultimately cause the plants to die [9,42,75]. Therefore, preventing formation of intracellular ice crystals and avoiding growth of ice crystals are important for plants to tolerate cold stress. The most popular approach used by plants to deal with LT stress is cold acclimation, which allows plants to survive freezing via accumulation of cryoprotective polypeptides (e.g., *COR15a*) and osmolytes (e.g., soluble sugars and proline). It has been reported that sugar content in *Euphorbia resinifera*, *Echinocactus grusonii*, *Aloe vera*, *Crassula lactea*, *Bryophyllum pinnatum*, *Yucca aloifolia*, and *Sansevieria*

trifasciata is increased after cold stress [76]. Cold adaptive plants always store more sugar (D-Glucose, D-Glucose 6 Phosphate, amylose, starch, and maltose) in their underground tissues [25,77].

A recent study of grapevine reveals that grapevine leaves have a watery appearance, indicating tissue damage and cell leakage after freezing treatment. After 4 days of recovery, damage was found in the leaves [25]. Necrosis of plants is normally caused by overproduction of Reactive Oxygen Species (ROS). The elevated H_2O_2 level in plants under LT stress is the result of increased oxygenation reaction in the chloroplasts, which leads to an increased glycolate content. The glycolate is converted to glyoxylate in peroxisomes by glycolate oxidase, which is accompanied by accumulation of H_2O_2 . The physiological process of ROS toxic concentration in plants could be relieved by developing a complicated and efficient ROS scavenging and antioxidant defense system. Plants require the use of low ROS concentrations as mediators for signal transduction. Nitric oxide (NO) is implicated in the response of plants to LT stress. ABA, Ca^{2+} , and H_2O_2 -associated NO are shared by signaling cold stress events [78]. Hemoglobin (Hb) is believed to be a modifier of low-temperature plant response through the transition of NO [79]. Hb over-expressing lines have demonstrated reduced cold-induced gene expression. However, a decrease was only seen in *CBF1* and *CBF3*, not *CBF2* [80]. Moreover, an increased malondialdehyde (MDA) content and Ca^{2+} in the cytosol characterized lipid degradation, while the activity of antioxidant enzymes, such as Catalase (CAT), superoxide dismutase (SOD), ascorbate peroxidase (APX), and peroxidase (POD), was minimized [22,42,81,82]. In addition, ABA and ROS can induce Ca^{2+} and will affect cold signaling [8].

After methyl jasmonate (MeJa) treatment in bell pepper [34] and ethylene treatment in *Arabidopsis* [42], bell pepper and *Arabidopsis* are more tolerant to cold stress and chilling stress. Their physiological function is changed, namely, via decrease of MDA content and increase of antioxidant enzyme activities, such as CAT, SOD, and POD. This proves that these plants have a high tolerance to cold stress [42]. Other research about cold stress revealed that cold could induce the inhibition of CO_2 assimilation in *Zea mays* and was also related to a persistent depression of the photochemical efficiency of PSII [83]. Moreover, NO is known as a signal in an early transduction network. Cold triggers NO a few hours after exposure to low temperature in *Arabidopsis* [84]. *Arabidopsis* hemoglobin 1 (*AHb1*) interferes with NO production before and after exposure to low temperature. However, *A. thaliana* over-expressing *AHb1* resists its capacity to produce NO during cold stress [84].

Nevertheless, lowering the temperature decreased the translocation of xylem N in *S. cereale* and *B. napus* by about 60% and 30%, respectively. It is suggested that low temperatures will directly affect the absorption mechanism of nitrates and N accumulation in the roots. This is caused by an obstruction of the N xylem flow greater than the NO absorption [85].

LT also contributed to decreasing chlorophyll content of rice. Putting rice at low temperatures modified the number of chloroplasts, the arrangement of grana (no normal stacked membranous structures), and the lamellar structures in chloroplasts. In addition, temperature-sensitive virescent (TSV) could improve the stability of *OsTrxZ* at low temperatures, which is critical to the production of chloroplasts during or after cold stress in *Oryza sativa* [86]. This is due to the abnormal development of chloroplasts during and after low-temperature stress [87].

4. Influence Factors

Plants can sense several parameters of light signals, such as light quality (wavelength), quantity, and duration (daylight), and even direction. The length of the daily photoperiod and moderate subfreezing temperature greatly affects the hardening and dehardening processes in Scots pine [81]. Short day (9 h) and long day (16 h) first frost temperatures are different with 16 h and 9 h daily photoperiod: the first frost is at about $-10\text{ }^{\circ}\text{C}$ and frozen at $-22\text{ }^{\circ}\text{C}$. This means that light has a pivotal role in the hardening process. A previous study suggested that light is one of the regulators of *FDA2-3* and *FDA2-4* gene expression in cotton (*Gossypium hirsutum*). Light and low temperature induces the expression of these two genes and allows the plant to tolerate cold stress [30]. Meanwhile, LT reduces the utilization of light [82]. Light has a pivotal effect

on the relationship between insects and plants, while temperature affects light performance [88]. However, the light also acts as an external signal that influences the growth of the plant [89].

