Research Article

Characterization and Expression Profiling Analysis of Calmodulin Genes in Response to Salt and Osmotic Stresses in Pear (Pyrus bretschneideri Rehd.) and in Comparison with Arabidopsis

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1. Introduction

Calcium (Ca\(^{2+}\)) is an important second messenger in eukaryotic cells. Ca\(^{2+}\) signaling plays diverse and essential functions in many aspects of plant development and stress responses. Many abiotic factors, including salt, temperature, light, and osmotic stress, modulate Ca\(^{2+}\) signals that are then recognized and translated into downstream responses by Ca\(^{2+}\) sensors [1–4]. Ca\(^{2+}\) sensors can bind Ca\(^{2+}\) and induce a conformational change in the sensor that promotes an interaction with downstream effectors or modulates its own catalytic activity [5]. Most Ca\(^{2+}\) sensors utilize the elongation factor- (EF) hand motif, a helix-loop-helix structure, to bind Ca\(^{2+}\); with each EF-motif binding a single Ca\(^{2+}\) ion [6]. Several families of Ca\(^{2+}\) sensors have been identified in higher plants based on the presence of EF-hand motifs including calmodulin proteins (CaMs) and calmodulin-like proteins (CMLs), calcineurin B-like proteins (CBLs), and Ca\(^{2+}\)-dependent protein kinases (CPKs) [4, 5, 7–12]. Due to their commonality, CaMs as a Ca\(^{2+}\) sensor in eukaryotes are well known. On the other hand, CMLs, CBLs, and CDPKs may be restricted to just plants [5, 6, 13]. CaMs lack effector modules such as the kinase domain in CDPK proteins and lack any other identifiable functional domain except the EF-hand motif. CaMs transduce Ca\(^{2+}\) signals through their interaction with a series of target proteins (CaM-binding proteins [CaMBP]), which control a multitude of cellular functions [5, 7, 14].

All of the typical plant CaM family members are highly similar to animal CaMs and contain four EF-hand motifs. CaMs are organized into two distinct globular domains connected by a long flexible helix, and each of the globular domains contains one pair of intimately linked EF-hands that serves as the basic functional unit [5]. Seven CaMs (AtCaM1–AtCaM7) have been identified in the Arabidopsis genome [5], that function as one of several intracellular transducers
that transmit information from diverse developmental and environmental stimuli [15, 16]. Studies have demonstrated that CaMs play an important role in active stress-related proteins and, thus by implication, play a role in augmenting abiotic stress tolerance in plants [3, 6, 16]. For instance, CaM can regulate the heat shock-induced expression of HSP90 and HSP70 in sorghum [17]. In Arabidopsis, CaM7 can physically interact with HY5 and regulate its expression to promote phomorphogenic growth [18]. AtCaM3 functions as a downstream factor of NO signal transduction, which is involved in heat shock signal transduction [19, 20]. Overexpression of CaM3 can decrease the level of COR (cold regulated) transcripts in transgenic Arabidopsis plants [21]. Moreover, CaMs reportedly can activate AtMPK8, which subsequently suppresses wound-induced ROS accumulation [15]. AtMYB2 was identified as a CaM-binding protein that regulates the response to salt and dehydration stress [14]. AtCaMBP25 (a CaM-binding protein) is targeted to the nucleus and acts as a negative effector of osmotic and salt stress responses [1]. Interestingly, recent study [14] indicated that CaMs can also interact with group IId proteins of the entire WRKY subfamily of transcription factors which contain conserved Ca2+-dependent CaM-binding domains in regulating abiotic stress adaptation [14, 22, 23] and those proteins contain conserved Ca2+-dependent CaM-binding domains [14]. In addition, some plant-specific CaM-binding proteins, such as At-BT1, AT-BT2, and At-BT5 are induced in AtBZIP60-overexpressed plants, conferring the salt tolerance, suggested these At-BT proteins may be involved in protecting plants from salt stress [10, 24]. These data show diverse functions of CaMs, CaM-binding proteins, and their synergistic effects to deal with multiple stresses, offering further encouragement to explore the function of CaM gene regulated abiotic stress responses in plants.

