Review

Insights on Calcium-Dependent Protein Kinases (CPKs) Signaling for Abiotic Stress Tolerance in Plants

Rana Muhammad Atif 1,2,+,†, Luqman Shahid 1,†, Muhammad Waqas 1,*, Babar Ali 1, Muhammad Abdul Rehman Rashid 1,3,†, Farrukh Azeem 4,*, Muhammad Amjad Nawaz 5,†, Shabir Hussain Wani 6, and Gyuhwa Chung 7,*,‡

1 Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad 38000, Pakistan; luqmanshahid73@gmail.com (L.S.); bhuttawaqas@gmail.com (M.W.); babar1292ali@gmail.com (B.A.); rashidpbg@hotmail.com (M.A.R.R.)
2 Center for Advanced Studies in Agriculture and Food Security, University of Agriculture, Faisalabad 38040, Pakistan
3 Industrial Crops Research Institute, Yunnan Academy of Agricultural Sciences, Kunming 650200, China
4 Department of Bioinformatics and Biotechnology, Government College University, Faisalabad 38040, Pakistan; azeuaf@hotmail.com
5 Education Scientific Center of Nanotechnology, Far Eastern Federal University, 690950 Vladivostok, Russia; amjad_ucauos@yahoo.com
6 Mountain Research Centre for Field Crops, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar 190001, India; shabirhussainwani@gmail.com
7 Department of Biotechnology, Chonnam National University, Chonnam 59626, Korea
* Correspondence: dratif@uaf.edu.pk (R.M.A.); chung@chonnam.ac.kr (G.C.)
† These authors contributed equally to this work.

Received: 28 June 2019; Accepted: 17 October 2019; Published: 24 October 2019

Abstract: Abiotic stresses are the major limiting factors influencing the growth and productivity of plants species. To combat these stresses, plants can modify numerous physiological, biochemical, and molecular processes through cellular and subcellular signaling pathways. Calcium-dependent protein kinases (CDPKs or CPKs) are the unique and key calcium-binding proteins, which act as a sensor for the increase and decrease in the calcium (Ca) concentrations. These Ca flux signals are decrypted and interpreted into the phosphorylation events, which are crucial for signal transduction processes. Several functional and expression studies of different CPKs and their encoding genes validated their versatile role for abiotic stress tolerance in plants. CPKs are indispensable for modulating abiotic stress tolerance through activation and regulation of several genes, transcription factors, enzymes, and ion channels. CPKs have been involved in supporting plant adaptation under drought, salinity, and heat and cold stress environments. Diverse functions of plant CPKs have been reported against various abiotic stresses in numerous research studies. In this review, we have described the evaluated functions of plant CPKs against various abiotic stresses and their role in stress response signaling pathways.

Keywords: calcium-dependent protein kinases; calcium signaling; ABA; drought; salinity

1. Introduction

Plants have several adaptive features to cope with biotic and abiotic stresses under challenging environmental situations. Plants respond to these stresses by inducing the expression of stress-responsive genes through a complex signaling pathway. The expression of these stress-responsive genes is induced
upon changes in calcium ion (Ca\(^{2+}\)) concentrations, due to various biotic and abiotic stimuli [1,2], which enable plant adaptations in a wide range of stressed environments.

Calcium (Ca) as a ubiquitous secondary messenger regulates the stress signaling mechanism in plants. Changes in Ca\(^{2+}\) concentration are sensed by several calcium-binding proteins, especially calcium-dependent protein kinases [3]. The calcium-dependent abiotic and biotic stress signaling mechanisms are most commonly dominated by calcium-dependent protein kinases, which play a pivotal role in the regulation of plant responsiveness to salt, drought, and cold and heat stresses as well as other environmental factors. Ca\(^{2+}\) is involved in abscisic acid (ABA)-dependent biotic and abiotic stress signals in various plant species [4,5]. The calcium-dependent protein kinases phosphorylate the ABA-responsive element-binding factors (ABFs). ABA regulation by Ca\(^{2+}\) is associated with plant defense systems through induction of antioxidants [6], including reactive oxygen species (ROS) [2], and other enzymes like superoxide dismutase (SOD), catalase 3 (CAT3), ascorbate peroxidase (APX), glutathione peroxidase (GPX), and glutathione reductase (GR) [6,7]. It is also involved in the induction of some nonenzymatic antioxidants like ascorbic acid, \(\alpha\)-tocopherol, carotenoids, and glutathione and controls multiple abiotic stress response processes [6,8–10]. This review will provide insight into the role of calcium-dependent protein kinases (CPKs) in abiotic stress tolerance in different plant species.

2. CPK Enzymes and Related Kinases

Several calcium-binding protein families have been identified in plants, which are potentially involved in the regulation of calcium-dependent abiotic stress response mechanisms. These Ca\(^{2+}\) sensors decode and transmit complex information, present in the form of calcium signal, to the phosphorylation events and regulate stress-responsive genes through protein interactions [11]. These Ca\(^{2+}\) signal-decoding groups include calcium-dependent protein kinases (CDPKs or CPKs), calmodulins (CaMs), calmodulin-like protein kinases (CMLs), calcineurin \(\beta\)-like proteins (CBLs), and Ca\(^{2+}\)/calmodulin-dependent protein kinase (CCaMK) [12,13]. Among all these kinases, CPKs, CMLs, and CBLs have only been discovered in plants and some protozoans, while CaMs are highly conserved among all eukaryotes [11,14]. CaMs, CBLs, and CMLs are small proteins that function as calcium signal communicators through binding to downstream effectors (EFs) [15,16]. CaMs evolved from CMLs, which are considered as the most primitive calcium-binding proteins [13]. Among all these, CPKs were identified in plants as well as green algae, oomycetes, and in some protozoans [17], but they are not present in animals. CPKs, through direct binding with Ca\(^{2+}\), have a predominant regulatory role for the Ca-sensing protein families [17].

3. CPK Family in Plants

CPKs are considered as the versatile player for the regulation of abiotic stress management in plants [17]. In 1984, the very first plant CPKs were identified in *Pisum sativum* [18]. These proteins were initially purified from soybeans in 1987. A CPK encoding gene was cloned from *Arabidopsis thaliana* in 1991, which opened new ways for CPK gene cloning in several other plant species [11,19,20]. The presence of CPKs in almost all parts of the plant demonstrates that these kinases have a high potential for regulating various signal transduction pathways and have a significant influence on plant growth and development [17,21–23].

3.1. CPK Distribution and Localization in Plants

CPKs show a widespread distribution in different plant species. The whole-genome sequencing of plant species (e.g., *Arabidopsis* [24]) enables researchers to conduct genome-wide identifications of variable CPK encoding genes. These studies identified 34 CPK-encoding genes in the genome of *Arabidopsis thaliana*, 20 in *Triticum aestivum* (wheat), and 31 in *Oryza sativa* (rice) [20,25,26]. *Solanum lycopersicum* (tomato), which is a model plant of the Solanaceae family, has 29 CPK-encoding genes [27]. Genome-wide exploration of some other plants such as *Zea mays* (maize), *Hordeum vulgare* (barley), *Cucumis melo* (melon), *Populus trichocarpa* (poplar), *Gossypium raimondii* (cotton), *Manihot esculenta*
(cassava), and *Vitis vinifera* (grapevine) revealed the presence of 40, 28, 18, 30, 41, 27, and 19 CPK-encoding genes, respectively [28–34] (Table 1). Mostly, CPK-encoding genes are expressed in leaves, meristems, roots, and flowers, while some are expressed only in specific tissues [25,35,36].

**Table 1.** Genome-wide identification of calcium-dependent protein kinases (CPKs) among various plant species.

| Sr. # | Common Name       | Botanical Name               | No. of CPKs | Genome Size (Mb) | Reference       |
|-------|-------------------|------------------------------|-------------|------------------|-----------------|
| 1     | Algae             | *Volvox carteri*             | 6           | 131.2            | [37]            |
| 2     | Apple             | *Malus domestica*            | 28          | 881.3            | [37]            |
| 3     | Arabidopsis       | *Arabidopsis italiana*       | 34          | 135              | [20]            |
| 4     | Banana            | *Musa acuminata*             | 44          | 523              | [38]            |
| 5     | Barley            | *Hordeum vulgare*            | 27          | 667              | [39]            |
| 6     | Barley            | *Hordeum vulgare*            | 28          | 667              | [31]            |
| 7     | Barrel clover     | *Medicago truncatula*        | 11          | 360              | [37]            |
| 8     | Black cottonwood  | *Populus trichocarpa*        | 28          | 422.9            | [37]            |
| 9     | Poplar            | *Populus trichocarpa*        | 30          | 500              | [34]            |
| 10    | Butcher           | *Micromonas pusilla*         | 22          | 2                | [13,37]         |
| 11    | Cacao tree        | *Theobroma cacao*            | 17          | 346              | [13,37]         |
| 12    | Canola            | *Brassica napus*             | 25          | 1130             | [40]            |
| 13    | Cassava           | *Manihot esculenta*          | 26          | 532.5            | [30]            |
| 14    | Caster bean       | *Ricinus communis*           | 15          | 400              | [37]            |
| 15    | Castor bean       | *Ricinus communis*           | 15          | 400              | [13,37]         |
| 16    | Chinese liquorice | *Glycyrrhiza uralensis*      | 23          | 379              | [41]            |
| 17    | Chlamydomonas     | *Chlamydomonas reinhardtii*  | 14          | 111.1            | [13,37]         |
| 18    | Clementine        | *Citrus clementina*          | 26          | 301.4            | [37]            |
| 19    | Cocoa tree        | *Theobroma cacao*            | 17          | 346              | [37]            |
| 20    | Columbine         | *Aquilegia coerulea*         | 16          | 306.5            | [13,37]         |
| 21    | Cotton            | *Gossypium raimondii*        | 41          | 880              | [28]            |
| 22    | Cotton            | *Gossypium hirsutum*         | 98          | 2250–2430        | [42]            |
| 23    | Cucumber          | *Cucumis sativus*            | 19          | 323.99           | [43]            |
| 24    | Cucumber          | *Cucumis sativus*            | 18          | 203              | [37]            |
| 25    | Finger Millet     | *Eleusine coracana*          | 4           | 1593             | [44]            |
| 26    | Flax              | *Linum usitatissimum*        | 47          | 318.3            | [37]            |
| 27    | Flooded gum       | *Eucalyptus grandis*         | 22          | 691              | [37]            |
| 28    | Foxtail Millet    | *Setaria italic*             | 27          | 405.7            | [37]            |
| 29    | Foxtail Millet    | *Setaria italic*             | 29          | 405.7            | [45]            |
| 30    | Foxtail millet    | *Setaria italic*             | 27          | 405.7            | [13,37]         |
| 31    | Grape             | *Vitis vinifera*             | 19          | 500              | [29]            |
| 32    | Grapevine         | *Vitis amurensis*            | 17          | 500              | [46]            |
| 33    | Grapevine         | *Vitis amurensis*            | 13          | 500              | [47]            |
| 34    | Green algae       | *Coccomyxa subellipsoidea*   | 2           | 49               | [13,37]         |
| 35    | Green algae       | *Ostreococcus lucimarinus*   | 3           | 13.2             | [13,37]         |
| 36    | Green bean        | *Phaeolus vulgaris*          | 25          | 521.1            | [37]            |
| 37    | Linseed           | *Linum usitatissimum*        | 47          | 318.3            | [13,37]         |
| 38    | Maize             | *Zea mays*                   | 35          | 2500             | [48]            |
| 39    | Maize             | *Zea mays*                   | 40          | 2500             | [49]            |
| 40    | Maize             | *Zea mays*                   | 47          | 2500             | [37]            |
Similarly, CPKs are also found in pollens, embryonic cells, guard cells, xylem, and meristem [36]. These Ca-dependent functional proteins are involved in biological functioning in cellular and subcellular compartments. Numerous CPKs of Arabidopsis are membrane-localized. It is considered that the myristylation causes CPKs to target the membrane [62]. This cellular and subcellular localization indicates a significant role of CPKs in several signaling transduction pathways under stress stimuli.