Similar to light, hormones also have a role in the activation process of TFs [35,37]. Although the ICE-CBF-COR pathway plays a key role in the cold tolerance in plants, researchers are currently focusing on the contribution of hormones to cold stress. Major hormones, such as ABA, GA, brassinosteroids (BR), jasmonates (JA), auxin, cytokinin (CK), melatonin, and polyamines, affect CBFs (Figure 2) [37]. One of the most important hormones in cold stress is ABA [90]. ABA increases when stress surge affects plants and, contrary to ABA, the TF is not affected. Furthermore, an overlapping linkage between the ABA-dependent pathway and the ICE-CBF-COR pathway was found in cold tolerance [37]. A number of studies suggest that ABA can induce increases in the transcript levels of CBF genes, perhaps via binding to the CRT/DRE element. It has the potential to encourage CBF activation. In addition, *AtHAP5A* regulates freezing stress tolerance through binding to the CCAAT motif of *AtXTH21* in *Arabidopsis*. *AtHAP5A* and *AtXTH21* overexpressing plants were more tolerant of freezing stress but less susceptible to ABA than WT plants [61]. Moreover, ABA also plays an important role in the acclimation process and can induce *COR* gene expression [26]. Some genes in *Pyrus ussuriensis* also collaborate with ABA, Gibberellin, and Ethylene to up-regulate genes [35]. The ABA signal transduction pathway also has a positive regulator, namely, the *BpUVR8* gene, which regulates the expression of a subset of ABA-responsive genes, both in *Arabidopsis* and *Betula platyphylla* under ABA treatment [60]. ABA pretreatment was also successful in increasing the mechanism of cold stress tolerance in the root level of *Brassica rapa* with phase <3 h and decreased the deleterious effect of Paclobutrazol (PBZ), which reduced the root hydraulic conductance of *B. rapa* [91].

Other studies have found plant mutants with altered levels of GA. GA will increase rice tolerance in stress. In research of *B. napus*, the gibberellin 2 oxidase gene was added into a transgenic plant and caused dwarfism. In comparison to the WT plants, the dwarf transgenic plants were 18.3–26.1% shorter in height and had 17.8–33.6% shorter internodes, and smaller and dark green leaves. GA and JA play an efficient role in the ICE-CBF-COR pathway [37]. Jasmonates activate TFs and then TFs will bind with the cis-acting element in the promoter of target genes [92].

Ethylene, ABA, and Jasmonates hormones can induce the expression of ethylene-responsive (*ERF*) genes [93]. These genes can be found in species such as *Arabidopsis* (*AtERF6*), *Citrus sinensis* (*CsERF*), *Lycopersicon esculentum* (*LeERF3b*; *SIERF5*), *Nicotiana tabacum* (*JERF1*; *JERF3*), *Triticum aestivum* (*TaERF1*), and *Triticum turgidum* (*TdSHN1*). At low temperature, *ERFs* will bind with the GCC box and DRE elements and provide some plants with tolerance to cold stress.

In addition, the *BpGH3.5* gene also affects Indole-3-acetic acid (IAA) in birch. This is shown by the decrease of auxin, which is indicated by a decrease in IAA. Some research results show that GH3 gene families play an important role in plant growth and development, and the short root phenotype in transgenic birch is caused by changes in IAA levels [94]. In another study, it was also mentioned that *BpGH3.5* causes primary short and lateral roots and more root hairs. More root hairs are caused by increased surface area for nutrient and water uptake, and finally lead to short root length (root dwarfism) [95].

Transgenic plants produce more anthocyanins in winter. It is well known that the anthocyanin content in plants will be higher in cold stress conditions. This means that the Gibberellin 2-oxidase gene perhaps has an important role in cold stress [96]. Carbon ion beam irradiation is one of the tools that can upregulate the expression levels of *CBFs*, *ICE1*, *ICE2*, *CAMTA3*, and *COR* genes in cold stress [22]. In addition, melatonin is also known as an influencer of the increase of the levels of mRNA, such as *COR15a* [37]. Expression of those genes is increased by 50 Gy of carbon ion beam irradiation for 6 h and 12 h at 4 °C. Nonetheless, in *Arabidopsis*, carbon ion beam irradiation of 50 Gy increases the content of AsA and GSH, which play important roles in alleviating ROS generation and oxidative stress under cold stress [22]. The level of soil moisture and stomatal conductivity has been determined by Rihan et al. [26]; these two factors can up-regulate the *CBF/DREB1* gene in cauliflower (*Brassica oleracea* var. botrytis). In fact, the addition of methyl jasmonate to bell pepper can induce POD, CAT,

stress takes place. The *COR* gene is a critical gene that is responsible for chilling tolerance and cold acclimation processes in plants. Under normal conditions, *CBFs* are regulated by the circadian clock and the photoperiod. Under cold stress conditions, however, *CBFs* induce several cold stress-related genes to regulate the cold tolerance of plants.

Author Contributions: F.N.R. had contributed to writing and original draft preparation, S.C. had contributed to supervision, project administration, funding acquisition, review, and editing manuscript. All authors have read and agreed to the published version of the manuscript.

Funding: This review is funded by The Fundamental Research Funds for The Central Universities, grant number 2572019CG08 and Heilongjiang Touyan Innovation Team Program (Tree Genetics and Breeding Innovation Team).

Acknowledgments: The authors sincerely thank State Key Laboratory of Tree Genetics and Breeding, Northeast Forestry University, especially for providing a good environment during the writing process. The authors appreciate the reviewers for comments and suggestions.