Due to the multiple functions of CaMs and the increase in the availability of sequenced plant genomes, many CaM genes have been identified at the whole genome level in several plant species including Arabidopsis [5, 7], rice [25], and several species in the Solanaceae family [26]. Pear (Pyrus bretschneideri), a species within Rosaceae, is cultivated worldwide as a fruit tree, whose growth, development, and productivity are frequently affected by abiotic stress, such as salinity and drought [27]. Although the pear genome has been released [28], an analysis of the CaM gene family at the whole genome level has not been conducted. Additionally, few studies on specific pear CaM genes have been published. The present study reported genome-wide analysis of the CaM gene family in pear. Analyses included an examination of gene structure, the presence of conserved motifs, phylogeny, chromosomal locations, synteny analysis, presence of cisregulatory elements, and expression profiles in response to salt and osmotic stress. A comparison with the expression of CaM in Arabidopsis was also conducted. Results indicated a conserved evolution of the CaM gene family in pear and that some PbCaM genes were obviously upregulated in response to salt and osmotic stresses. These data provide new insight into the conserved evolution and expression of the pear CaM gene family and their potential role in the response of pear to abiotic stress.

2. Materials and Methods

2.1. Identification and Characterization of CaM Genes in Pear. The genome sequence of pear (P. bretschneideri) was obtained from the pear genome project website (https://peargenome.njau.edu.cn). The Arabidopsis CaM protein sequences [5, 7] were from The Arabidopsis Information Resource (TAIR; http://www.arabidopsis.org). BLASTP and TBLASTN were used to identify putative CaM family proteins in the pear proteome and genome using Arabidopsis CaM proteins as queries with default parameters. Sequences with an identity >80% against the queries [7, 12] were collected and analyzed using Pfam (http://pfam.xfam.org/) [29] and SMART (http://smart.embl-heidelberg.de/) [30] to identify the proteins with four conserved EF-hand domains and without other known functional domains. Then, the remaining nonredundant sequences were as putative CaM candidates in pear. Simultaneously, to avoid false positives and erroneous assembly errors, the full-length cDNA sequence was cloned for each of the putative PbCaM genes using genespecific primers (Table S1 in Supplementary Material available online at https://doi.org/10.1155/2017/7904162) based on cDNA templates obtained from pear (P. bretschneideri cv “Dangshansuli”) leaves. PCR products were cloned and sequenced to confirm the identity of each PbCaM gene. A total of four sequenced genes were collected as true CaM genes in pear and named according to their genomic locations (Table 1).

2.2. Sequence Alignments, Structure Analysis, and Phylogenetic Analyses. Multiple sequence alignments were carried out using CLUSTALW 2.0 software [31] and conserved sequences were viewed and edited using GeneDoc (http://genedoc .software.informer.com/2.7/). Phylogenetic trees that included CaM sequences from pear (P. bretschneideri), Arabidopsis (A. thaliana), rice (Oryza sativa), tomato (Solanum lycopersicum), tobacco (Nicotiana benthamiana), and potato (Solanum tuberosum) were generated using the maximum-likelihood (ML) method and bootstrap analysis with 1000 replicates in MEGA7 software [31, 32]. Data for CaM proteins from rice, tomato, tobacco, and potato were obtained from Zhao et al. [26]. Gene structures were analyzed through aligning their coding sequences and their corresponding genomic sequences with the online tool GSDS2.0 (http://gsds.cbi.pku.edu.cn/index.php) [33]. Secondary structure analysis of CaM proteins was performed using JPred 4 (http://www.compbio.dundee.ac.uk/jpred4/index.html).