Table 1. Cont.

| Sr. # | Common Name      | Botanical Name       | No. of CPKs | Genome Size (Mb) | Reference |
|-------|-------------------|----------------------|-------------|------------------|-----------|
| 41    | Melon             | Cucumis melo         | 18          | 375              | [32]      |
| 42    | Monkey flower     | Minulius gattatus    | 25          | 321.7            | [37]      |
| 43    | Mustard           | Brassica rapa        | 49          | 283.8            | [37]      |
| 44    | Norway spruce     | Picea abies          | 11          | 1960             | [37]      |
| 45    | Oilseed rape      | Brassica rapa        | 49          | 283.8            | [13,37]   |
| 46    | Orange            | Citrus sinensis      | 24          | 319              | [13,37]   |
| 47    | Papaya            | Carica papaya        | 15          | 135              | [13,37]   |
| 48    | Papaya            | Carica papaya        | 15          | 135              | [37]      |
| 49    | Peach             | Prunus persica       | 17          | 227.3            | [37]      |
| 50    | Pepper            | Capsicum annuum      | 31          | 407.5            | [50]      |
| 51    | Pigeon Pea        | Cajanus cajan        | 23          | 852              | [51]      |
| 52    | Potato            | Solanum tubersum     | 21          | 800              | [37]      |
| 53    | Potato            | Solanum tubersum     | 23          | 800              | [52]      |
| 54    | Purple false brome| Brachypodium distachyon| 27          | 272              | [37]      |
| 55    | Purple false brome| Brachypodium distachyon| 27          | 272              | [37]      |
| 56    | Red Shepherd’s Purse| Capsella rubella    | 32          | 134.8            | [37]      |
| 57    | Rice              | Oryza sativa         | 29          | 430              | [53]      |
| 58    | Rice              | Oryza sativa         | 22          | 430              | [54]      |
| 59    | Rice              | Oryza sativa         | 30          | 372              | [37]      |
| 60    | Rubber tree       | Hevea brasiliensis   | 30          | 1332             | [55]      |
| 61    | Salt cress        | Thellungiella halophile| 31          | 238.5            | [13,37]   |
| 62    | Shepherd’s Purse  | Capsella rubella     | 32          | 134.8            | [37]      |
| 63    | Sorghum           | Sorghum bicolor      | 28          | 697.5            | [37]      |
| 64    | Soybean           | Glycine max          | 39          | 1115             | [56]      |
| 65    | Soybean           | Glycine max          | 50          | 1115             | [57]      |
| 66    | Soybean           | Glycine max          | 39          | 1115             | [58]      |
| 67    | Soybean           | Glycine max          | 41          | 978              | [13,37]   |
| 68    | Spikemosses       | Selaginella moellendorffii| 11          | 212.5            | [13,37]   |
| 69    | Spreading earthmoss| Physcomitrella patens| 25          | 480              | [13,37]   |
| 70    | Sweet orange      | Citrus sinensis      | 24          | 319              | [37]      |
| 71    | Switchgrass       | Panicum virgatum     | 53          | 1358             | [37]      |
| 72    | Tobacco           | Nicotiana tabacum    | 15          | 323.75           | [59]      |
| 73    | Tomato            | Solanum lycopersicum| 29          | 900              | [60]      |
| 74    | Tomato            | Solanum lycopersicum| 28          | 900              | [37]      |
| 75    | Tomato            | Solanum lycopersicum| 29          | 900              | [61]      |
| 76    | Wheat             | Triticum aestivum    | 20          | 2125             | [26]      |
| 77    | Wild Strawberry   | Fragaria vesca       | 14          | 240              | [37]      |
3.2. CPK Domain Organization and Calcium Ion Signal Decryption

On account of specific abiotic stress stimuli, the plant activates distinct physiological and biochemical response pathways. These stimuli are perceived by some protein and nonprotein elements. Protein elements include enzymes, transcription factors, and disparate receptors, while nonproteins comprise some secondary messengers such as calcium ion cyclic nucleotides, hydrogen ions, lipids, and active oxygen species [17,63]. Among them, Ca is a crucial secondary messenger involved in the signal transduction in all eukaryotes. It regulates the cell polarity and is essential for the regulation of stress-responsive cellular processes, cell morphogenesis, as well as plant growth and development [3,11,64,65]. These calcium signals are recognized by several protein kinases (CPKs), which regulate the response of downstream factors.

The CPK-encoding protein commonly has four functional domains, viz., calcium-binding domain (CBD), N terminus variable domain (NTD), protein kinase domain (PKD), and autoinhibitory junction (AJ), but many CPKs also contain an amino-terminal domain with varying sequence lengths, which is a source of functional diversity in the CPK family [62]. Sometimes, the C-terminus variable domain (CTD) also considered as a distinct domain instead of NTD. Different plant species contain varying numbers of CPK genes that are functionally important. The CBD contains four loops where calcium ions directly bind, called EF-hands, and are 20 amino acids in length [20,66–68]. The PKD domain has a characteristic serine/threonine phosphorylation site, which responds during regulation of CBD and AJ through Ca signals [68,69]. Among the number of CPK proteins, the majority of them have a myristylation site upstream from their N-terminal variable domain, showing that no CPKs appear in the form of membrane integral proteins [23]. The N-terminus of CPKs has a greater percentage of proline, glutamine, serine, and threonine (PEST) sequences, which carry out swift proteolytic degradation. There is an auto-inhibitory domain adjacent to the conserved domains, having a pseudo-substrate domain activity, and can cause inhibition of the regulatory pathways [68]. The variation in the length of CPK genes is due to the NTD, CT domain, and EF hand of the calcium-binding domain. Ca$^{2+}$ through binding with the EF-hand motif, carries out the phosphorylation of the CPK substrate by removing autoinhibition of kinase activity [22,70]. The highly conserved calmodulin-like domain regulates all the activities of the CPKs by binding the four Ca$^{2+}$ ions to four EF hands at its downstream end. Proteomics of most of the CPKs show that the autophosphorylation of proteins at serine and threonine through a calcium-dependent manner regulate the kinase activity (Figure 1).

![Structure and activation process of plant CPKs](image)

**Figure 1.** Structure and activation process of plant CPKs. (A) CPK domain structure under the inactive state, (B) activation of CPKs after the binding of Ca$^{2+}$ to the active site of the protein kinase domain (PKD), the autoinhibitory junction (AJ), and calmodulin-like domain (CaM-like domain, CaM-LD).
CPKs are monomolecular Ca-signaling protein kinases that regulate protein phosphorylation. In response to extrinsic and intrinsic cues, the variation in \( \text{Ca}^{2+} \) concentration, also called “\( \text{Ca}^{2+} \) signatures”, is recognized, interpreted, and transduced to the downstream toolkit by a group of \( \text{Ca}^{2+} \)-binding proteins. Phosphorylation events cause the activation of CPKs.

3.3. Functional Characterization of Plant CPKs

CPKs are differentially involved in diverse and indispensable functions in various plant species. CPKs show their role against biotic and abiotic stress tolerance upon interaction with specific calcium signals. With respect to abiotic stresses, CPKs are involved in drought \[71\], salinity \[72\], and heat \[73\] and cold \[74\] stress response signaling by regulating the ABA-responsive transcriptional factors and ion channel regulation \[75\]. Some \textit{Arabidopsis} CPKs (e.g., \textit{CPK13}) are also involved in potassium ion (K\(^+\)) channel regulation and other ion transportation in guard cells \[11\]. CPKs are also a major participant for providing pathogen-related immunity to plants. In several plant species, CPKs enhance the resistance against fungal elicitors \[1,76,77\], bacterial invasions \[78\], and many other pathogen-related diseases \[60,79\]. Some CPKs are involved in the regulation of the jasmonic acid (JA)-dependent pathway during insect and plant interaction and indirectly regulate plant resistance against insects \[80\]. The crucial role of CPKs have also been reported in various growth and developmental processes in plants. CPK-encoding genes (\textit{AtCPK28}) in \textit{Arabidopsis} play a positive role in stem elongation and contribute to secondary growth by interacting with the gibberellic acid (GA) pathway \[81,82\]. Similarly, some CPKs regulate pollen tube growth \[83\], latex biosynthesis \[55,84\], higher biomass accumulation \[85\], wounding and herbivory attack \[80,86\], germination and seedling growth \[87\], early maturity \[88,89\], pigmentation and fruit development \[90\], and several other metabolic and developmental pathways \[91\]. Still, the role and functionality of various CPK-encoding genes against biotic and abiotic stresses are veiled.

4. Role of CPKs in Abiotic Stress Tolerance

CPKs are recognized as a key Ca sensor group of protein kinase, having a multigene family in the whole plant kingdom \[55,92\]. The functions of these CPKs are completely dependent on \( \text{Ca}^{2+} \) signatures. Most of CPK functionality has been identified only in vitro, which is why only specific stress response-associated functions are known \[93\]. CPKs are not only involved in ion channel regulation but also respond to multiple stress-related pathways through interactions with other distant transcription factors through phosphorylation. Several loss-of-function and gain-of-function studies have confirmed the role of CPKs in abiotic stress tolerance. The cytosolic \( \text{Ca}^{2+} \) concentration fluxes, induced by various environmental stresses, viz., heat \[47\], cold \[94\] light \[95\], drought \[96,97\], salt \[72,98\], and osmotic \[99\] and pathogen-related factors \[100\], activate the plant’s transcriptional and metabolic activities \[101\]. Expression analyses and genome-wide studies have discovered the CPKs transcript activity, protein, and substrate recognition in different plant parts \[93\]. CPKs are also involved in the ABA-dependent abiotic stress signaling in various plant species. Several CPK genes are involved in the regulation of ABA signaling pathways in plants. Transient gene expression analyses in protoplasts of maize show that \textit{CPK11} (closely related to \textit{AtCPK4} and \textit{AtCPK11}) acts upstream of mitogen-activated proteins (MPK5) and is required for the activation of defense functions and antioxidant enzyme activity by regulating the expression of MPK5 genes. Similarly, \textit{CPK11} induced by hydrogen peroxide (H\(_2\)O\(_2\)) regulates and controls the activity of SOD and APX production induced by the ABA signaling pathway \[102,103\]. CPK activity confirmed by global expression analyses, shows that several CPK members are expressed differentially under varying ABA, salinity, drought, and heat and cold levels \[93\]. The change in the expression of CPK genes indicates the role of CPKs in plant adaptation against abiotic stress environments.
4.1. CPK-Mediated Drought Response Signaling

Drought stress is a major destructive factor affecting plant growth and development. It decreases water potential in plants as a result, where ABA accumulation controls the opening and closing of stomata, which leads to a lower photosynthetic activity [104]. It decreases the biomass and grain yield in plants. Under drought, plants adopt several conformational changes in the cell. These include ABA-dependent stomatal movement through regulation of guard cells, osmotic adjustments through the accumulation of osmolytes, regulating the oxidative damage by ROS homeostasis, and so on [93,105]. Changes in cytosolic Ca\(^{2+}\) concentrations due to water deficiency initiates CPK activity, resulting in the release of ABA in the cell [97]. ABA induces the injection of a calcium chelator (i.e., 1,2-bis (2-aminophenoxy) ethane-\(N,N',N''\)-tetra acetic acid; BAPTA), into the guard cell, which causes the closing of the stomata and, eventually, control of the transpiration process. Several plant CPKs are involved in drought stress-response mechanisms through an ABA-dependent manner. The CPK-encoding gene (CPK10) of Arabidopsis and an identified interacting heat shock protein (HSP1) lead to a drought-sensitive genotype. CPK10 T-DNA insertion mutants show sensitivity to drought stress as compared to the wild types. AtCPK9 and AtCPK10 are involved in Ca\(^{2+}\)-dependent ABA-mediated stomatal regulation through interaction with AtCPK33 [106]. The light-induced Arabidopsis encoding gene (CPK13) is involved in inhibiting stomatal opening and contributes to the drought stress responsiveness [11]. Some drought-responsive CPKs also have some associated functions. In rice, for example, OsCPK9 controls both drought stress tolerance and spikelet fertility through an ABA-dependent manner. Results of overexpression of OsCPK9 (OsCPK9-OX) induces stomatal closure through osmotic adjustment and increases the pollen viability and spikelet fertility under polyethylene glycol (PEG-6000)-induced drought stress [71]. Another CPK-encoding gene from the wild grapevine (CPK20) acts as a regulator for drought and its associated with heat/cold responsive pathways. Expression of these genes studied in transgenic Arabidopsis reveals that VaCPK20 overexpression exhibits a high level of tolerance to drought and cold stress through regulation of stress responder genes, viz., ABA-responsive element binding factor 3 (ABF3) or sodium/hydrogen exchanger 1 (NHX1), and cold regulator gene (COR47) [107]. While a CPK-encoding gene of broad bean (VfCPK1) reported being highly expressed in leaf epidermal peels, it is not considered a tissue-specific gene and is only expressed under drought stress [108]. This CPK-encoding gene shows no relationship with both high (37 °C) and low (4 °C) temperatures. The increase in the number of transcripts of VfCPK1 under drought stress only plays a role in the up-regulation of ABA-responsive genes and other kinases that are involved in the signal transduction pathway [108].