Conflicts of Interest: The authors declare no conflict of interest.

References

- Mboup, M.; Fischer, I.; Lainer, H.; Stephan, W. Trans-species polymorphism and allele-specific expression in the *cbf* gene family of wild tomatoes. *Mol. Biol. Evol.* **2012**, *29*, 3641–3652. [[CrossRef](#)] [[PubMed](#)]
- Theocharis, A.; Clément, C.; Barka, E.A. Physiological and molecular changes in plants grown at low temperatures. *Planta* **2012**, *235*, 1091–1105. [[CrossRef](#)] [[PubMed](#)]
- Zhou, M.; Chen, H.; Wei, D.; Ma, H.; Lin, J. Arabidopsis I3 and DELLAs positively regulate each other in response to low temperature. *Sci. Rep.* **2017**, *7*, 1–13. [[CrossRef](#)]
- Mickelbart, M.V.; Hasegawa, P.M.; Bailey-Serres, J. Genetic mechanisms of abiotic stress tolerance that translate to crop yield stability. *Nat. Rev. Genet.* **2015**, *16*, 237–251. [[CrossRef](#)] [[PubMed](#)]
- Guo, X.; Zhang, L.; Zhu, J.; Liu, H.; Wang, A. Cloning and characterization of SiDHN, a novel dehydrin gene from *Saussurea involucreata* Kar. et Kir. that enhances cold and drought tolerance in tobacco. *Plant Sci.* **2017**, *256*, 160–169. [[CrossRef](#)]
- Liu, Y.; Zhou, J. MAPping Kinase Regulation of ICE1 in Freezing Tolerance. *Trends Plant Sci.* **2018**, *23*, 91–93. [[CrossRef](#)]
- Shi, Y.; Ding, Y.; Yang, S. Molecular Regulation of CBF Signaling in Cold Acclimation. *Trends Plant Sci.* **2018**, *23*, 623–637. [[CrossRef](#)]
- Chinnusamy, V.; Zhu, J.; Zhu, J.-K. Cold stress regulation of gene expression in plants. *Trends Plant Sci.* **2007**, *12*, 444–451. [[CrossRef](#)]
- Zhang, F.; Jiang, Y.; Bai, L.-P.; Zhang, L.; Chen, L.-J.; Li, H.G.; Yin, Y.; Yan, W.-W.; Yi, Y.; Guo, Z.-F. The ICE-CBF-COR Pathway in Cold Acclimation and AFPs in Plants. *Middle-East J. Sci. Res.* **2011**, *8*, 493–498.
- Zhao, C.; Lang, Z.; Zhu, J.K. Cold responsive gene transcription becomes more complex. *Trends Plant Sci.* **2015**, *20*, 466–468. [[CrossRef](#)]
- Zhang, X.; Da Silva, J.A.T.; Niu, M.; Li, M.; He, C.; Zhao, J.; Zeng, S.; Duan, J.; Ma, G. Physiological and transcriptomic analyses reveal a response mechanism to cold stress in *Santalum album* L. Leaves. *Sci. Rep.* **2017**, *7*, 42165. [[CrossRef](#)] [[PubMed](#)]
- Pandey, S.; Carrer, M.; Castagneri, D.; Petit, G. Xylem anatomical responses to climate variability in Himalayan birch trees at one of the world's highest forest limit. *Perspect. Plant Ecol. Evol. Syst.* **2018**, *33*, 34–41. [[CrossRef](#)]
- Hao, X.; Wang, B.; Wang, L.; Zeng, J.; Yang, Y.; Wang, X. Comprehensive transcriptome analysis reveals common and specific genes and pathways involved in cold acclimation and cold stress in tea plant leaves. *Sci. Hortic.* **2018**, *240*, 354–368. [[CrossRef](#)]
- Mata, C.I.; Hertog, M.L.; Van Raemdonck, G.; Baggerman, G.; Tran, D.; Nicolai, B.M. Omics analysis of the ethylene signal transduction in tomato as a function of storage temperature. *Postharvest Biol. Technol.* **2019**, *155*, 1–10. [[CrossRef](#)]
- Rubio, S.; Pérez, F.J. ABA and its signaling pathway are involved in the cold acclimation and deacclimation of grapevine buds. *Sci. Hortic.* **2019**, *256*, 108565. [[CrossRef](#)]
- Zheng, Y.; Luo, L.; Wei, J.; Chen, Q.; Yang, Y.; Hu, X.; Kong, X. The glutamate receptors AtGLR1. 2 and AtGLR1. 3 increase cold tolerance by regulating jasmonate signaling in *Arabidopsis thaliana*. *Biochem. Biophys. Res. Commun.* **2018**, *506*, 895–900. [[CrossRef](#)]