2.3. Protein Properties, Conserved Motifs, and Cis-Element Analysis. The molecular weight (MW) and isoelectric point (pI) of CaM proteins were calculated using ProtParam (http://web.expasy.org/protparam/). The distribution of conserved motifs within the CaM proteins was determined using MEME Suite software (http://meme-suite.org/index .html) [34] with default settings. A 1000 bp upstream genomic sequence above the transcription start site (ATG) was obtained for all of the identified CaM genes from the pear and the Arabidopsis genome sequence. The obtained sequences were submitted to the PlantCARE database.
| Gene name | Gene ID   | Accession ID | Position          | CDS (bp) | Size (aa) | Number of introns | MW (KDa) | PI  | Number of EF-hands | % identity to AtCaM2 |
|-----------|-----------|--------------|-------------------|----------|-----------|-------------------|----------|-----|--------------------|---------------------|
| PbCaM1    | Pbr0283272| KU950328     | Chr6: 2648292...2650176 (+) | 564      | 187       | 4                 | 21.20    | 4.31| 4                  | 88.62               |
| PbCaM2    | Pbr039046.1| KU950329     | Chr12: 10152516...10154840 (−) | 450      | 149       | 3                 | 16.85    | 3.88| 4                  | 99.33               |
| PbCaM3    | Pbr038169.1| KU950330     | Chr14: 7176273...7178095 (−) | 450      | 149       | 1                 | 16.85    | 3.88| 4                  | 99.33               |
| PbCaM4    | Pbr038805.1| KU950331     | Chr14: 16928793...16930245 (+) | 450      | 149       | 3                 | 16.97    | 3.90| 4                  | 87.92               |

**Table 1**: Characteristics of CaM genes in pear (*P. bretschneideri*).
2.4. Chromosomal Location and Synteny Analysis. To map the corresponding CaM loci on pear and Arabidopsis chromosomes, the genome annotation files of pear and Arabidopsis were obtained from the pear genome project website (https://peargenome.njau.edu.cn) and TAIR (http://www.arabidopsis.org/), respectively. To detect synteny of the CaM genes in pear and Arabidopsis, the whole genome synteny block data within/between pear and Arabidopsis genomes were collected from the Plant Genome Duplication Database (http://chibba.agtec.uga.edu/duplication/) [36]. Chromosomal locations and synteny relationships for the CaM family genes within and between the pear and Arabidopsis genome were examined to show their duplications and synteny relationships using Circos [37].

2.5. Plant Material and Treatments. The newly growing shoots with young leaves were collected from the 20-old-year pear (P. bretschneideri "Dangshansuli") in the national germplasm orchard of the Institute of Horticulture, Jiangsu Academy of Agricultural Sciences, Nanjing, China. The samples were treated according to methods previously described [38]. Briefly, the shoots with young leaves were firstly placed in hydroponic containers containing 1/2 MS [39] solution (pH 5.8) for pretreatment of 14 days at 22 ± 2 °C, 16 h light/8 h dark photoperiod, and 60–70% humidity conditions in growth chambers. The robust shoots with young leaves were used for stress treatments, and then the shoots were exposed to a 1/2 MS solution (pH 5.8) containing 200 mM NaCl and 15% (w/v) polyethylene glycol (PEG6000), respectively. Control was exposed to the same growth conditions but were grown only in 1/2 MS solution (pH 5.8) without the addition of any salt or polyethylene glycol. Young leaves were sampled according to [40] after 0, 12, 24, and 48 h of each treatment, respectively. For each treatment, three biological replicates were included and all samples were flash frozen in liquid nitrogen and stored at −80 °C until further analysis.

2.6. RNA Isolation, cDNA Synthesis, and Cloning of PbCaM Genes. Total RNA was isolated from treated leaves using the TaKaRa MiniBEST Plant RNA Extraction Kit (TaKaRa, Dalian, China; Code no. 9769) according to the manufacturer’s instructions. RNA concentration and integrity was quantified using a Nanodrop1000 (Thermo Scientific, Wilmington, DE) and its integrity was checked by electrophoresis in a 1.5% (w/v) agarose gel. Total RNA (2 μg) from pear leaves was reverse transcribed into cDNA by PrimeScript™ 1st Strand cDNA Synthesis Kit (TaKaRa, Dalian, China; Code number 6110A) in order to clone PbCaM genes. PCR was performed with PrimeSTAR® Max DNA Polymerase (TaKaRa, Code no. R045A), and amplification conditions were as follows: 95 °C for 5 min, followed by 35 cycles of 95 °C for 30 s, 55–58 °C for 2 min, and 72 °C for 30 s and a final extension at 72 °C for 10 min. PCR products were purified and cloned into the pMD19-T vector (TaKaRa). Positive clones were sequenced in order to confirm the identity and sequence length of the cloned PbCaM genes.