Some CPKs are involved in the regulation of antioxidant production and osmolyte homeostasis to combat drought stress. AtCPK8 regulates the movement of the stomatal guard cell and \(H_2O_2\) homeostasis in response to cellular Ca\(^{2+}\). An Arabidopsis T-DNA insertion mutant of CPK8 was found to be more sensitive to drought stress as compared to the wild-type plant, which reveals its drought response functionality [97]. CPKs phosphorylate some interactional proteins and perform interactive functioning in plants. Under drought stress, AtCPK8 with an interacting protein CAT3 controls the Ca\(^{2+}\)-dependent ABA-mediated regulation of stomatal guard cells. The CPK8 mutant was more sensitive to drought stress, while overexpressing CPK8 in transgenic plants exhibited tolerance [97,109]. CaCPK1 activity increases the chickpea responsiveness to drought stress, and its activity is ubiquitous in all tissues of the plant [110]. The activation of drought-responsive CPK-encoding genes is also triggered by various biochemical pathways. A rice CPK-encoding gene (OsCPK1) specifically activated by sucrose starvation was involved in mechanism to prevent drought stress injury during germination by negatively regulating the expression of GA biosynthesis and activating the expression of a 14-3-3 protein ‘GF14c’ [111].

Some closely related CPK-encoding isoforms show functional diversity in response to drought stress. For example, functional divergence is present between two closely homologous (TaCPK7 and TaCPK12) genes of wheat [112]. Functional analysis of TaCPK7 and TaCPK12 reveals that TaCPK7 responded to \(H_2O_2\), drought, salt, and low temperature, while TaCPK12 responded only
through the ABA signaling pathway [112]. Several transgenic studies have been conducted to characterize the functions of CPKs in different plant species in relation to drought stress response signaling in plants. The ZoCDPK1 genes from ginger overexpressed in tobacco (Nicotiana tabacum) conferred drought as well as salinity tolerance by improving the photosynthesis and growth of the plant [113]. Enhanced expression of ZoCDPK1 under drought and JA treatment was observed, but no variation was found in expression because of low-temperature stress and abscisic acid treatment. ZoCDPK1 induces the expression of stress-responsive genes (i.e., early responsive to dehydration stress (ERD1) and responsive to dehydration (RD21A)). In ginger, it controls the stress signaling pathway and works in a CTR/DRE-independent manner [113]. Expression of CPK encoding genes of maize studied in Arabidopsis shows that ZmCPK4 is involved in resistance to drought stress through ABA-regulated stomatal regulation. ZmCPK4 induced by H2O2 and ABA treatment shows that there might be an association between mitogen-activated protein kinase (MAPKs) members and ZmCPK4 in the upregulation of ABA-regulatory components, especially ABA-insensitive (ABI5), ABF3, and Ras-associated binding protein (RAB18) [87]. The functions of several drought-responsive CPK-encoding genes are summarized in Table 2. (Details of all the genes are given in Table S1)

**Table 2. Various functions of CPKs in biotic and abiotic stresses in different plant species.**

| Sr. # | Specie Name | Gene   | Function                                                                 | Reference               |
|-------|-------------|--------|--------------------------------------------------------------------------|-------------------------|
| 1     | Arabidopsis thaliana | AtCPK1 | Cellular homeostasis, resistance fungal elicitor.                         | [76,78,114–116]         |
| 2     |             | AtCPK3 | Salt resistance.                                                          | [117,118]               |
| 3     |             | AtCPK4 | Regulate ABA-regulatory transcription factors (e.g., ABF, ABF4, drought resistance). | [98]                    |
| 4     |             | AtCPK5 | Regulate immunity responses, ROS-dependent cell-to-cell communication.    | [78]                    |
| 5     |             | AtCPK6 | Drought tolerance, ABA-dependent osmotic adjustment.                      | [119]                   |
| 6     |             | AtCPK8 | Drought tolerance through interaction with protein CAT3.                 | [97,109]                |
| 7     |             | AtCPK9 | Regulate the ABA-dependent signaling pathway interacting with CPK33.      | [75]                    |
| 8     |             | AtCPK10| Drought responsiveness, ABA-mediated stomatal movements.                 | [106]                   |
| 9     |             | AtCPK11| Phosphorylation of AtDi19, ABA signaling.                                 | [120]                   |
| 10    |             | AtCPK12| Seed germination, activation of ABA regulators.                           | [72,121]                |
| 11    |             | AtCPK16| Root-gravitropism phosphorylate AtACS7.                                   | [122]                   |
| 12    |             | AtCPK21| Hyperosmotic adjustments.                                                 | [123]                   |
| 13    |             | AtCPK23| Salt stress, drought stress.                                              | [124]                   |
| 14    |             | AtCPK27| Salinity resistance, H2O2 and ionic homeostasis.                         | [125]                   |
| 15    |             | AtCPK28| Vascular development, stem elongation, ethylene synthesis, lignin deposition. | [81,82]                |
| 16    |             | AtCPK32| ABA-regulatory gene activation.                                           | [126]                   |
| 17    |             | AtCPK33| Regulates flowering, biosynthesis of florigen and flowering locus T protein. | [127]                   |
| 18    | Cicer arietinum (Chickpea) | CaCPK1 | Salt stress, drought stress, phytohormones, and defense signaling pathways. | [110]                   |
| 19    |             | CaCPK2 |                                                                        |                         |
| Sr. # | Specie Name                  | Gene       | Function                                                                                      | Reference |
|-------|----------------------------|------------|----------------------------------------------------------------------------------------------|-----------|
| 20    | Capsicum annuum (Peppers)   | CaCPK3     | Pathogen resistance, defense functioning (i.e., regulates jasmonic and salicylic acid), ethephon. | [79]      |
| 21    | Fragaria x ananassa (Garden strawberry) | FaCPK1    | low-temperature tolerance, fruit ripening.                                                   | [128]     |
| 22    | Medicago sativa (Alfalfa)   | MsCPK3     | Heat stress resistance, embryogenesis.                                                        | [129]     |
| 23    | Oryza sativa (Rice)         | OsCPK1     | Drought stress, seed germination, and GA biosynthesis.                                       | [111]     |
| 24    | Oryza sativa (Rice)         | OsCPK4     | Microbial-associated immunity, OsRLCK176 degradation.                                        | [130]     |
| 25    | Oryza sativa (Rice)         | OsCDPK5    | Fungal attacks phosphorylate OsERG1 and OsERG3.                                               | [131]     |
| 26    | Oryza sativa (Rice)         | OsCPK9     | Drought stress tolerance, ABA sensitivity spikelet fertility.                                | [71]      |
| 27    | Oryza sativa (Rice)         | OsCPK10    | Pseudomonas syringae pv resistance, SA and JA regulator.                                      | [132]     |
| 28    | Oryza sativa (Rice)         | OsCPK12    | Salt tolerance, blast disease resistance, induce ROS production, leaf senescence,            | [1,133]   |
| 29    | Oryza sativa (Rice)         | OsCDPK13   | Regulate cold, salt, dehydration responses.                                                   | [134]     |
| 30    | Oryza sativa (Rice)         | OsCPK17    | Cold stress interacts with sucrose synthase and plasma membrane intrinsic proteins.          | [135]     |
| 31    | Oryza sativa (Rice)         | OsCPK21    | Salt tolerance, ABA pathway activation.                                                       | [136]     |
| 32    | Oryza sativa (Rice)         | OsCPK24    | Cold stress tolerance, inhibition of OsGrx10.                                                | [74]      |
| 33    | Oryza sativa (Rice)         | OsCPK31    | Starch accumulation, early grain filling.                                                     | [137]     |
| 34    | Nicotiana tabacum (Tobacco) | NicPK1     | Signaling localization for repression of shoot growth, GA biosynthesis.                      | [138]     |
| 35    | Nicotiana tabacum (Tobacco) | NicPK2     | Biotic stress immunity.                                                                      | [139]     |
| 36    | Nicotiana tabacum (Tobacco) | NicPK32    | Pollen tube growth interacts with CNGC18.                                                    | [83]      |
| 37    | Hevea brasiliensis (Rubber tree) | HbCDPK1  | Latex biosynthesis, rubber production.                                                       | [84]      |
| 38    | Panax ginseng (Chinese ginseng) | PgCDPK1a  | Regulate ginseng growth.                                                                     | [85]      |
| 39    | Phalaenopsis amabilis (Moth orchid) | PaCPK1   | Cold stress sensitivity, wounding, pathogen attack.                                          | [86]      |
| 40    | Triticum aestivum (Wheat)   | TaCDPK1    | Regulate metabolic and developmental pathways.                                                | [91]      |
| 41    | Triticum aestivum (Wheat)   | TaCPK7     | Drought stress, salt stress, ABA signaling pathway.                                          | [112]     |
| 42    | Triticum aestivum (Wheat)   | TaCPK12    |                                                                                              |           |
| 43    | Zingiber officinale (Ginger) | ZoCDPK1    | Salinity and drought stress tolerance.                                                        | [113]     |
| 44    | Zea mays (Maize)            | ZmCPK1     | Cold stress regulates ZmERF3 expression.                                                      | [33]      |
| 45    | Zea mays (Maize)            | ZmCPK4     | Upregulate ABA-regulatory components (i.e., ABI5, ABI3, and RAD5) with MAPKs.                 | [87]      |
| 46    | Zea mays (Maize)            | ZmCPK11    | Superoxide dismutase and ascorbate peroxidase production, ABA pathway.                       | [103]     |
| Sr. # | Specie Name                  | Gene    | Function                                  | Reference |
|-------|-----------------------------|---------|-------------------------------------------|-----------|
| 47    | *Vigna radiata* (Mung bean) | VrCPK1  | Salt stress tolerance.                    | [140]     |
| 48    | *Vicia faba* (Broad bean)   | VFCPK1  | Drought stress resistance.                | [108]     |
| 49    | *Solanum lycopersicum* (Tomato) | SICDPK2 | Flowering.                                | [141]     |
| 50    | *Solanum lycopersicum* (Tomato) | SICDPK10 | Xanthomonas oryzae pv. oryzae and Pseudomonas syringae resistance. | [141]     |
| 51    | *Solanum lycopersicum* (Tomato) | SICDPK18 | Xanthomonas oryzae pv. oryzae and Pseudomonas syringae resistance. | [60]      |
| 52    | *Solanum lycopersicum* (Tomato) | StCPK1  | Tuber formation.                          | [142]     |
| 53    | *Solanum tuberosum* (Potato) | StCPK4  | Fungal pathogen resistance, ROS production. | [143]     |
| 54    | *Solanum tuberosum* (Potato) | StCPK5  | Blight resistance and susceptibility, ROS defense functioning. | [100]     |
| 55    | *Nicotiana attenuate* (Coyote tobacco) | NaCDPK4 | Wound-induced jasmonic acid (JA) accumulation, insect resistance. | [80]      |
| 56    | *Nicotiana attenuate* (Coyote tobacco) | NaCDPK5 |                                      |           |
| 57    | *Camellia sinensis* (Tea plant) | CsCDPK20 | High-temperature stress resistance.        | [144]     |
| 58    | *Camellia sinensis* (Tea plant) | CsCDPK26 |                                      |           |
| 59    | *Hordeum vulgare* (Barley)   | HvCPK3  | Resistance against powdery mildew.         | [145]     |
| 60    | *Hordeum vulgare* (Barley)   | HvCPK4  |                                      |           |
| 61    | *Brassica napus* (Oilseed rape) | BnaCPK2 | ROS accumulation, cell death.             | [2]       |
| 62    | *Musa acuminate* (Banana)    | MaCDPK7 | Heat-induced fruit ripening, chilling, stress tolerance. | [146]     |
| 63    | *Musa acuminate* (Banana)    | MaCDPK2 | Sensitive to Foc-TR4 infection, biotic stress tolerance. | [147]     |
| 64    | *Musa acuminate* (Banana)    | MaCDPK4 | Sensitive to Foc-TR4 infection, biotic stress tolerance. | [147]     |
| 65    | *Musa acuminate* (Banana)    | MaCDPK3 | Responsive for drought, cold, and salinity. |           |
| 66    | *Vitis amurensis* (Grapevine) | VaCPK1  | Salt stress, heat-responsiveness, stilbene bio-synthesis. | [89,148] |
| 67    | *Vitis amurensis* (Grapevine) | VaCPK26 | Salt stress, Stilbene bio-synthesis, through the induced expression of stilbene synthase (STS) genes. | [89,148] |
| 68    | *Pharbitis nil* (Picotee)    | PnCPK1  | Seed germination, seedling growth, flowering, regulation of light-dependent pathways, embryogenesis. | [90]      |
| 69    | *Pharbitis nil* (Picotee)    | PnCPK21 | Salt stress signaling.                    | [149]     |
| 70    | *Populus euphratica* (Desert poplar) | PrCPK10 | Drought and cold stress tolerance, ABA-responsive genes regulator. | [150]     |
| 71    | *Cucumis melo* (Hami melon)  | HmCDPK2 | Resistance against Penicillium infection.   | [151]     |

### 4.2. CPKs-Mediated Salt Response Signaling

Salt stress is also a major abiotic factor limiting plant growth and global agricultural productivity. Salinity, mostly due to the accumulation of sodium Na\(^+\) and chloride Cl\(^-\) ions, causes an ion imbalance that leads the plants toward oxidative stress [152]. These ions also induce the toxicity of other ions in plants. Salts also increases the production of ROS in plants. Several studies have presented the
functioning of CPK-encoding genes in plants against salt stresses. In *Arabidopsis*, AtCPK27 genes were found in favor of plant adaptation against salt stress [125]. Disruption in the expression of CPK27 in a T-DNA insertional mutant shows salt hypersensitivity at early growth stages in *Arabidopsis*. CPK27 regulated H$_2$O$_2$ and ionic homeostasis. AtCPK3 functions in guard cell movement through osmotic adjustment and ion channel regulation during salt accumulation [11,117,118]. The overexpression of AtCPK3 also increases ABA sensitivity and salt hypersensitivity, affecting the seedling growth and stomatal regulation [98,117]. AtCPK6 belongs to a subclass of the CPK gene family in *Arabidopsis* whose expression is induced under salt-stressed conditions. AtCPK6 and other kinases are activated because of cytoplasmic Ca$^{2+}$ elevation in the calcium-dependent pathway, which depends on ABA. These kinases combined with AtCPK6 trigger the salt and osmotic stress tolerance. Overexpression of AtCPK6 in *Arabidopsis* increases the drought and salt tolerance in transgenic plants. RT-PCR analyses showed an increase in the expression of salt-regulated genes in plants, in which the AtCPK6 gene was over-expressed [119].