17. Xu, Y.; Hu, W.; Liu, J.; Song, S.; Hou, X.; Jia, C.; Li, J.; Miao, H.; Wang, Z.; Tie, W. An aquaporin gene MaPIP2-7 is involved in tolerance to drought, cold and salt stresses in transgenic banana (*Musa acuminata* L.). *Plant Physiol. Biochem.* **2020**, *147*, 66–76. [[CrossRef](#)]
18. Tolosa, L.N.; Zhang, Z. The Role of Major Transcription Factors in Solanaceous Food Crops under Different Stress Conditions: Current and Future Perspectives. *Plants* **2020**, *9*, 56. [[CrossRef](#)]
19. Puijalon, S.; Bouma, T.J.; Douady, C.J.; Groenendael, J.V.; Anten, N.P.R.; Martel, E.; Bornette, G. Plant resistance to mechanical stress: Evidence of an avoidance—Tolerance trade-off. *New Phytol.* **2011**, *191*, 1141–1149. [[CrossRef](#)]
20. Jutsz, A.M.; Gnida, A. Mechanisms of stress avoidance and tolerance by plants used in phytoremediation of heavy metals. *Arch. Environ. Prot.* **2015**, *41*, 104–114. [[CrossRef](#)]
21. Zarka, D.G.; Vogel, J.T.; Cook, D.; Thomashow, M.F. Cold Induction of Arabidopsis. *Plant Physiol.* **2003**, *133*, 910–918. [[CrossRef](#)] [[PubMed](#)]
22. Wang, L.; Ma, R.; Yin, Y.; Jiao, Z. Role of carbon ion beams irradiation in mitigating cold stress in Arabidopsis thaliana. *Ecotoxicol. Environ. Saf.* **2018**, *162*, 341–347. [[CrossRef](#)] [[PubMed](#)]
23. Zhen, Y.; Ungerer, M.C. Relaxed selection on the CBF/DREB1 regulatory genes and reduced freezing tolerance in the southern range of Arabidopsis thaliana. *Mol. Biol. Evol.* **2008**, *25*, 2547–2555. [[CrossRef](#)]
24. Borba, A.R.; Serra, T.S.; Górska, A.; Gouveia, P.; Cordeiro, A.M.; Reyna-Llorens, I.; Kneřová, J.; Barros, P.M.; Abreu, I.A.; Oliveira, M.M.; et al. Synergistic binding of bHLH transcription factors to the promoter of the maize NADP-ME gene used in C4 photosynthesis is based on an ancient code found in the ancestral C3 state. *Mol. Biol. Evol.* **2018**, *35*, 1690–1705. [[CrossRef](#)]
25. Londo, J.P.; Kovalski, A.P.; Lillis, J.A. Divergence in the transcriptional landscape between low temperature and freeze shock in cultivated grapevine (*Vitis vinifera*). *Hortic. Res.* **2018**, *5*. [[CrossRef](#)] [[PubMed](#)]
26. Rihan, H.Z.; Al-Issawi, M.; Fuller, M.P. Upregulation of CBF/DREB1 and cold tolerance in artificial seeds of cauliflower (*Brassica oleracea* var. botrytis). *Sci. Hortic.* **2017**, *225*, 299–309. [[CrossRef](#)]
27. Lata, C.; Prasad, M. Role of DREBs in regulation of abiotic stress responses in plants. *J. Exp. Bot.* **2011**, *62*, 4731–4748. [[CrossRef](#)]
28. Yadav, S.K. Cold stress tolerance mechanisms in plants. *Sustain. Agric.* **2009**, *2*, 605–620. [[CrossRef](#)]
29. Azzeme, A.M.; Abdullah, S.N.A.; Aziz, M.A.; Wahab, P.E.M. Oil palm drought inducible DREB1 induced expression of DRE/CRT- and non-DRE/CRT-containing genes in lowland transgenic tomato under cold and PEG treatments. *Plant Physiol. Biochem.* **2017**, *112*, 129–151. [[CrossRef](#)]
30. Kargiotidou, A.; Deli, D.; Galanopoulou, D.; Tsafaris, A.; Farmaki, T. Low temperature and light regulate delta 12 fatty acid desaturases (FAD2) at a transcriptional level in cotton (*Gossypium hirsutum*). *J. Exp. Bot.* **2008**, *59*, 2043–2056. [[CrossRef](#)] [[PubMed](#)]
31. Yao, P.; Sun, Z.; Li, C.; Zhao, X.; Li, M.; Deng, R.; Huang, Y.; Zhao, H.; Chen, H.; Wu, Q. Overexpression of *Fagopyrum tataricum* FtbHLH2 enhances tolerance to cold stress in transgenic Arabidopsis. *Plant Physiol. Biochem.* **2018**, *125*, 85–94. [[CrossRef](#)] [[PubMed](#)]
32. Kindgren. Transcriptional read-through of the long non-coding RNA SVALKKA governs plant cold acclimation. *bioRxiv* **2018**, 77058, 1–31. [[CrossRef](#)] [[PubMed](#)]
33. Jia, Y.; Ding, Y.; Shi, Y.; Zhang, X.; Gong, Z.; Yang, S. The cbfs triple mutants reveal the essential functions of CBFs in cold acclimation and allow the definition of CBF regulons in Arabidopsis. *New Phytol.* **2016**, *212*, 345–353. [[CrossRef](#)] [[PubMed](#)]
34. Wang, S.; Yang, C.; Zhao, X.; Chen, S.; Qu, G.-z. Complete chloroplast genome sequence of *Betula platyphylla*: Gene organization, RNA editing, and comparative and phylogenetic analyses. *BMC Genomics* **2018**, *19*, 950. [[CrossRef](#)]
35. Yang, T.; Huang, X.S. Deep sequencing-based characterization of transcriptome of *Pyrus ussuriensis* in response to cold stress. *Gene* **2018**, *661*, 109–118. [[CrossRef](#)]
36. Barrero-Gil, J.; Salinas, J. CBFs at the Crossroads of Plant Hormone Signaling in Cold Stress Response. *Mol. Plant* **2017**, *10*, 542–544. [[CrossRef](#)]
37. Wang, D.-Z.; Jin, Y.-N.; Ding, X.-H.; Wang, W.-J.; Zhai, S.-S.; Bai, L.-P.; Guo, Z.-F. Gene regulation and signal transduction in the ICE–CBF–COR signaling pathway during cold stress in plants. *Biochem. (Mosc.)* **2017**, *82*, 1103–1117. [[CrossRef](#)]
38. Franco-Zorrilla, J.M.; Solano, R. Identification of plant transcription factor target sequences. *Biochim. Biophys. Acta-Gene Regul. Mech.* **2017**, *1860*, 21–30. [[CrossRef](#)]