2.7. Quantitative Real-Time RT-PCR (qRT-PCR) and Expression Profiling Analysis. A total of 2 μg of total RNA was used to synthesize cDNA with the PrimeScript RT reagent Kit with gDNA Eraser (Perfect Real Time) Kit (TaKara, Code no. RR047A) according to the manufacturer’s instructions. The cDNA reaction mixture was diluted 1:10 with EASY Dilution for Real-Time PCR (TaKara). SYBR® Premix Ex Taq™II (TaKara, Code no. RR820A) was used to analyze gene expression with a 7500 Fast Real-Time PCR System (Applied Biosystems, USA). qRT-PCR was carried out in 96-well, optical reaction plates. The PCR reaction was performed in a total volume of 20 μL containing 0.5 μM of each primer (1 μL), 20 ng/μL cDNA (1 μL), and 1x SYBR Premix Ex Taq II (10 μL) and additional ddH2O to make a final volume of 20 μL. The gene-specific primers were designed according to nonconserved region sequences of each PbCaM gene using the program Beacon Designer 8.10 (http://www.premierbiosoft.com/), and then the hit primer pairs of each gene were subjected to realignment with the coding sequences of the whole pear genome using BLASTn. Finally, the primer pair was collected for qRT-PCR only when they both matched the same PbCaM gene (Table S1). Pear Actin2/7 and UB1 genes were used as internal standards for subsequent normalization of the data as previously described by Xu et al. [41]. The settings of qRT-PCR conditions and the calculation of relative gene expression are performed according to methods described previously [38]. All of the experiments were examined using three biological replicates and three technical replicates for all of the genes. The relative expression levels were normalized to a value of 1 in the respective 0 h treated samples. The data of each gene was shown using the mean ± standard deviation (SD).

In addition, the expressions of CaM genes in Arabidopsis were analyzed based on the AtGenExpress (http://jsp.weigelworld.org/AtGenExpress/resources/) [42] and the heat map was generated using Cluster 3.0 software [43].

3. Results and Discussion

3.1. Identification and Characterization of CaM Genes in Pear. Through combination of the local BLASTP and TBLASTN searches using typical CaM protein sequences from Arabidopsis as queries, nonredundant hit sequences with >80% identity [7, 12] were collected and examined for the presence of conserved domains using Pfam [29] and SMART [30]. Sequences containing four EF-hand domains and having no other known functional domains were considered as putative PbCaM genes. Table 1 listed these four genes which displayed similar characteristics with all of the common CaM protein properties in Arabidopsis [4, 5, 7, 12]. These four putative CaM genes were cloned to confirm the reliability of genome-wide identification of CaM genes in pear. Sequencing of the cloned cDNA further showed complete consistency with those obtained from the genome-wide prediction. These four genes were named and submitted to the NCBI database under the accession numbers KU950328, KU950329, KU950330,
proteins from pear and genomic and coding sequences were used to construct a ML designated (Table S). (Table 1). Although there are several criteria for classifying CaM proteins [4, 7, 12], based on high degree of sequence similarity of the CaMs to known CaMs from different species [4–7, 12], the four pear CaM proteins are considered as canonical CaM proteins in pear (Table 1), which can well fit the trend of expansion of CaM in the green lineage ranged from 1 to 7 previously reported [12]. The sequence identity of PbCaM proteins versus AtCaM2 was within 88.6–99.3% (Table 1). Notably, each PbCaM protein contained four EF-hand domains and possessed similar secondary structure elements than Arabidopsis CaMs (Figure 1(a) and Figure S1).