OsCPK12 positively modulates salt stress tolerance, and it is associated with decreases in the resistance against blast disease by increasing the sensitivity to ABA and inducing the accumulation of ROS in rice [1]. In *Arabidopsis*, AtCPK27 was found to be favorable for plant adaptation against salt stress. Disruption in the expression of CPK27 in T-DNA insertional mutant shows salt hypersensitivity at early growth stages. Under salt stress, CPK27 regulates H$_2$O$_2$ and ionic homeostasis and makes plants resistant to salt stress (Figure 2) [125].

![Figure 2](#)

**Figure 2.** Role of different CPKs under various abiotic stresses; (A) Ca$^{2+}$-dependent ABA-mediated drought and salt stress signal recognition by CPKs; (B) Ca$^{2+}$ binding at the active site of protein kinase domain (PKD); (C) some drought-responsive genes involved in metabolite regulation and signal transduction pathways; (D) some salt-responsive genes and their role in antioxidant production (i.e., H$_2$O$_2$), as well as ROS detoxification; (E) some cold stress-responsive genes and their interaction genes activation; and (F) phosphorylation events controlling the anion channel regulation, K$^+$-inward channel regulation, Ca$^{2+}$-concentration, and channel regulation in the cell, and ABA-mediated CATALASE 3 regulation in plant cells.

OsCPK21 genes regulate the ABA-dependent salt stress signaling pathway. The high survival rate of transgenic rice seedlings developed by a mini scale, full-length cDNA over-expresser (FOX) gene hunting system was found due to the overexpression of OsCPK21-FOX under salt stress. In these plants, many salt-induced and ABA-regulating genes were expressed more as compared to wild-type plants.
Overexpression of OsCPK21 increases exogenous ABA and enhances salt tolerance by regulating and inducing the salt tolerance genes [136].

VaCPK21 gene up-regulation is positively involved in salt stress-response signaling mechanisms in grapevines. Overexpression of this gene in transgenic Arabidopsis and V. amurensis callus cell lines shows that under the salt stress, VaCPK21 acts as a regulator for genes that respond to salt stress (i.e., AtRD26, kinase-like protein (AtKIN1), AtRD29B, AtNHX1, catalase (AtCATT), copper superoxide dismutase (AtCSD1), cold regulator (AtCOR15 and AtCOR15)), and are found functionally important for salt stress tolerance [149]. Similarly, CaCPK1 and CaCPK2 activities are enhanced during high salt stress in leaves of chickpea plants. These isoforms play a role in the regulation of phytohormones and defense signaling pathways [110].

4.3. CPK-Dependent Cold and Heat Stress Signaling

Several CPK-encoding genes are differentially expressed under cold and heat treatments, but their exact molecular response mechanism is still unknown. OsCPK17 was reported to be important for the cold stress response by targeting the sucrose synthase and plasma membrane intrinsic proteins in rice [135]. OsCPK24 causes inhibition of glutaredoxin (OsGrx10) to sustain higher glutathione levels and phosphorylation, through the Ca$^{2+}$ signaling pathway, and responds positively to cold stress tolerance in rice [74]. MacDPK7 was found as a positive regulator of heat-induced fruit ripening and chilling stress tolerance in bananas [146].

PeCPK10 provides cold and drought stress tolerance through ABA-induced stomatal closing in P. euphratica. Its constitutive expression regulates ABA-responsive genes (i.e., RD29B and COR15A) that regulate the cellular functioning. Transgenic Arabidopsis with over-expressed PeCPK10 showed lower water loss under drought stress and tolerance against freezing. Expression analyses reveal that PeCPK10 localizes in cytoplasm quickly in response to changes in Ca$^{2+}$ concentrations and regulates the stomata guard cells, while nuclear-localized PeCPK10 only regulates the transcriptional factors [150]. CPK16 and CPK32 in grapevine plants positively regulate stilbene (a phenolic secondary metabolite) biosynthesis and CPK30 individually involved in both cold and drought tolerance [153]. In maize, ZmCPK1 and ZmCPK25 gene expressions were increased or decreased, respectively, upon exposure to cold stress. ZmCPK1 is negatively related with the regulation of the cold stress signaling mechanism. Studies of transgenic Arabidopsis also show that ZmCPK1 inversely regulates the expression of ethylene response factor (ZmERF3) genes and impairs cold stress tolerance [53]. CsCDPK20 and CsCDPK26 act as regulatory factors for heat stress-responsive genes and control positive heat stress signaling in the tea plant [144].

4.4. Role of CPKs in ROS Detoxification

Drought, salt, and heat stress triggers ROS production in plants, which must be detoxified by the plant to prevent itself from oxidative stress. Mitochondria, chloroplasts, and peroxisomes are the central organelles for ROS accumulation [105,154]. ABA-induced ROS production in plants is reported to be dependent on nicotinamide adenine dinucleotide phosphate hydrogen (NADPH) oxidase [105], which plays a vital role in oxidative bursting and activating plant defense responses [155,156]. Plant CPKs have been reported to regulate ROS production [2]. For instance, StCPK4 functions in the phosphorylation of NADPH oxidase and indirectly regulates ROS accumulation [143]. In B. napus, BnaCPK2 controls the activity of the respiratory burst oxidase homolog protein D (RbohD) during cell death and ROS production [2]. Arabidopsis CPK32 interacts with ABF4 in the ABA signaling pathway [126]. AtCPK6 from Arabidopsis decreases ROS production by reducing lipid peroxidation and confers drought stress [119]. Likewise, OsCPK12 promotes salt stress tolerance in rice through decreasing ROS accumulation [1]. The other CPKs and ROS responses are summarized in Table 2.
5. Functional Interaction of CPKs with Other Kinases in Abiotic Stress Signaling

CPK crosstalk and several interactions have been revealed in molecular regulatory pathways by functional studies. CPKs are not only involved in specific stress responses but also in multiple stress-related pathways by interacting with other distant proteins and regulating phosphorylation events. In Arabidopsis, CPK28 supports the turnover and phosphorylation of plasma membrane-related receptor-like cytoplasmic kinase (botrytis-induced kinase 1, BIK1), an important convergent substrate of multiple pattern recognition receptor (PRR) complexes for plant immunity [36]. AtCPK8 regulates and phosphorylates CAT3. It is involved in Ca^{2+}-dependent ABA and H_{2}O_{2}-induced guard cell regulation and provides drought resistance [97,109]. Molecular responses of AtCPK1 studied by using real-time PCR (RT-PCR) show that the investigated gene expressions, viz., pyrroline-5-carboxylate synthetase 1 (P5CS1), galactinol synthase 1 (GOLS1), RD22 (dehydration-responsive protein), RD29A, C-repeat binding factor (CBF4), and KIN2 (kinases), were upregulated by ATCPK1 and conferred salinity stress tolerance [157]. Further, ATCPK1 in loss-of-function and gain-of-function mutants were studied. It provides salt and drought stress resistance by up and down-regulation of stress responder genes, viz., zinc finger protein (ZAT10), APX2, COR15A, and RD29A [157]. AtCPK12 phosphorylates several salt stress response-related proteins during regulatory functioning [72]. Another grapevine gene (VaCPK21) transgenically expressed in Arabidopsis interacts with several salt stress-related genes (i.e., AtRD29A, AtRD26, AtKIN1, AtNHX1, AtCSD1, AtCAT1, AtCOR15A, and AtCOR47). Likewise, VaCPK20 responds to cold and drought stress tolerance by regulating COR47, NHX1, KIN1, or ABF3 in transgenic Arabidopsis [107,149].

In vivo interaction validated by co-immunoprecipitation assays (Co-IP) revealed that OsCPK4, a dual-face protein, was involved in the regulation of the stability of cytoplasmic kinase (CPK176) in rice. OsCPK4 plays a vital role in the negative regulation of receptor-like OsCPK176 accumulation. OsCPK4 and OsCPK176 phosphorylation events provide pattern-triggered immunity [130]. OsCPK17 phosphorylates the sucrose-phosphate synthase (OsSPS4) and plasma membrane intrinsic proteins (OsPIP2:1 and OsPIP2:6) (aquaporin), which are essential in sugar metabolism and membrane channel activity against cold stress responses in rice [135]. Moreover, OsCPK24 is involved in the phosphorylation of glutathione-dependent thioltransferase and inhibition of OsGRX10 to maintain a higher level of glutathione. This regulatory pathway induces the overall cold stress responsiveness in rice [74]. The plant CPK-encoding genes also induce the regulation of other stress-responsive genes, viz., AtRBOHF, AtRBOHD, AtABI1, AtRAB18, AtRD29B, AtHSP101, AtHSP70, Arabidopsis heat stress transcription factor A2 (AtHSF A2), AtP5CS2, proline transporter (AtProT1), AtPOD, and AtAPX1 for drought, salt, heat and cold stresses [11]. In tea plants, CsCPK20 and CsCPK26 have an interactive function for thermo-tolerance [144]. BnaCPK2 interacts with NADPH oxidase-like RbohD and controls ROS accumulation and cell death in oilseed rape [2]. In Arabidopsis, CPK9 controls the ABA ion channel regulation through a Ca^{2+}-dependent manner. Overexpression studies revealed that CPK9 and CPK33 mutually controlled the regulation of guard cells and stomatal movement [75]. CPK16 and CPK32 in grapevine plants positively regulate stilbene (a phenolic secondary metabolite) biosynthesis and CPK30 individually involved in both drought and cold tolerance [153]. Moreover, VaCPK1 and VaCPK26 genes are also involved in the same regulatory pathway [89]. The overexpression of VaCPK29 up-regulates stress-responsive genes (i.e., dehydration elements (DREs) AtABF3, AtDREB1A, AtDREB2A, AtRD29A, and AtRD29B), which provide resistance to heat as well as osmotic stress [73]. Under in vitro conditions, post-translationally miR390-regulated StCDPK1 controls the downstream auxin efflux carrier of PIN-proteins (STIPIN4), which are involved in potato tuber development [142].