39. Yanagisawa, S. Dof Domain Proteins: Plant-Specific Transcription Factors Associated with Div. *Library* **2004**, *45*, 386–391.
40. Matsukura, S.; Mizoi, J.; Yoshida, T.; Todaka, D.; Ito, Y.; Maruyama, K.; Shinozaki, K.; Yamaguchi-Shinozaki, K. Comprehensive analysis of rice DREB2-type genes that encode transcription factors involved in the expression of abiotic stress-responsive genes. *Mol. Genet. Genom.* **2010**, *283*, 185–196. [[CrossRef](#)]
41. Ying, M.; Kidou, S.i. Discovery of novel cold-induced CISP genes encoding small RNA-binding proteins related to cold adaptation in barley. *Plant Sci.* **2017**, *260*, 129–138. [[CrossRef](#)] [[PubMed](#)]
42. Sun, X.; Zhu, Z.; Zhang, L.; Fang, L.; Zhang, J.; Wang, Q.; Li, S.; Liang, Z.; Xin, H. Overexpression of ethylene response factors VaERF080 and VaERF087 from *Vitis amurensis* enhances cold tolerance in *Arabidopsis*. *Sci. Hortic.* **2019**, *243*, 320–326. [[CrossRef](#)]
43. Hao, J.; Yang, J.; Dong, J.; Fei, S.z. Characterization of BdCBF genes and genome-wide transcriptome profiling of BdCBF3-dependent and -independent cold stress responses in *Brachypodium distachyon*. *Plant Sci.* **2017**, *262*, 52–61. [[CrossRef](#)] [[PubMed](#)]
44. Lou, X.; Wang, H.; Ni, X.; Gao, Z.; Iqbal, S. Integrating proteomic and transcriptomic analyses of loquat (*Eriobotrya japonica* Lindl.) in response to cold stress. *Gene* **2018**, *677*, 57–65. [[CrossRef](#)] [[PubMed](#)]
45. Chan, Z.; Wang, Y.; Cao, M.; Gong, Y.; Mu, Z.; Wang, H.; Hu, Y.; Deng, X.; He, X.J.; Zhu, J.K. RDM 4 modulates cold stress resistance in *Arabidopsis* partially through the CBF-mediated pathway. *New Phytol.* **2016**, *209*, 1527–1539. [[CrossRef](#)]
46. Du, H.; Wu, N.; Fu, J.; Wang, S.; Li, X.; Xiao, J.; Xiong, L. A GH3 family member, OsGH3-2, modulates auxin and methylation and chromatin patterning abscisic acid levels and differentially affects drought and cold tolerance in rice. *J. Exp. Bot.* **2012**, *63*, 6467–6480. [[CrossRef](#)]
47. Chen, L.; Zhao, Y.; Xu, S.; Zhang, Z.; Xu, Y.; Zhang, J.; Chong, K. Os MADS 57 together with Os TB 1 coordinates transcription of its target Os WRKY 94 and D14 to switch its organogenesis to defense for cold adaptation in rice. *New Phytol.* **2018**, *218*, 219–231. [[CrossRef](#)]
48. Shan, D.P.; Huang, J.G.; Yang, Y.T.; Guo, Y.H.; Wu, C.A.; Yang, G.D.; Gao, Z.; Zheng, C.C. Cotton GhDREB1 increases plant tolerance to low temperature and is negatively regulated by gibberellic acid. *New Phytol.* **2007**, *176*, 70–81. [[CrossRef](#)]
49. Ortiz, D.; Hu, J.; Salas Fernandez, M.G. Genetic architecture of photosynthesis in *Sorghum bicolor* under non-stress and cold stress conditions. *J. Exp. Bot.* **2017**, *68*, 4545–4557. [[CrossRef](#)]
50. Hu, Y.; Wu, Q.; Sprague, S.A.; Park, J.; Oh, M.; Rajashekar, C.B.; Koiwa, H.; Nakata, P.A.; Cheng, N.; Hirschi, K.D.; et al. Tomato expressing *Arabidopsis* glutaredoxin gene AtGRXS17 confers tolerance to chilling stress via modulating cold responsive components. *Hortic. Res.* **2015**, *2*, 1–11. [[CrossRef](#)]
51. Gang, H.; Liu, G.; Zhang, M.; Zhao, Y.; Jiang, J.; Chen, S. Comprehensive characterization of T-DNA integration induced chromosomal rearrangement in a birch T-DNA mutant. *BMC Genom.* **2019**, *20*, 311. [[CrossRef](#)] [[PubMed](#)]
52. Gang, H.; Li, R.; Zhao, Y.; Liu, G.; Chen, S.; Jiang, J. Loss of GLK1 transcription factor function reveals new insights in chlorophyll biosynthesis and chloroplast development. *J. Exp. Bot.* **2019**, *70*, 3125–3138. [[CrossRef](#)]
53. Chen, S.; Lin, X.; Zhang, D.; Li, Q.; Zhao, X.; Chen, S. Genome-Wide Analysis of NAC Gene Family in *Betula pendula*. *Forests* **2019**, *10*, 741. [[CrossRef](#)]
54. Wang, F.; Chen, S.; Liang, D.; Qu, G.-Z.; Chen, S.; Zhao, X. Transcriptomic analyses of *Pinus koraiensis* under different cold stresses. *BMC Genom.* **2020**, *21*, 1–14. [[CrossRef](#)]
55. Wang, S.; Huang, H.; Han, R.; Liu, C.; Qiu, Z.; Liu, G.; Chen, S.; Jiang, J. Negative feedback loop between BpAP1 and BpPI/BpDEF heterodimer in *Betula platyphylla* × *B. pendula*. *Plant Sci.* **2019**, *289*, 110280. [[CrossRef](#)]
56. Jyoti, A.; Kaushik, S.; Srivastava, V.K.; Datta, M.; Kumar, S.; Yugandhar, P.; Kothari, S.L.; Rai, V.; Jain, A. The potential application of genome editing by using CRISPR/Cas9, and its engineered and ortholog variants for studying the transcription factors involved in the maintenance of phosphate homeostasis in model plants. *Semin. Cell Dev. Biol.* **2019**, *96*, 77–90. [[CrossRef](#)]
57. Yubing, H.; Min, Z.; Lihao, W.; Junhua, W.; Qiaoyan, W.; Rongchen, W.; Yunde, Z. Improvements of TKC technology accelerate isolation of transgene-free CRISPR/Cas9-edited rice plants. *Rice Sci.* **2019**, *26*, 109–117. [[CrossRef](#)]