3.2. Sequence Features and Organization of PbCaM Genes. Multiple sequence alignments of CaMs proteins from pear and Arabidopsis indicated that both pear and Arabidopsis CaMs contain highly similar distributions of conserved domains and motifs (Figure 1). The four conserved common helix-loop-helix structural motifs (the EF-hands), which act as Ca2+ binding sites of PbCaMs and AtCaMs, are illustrated in Figure 1(a). This architecture is consistent with the canonical “EF-hand” domain, which is composed of two alpha helices linked by a loop of 12 residues that usually binds Ca2+ [6, 7]. In an EF-hand loop, the calcium ion is coordinated in a pentagonal bipyramidal configuration through six residues in positions of 1, 3, 5, 7, 9, and 12 of loop. When an EF-hand motif binds to Ca2+, a conformational change of the EF-hand will be induced, leading to the activation or inactivation of target proteins [6, 7]. All of the pear and Arabidopsis CaM proteins possess four conserved motifs and similar distributions of motifs (Figure 1(b)), further supporting that the structural characteristics of CaMs in pear and Arabidopsis are highly conserved. Moreover, each CaM protein possesses four kinds of different motifs containing two motifs 1s, two motifs 2s, one motif 3, and one motif 4 (Figure 1(b)). The motif length ranged from 6 to 50, and the corresponding site number ranged from 12 to 24 (Table S2). Among the four motifs, motif 2, which is 50 amino acids in length, has been annotated as a CaM-binding domain with two EF-hands. The functional annotations of motifs 2, 3, and 4, however, have not been designated (Table S2). Although the functional annotation of motif 1 is unclear, its presence is closely adjacent to a CaM-binding domain (Figure 1(b)), suggesting that it may be related to recognition of calcium binding.

The full-length alignment of CaM family protein sequences in pear and Arabidopsis and their associated genomic and coding sequences were used to construct a ML phylogenetic tree and to examine gene structure. The II CaM proteins from pear and Arabidopsis can be divided into two major groups (I and II) based on the basis of their phylogeny and gene structure (Figure 2). Phylogenetic analysis indicated that group I contains two PbCaM members (PbCaM2 and PbCaM3) and two AtCaM members (AtCaM6 and AtCaM7), while group II contains two PbCaM members (PbCaM1 and PbCaM4) and five AtCaM members (AtCaM1, AtCaM2, AtCaM3, AtCaM4, and AtCaM5), supported by the structures of CaM family members in each group. CaMs within the same group had a similar intron-exon distribution in CaM genes of both species. Most of the CaM genes (9/11) in Arabidopsis and pear contained two exons and one intron, with the exception of PbCaM1 and PbCaM4, which contained four exons and three introns. Group I genes contained one intron, two exons, and four EF-hands, and the intron was inserted in the first EF-hand (Figure 2), which is similar to AtCaM1–5 from group II, while in group II PbCaM1 and PbCaM4 contained three introns, four exons, and four EF-hands, respectively. Within group I, two introns were inserted in the architecture region of first EF-hand and third EF-hand, while AtCaM1–5 only contained one intron, two exons, and four EF-hands, and the intron was placed in the region of first EF-hand (Figure 2). However, the member from group I has a longer intron inserted than the ones from group II. Those data show that two subgroups of CaM proteins may possess different expansion patterns, group I only by changing size of inserting intron in the first EF-hand and group II by insertion of intron in the first EF-hand or the third EF-hand. These results revealed that the orthologous expansion of these subfamily members is highly restricted, especially in group I, which may possess more conserved functions. Interestingly, all CaMs genes in pear were disrupted by the first intron at the Gly26 codon, which has been previously reported in Arabidopsis and solanaceous CaMs [7, 26]. The majority of the first intron is located in the region of the EF-hand 1, while the second exon encodes multiple EF-hands (Figure 2). Although the size of the introns in pear CaM genes is generally greater than those found within Arabidopsis CaM genes (Figure 2), the lengths of encoded proteins, however, are similar (Figure 1). Altogether the conserved exon/intron structure and motif distributions in CaM genes in pear and Arabidopsis testify the conserved expansion of CaM family members between pear and Arabidopsis.