Arabidopsis CPKs interact and phosphorylate the basic leucine zipper domain (bZIP) transcription factor FD and have a crucial role in floregen complex formation, which induces late flowering in plants [127]. Biochemical analyses show that the cold-induced marker gene (Zmerf3), which is a type II ethylene response factor, is suppressed by ZmCPK1 in maize. It is supposed that the ZmCPK1 directly phosphorylates the ERF3 protein and, as a result, inactivates ERF and has a negative role in the cold stress response [33]. ZmCPK11 controls the upstream ZmMPK5, which is involved in ABA-dependent
defense-related signaling in maize. CPK-encoding genes also have several interactive functions concerning plant growth and development. In *Xenopus* oocytes, AtCPK32 potentially regulates the cyclic nucleotide-gated ion channel regulating gene (CNGC18). AtCPK32 stimulation of CNGC18 regulates pollen tube depolarization in *Arabidopsis* [83]. Constitutively active OsCDPK1 in gain and loss-of-function transgenic rice targets the G-box factor 14-3-3c protein (GF14c). The expression of this protein causes the biosynthesis of GA and improves drought tolerance in rice seedlings [111]. AtCPK28 seems to be a regulatory component for the control of stem length and vascular development in *Arabidopsis*. The mutant of CPK28 (i.e., cpk28) was involved in the altered expression of NAC transcriptional regulators, such as NST1 and NST3, as well as gibberellin-3-beta-oxidogenase 1 (GA3ox1), a regulator of gibberellin homeostasis [81]. After ABA treatment, the dual functioning OsCPK9-OX in rice increases the transcript levels of drought and spikelet fertility-responsive genes, viz., OsRSUS, Rab21, Osbzip66, and OsNAC45. The results confirmed by quantitative reverse transcription polymerase chain reaction (qRT-PCR) demonstrate that OsCPK9 in interacting with these genes switches on the molecular regulation of ABA and stress-associated pathways [71]. The ZoCDPK1 gene from ginger promotes the expression of drought and salinity stress-associated genes, viz., RD2A (dehydration responsive protein 2A) and ERD1 (early responsive to dehydration stress 1) in tobacco. This DRE/CRT-independent regulatory pathway improves photosynthesis and plant growth as well [113]. Constitutive expression of calcium-dependent protein kinase of *Populus euphratica* (PeCPK10) regulates (RD29B and COR15A) cold and drought genes [150]. This cross-talk between CPK isoforms and the interactive partners increases the complexities among the signaling pathways.

6. Conclusions

The multifaceted role of CPKs in plants is consequential for abiotic stress tolerance in plants. Regardless of the reported functional detail on CPK-encoding genes, there are many other important isoforms identified whose expression profiles and involvement in abiotic stress signal transduction pathways in plants are still not clearly known. Future research is required to extend and identify the remaining CPK-encoding genes, their interactional regulators, and their functional exploration with respect to abiotic stress responses. These research studies are helpful to improve the plant’s adaptation under unpredictable environments and to minimize threats to the world’s food security.

**Supplementary Materials:** Supplementary materials can be found at [http://www.mdpi.com/1422-0067/20/21/5298/s1](http://www.mdpi.com/1422-0067/20/21/5298/s1).

**Author Contributions:** Conceptualization, R.M.A. and L.S.; Validation, G.C., M.W., M.A.R.R., F.A., and S.H.W.; Investigation, L.S., M.W., and F.A.; Resources, M.W., B.A., M.A.R.R., M.A.N., and S.H.W.; Writing—original draft preparation, R.M.A. and L.S.; Writing—review and editing, M.A.R.R., L.S. and M.A.N.; Visualization, G.C., M.W., M.A.R.R.; Supervision, L.S.; Project administration, R.M.A.; Funding acquisition, R.M.A.

**Funding:** This research was funded by the Punjab Agricultural Research Board (PARB) of Pakistan under the project grant # PARB-938.

**Acknowledgments:** The authors wish to acknowledge the Center for Advance Studies in Agriculture and Food Security (CAS-AFS) at the University of Agriculture, Faisalabad Pakistan for providing the research opportunity to the Master’s Candidates of Plant Breeding and Genetics.

**Conflicts of Interest:** The authors declare no conflicts of interest.
### Abbreviations

| Abbreviation | Description |
|--------------|-------------|
| ABA          | Abscisic acid |
| AJ           | Autoinhibitory junction |
| APX          | Ascorbate peroxidase |
| AtABI1       | *Arabidopsis thaliana* ABA-insensitive-1 |
| AtCDPK/AtCPK | *Arabidopsis thaliana*-calcium dependent protein |
| AtCSD1       | *Arabidopsis thaliana* copper superoxide dismutase 1 |
| AtHSP101 and 70 | *Arabidopsis thaliana* heat shock protein 101 and 70 |
| AtProT1      | *Arabidopsis thaliana* proline transporter 1 |
| AtRBOHD      | *Arabidopsis thaliana* respiratory burst oxidase protein D |
| AtRBOHF      | *Arabidopsis thaliana* respiratory burst oxidase protein F |
| BaCDPK/BaCPK | *Brassica napus* calcium dependent protein kinase |
| BIK1         | Botrytis-induced kinase 1 |
| bZIP         | Basic leucine zipper domain |
| Ca           | Calcium |
| Ca2+         | Calcium ion |
| CaCDPK/CaCPK | *Cicer arietinum* calcium dependent protein kinase |
| CaMs         | Calmodulins |
| CAT          | Catalase |
| CAT3         | Catalase-3 |
| CBD          | Calcium binding domain |
| CBF4         | C-repeat binding factor 4 |
| CBLs         | Calcineurin β-like proteins |
| CCoMK        | Calcium/Calmodulin-dependent protein kinase |
| CDPKs/CPKs   | Calcium dependent protein kinases |
| CMLs         | Calmodulin-like Protein Kinase |
| CNGC18       | Cyclic nucleotide-gated ion channel 18 |
| Co-IP        | Co-immunoprecipitation assay |
| COR          | Cold regulator |
| CT           | C-terminus |
| CTR          | C-repeat |
| DRE          | Dehydration elements |
| EF           | Elongation Factor |
| ERD1         | Early responsive to dehydration stress 1 |
| ERF3         | Ethylene response factor 3 |
| FaCDPK/FaCPK | *Fragaria x ananassa* calcium dependent protein kinase |
| GA           | Gibberellic acid |
| Ga3ox1       | Gibberellin-3-betaoxigenase 1 |
| GOLS1        | Galactinol synthase 1 |
| GPX          | Glutathione peroxidase |
| GR           | Glutathione reductase |
| H$_2$O$_2$   | Hydrogen peroxide |
| HSF          | Heat stress transcription factor |
| HSP          | Heat shock protein |
| HvCDPK/HvCPK | *Hordeum vulgare* calcium dependent protein kinase |
| JA           | Jasmonic acid |
| K*           | Potassium ion |
| LeCDPK/LeCPK | *Solanum lycopersicum* calcium dependent protein kinase |
| MaCDPK/MaCPK | *Musa acuminate* calcium dependent protein kinase |
| MPK5         | Mitogen-activated protein kinase 5 |
| MsCPK        | *Medicago sativa* calcium dependent protein kinase |
| NaCDPK/NaCPK | *Nicotiana attenuate* calcium dependent protein kinase |
NADPH Nicotinamide Adenine Dinucleotide Phosphate Hydrogen

NHX Sodium/Hydrogen exchanger

NST NAC-transcription factors

NtCDPK/NtCPK Nicotiana tabacum calcium dependent protein kinase

N-VD N-terminus variable domain

OsCPK/OsCDPK Oryza sativa calcium dependent protein kinase

OsGrx10 Oryza sativa glutaredoxin 10

OX Overexpression

P5CS1 Pyrroline-5-carboxylate synthetase 1

PaCDPK/PaCPK Phalaenopsis amabilis calcium dependent protein kinase

PeCDPK/PeCPK Populus euphratica calcium dependent protein kinase

PEG Polyethylene glycol

PEST Proline, glutamine, serine and threonine

PgCDPK/PgCPK Panax ginseng calcium dependent protein kinase

PIP Plasma membrane intrinsic protein

PKD Protein kinase domain

PnCDPK/PnCPK Populus euphratica calcium dependent protein kinase

PRR Pattern recognition receptor

qRT-PCR Quantitative reverse transcription Polymerase chain reaction

RAB18 Ras-associated binding protein 18

RbohD Respiratory burst oxidase homolog protein D

RD2A Dehydration responsive protein 2A

RD29A Dehydration responsive protein 29A

ROS Reactive oxygen species

RT-PCR Real-time PCR

SiCDPK/SiCPK Setaria italic calcium dependent protein kinase

SOD Superoxide dismutase

StCDPK/StCPK Solanum tuberosum calcium dependent protein kinase

TaCDPK/TaCPK Triticum aestivum calcium dependent protein kinase

T-DNA Transfer DNA

VaCDPK/VaCPK Vitis amurensis calcium dependent protein kinase

VaCPK/VaCDPK Vitis amurensis calcium dependent protein kinase

VfCPK/VfCDPK Vicia faba calcium dependent protein kinase

VrCDPK/VrCPK Vigna radiata calcium dependent protein kinase

ZmCDPK1/ZmCPK1 Zea mays calcium dependent protein kinase 1

ZoCDPK/ZoCPK Zingiber officinale calcium dependent protein kinase

References

1. Asano, T.; Hayashi, N.; Kobayashi, M.; Aoki, N.; Miyao, A.; Mitsuhara, I.; Ichikawa, H.; Komatsu, S.; Hirochika, H.; Kikuchi, S. A rice calcium-dependent protein kinase OsCPK12 oppositely modulates salt-stress tolerance and blast disease resistance. *Plant J.*, 2012, 69, 26–36. [CrossRef] [PubMed]

2. Wang, W.; Zhang, H.; Wei, X.; Yang, L.; Yang, B.; Zhang, L.; Li, J.; Jiang, Y-Q. Functional characterization of calcium-dependent protein kinase (CPK) 2 gene from oilseed rape (*Brassica napus* L.) in regulating reactive oxygen species signaling and cell death control. *Gene* 2018, 651, 49–56. [CrossRef] [PubMed]

3. Sanders, D.; Pelloux, J.; Brownlee, C.; Harper, J.F. Calcium at the crossroads of signaling. *Plant Cell* 2002, 14, S401–S417. [CrossRef] [PubMed]

4. Li, A.; Wang, X.; Leseberg, C.H.; Jia, J.; Mao, L. Biotic and abiotic stress responses through calcium-dependent protein kinase (CDPK) signaling in wheat (*Triticum aestivum* L.). *Plant Sig. Behav.* 2008, 3, 654–656. [CrossRef]

5. Asano, T.; Hayashi, N.; Kikuchi, S.; Ohsugi, R. CDPK-mediated abiotic stress signaling. *Plant Sig. Behav.* 2012, 7, 817–821. [CrossRef]

6. Miao, Y.; Lv, D.; Wang, P.; Wang, X.-C.; Chen, J.; Miao, C.; Song, C.-P. An *Arabidopsis* glutathione peroxidase functions as both a redox transducer and a scavenger in abscisic acid and drought stress responses. *Plant Cell* 2006, 18, 2749–2766. [CrossRef]
Ahmad, P.; Jaleel, C.A.; Salem, M.A.; Nabi, G.; Sharma, S. Roles of enzymatic and nonenzymatic antioxidants in plants during abiotic stress. *Crit. Rev. Biotechnol.* 2010, 30, 161–175. [CrossRef]

Jiang, M.; Zhang, J. Water stress-induced abscisic acid accumulation triggers the increased generation of reactive oxygen species and up-regulates the activities of antioxidant enzymes in maize leaves. *J. Exp. Bot.* 2002, 53, 2401–2410. [CrossRef]

Hu, X.; Jiang, M.; Zhang, A.; Lu, J. Abscisic acid-induced apoplastic H₂O₂ accumulation up-regulates the activities of chloroplastic and cytosolic antioxidant enzymes in maize leaves. *Planta* 2005, 223, 57. [CrossRef]

Baba, A.I.; Rigo, G.; Andräsi, N.; Tietz, O.; Palme, K.; Szabados, L.; Csépeli, Á. Striving Towards Abiotic Stresses: Role of the Plant CDPK Superfamily Members; Springer: Berlin, Germany, 2019; pp. 99–105.

Shi, S.; Li, S.; Asim, M.; Mao, J.; Xu, D.; Ullah, Z.; Liu, G.; Wang, Q.; Liu, H. The *Arabidopsis* calcium-dependent protein kinases (CDPKs) and their roles in plant growth regulation and abiotic stress responses. *Int. J. Mol. Sci.* 2018, 19, 1900. [CrossRef]

Ray, S.D. Decrypting Calcium Signaling in Plants: The Kinase Way; Springer: Berlin, Germany, 2015; pp. 119–174.