58. Abdelrahman, M.; Al-Sadi, A.M.; Pour-Aboughadareh, A.; Burritt, D.J.; Tran, L.-S.P. Genome editing using CRISPR/Cas9–targeted mutagenesis: An opportunity for yield improvements of crop plants grown under environmental stresses. *Plant Physiol. Biochem.* **2018**, *131*, 31–36. [[CrossRef](#)] [[PubMed](#)]
59. Ma, X.; Zhu, Q.; Chen, Y.; Liu, Y.-G. CRISPR/Cas9 platforms for genome editing in plants: Developments and applications. *Mol. Plant* **2016**, *9*, 961–974. [[CrossRef](#)] [[PubMed](#)]
60. Li, X.; Ma, M.; Shao, W.; Wang, H.; Fan, R.; Chen, X.; Wang, X.; Zhan, Y.; Zeng, F. Molecular cloning and functional analysis of a UV-B photoreceptor gene, BpUVR8 (UV Resistance Locus 8), from birch and its role in ABA response. *Plant Sci.* **2018**, *274*, 294–308. [[CrossRef](#)]
61. Shi, H.; Ye, T.; Zhong, B.; Liu, X.; Jin, R.; Chan, Z. At HAP 5A modulates freezing stress resistance in Arabidopsis through binding to CCAAT motif of AtXTH21. *New Phytol.* **2014**, *203*, 554–567. [[CrossRef](#)] [[PubMed](#)]
62. Wang, X.; Zeng, W.; Ding, Y.; Wang, Y.; Niu, L.; Yao, J.-l.; Pan, L.; Lu, Z.; Cui, G.; Li, G.; et al. Plant Science Peach ethylene response factor PpeERF2 represses the expression of ABA biosynthesis and cell wall degradation genes during fruit ripening. *Plant Sci.* **2019**, *283*, 116–126. [[CrossRef](#)] [[PubMed](#)]
63. Ding, C.; Lei, L.; Yao, L.; Wang, L.; Hao, X.; Li, N.; Wang, Y.; Yin, P.; Guo, G.; Yang, Y. The involvements of calcium-dependent protein kinases and catechins in tea plant [*Camellia sinensis* (L.) O. Kuntze] cold responses. *Plant Physiol. Biochem.* **2019**, *143*, 190–202. [[CrossRef](#)] [[PubMed](#)]
64. Guo, X.; Zhang, L.; Dong, G.; Xu, Z.; Li, G.; Liu, N.; Wang, A.; Zhu, J. A novel cold-regulated protein isolated from *Saussurea involucreta* confers cold and drought tolerance in transgenic tobacco (*Nicotiana tabacum*). *Plant Sci.* **2019**, *289*, 110246. [[CrossRef](#)] [[PubMed](#)]
65. Liu, G.; Khan, N.; Ma, X.; Hou, X. Identification, Evolution, and Expression Profiling of Histone Lysine Methylation Moderators in *Brassica rapa*. *Plants* **2019**, *8*, 526. [[CrossRef](#)]
66. Liu, X.; Fu, L.; Qin, P.; Sun, Y.; Liu, J.; Wang, X. Overexpression of the wheat trehalose 6-phosphate synthase 11 gene enhances cold tolerance in Arabidopsis thaliana. *Gene* **2019**, *710*, 210–217. [[CrossRef](#)]
67. Valitova, J.; Renkova, A.; Mukhitova, F.; Dmitrieva, S.; Beckett, R.P.; Minibayeva, F.V. Membrane sterols and genes of sterol biosynthesis are involved in the response of *Triticum aestivum* seedlings to cold stress. *Plant Physiol. Biochem.* **2019**, *142*, 452–459. [[CrossRef](#)]