3.3. Phylogenetic Analysis of CaM Orthologs during Several Plant Species. To further examine the evolution of the CaM protein family, full-length amino acid sequences of pear, Arabidopsis, rice, tomato, potato, and tobacco CaMs that all contained four EF-hand domains, were aligned and then used to conduct a phylogenetic analysis. In a maximum-likelihood (ML) phylogenetic tree, the 30 CaM proteins included four CaMs from pear, four CaMs from Arabidopsis (seven CaM genes encode four proteins: AtCaM2, -3, -5 are homologous and AtCaM1 and AtCaM2 are homologous), five from rice, seven from tobacco, six from tomato, and four from potato. Collectively, the CaM proteins clustered into two major groups: I and II (Figure 3). The phylogenetic clusters of pear and Arabidopsis CaMs are consistent with the phylogenetic groups constructed from all six plant species. As shown in Figure 3, five of the six species contained two clusters, with rice being the exception. In the clustering analysis of the six species, group II included two of the four PbCaMs, two of the four AtCaMs, two of the six StCaMs; two of the four StCaMs, and one of the seven NbCaMs. All five of the rice CaMs
that the plantspecies evolved from two ancestral forms. It is plausible II. These observations suggest that the CaM proteins in the six withinasinglephylogeneticclade[26]. It is notable that pear, that CaM proteins from Solanaceous species tend to cluster and tobacco that clustered intotwogroupsmay have evolved the others from group I (Figure 3). The clustering analysis conducted in the present study supports a previous report the others from group I or II, (Figure 3). The clustering analysis conducted in the present study supports a previous report that CaM proteins from Solanaceous species tend to cluster within asinglephylogenetic clade [26]. It is notable that pear, Arabidopsis, and rice CaMs clustered differently. All of the pear and Arabidopsis CaMs clustered in either group I or II, while all of the rice CaMs were clustered exclusively in group II. These observations suggest that the CaM proteins in the six plant species evolved from two ancestral forms. It is plausible that the CaM genes from pear, Arabidopsis, tomato, potato, and tobacco that clustered into two groups may have evolved from the two ancestral forms of CaMs, whereas the species that cluster into just one of the phylogenetic groups may have been derived from either one of the two ancestral forms. A final determination of whether CaMs have evolved from two ancestral genes, however, still requires more supportive data.

3.4. Chromosome Locations and Synteny Analysis of PbCaM and AtCaM Genes. Chromosome localization analysis revealed that the four PbCaMs and seven AtCaMs mapped to four chromosomes in the pear and Arabidopsis genomes. Synteny analysis indicated seven paralogous duplications and one orthologous duplication within pear and Arabidopsis, and between pear and Arabidopsis (Table 2). The chromosome locations and synteny relationships of duplicated CaM gene pairs are shown in Figure 4 using Circos [37]. PbCaM3 and PbCaM4 are located on chromosome 14, while the other two PbCaM genes (PbCaM1 and PbCaM2) mapped onto chromosomes 6 and 12, respectively (Figure 4 and Table 1). In comparison, Arabidopsis chromosomes 2, 3, and 5 possessed two CaM genes, respectively, while only
AtCaM4 was located on chromosome 1 (Figure 4). The PbCaM gene family contained two pairs of paralogous duplications (PbCaM1–PbCaM4 and PbCaM2–PbCaM3), while the AtCaM gene family contained four pairs of paralogous duplications (AtCaM1–AtCaM2, AtCaM1–AtCaM4, AtCaM2–AtCaM3, and AtCaM3–AtCaM5). Only one orthologous duplication pair (AtCaM7-PbCaM3) was found between pear and *Arabidopsis* (Table 2). The different number of CaM gene duplication events in pear and *Arabidopsis* (Table 2) suggests that the CaM genes may undergo different duplications in two species. However, the presence of the orthologous duplication event between two species implies that the orthologous duplication or vertical evolution of CaM genes in two species has occurred during the long-term plant evolution processes. The paralogous and orthologous duplications of the CaMs within/between pear and *Arabidopsis* demonstrate the conserved relationships of CaM genes in pear and *Arabidopsis*, further suggesting that the CaM orthologs in pear may have similar or identical biological roles to mediate the transduction of calcium signals in plant cells.