Mohanta, T.K.; Yadav, D.; Khan, A.L.; Hashem, A.; Abd Allah, E.F.; Al-Harrasi, A. Molecular Players of EF-hand Containing Calcium Signaling Event in Plants. *Int. J. Mol. Sci.* 2019, 20, 1476. [CrossRef] [PubMed]

Reddy, A.S.; Ali, G.S.; Celesnik, H.; Day, I.S. Coping with stresses: Roles of calcium-and calcium/calmodulin-regulated gene expression. *Plant Cell* 2011, 23, 2010–2032. [CrossRef] [PubMed]

Luan, S.; Kudla, J.; Rodriguez-Concepcion, M.; Yalovsky, S.; Gruissem, W. Calmodulins and calcineurin B-like proteins: Calcium sensors for specific signal response coupling in plants. *Plant Cell* 2002, 14, S389–S400. [CrossRef] [PubMed]

Hashimoto, K.; Kudla, J. Calcium decoding mechanisms in plants. *Biochimie* 2011, 93, 2054–2059. [CrossRef]

Valmonte, G.R.; Arthur, K.; Higgins, C.M.; MacDiarmid, R.M. Calcium-dependent protein kinases in plants: Evolution, expression and function. *Plant Cell Physiol.* 2014, 55, 551–569. [CrossRef] [PubMed]

Hetherington, A.; Trewavas, A. Activation of a pea membrane protein kinase by calcium ions. *Planta* 1984, 161, 409–417. [CrossRef]

Harmon, A.C.; Gribskov, M.; Harper, J.F. CDPKs–A kinase for every Ca²⁺ signal? *Trends Plant Sci.* 2000, 5, 154–159. [CrossRef] [PubMed]

Cheng, S.-H.; Willmann, M.R.; Chen, H.-C.; Sheen, J. Calcium signaling through protein kinases. The *Arabidopsis* calcium-dependent protein kinase gene family. *Plant Physiol.* 2002, 129, 469–485. [CrossRef]

Rudd, J.J.; Franklin-Tong, V.E. Unravelling response-specificity in Ca²⁺ signalling pathways in plant cells. *New Phytol.* 2001, 151, 7–33. [CrossRef]

Boudsocq, M.; Sheen, J. CDPKs in immune and stress signaling. *Trends Plant Sci.* 2013, 18, 30–40. [CrossRef] [PubMed]

Simeunovic, A.; Mair, A.; Wurzinger, B.; Teige, M. Know where your clients are: Subcellular localization and targets of calcium-dependent protein kinases. *J. Exp. Bot.* 2016, 67, 3855–3872. [CrossRef] [PubMed]

Initiative, A.G. Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* 2000, 408, 796. [CrossRef] [PubMed]

Ray, S.; Agarwal, P.; Arora, R.; Kapoor, S.; Tyagi, A.K. Expression analysis of calcium-dependent protein kinase gene family during reproductive development and abiotic stress conditions in rice (*Oryza sativa* L. ssp. *indica*). *Mol. Genet. Genom.* 2007, 278, 493–505. [CrossRef] [PubMed]

Li, A.-L.; Zhu, Y.-F.; Tan, X.-M.; Wang, X.; Wei, B.; Guo, H.-Z.; Zhang, Z.-L.; Chen, X.-B.; Zhao, G.-Y.; Kong, X.-Y. Evolutionary and functional study of the CDPK gene family in wheat (*Triticum aestivum* L.). *Plant Mol. Biol.* 2008, 66, 429–443. [CrossRef] [PubMed]

Wang, N.; Xia, E.-H.; Gao, L.-Z. Genome-wide analysis of WRKY family of transcription factors in common bean, *Phaseolus vulgaris*: Chromosomal localization, structure, evolution and expression divergence. *Plant Gene* 2016, 5, 22–30. [CrossRef]

Liu, W.; Li, W.; He, Q.; Daud, M.K.; Chen, J.; Zhu, S. Genome-wide survey and expression analysis of calcium-dependent protein kinase in *Gossypium raimondii*. *PLoS ONE* 2014, 9, e98189. [CrossRef]

Zhang, K.; Han, Y.-T.; Zhao, F.-L.; Hu, Y.; Gao, Y.-R.; Ma, Y.-F.; Zheng, Y.; Wang, Y.-J.; Wen, Y.-Q. Genome-wide identification and expression analysis of the CDPK gene family in grape, *Vitis* spp. *BMC Plant Biol.* 2015, 15, 164. [CrossRef]

Hu, W.; Hou, X.; Xia, Z.; Yan, Y.; Wei, Y.; Wang, L.; Zou, M.; Lu, C.; Wang, W.; Peng, M. Genome-wide survey and expression analysis of the calcium-dependent protein kinase gene family in cassava. *Mol. Genet. Genom.* 2016, 291, 241–253. [CrossRef]
31. Yang, Y.; Wang, Q.; Chen, Q.; Yin, X.; Qian, M.; Sun, X.; Yang, Y. Genome-wide survey indicates diverse physiological roles of the barley (Hordeum vulgare L.) calcium-dependent protein kinase genes. Sci. Rep. 2017, 7, 5306. [CrossRef]

32. Zhang, H.; Wei, C.; Yang, X.; Chen, H.; Yang, Y.; Mo, Y.; Li, H.; Zhang, Y.; Ma, J.; Yang, J. Genome-wide identification and expression analysis of calcium-dependent protein kinase and its related kinase gene families in melon (Cucumis melo L.). PLoS ONE 2017, 12, e0176352. [CrossRef]

33. Weckwerth, P.; Ehret, B.; Romeis, T. Zm CPK 1, a calcium-independent kinase member of the Zea mays CDPK gene family, functions as a negative regulator in cold stress signalling. Plant Cell Environ. 2015, 38, 544–558. [CrossRef] [PubMed]

34. Ye, S.; Wang, L.; Xie, W.; Wan, B.; Li, X.; Lin, Y. Expression profile of calcium-dependent protein kinase (CDPKs) genes during the whole lifespan and under phytohormone treatment conditions in rice (Oryza sativa L. ssp. indica). Plant Mol. Biol. 2009, 70, 311–325. [CrossRef] [PubMed]

35. Monaghan, J.; Matschi, S.; Shorinola, O.; Rovenich, H.; Matea, A.; Segonzac, C.; Malinovsky, F.G.; Rathjen, J.P.; MacLean, D.; Romeis, T. The calcium-dependent protein kinase CPK28 buffers plant immunity and regulates BIK1 turnover. Cell Host Microbe 2014, 16, 605–615. [CrossRef]

36. Mohanta, T.K.; Mohanta, N.; Mohanta, Y.K.; Bae, H. Genome-wide identification of calcium dependent protein kinase gene family in plant lineage shows presence of novel DxD and DEL motifs in EF-hand domain. Front. Plant Sci. 2015, 6, 1146. [CrossRef]

37. Li, M.; Hu, W.; Ren, L.; Jia, C.; Liu, J.; Miao, H.; Guo, A.; Xu, B.; Jin, Z. Identification, Expression, and Interaction Network Analyses of the CDPK Gene Family Reveal Their Involvement in the Development, Ripening, and Abiotic Stress Response in Banana. Biochem. Genet. 2019, 1–23. [CrossRef]

38. Fedorowicz-Strońska, O.; Koczyk, G.; Kaczmarek, M.; Krajewski, P.; Sadowski, J. Genome-wide identification, characterisation and expression profiles of calcium-dependent protein kinase genes in barley (Hordeum vulgare L.). J. App. Genet. 2017, 58, 11–22. [CrossRef]

39. Zhang, H.; Liu, W.-Z.; Zhang, Y.; Deng, M.; Niu, F.; Yang, B.; Wang, X.; Wang, B.; Liang, W.; Deyholos, M.K. Identification, expression and interaction analyses of calcium-dependent protein kinase (CPK) genes in canola (Brassica napus L.). BMC Genom. 2014, 15, 211. [CrossRef]

40. Tong, X.; Cao, A.; Wang, F.; Chen, X.; Xie, S.; Shen, H.; Jin, X.; Li, H. Calcium-Dependent Protein Kinase Genes in Glycrrhiza Uralensis Appear to be Involved in Promoting the Biosynthesis of Glycyrrhizic Acid and Flavonoids under Salt Stress. Molecules 2019, 24, 1837. [CrossRef]

41. Gao, W.; Xu, F.-C.; Guo, D.-D.; Zhao, J.-R.; Liu, J.; Guo, Y.-W.; Singh, P.K.; Ma, X.-N.; Long, L.; Botella, J.R. Calcium-dependent protein kinases in cotton: Insights into early plant responses to salt stress. BMC Plant Biol. 2018, 18, 15. [CrossRef]

42. Xu, X.; Liu, M.; Lu, L.; He, M.; Qu, W.; Xu, Q.; Qi, X.; Chen, X. Genome-wide analysis and expression of the calcium-dependent protein kinase gene family in cucumber. Mol. Genet. Genom. 2015, 290, 1403–1414. [CrossRef] [PubMed]

43. Singh, U.M.; Chandra, M.; Shankhdhar, S.C.; Kumar, A. Transcriptome wide identification and validation of calcium sensor gene family in the developing spikes of finger millet genotypes for elucidating its role in grain calcium accumulation. PLoS ONE 2014, 9, e103963. [CrossRef] [PubMed]

44. Yu, T.-F.; Zhao, W.-Y.; Fu, J.-D.; Liu, Y.-W.; Chen, M.; Zhou, Y.-B.; Ma, Y.-Z.; Xu, Z.-S.; Xi, Y.-J. Genome-wide analysis of CDPK family in foxtail millet and determination of SiCDPK24 functions in drought stress. Front. Plant Sci. 2018, 9, 651. [CrossRef]

45. Chen, F.; Fasoli, M.; Tornielli, G.B.; Dal Santo, S.; Pezzotti, M.; Zhang, L.; Cai, B.; Cheng, Z.-M. The evolutionary history and diverse physiological roles of the grapevine calcium-dependent protein kinase gene family. PLoS ONE 2013, 8, e80818. [CrossRef]

46. Dubrovina, A.S.; Kiselev, K.V.; Kristensen, V.S. Expression of calcium-dependent protein kinase (CDPK) genes under abiotic stress conditions in wild-growing grapevine Vitis amurensis. J. Plant Physiol. 2013, 170, 1491–1500. [CrossRef]

47. Ma, P.; Liu, J.; Yang, X.; Ma, R. Genome-wide identification of the maize calcium-dependent protein kinase gene family. App. Biochem. Biotechnol. 2013, 169, 2111–2125. [CrossRef]
49. Kong, X.; Lv, W.; Jiang, S.; Zhang, D.; Cai, G.; Pan, J.; Li, D. Genome-wide identification and expression analysis of calcium-dependent protein kinase in maize. *BMC Genom.* 2013, 14, 433. [CrossRef]

50. He, S. Genome-wide identification and expression analysis of calcium-dependent protein kinase and its closely related kinase genes in *Capsicum annuum*. *Front. Plant Sci.* 2015, 6, 737.

51. Wankhede, D.P.; Kumari, M.; Richa, T.; Aravind, J.; Rajkumar, S. Genome-wide identification and characterization of Calcium Dependent Protein Kinase Gene family in *Cajanus cajan*. *J. Environ. Biol.* 2017, 38, 167. [CrossRef]

52. Gromadka, R.; Cieśla, J.; Olszak, K.; Szczegielniak, J.; Muszyńska, G.; Polkowska-Kowalczyk, L. Genome-wide analysis and expression profiling of calcium-dependent protein kinases in potato (*Solana tuberosa*). *Plant Growth Reg.* 2018, 84, 303–315. [CrossRef]

53. Asano, T.; Tanaka, N.; Yang, G.; Hayashi, N.; Komatsu, S. Genome-wide identification of the rice calcium-dependent protein kinase and its closely related kinase gene families: Comprehensive analysis of the CDPKs gene family in rice. *Plant Cell Physiol.* 2005, 46, 356–366. [CrossRef] [PubMed]

54. Wan, B.; Lin, Y.; Mou, T. Expression of rice Ca$^{2+}$-dependent protein kinases (CDPKs) genes under different environmental stresses. *FEBS Lett.* 2007, 581, 1179–1189. [CrossRef] [PubMed]

55. Xiao, X.H.; Yang, M.; Sui, J.L.; Qi, J.Y.; Fang, Y.J.; Hu, S.N.; Tang, C.R. The calcium-dependent protein kinase (CDPK) and CDPK-related kinase gene families in *Hevea brasiliensis*—Comparison with five other plant species in structure, evolution, and expression. *FEBS Open Biol.* 2017, 7, 4–24. [CrossRef] [PubMed]

56. Liu, F. Calcium-Dependent Protein Kinase Regulates Soybean Serine Acetyltransferase in Response to Oxidative Stress. Ph.D. Thesis, University of Florida, Gainesville, FL, USA, 2002.