68. Visconti, S.; D’Ambrosio, C.; Fiorillo, A.; Arena, S.; Muzi, C.; Zottini, M.; Aducci, P.; Marra, M.; Scaloni, A.; Camoni, L. Overexpression of 14-3-3 proteins enhances cold tolerance and increases levels of stress-responsive proteins of Arabidopsis plants. *Plant Sci.* **2019**, *289*, 110215. [[CrossRef](#)]
69. Wang, W.; Gao, T.; Chen, J.; Yang, J.; Huang, H.; Yu, Y. The late embryogenesis abundant gene family in tea plant (*Camellia sinensis*): Genome-wide characterization and expression analysis in response to cold and dehydration stress. *Plant Physiol. Biochem.* **2019**, *135*, 277–286. [[CrossRef](#)]
70. Wang, Y.; Mao, Z.; Jiang, H.; Zhang, Z.; Chen, X. A feedback loop involving MdMYB108L and MdHY5 controls apple cold tolerance. *Biochem. Biophys. Res. Commun.* **2019**, *512*, 381–386. [[CrossRef](#)]
71. Yang, X.; Wang, R.; Hu, Q.; Li, S.; Mao, X.; Jing, H.; Zhao, J.; Hu, G.; Fu, J.; Liu, C. DICE1, a stress-responsive gene from *Dimocarpus longan*, enhances cold tolerance in transgenic Arabidopsis. *Plant Physiol. Biochem.* **2019**, *142*, 490–499. [[CrossRef](#)] [[PubMed](#)]
72. Zuo, Z.-F.; Kang, H.-G.; Park, M.-Y.; Jeong, H.; Sun, H.-J.; Song, P.-S.; Lee, H.-Y. Zoysia japonica MYC type transcription factor ZjICE1 regulates cold tolerance in transgenic Arabidopsis. *Plant Sci.* **2019**, *289*, 110254. [[CrossRef](#)] [[PubMed](#)]
73. Yu, H.; Kong, X.; Huang, H.; Wu, W.; Park, J.; Yun, D.-J.; Lee, B.-h.; Shi, H.; Zhu, J.-K. STCH4/REIL2 Confers Cold Stress Tolerance in Arabidopsis by Promoting rRNA Processing and CBF Protein Translation. *Cell Rep.* **2020**, *30*, 229–242.e225. [[CrossRef](#)] [[PubMed](#)]
74. Puhakainen, T. Short-Day Potentiation of Low Temperature-Induced Gene Expression of a C-Repeat-Binding Factor-Controlled Gene during Cold Acclimation in Silver Birch. *Plant Physiol.* **2004**, *136*, 4299–4307. [[CrossRef](#)]
75. Demidchik, V.; Straltsova, D.; Medvedev, S.S.; Pozhvanov, G.A.; Sokolik, A.; Yurin, V. Stress-induced electrolyte leakage: The role of K⁺-permeable channels and involvement in programmed cell death and metabolic adjustment. *J. Exp. Bot.* **2014**, *65*, 1259–1270. [[CrossRef](#)]
76. Khan, H.; Shah, S.H.; Uddin, N.; Azhar, N.; Asim, M.; Syed, S.; Ullah, F.; Tawab, F.; Inayat, J. Biochemical and Physiological Changes of Different Plants Species in Response To Heat and Cold Stress. *ARPJ. Agric. Biol. Sci.* **2015**, *10*, 213–216.