### Table 2: Gene duplication and synteny analysis of CaM genes among *P. bretschneideri* and *A. thaliana*.

| Duplicated gene 1       | Duplicated gene 2       | Synteny relationship |
|-------------------------|-------------------------|----------------------|
| AtCaM1 (AT5G37780)     | AtCaM2 (AT2G41110)     | Paralogous           |
| AtCaM2 (AT2G41110)     | AtCaM3 (AT3G56800)     | Paralogous           |
| AtCaM3 (AT3G56800)     | AtCaM4 (AT2G41110)     | Paralogous           |
| AtCaM4 (AT2G41110)     | AtCaM5 (AT2G27030)     | Paralogous           |
| AtCaM5 (AT2G27030)     | AtCaM2 (AT2G41110)     | Paralogous           |
| PbCaM1 (Pbr012900.1)   | PbCaM5 (Pbr018864-1.1) | Paralogous           |
| PbCaM2 (Pbr039046.1)   | PbCaM3 (Pbr038169.1)   | Paralogous           |
| AtCaM7 (AT3G43810)     | PbCaM3 (Pbr038169.1)   | Orthologous          |

3.5. Cis-Regulatory Element Analysis of PbCaM and AtCaM Genes. Stress-related cis-acting elements such as MBS (MYB transcription factor binding site), HSE (heat shock element), ABRE (ABA-responsive element), LTRE (low-temperature responsive element), CE3 (coupling element 3), and W-box (WRKY transcription factor binding site) have been demonstrated to play a key role in the response of plants to stresses [44–48]. The promoter regions (1000 bp upstream of the translation start site) of pear and *Arabidopsis* CaM genes were analyzed to exhibit distributions of conserved stress-related cis-elements on the promoter region of four of the PbCaM and seven of the AtCaM genes (Figure 5 and Table S3). Results indicated that the promoters of CaM genes from the same phylogenetic cluster contained similar distribution of stress-related cis-elements (Figure 5 and Table S3), which may be associated with the similar functions within the
same group. Among the total of 44 occurrences of stress-related cis-elements, the ranked three were MBS (19), HSE (11), and ABRE (6) elements, followed by four LTR, three W-box, and one CE3, respectively (Figure 5 and Table S3). The number of stress-responsive elements in the promoter region of the four PbCaMs ranged from a maximum of six in PbCaM3 to a minimum of three in PbCaM1 and PbCaM2, while the numbers ranged from 2 to 7 in Arabidopsis, which indicated that CaM gene promoter regions possessed the similar components of cis-elements in pear and Arabidopsis. Interestingly, a total of 19 MBS elements were found in the promoter region of the pear and Arabidopsis CaM genes (Table S3) of eight MBS elements were present in four PbCaMs (one in AtCaM1, AtCaM2, AtCaM3 or AtCaM7, four in AtCaM4, three in AtCaM6) and the remaining 11 MBS elements in six AtCaMs (two in AtCaM1, two in AtCaM3, and one in AtCaM7). This result suggests that the expression of AtCaMs and PbCaMs may be similarly induced by abiotic stresses. Moreover, only one CE3 element, involved in ABA signal transduction [44], was found in the promoter region of AtCaM3 and none in PbCaM genes (Figure 5 and Table S2). These data suggest that the consistent or similar distribution of stress-related cis-elements in the promoter regions of both PbCaMs and AtCaMs may respond to similar environmental stimuli.

3.6. Expression Pattern of PbCaM Genes in Response to Salt and Osmotic Stress. The temporal expression pattern of genes or gene families has been widely used to identify candidate genes in response to salt stress and osmotic stress [38, 49–51]. The qRT-PCR data indicated that the expression profiles of PbCaM genes varied over time (0, 12, 24, and 48 h) in
response to salt and osmotic stress (Figure 6). All four \( \text{PbCaM} \) genes were upregulated with different degrees in response to salt and osmotic stresses. Two \( \text{PbCaM} \) genes (\( \text{PbCaM1} \) and \( \text{PbCaM4} \)) were significantly upregulated in response to salt or osmotic stress (Figure 6). Moreover, \( \text{PbCaM1} \), \( \text{PbCaM3} \), and \( \text{PbCaM4} \) exhibited similar upregulatory patterns from 0 h to 48 h after being exposed to the salt or osmotic stress, while \( \text{PbCaM2} \) was induced with different degrees of upregulation during salt and osmotic from 0 h to 48 (Figure 6(a)), which may imply the subfunctionalization of \( \text{CaM} \) genes in pear.