57. Hettenhausen, C.; Sun, G.; He, Y.; Zhuang, H.; Sun, T.; Qi, J.; Wu, J. Genome-wide identification of calcium-dependent protein kinase genes in soybean and analyses of their transcriptional responses to insect herbivory and drought stress. *Sci. Rep.* 2016, 6, 18973. [CrossRef] [PubMed]

58. Liu, H.; Che, Z.; Zeng, X.; Zhou, X.; Sitoe, H.M.; Wang, H.; Yu, D. Genome-wide analysis of calcium-dependent protein kinases and their expression patterns in response to herbivore and wounding stresses in soybean. *Funct. Integr. Genom.* 2016, 16, 481–493. [CrossRef] [PubMed]

59. Tai, S.-S.; Liu, G.-S.; Sun, Y.-H.; Jia, C. Cloning and expression of calcium-dependent protein kinase (CDPK) gene family in common tobacco (*Nicotiana tabacum*). *Agric. Sci. China* 2009, 8, 1448–1457. [CrossRef]

60. Wang, J.-P.; Xu, Y.-P.; Munyampundu, J.-P.; Liu, T.-Y.; Cai, X.-Z. Calcium-dependent protein kinase (CDPK) and CDPK-related kinase (CRK) gene families in tomato: Genome-wide identification and functional analyses in disease resistance. *Mol. Genet. Genom.* 2016, 291, 661–676. [CrossRef]

61. Hu, Z.; Lv, X.; Xia, X.; Zhou, J.; Shi, K.; Yu, J.; Zhou, Y. Genome-wide identification and expression analysis of calcium-dependent protein kinase in tomato. *Front. Plant Sci.* 2016, 7, 469. [CrossRef]

62. Podell, S.; Gribskov, M. Predicting N-terminal myristoylation sites in plant proteins. *BMC Genom.* 2004, 5, 37. [CrossRef]

63. Lisee, A.; Romeis, T. Biochemical regulation of in vivo function of plant calcium-dependent protein kinases (CDPK). *Biochim. Biophys. Acta BBA Mol. Cell Res.* 2013, 1833, 1582–1589. [CrossRef]

64. White, P.J.; Broadley, M.R. Calcium in plants. *Ann. Bot.* 2003, 92, 487–511. [CrossRef] [PubMed]

65. Himschoot, E.; Beeckman, T.; Friml, J.; Vanneste, S. Calcium is an organizer of cell polarity in plants. *Biochim. Biophys. Acta BBA Mol. Cell Res.* 2015, 1853, 2168–2172. [CrossRef] [PubMed]

66. Harmon, A.C.; Gribskov, M.; Gabrini, E.; Harper, J.F. The CDPK superfamily of protein kinases. *New Phytol.* 2001, 151, 175–183. [CrossRef]

67. Grabarek, Z. Structural basis for diversity of the EF-hand calcium-binding proteins. *J. Mol. Biol.* 2006, 359, 509–525. [CrossRef]

68. Klimecka, M.; Muszynska, G. Structure and functions of plant calcium-dependent protein kinases. *Acta Biochim. Pol. Eng. Edi.* 2007, 54, 219.

69. Wernimont, A.K.; Arzt, J.D.; Finerty, P.J.; Lin, Y.-H.; Amani, M.; Allali-Hassani, A.; Senisterra, G.; Vedadi, M.; Tempel, W.; Mackenzie, F. Structures of apicomplexan calcium-dependent protein kinases reveal mechanism of activation by calcium. *Nat. Struct. Mol. Biol.* 2010, 17, 596. [CrossRef]

70. Parvathy, S.T. Versatile roles of ubiquitous calcium-dependent protein kinases (CDPKs) in plants. *Indian Soc. Oilseeds Res.* 2018, 35, 1–11.
Wei, S.; Hu, W.; Deng, X.; Zhang, Y.; Liu, X.; Zhao, X.; Luo, Q.; Jin, Z.; Li, Y.; Zhou, S. A rice calcium-dependent protein kinase OsCPK9 positively regulates drought stress tolerance and spikelet fertility. BMC Plant Biol. 2014, 14, 133. [CrossRef]

Zhang, H.; Zhang, Y.; Deng, C.; Deng, S.; Li, N.; Zhao, C.; Zhao, R.; Liang, S.; Chen, S. The Arabidopsis Cyt25-Dependent Protein Kinase CPK12 Is Involved in Plant Response to Salt Stress. Int. J. Mol. Sci. 2018, 19, 4062. [CrossRef]

Dubrovina, A.S.; Kiselev, K.V.; Khristenko, V.S.; Aleyanova, O.A. The calcium-dependent protein kinase gene VaCPK29 is involved in grapevine responses to heat and osmotic stresses. Plant Growth Reg. 2017, 82, 79–89. [CrossRef]

Liu, Y.; Xu, C.; Zhu, Y.; Zhang, L.; Chen, T.; Zhou, F.; Chen, H.; Lin, Y. The calcium-dependent kinase OsCPK24 functions in cold stress responses in rice. J. Integr. Plant Biol. 2018, 60, 173–188. [CrossRef] [PubMed]

Chen, D.-H.; Liu, H.-P.; Li, C.-L. Calcium-dependent protein kinase CPK9 negatively functions in stomatal abscisic acid signaling by regulating ion channel activity in Arabidopsis. Plant Mol. Biol. 2019, 99, 113–122. [CrossRef] [PubMed]

Fantino, E.; Segretin, M.E.; Santin, F.; Mirkin, F.G.; Ulloa, R.M. Analysis of the potato calcium-dependent protein kinase family and characterization of SCDPK7, a member induced upon infection with Phytophthora infestans. Plant Cell Rep. 2017, 36, 1137–1157. [CrossRef] [PubMed]

Dubrovina, A.S.; Kiselev, K.V.; Khristenko, V.S.; Aleynova, O.A. The calcium-dependent protein kinase gene VaCPK29 is involved in grapevine responses to heat and osmotic stresses. Plant Growth Reg. 2017, 82, 79–89. [CrossRef]

Jin, Y.; Ye, N.; Zhu, F.; Li, H.; Wang, J.; Jiang, L.; Zhang, J. Calcium-dependent protein kinase CPK28 targets the methionine adenosyltransferases for degradation by the 26S proteasome and affects ethylene biosynthesis and lignin deposition in Arabidopsis. Plant Physiol. 2014, 165, 1391–1407. [CrossRef]

Jiang, S.; Zhang, D.; Wang, L.; Pan, J.; Liu, Y.; Kong, X.; Zhou, Y.; Li, D. A maize calcium-dependent protein kinase gene, ZmCPK4, positively regulated abscisic acid signaling and enhanced drought stress tolerance in transgenic Arabidopsis. Plant Physiol. Biochem. 2013, 71, 112–120. [CrossRef] [PubMed]

Kiselev, K.; Dubrovina, A.; Shumakova, O.; Karetin, Y.; Manyakhin, A. Structure and expression profiling of a novel calcium-dependent protein kinase gene, CDPK3a, in leaves, stems, grapes, and cell cultures of wild-growing grapevine Vitis amurensis Rupr. Plant Cell Rep. 2013, 32, 431–442. [CrossRef] [PubMed]
98. Zhu, S.-Y.; Yu, X.-C.; Wang, X.-J.; Zhao, R.; Li, Y.; Fan, R.-C.; Shang, Y.; Du, S.-Y.; Wang, X.-F.; Wu, F.-Q.; Liu, G.; Chen, J.; Wang, X. VfCPK1, a gene encoding calcium-dependent protein kinase from Vicia faba, is induced by drought and abscisic acid. Plant Cell Environ. 2006, 29, 2091–2099. [CrossRef]

99. Takahashi, K.; Isobe, M.; Muto, S. An increase in cytosolic calcium ion concentration precedes hypoosmotic shock-induced activation of protein kinases in tobacco suspension culture cells. FEBS Lett. 1997, 401, 202–206. [CrossRef]

100. Kobayashi, M.; Yoshioka, M.; Asai, N.; Nomura, H.; Doke, N.; Yoshioka, H. StCDPK5 confers resistance to late blight pathogen but increases susceptibility to early blight pathogen in potato via reactive oxygen species burst. New Phytol. 2012, 196, 223–237. [CrossRef]

101. Perochon, A.; Aldon, D.; Galaud, J.-P.; Ranty, B. Calmodulin and calmodulin-like proteins in plant calcium signaling. Biochimie 2011, 93, 2048–2053. [CrossRef]

102. Szczegielniak, J.; Borkiewicz, L.; Lewandowska-Gnatowska, E.; Statkiewicz, M.; Klimecka, M.; Ciesla, J.; Muszyńska, G. Maize calcium-dependent protein kinase (ZmCPK11): Local and systemic response to wounding, regulation by touch and components of jasmonate signaling. Physiol. Plant. 2012, 146, 1–14. [CrossRef]

103. Ding, Y.; Cao, J.; Ni, L.; Zhu, Y.; Zhang, A.; Tan, M.; Jiang, M. ZmCPK11 is involved in abscisic acid-induced antioxidant defence and functions upstream of ZmMPK5 in abscisic acid signalling in maize. J. Exp. Bot. 2012, 64, 871–884. [CrossRef]

104. Zandalinas, S.I.; Mittler, R.; Ballagón, D.; Arbó, V.; Gómez-Cadenas, A. Plant adaptations to the combination of drought and high temperatures. Physiol. Plant. 2018, 162, 2–12. [CrossRef] [PubMed]

105. Foyer, C.H.; Noctor, G. Redox homeostasis and antioxidant signaling: A metabolic interface between stress perception and physiological responses. Plant Cell 2005, 17, 1866–1875. [CrossRef] [PubMed]

106. Zhou, J.J.; Wei, F.J.; Wang, C.; Wu, J.J.; Ratnasekera, D.; Liu, W.X.; Wu, W.H. Arabidopsis calcium-dependent protein kinase CPK10 functions in abscisic acid-and Ca^{2+}-mediated stomatal regulation in response to drought stress. Plant Physiol. 2010, 154, 1232–1243. [CrossRef] [PubMed]

107. Dubrovina, A.S.; Kiselev, K.V.; Kristensen, V.S.; Aleyanova, O.A. VaCPK20, a calcium-dependent protein kinase gene of wild grapevine Vitis amurensis Rupr., mediates cold and drought stress tolerance. J. Plant Physiol. 2015, 185, 1–12. [CrossRef]

108. Liu, G.; Chen, J.; Wang, X. VfCPK1, a gene encoding calcium-dependent protein kinase from Vicia faba, is induced by drought and abscisic acid. Plant Cell Environ. 2006, 29, 2091–2099. [CrossRef]
109. Ratnasekera, D. A calcium dependent protein kinase involves H$_2$O$_2$ mediated guard cell signaling in Arabidopsis. *Trop. Agric. Res. Exten.* 2015, 16, 7–14. [CrossRef]

110. Syam Prakash, S.R.; Jayabaskaran, C. Heterologous expression and biochemical characterization of two calcium-dependent protein kinase isoforms CaCPK1 and CaCPK2 from chickpea. *J. Plant Physiol.* 2006, 163, 1083–1093. [CrossRef]

111. Ho, S.-L.; Huang, S.-J.; Lu, C.-A.; He, S.-L.; Wang, C.-C.; Wu, S.-P.; Chen, J.; Yu, S.-M. Sugar starvation-and GA-inducible calcium-dependent protein kinase 1 feedback regulates GA biosynthesis and activates a 14-3-3 protein to confer drought tolerance in rice seedlings. *Plant Mol. Biol.* 2013, 81, 347–361. [CrossRef]

112. Geng, S.; Zhao, Y.; Tang, L.; Zhang, R.; Sun, M.; Guo, H.; Kong, X.; Li, A.; Mao, L. Molecular evolution of two duplicated CDPK genes CPK7 and CPK12 in grass species: A case study in wheat (*Triticum aestivum* L.). *Gene* 2011, 475, 94–103. [CrossRef]

113. Vivek, P.J.; Tuteja, N.; Soniya, E.V. CDPK1 from ginger promotes salinity and drought stress tolerance without yield penalty by improving growth and photosynthesis in *Nicotiana tabacum*. *PLoS ONE* 2013, 8, e76392. [CrossRef]

114. Huang, K.; Peng, L.; Liu, Y.; Yao, R.; Liu, Z.; Li, X.; Yang, Y.; Wang, J. Arabidopsis calcium-dependent protein kinase AtCPK1 plays a positive role in salt/drought-stress response. *Biochem. Biophys. Res. Commun.* 2018, 498, 92–98. [CrossRef] [PubMed]

115. Brandt, B. Specific Calcium and Abscisic Acid Regulation of Anion Channels in Arabidopsis Guard Cells. Ph.D. Thesis, Eberhard Karls University Tübingen, Tübingen, Germany, 2014.