77. Janská, A.; Maršík, P.; Zelenková, S.; Ovesná, J. Cold stress and acclimation—What is important for metabolic adjustment? *Plant Biol.* **2010**, *12*, 395–405. [[CrossRef](#)]
78. Ding, Y.; Shi, Y.; Yang, S. Advances and challenges in uncovering cold tolerance regulatory mechanisms in plants. *New Phytol.* **2019**, *222*, 1690–1704. [[CrossRef](#)]
79. Abiri, R.; Azmi, N.; Maziah, M.; Norhana, Z.; Yusof, B.; Atabaki, N.; Sahebi, M.; Valdiani, A.; Kalhori, N.; Azizi, P.; et al. Role of ethylene and the APETALA 2/ethylene response factor superfamily in rice under various abiotic and biotic stress conditions. *Environ. Exp. Bot.* **2017**, *134*, 33–44. [[CrossRef](#)]
80. Gupta, K.J.; Hinch, D.K.; Mur, L.A. NO way to treat a cold. *New Phytol.* **2011**, *189*, 360–363. [[CrossRef](#)]
81. Beck, E.H.; Heim, R.; Hansen, J. Plant resistance to cold stress: Mechanisms and environmental signals triggering frost hardening and dehardening. *J. Biosci.* **2004**, *29*, 449–459. [[CrossRef](#)]
82. Longo, V.; Kamran, R.V.; Michaletti, A.; Toorchi, M.; Zolla, L.; Rinalducci, S. Proteomic and Physiological Response of Spring Barley Leaves to Cold Stress. *Int. J. Plant Biol. Res.* **2017**, *5*, 1–10.
83. Savitch, L.V.; Ivanov, A.G.; Gudynaite-Savitch, L.; Huner, N.P.A.; Simmonds, J. Cold stress effects on PSI photochemistry in Zea mays: Differential increase of FQR-dependent cyclic electron flow and functional implications. *Plant Cell Physiol.* **2011**, *52*, 1042–1054. [[CrossRef](#)] [[PubMed](#)]
84. Cantrel, C.; Vazquez, T.; Puyaubert, J.; Rezé, N.; Lesch, M.; Kaiser, W.M.; Dutilleul, C.; Guillas, I.; Zachowski, A.; Baudouin, E. Nitric oxide participates in cold-responsive phosphosphingolipid formation and gene expression in Arabidopsis thaliana. *New Phytol.* **2011**, *189*, 415–427. [[CrossRef](#)] [[PubMed](#)]
85. Laine, P.; Bigot, J.; Ourry, A.; Boucaud, J. Effects of low temperature on nitrate uptake, and xylem and phloem flows of nitrogen, in Secale cereale L. and Brassica napus L. *New Phytol.* **1994**, *127*, 675–683. [[CrossRef](#)]
86. Sun, J.; Zheng, T.; Yu, J.; Wu, T.; Wang, X.; Chen, G.; Tian, Y.; Zhang, H.; Wang, Y.; Terzaghi, W. TSV, a putative plastidic oxidoreductase, protects rice chloroplasts from cold stress during development by interacting with plastidic thioredoxin Z. *New Phytol.* **2017**, *215*, 240–255. [[CrossRef](#)]
87. Cui, X.; Wang, Y.; Wu, J.; Han, X.; Gu, X.; Lu, T.; Zhang, Z. The RNA editing factor DUA 1 is crucial to chloroplast development at low temperature in rice. *New Phytol.* **2019**, *221*, 834–849. [[CrossRef](#)]
88. Garsed, S.; Davey, H.; Galley, D. The Effects of Light and Temperature on the Growth of and Balances of Carbon, Nitrogen and Potassium between Vicia faba L. and Aphis fabae Scop. *New Phytol.* **1987**, *107*, 77–102. [[CrossRef](#)]
89. Maibam, P.; Nawkar, G.M.; Park, J.H.; Sahi, V.P.; Lee, S.Y.; Kang, C.H. The influence of light quality, circadian rhythm, and photoperiod on the CBF-mediated freezing tolerance. *Int. J. Mol. Sci.* **2013**, *14*, 11527–11543. [[CrossRef](#)]
90. Shinozaki, K.; Kazuko, Y. Molecular responses to drought and cold stress. *Biotechnology* **1996**, *7*, 161–167. [[CrossRef](#)]
91. Bigot, J.; Boucaud, J. Effects of synthetic plant growth retardants and abscisic acid on root functions of Brassica rapa plants exposed to low root-zone temperature. *New Phytol.* **1998**, *139*, 255–265. [[CrossRef](#)]
92. Zhou, M.; Memelink, J. Jasmonate-responsive transcription factors regulating plant secondary metabolism. *Biotechnol. Adv.* **2016**, *34*, 441–449. [[CrossRef](#)] [[PubMed](#)]
93. Müller, M.; Munné-Bosch, S. Ethylene Response Factors: A Key Regulatory Hub in Hormone and Stress Signaling. *Plant Physiol.* **2015**, *169*, 32–41. [[CrossRef](#)] [[PubMed](#)]
94. Yang, G.; Chen, S.; Jiang, J. Transcriptome analysis reveals the role of BpGH3.5 in root elongation of Betula platyphylla × B. pendula. *Plant Cell Tissue Organ Cult.* **2015**, *121*, 605–617. [[CrossRef](#)]
95. Yang, G.; Chen, S.; Wang, S.; Liu, G.; Li, H.; Huang, H.; Jiang, J. BpGH3.5, an early auxin-response gene, regulates root elongation in Betula platyphylla × Betula pendula. *Plant Cell Tissue Organ Cult.* **2015**, *120*, 239–250. [[CrossRef](#)]
96. Zhou, B.; Lin, J.; Peng, W.; Peng, D.; Zhuo, Y.; Zhu, D.; Huang, X.; Tang, D.; Guo, M.; He, R.; et al. Dwarfism in Brassica napus L. induced by the over-expression of a gibberellin 2-oxidase gene from Arabidopsis thaliana. *Mol. Breed.* **2012**, *29*, 115–127. [[CrossRef](#)]
97. Nohales, M.A.; Kay, S.A. Molecular mechanisms at the core of the plant circadian oscillator. *Nat. Struct. Mol. Biol.* **2016**, *23*, 1061–1069. [[CrossRef](#)]