All four \( \text{PbCaM} \) genes were differentially upregulated in response to salt and osmotic treatments from 0 h to 48 h. Although two of four genes (\( \text{PbCaM1} \) and \( \text{PbCaM3} \)) were consistently upregulated by both salt and osmotic stresses, they showed higher inductive expression under osmotic stress treatment than under salt stress treatment (Figure 6), suggesting that these two \( \text{PbCaM} \) genes may be more sensitive to osmotic stress than to salt stress. The similar cis-element distributions in the \( \text{PbCaM} \) promoters further support this inference (Figure 5). Therefore, it is reasonable to consider that both \( \text{PbCaM1} \) and \( \text{PbCaM3} \) may play critical roles in the response to osmotic and/or salt stress. This is further supported by the fact that the expressions of \( \text{PbCaM} \) orthologs in \( \text{Arabidopsis} \), based on data available from AtGenExpress (http://jsp.weigelworld.org/AtGenExpress/resources/) [42], \( \text{AtCaM1} \) (\( \text{PbCaM1} \) ortholog), and \( \text{AtCaM7} \) (\( \text{PbCaM3} \) ortholog) were also obviously induced from 0 to 24 h during salt and osmotic stress (Figure 7 and Table S4), further suggesting that \( \text{PbCaM1} \) and \( \text{PbCaM3} \) have evolved similar role or subfunctionalization in response to salt and osmotic stress in pear. In Figure 7, the other five genes in \( \text{Arabidopsis} \) were induced and expressed under salt and osmotic stresses, indicating that the most \( \text{AtCaM} \) genes exhibited similar or
Figure 5: Stress-related cis-element analysis of the promoter regions of pear (Pyrus bretschneideri) and Arabidopsis CaM genes. Stress-related cis-elements including ABRE (involved in the response to ABA), CE3 (involved in ABA and VP1 responsiveness), HSE (involved in response to heat and oxidative stress), LTR (involved in response to low temperature), MBS (MYB binding site involved in response to ABA and drought), and W-box (WRKY binding site involved in abiotic stress and defense response) are shown in the promoter region (1000 bp upstream) of pear and Arabidopsis CaM genes. The colored boxes present above or below the line indicate the plus or minus strand for the distribution of PbCaM genes.

Figure 6: Expression of PbCaM genes in response to salt and osmotic stress. Shoots with young leaves were exposed to 1/2 MS solution containing 200 mM NaCl or 15% (w/v) polyethylene glycol (PEG6000) for the salt treatment (a) or osmotic treatment (b). Leaves were sampled at 0, 12, 24, and 48 h and were subsequently used for QRT-qPCR analysis. All of the experiments were examined using three biological replicates and three technical replicates for all of the genes. The data was shown using the mean ± standard deviation (SD). The error bars represent the SDs of nine replicates.

differential expression trends after being exposed to the same treatments in different treatment times. These data further indicated that CaM genes play conserved roles in response to abiotic stresses in plants.

4. Conclusions

Through comprehensive analysis of CaM genes in pear, we identified and cloned and four putative canonical CaM genes in pear. We further performed a genome-wide analysis of gene structure, gene duplication, synteny, and stress-responsive expression for putative PbCaM genes in comparison to Arabidopsis CaM genes to elucidate the possible expansion patterns of pear CaM genes in pear. Phylogenetic analysis of CaM genes from several sequenced species indicated a conserved evolution of the CaM gene family. Results also indicated that pear CaM genes were more closely related to Arabidopsis CaM genes then they were
to CaM genes in other plant species. PbCaM and AtCaM had a similar distribution of cis-elements and expressions in responses to salt and osmotic stress. All four PbCaMs had been differentially upregulated expression under salt stress and osmotic stress. In particular, PbCaM1 and PbCaM3 were both significantly upregulated in response to salt and osmotic stress, suggesting they may play an important role in the common response of pear to these stresses. The present study provides basic information on the composition, structure, and expression of pear CaM genes in response to salt and osmotic stresses, which can be used as a foundation for future studies regarding the specific function of CaM genes in pear.

Competing Interests

The authors declare that they have no any conflict of interest.

Authors’ Contributions

Jing Lin Zong-Ming (Max) Cheng and Youhong Chang conceived and designed the experiments. Jun Tang, Jing Lin, Xiaogang Li, Qiongsong Yang, and Qunkang Cheng performed the experiments and analyzed the data. Jun Tang wrote the manuscript. All authors read and approved the final version of the manuscript.

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