116. Baba, A.; Rigó, G.; Ayaydin, F.; Rehman, A.; András, N.; Zsigmond, L.; Vass, I.; Pasternak, T. Functional Analysis of the Arabidopsis thaliana CDPK-Related Kinase Family: AtCRK1 Regulates Responses to Continuous Light. *Int. J. Mol. Sci.* 2018, 19, 1282. [CrossRef] [PubMed]

117. Mori, I.C.; Murata, Y.; Munemasa, S.; Wang, Y.-F.; Andreoli, S.; Tiriac, H.; Alonso, J.M.; Harper, J.F.; Ecker, J.R. CDPKs CPK6 and CPK3 function in ABA regulation of guard cell S-type anion-and Ca$^{2+}$-permeable channels and stomatal closure. *PLoS Biol.* 2006, 4, e327. [CrossRef] [PubMed]

118. Mehlmer, N.; Wurzinger, B.; Stael, S.; Hofmann-Rodrigues, D.; Csaszar, E.; Pfister, B.; Bayer, R.; Teige, M. The Ca$^{2+}$-dependent protein kinase CPK3 is required for MAPK-independent salt-stress acclimation in Arabidopsis. *Plant J.* 2010, 63, 484–498. [CrossRef] [PubMed]

119. Xu, J.; Tian, Y.-S.; Peng, R.-H.; Xiong, A.-S.; Zhu, B.; Jin, X.-F.; Gao, F.; Fu, X.-Y.; Hou, X.-L.; Yao, Q.-H. AtCPK6, a functionally redundant and positive regulator involved in salt/drought stress tolerance in Arabidopsis. *Plant Sci.* 2010, 231, 1251–1260. [CrossRef] [PubMed]

120. Milla, M.A.R.; Townsend, J.; Chang, F.; Cushman, J.C. The Arabidopsis AtDi19 gene family encodes a novel type of Cys2/His2 zinc-finger protein implicated in ABA-independent dehydration, high-salinity stress and light signaling pathways. *Plant Mol. Biol.* 2006, 61, 13–30. [CrossRef]

121. Zhao, R.; Sun, H.; Mei, C.; Wang, X.; Yan, L.; Liu, R.; Zhang, X.F.; Wang, X.F.; Zhang, D.P. The Arabidopsis Ca$^{2+}$-dependent protein kinase CPK12 negatively regulates abscisic acid signaling in seed germination and post-germination growth. *New Phytol.* 2011, 192, 61–73. [CrossRef]

122. Huang, S.-J.; Chang, C.-L.; Wang, P.-H.; Tsai, M.-C.; Hsu, P.-H.; Chang, I.-F. A type III ACC synthase, ACS7, is involved in root gravitropism in Arabidopsis thaliana. *J. Exp. Bot.* 2013, 64, 4343–4360. [CrossRef]

123. Franz, S.; Ehler, B.; Liese, A.; Kurth, J.; Cazalé, A.-C.; Romeis, T. Calcium-dependent protein kinase CPK21 functions in abiotic stress response in Arabidopsis thaliana. *Mol. Plant* 2011, 4, 83–96. [CrossRef]

124. Ma, S.-Y.; Wu, W.-H. AtCPK23 functions in Arabidopsis responses to drought and salt stresses. *Plant Mol. Biol.* 2007, 65, 511–518. [CrossRef]

125. Zhao, R.; Sun, H.; Zhao, N.; Jing, X.; Shen, X.; Chen, S. The Arabidopsis Ca$^{2+}$-dependent protein kinase CPK27 is required for plant response to salt-stress. *Gene* 2015, 563, 203–214. [CrossRef]

126. Choi, H.-I.; Park, H.-J.; Park, J.H.; Kim, S.; Im, M.-Y.; Seo, H.-H.; Kim, Y.-W.; Hwang, I.; Kim, S.Y. Arabidopsis calcium-dependent protein kinase AtCPK32 interacts with ABF4, a transcriptional regulator of abscisic acid-responsive gene expression, and modulates its activity. *Plant Physiol.* 2005, 139, 1750–1761. [CrossRef] [PubMed]

127. Kawamoto, N.; Sasabe, M.; Endo, M.; Machida, Y.; Araki, T. Calcium-dependent protein kinases responsible for the phosphorylation of a bZIP transcription factor FD crucial for the florigen complex formation. *Sci. Rep.* 2015, 5, 8341. [CrossRef] [PubMed]
128. Llop-Tous, I.; Dominguez-Puigjaner, E.; Vendrell, M. Characterization of a strawberry cDNA clone homologous to calcium-dependent protein kinases that is expressed during fruit ripening and affected by low temperature. *J. Exp. Bot.* 2002, 53, 2283–2285. [CrossRef] [PubMed]

129. Davletova, S.; Mészáros, T.; Miskolczi, P.; Oberschall, A.; Török, K.; Magyar, Z.; Dudits, D.; Deák, M. Auxin and heat shock activation of a novel member of the calmodulin like domain protein kinase gene family in cultured alfalfa cells. *J. Exp. Bot.* 2001, 52, 215–221. [CrossRef] [PubMed]

130. Wang, J.; Wang, S.; Hu, K.; Yang, J.; Xin, X.; Zhou, W.; Fan, J.; Cui, F.; Mou, B.; Zhang, S. The kinase OsCPK4 regulates a buffering mechanism that fine-tunes innate immunity. *Plant Physiol.* 2018, 176, 1835–1849. [CrossRef]

131. Kang, C.H.; Moon, B.C.; Park, H.C.; Koo, S.C.; Chi, Y.H.; Cheong, Y.H.; Yoon, B.-D.; Lee, S.Y.; Kim, C.Y. Rice small C2-domain proteins are phosphorylated by calcium-dependent protein kinase. *Mol. Cells* 2013, 35, 381–387. [CrossRef]

132.Fu, L.; Yu, X.; An, C. Overexpression of constitutively active OsCPK10 increases *Arabidopsis* resistance against *Pseudomonas syringae* pv. tomato and rice resistance against *Magnaporthe grisea*. *Plant Physiol. Biochem.* 2013, 73, 202–210. [CrossRef]

133. Wang, B.; Zhang, Y.; Bi, Z.; Liu, Q.; Xu, T.; Yu, N.; Cao, Y.; Zhu, A.; Wu, W.; Zhan, X. Impaired function of the calcium-dependent protein kinase, OsCPK12, leads to early senescence in Rice (*Oryza sativa* L.). *Front. Plant Sci.* 2019, 10, 52. [CrossRef]

134. Abbasi, F.; Onedera, H.; Toki, S.; Tanaka, H.; Komatsu, S. OsCDPK13, a calcium-dependent protein kinase gene from rice, is induced by cold and gibberellin in rice leaf sheath. *Plant Mol. Biol.* 2004, 55, 541–552. [CrossRef]

135. Almadanum, M.C.; Alexandre, B.M.; Rosa, M.T.; Sapeta, H.; Leitão, A.E.; Ramalho, J.C.; Lam, T.T.; Negrão, S.; Abreu, I.A.; Oliveira, M.M. Rice calcium-dependent protein kinase OsCPK17 targets plasma membrane intrinsic protein and sucrose-phosphate synthase and is required for a proper cold stress response. *Plant Cell Environ.* 2017, 40, 1197–1213. [CrossRef]

136. Asano, T.; Hakata, M.; Nakamura, H.; Aoki, N.; Komatsu, S.; Ichikawa, H.; Hirochika, H.; Ohsugi, R. Functional characterisation of OsCPK21, a calcium-dependent protein kinase that confers salt tolerance in rice. *Plant Mol. Biol.* 2011, 75, 179–191. [CrossRef]

137. Manimaran, P.; Mangruthia, S.K.; Sundaram, R.; Balachandran, S. Constitutive expression and silencing of a novel seed specific calcium dependent protein kinase gene in rice reveals its role in grain filling. *J. Plant Physiol.* 2015, 174, 41–48. [CrossRef]

138. Ishida, S.; Yuasa, T.; Nakata, M.; Takahashi, Y. A tobacco calcium-dependent protein kinase, CDPK1, regulates the transcription factor repression of shoot growth in response to gibberellins. *Plant Cell* 2008, 20, 3273–3288. [CrossRef]

139. Romeis, T.; Ludwig, A.A.; Martin, R.; Jones, J.D. Calcium-dependent protein kinases play an essential role in a plant defence response. *EMBO J.* 2001, 20, 5556–5567. [CrossRef]

140. Botella, J.R.; Arteca, J.M.; Arteca, R.N. Calcium-dependent protein kinase expression is modulated during fruit ripening and affected by low temperature. *J. Exp. Bot.* 2002, 53, 2283–2285. [CrossRef] [PubMed]

141. Kobayashi, M.; Ohura, I.; Kawakita, K.; Yokota, N.; Fujiwara, M.; Shimamoto, K.; Doke, N.; Yoshikoa, H. Calcium-dependent protein kinases regulate the production of reactive oxygen species by potato NADPH oxidase. *Plant Cell* 2007, 19, 1065–1080. [CrossRef]

142. Wang, M.; Li, Q.; Sun, K.; Chen, X.; Zhou, Q.; Li, H.; Zhang, X.; Li, X. Involvement of CsCDPK20 and CsCDPK26 in Regulation of Thermotolerance in Tea Plant (*Camellia sinensis*). *Plant Mol. Biol. Rep.* 2018, 36, 176–187. [CrossRef]
145. Freymark, G.; Diehl, T.; Miklis, M.; Romeis, T.; Panstruga, R. Antagonistic control of powdery mildew host cell entry by barley calcium-dependent protein kinases (CDPKs). *Mol. Plant Microbe Interact.* 2007, 20, 1213–1221. [CrossRef] [PubMed]

146. Wang, H.; Gong, J.; Su, X.; Li, L.; Pang, X.; Zhang, Z. MaCDPK7, a calcium-dependent protein kinase gene from banana is involved in fruit ripening and temperature stress responses. *J. Hort. Sci. Biotechnol.* 2017, 92, 240–250. [CrossRef]

147. Wang, Z.; Li, J.; Jia, C.; Xu, B.; Jin, Z. Molecular cloning and expression analysis of eight calcium-dependent protein kinase (CDPK) genes from banana (*Musa acuminata* L. AAA group, cv. Cavendish). *S. Afr. J. Bot.* 2016, 104, 134–141. [CrossRef]

148. Dubrovina, A.; Kiselev, K. The Role of Calcium-Dependent Protein Kinase Genes VaCPK1 and VaCPK26 in the Response of *Vitis amurensis* (in vitro) and *Arabidopsis thaliana* (in vivo) to Abiotic Stresses. *Russian J. Genet.* 2019, 55, 319–329. [CrossRef]

149. Dubrovina, A.S.; Kiselev, K.V.; Khristenko, V.S.; Aleyanova, O.A. VaCPK21, a calcium-dependent protein kinase gene of wild grapevine *Vitis amurensis* Rupr., is involved in grape response to salt stress. *Plant Cell. Tissue Organ Cult.* 2016, 124, 137–150. [CrossRef]

150. Chen, J.; Xue, B.; Xia, X.; Yin, W. A novel calcium-dependent protein kinase gene from *Populus euphratica*, confers both drought and cold stress tolerance. *Biochem. Biophys. Res. Commun.* 2013, 441, 630–636. [CrossRef]

151. Ning, M.; Tang, F.; Zhang, Q.; Zhao, X.; Yang, L.; Cai, W.; Shan, C. Effects of Penicillium infection on the expression and activity of CDPK2 in postharvest Hami melon treated with calcium chloride. *Physiol. Mol. Plant Pathol.* 2019, 106, 175–181. [CrossRef]

152. AbdElgawad, H.; Zinta, G.; Hegab, M.M.; Pandey, R.; Asard, H.; Abuelsoud, W. High salinity induces different oxidative stress and antioxidant responses in maize seedlings organs. *Front. Plant Sci.* 2016, 7, 276. [CrossRef]

153. Dubrovina, A.; Aleyanova, O.; Manyakhin, A.; Kiselev, K. The Role of Calcium-Dependent Protein Kinase Genes CPK16, CPK25, CPK30, and CPK32 in Stilbene Biosynthesis and the Stress Resistance of Grapevine *Vitis amurensis* Rupr. *App. Biochem. Microbiol.* 2018, 54, 410–417. [CrossRef]

154. Miller, G.; Suzuki, N.; Ciftci-Yilmaz, S.; Mittler, R. Reactive oxygen species homeostasis and signalling during drought and salinity stresses. *Plant Cell Environ.* 2010, 33, 453–467. [CrossRef]

155. Kwak, J.M.; Mori, I.C.; Pei, Z.M.; Leonhardt, N.; Torres, M.A.; Dangl, J.L.; Bloom, R.E.; Bodde, S.; Jones, J.D.; Schroeder, J.I. NADPH oxidase AtrbohD and AtrbohF genes function in ROS-dependent ABA signaling in *Arabidopsis*. *EMBO J.* 2003, 22, 2623–2633. [CrossRef] [PubMed]

156. Mittler, R. ROS are good. *Trends Plant Sci.* 2017, 22, 11–19. [CrossRef] [PubMed]

157. Tao, X.-C.; Lu, Y.-T. Loss of AtCRK1 gene function in *Arabidopsis thaliana* decreases tolerance to salt. *J. Plant Biol.* 2013, 56, 306–314. [CrossRef]

© 2019 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).