Research Article

Genome-Wide Identification and Characterization of the Shaker-Type $K^+$ Channel Genes in *Prunus persica* (L.) Batsch

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Shaker-type $K^+$ channels are critical for plant $K^+$ acquisition and translocation that play key roles during plant growth and development. However, molecular mechanisms towards $K^+$ channels are extremely rare in fruit trees, especially in peach. In this study, we identified 7 putative shaker-type $K^+$ channel genes from peach, which were unevenly distributed on 5 chromosomes. The peach shaker $K^+$ channel proteins were classified into 5 subfamilies, I-V, and were tightly clustered with pear homologs in the phylogenetic tree. Various cis-acting regulatory elements were detected in the promoter region of the shaker-type $K^+$ channel genes, including phytohormone-responsive, abiotic stress-responsive, and development regulatory elements. The peach shaker $K^+$ channel genes were expressed differentially in distinct tissues, and $PpSPIK$ was specifically expressed in the full-bloom flowers; $PpKAT1$ and $PpGORK$ were predominantly expressed in the leaves, while $PpAKT1$, $PpKC1$, and $PpSKOR$ were majorly expressed in the roots. The peach shaker $K^+$ channel genes were differentially regulated by abiotic stresses in that $K^+$ deficiency, and ABA treatment mainly increased the shaker $K^+$ channel gene expression throughout the whole seedling, whereas NaCl and PEG treatment reduced the shaker $K^+$ channel gene expression, especially in the roots. Moreover, electrophysiological analysis demonstrated that $PpSKOR$ is a typical voltage-dependent outwardly rectifying $K^+$ channel in peach. This study lays a molecular basis for further functional studies of the shaker-type $K^+$ channel genes in peach and provides a theoretical foundation for $K^+$ nutrition and balance research in fruit trees.

1. Introduction

Potassium ($K^+$) is an essential macronutrient for plants to maintain crucial roles in a number of biochemical and physiological processes [1–3]. Xylem is the transport organization of vascular plants, which is responsible for the upward transport of $K^+$ absorbed by the roots. Phloem is a complex tissue that transports, supports, and stores nutrients, including $K^+$, especially in ferns and seed plants [1, 2, 4]. The $K^+$ from the soil solution was taken up via the root’s surface and then transported to the shoots, distributed within cells into different compartments, and recycled in storage organs by various $K^+$ transport systems, including the shaker-type $K^+$ channels, KT/HAK/KUP transporters, tandem-pore $K^+$ (TPK) channels, and cation-proton antiporters (CPAs) [2, 4, 5].

In plants, there are two kinds of $K^+$ uptake and transport mechanisms, i.e., the high-affinity $K^+$ absorption system (mechanism I) and the low-affinity $K^+$ absorption system (mechanism II). The mechanism I system plays a crucial role just when the external $K^+$ status is less than 200 $\mu$mol·L$^{-1}$, while the mechanism II system plays an important role when the external $K^+$ status is more than 1 mmol·L$^{-1}$ [6, 7]. In particular, the long-distance $K^+$ distribution and dynamic balance are mainly mediated by 3 categories of $K^+$ channels, including shaker-type channels, TPK family channels, and...
other K⁺ channels, which have been functionally verified via electrophysiological systems [2, 4, 5, 8, 9]. Notably, shaker K⁺ channels were the first K⁺ channels identified in plants at the molecular level [10]. According to the voltage dependence and K⁺ movement direction, there are 9 shaker-like K⁺ channels in Arabidopsis, including the inward-rectifying K⁺ channels AtKAT1, AtKAT2, AtAKT1, AtAKT5, and AtSPIK, the weak-rectifying K⁺ channel AtAKT2, the outward-rectifying K⁺ channels AtSKOR and AtGORK, and regulatory subunit AtKC1 [1, 8, 11–21]. Several members of the shaker K⁺ channel gene family have been cloned and functionally determined by heterologous expression system or electrophysiological system from tomato [12, 13], barley [14], maize [15], rice [16], carrot [17], A. fruticosa var. mongolicus [18], grape [19–21], strawberry [11], pear [8], and osier willow [9].

Peach (Prunus persica (L.) Batsch) is one of the most important fruit crops in the world [22]. K⁺ is the most abundant cation within the fruit that plays an important role in all developmental stages, and K⁺ deficiency negatively affects fruit productivity and fruit quality [23–25]. However, molecular mechanism towards K⁺ transport and distribution in fruits is unclear. In this study, 7 putative shaker-type K⁺ channel genes were identified in peach, and the detailed gene location, phylogenetic relationships, gene structures, and tissue expression profiles were further investigated. This study provides a foundation for further functional characterization of the shaker-like K⁺ channels in peach.

2. Materials and Methods

2.1. Identification and Classification of Putative Peach Shaker K⁺ Channel Genes. Peach genome datasets were downloaded from the Phytozone v 13 peach genome database (http://phytozone-next.jgi.doe.gov). The protein sequences of the 9 shaker K⁺ channel genes of Arabidopsis were obtained from the Arabidopsis Information Resource (TAIR) (http://www.arabidopsis.org). BLASTP searches against the peach genome database were performed using the full-length sequences of Arabidopsis shaker K⁺ channel proteins as queries. To confirm the existence of the shaker K⁺ channel protein domains (PF00027, PF00520, and PF11834) [7–9], the candidate proteins were analyzed using Pfam (http://pfam.xfam.org) and Simple Modular Architecture Research Tool (http://smart.embl-heidelberg.de/). To distinguish the candidate peach shaker K⁺ channel genes, we entailed them in accordance with the order of the corresponding phylogenetic locations. The molecular weights, isoelectric points (pl), aliphatic index, and grand average of hydropathy (GRAVY) of the peach shaker K⁺ channel proteins were calculated by the ExPasy website (https://web.expasy.org/protparam/). The subcellular locations of the peach shaker K⁺ channel proteins were predicted by WoLF PSORT (http://www.genscript.com/psort/wolf_psort.html). The exon-intron structure was determined using the online program Gene Structure Display Server: GSDS 2.0 (http://gsds.gao-lab.org), and transmembrane domains were predicted by the online program TMpredict (http://sbcb.bioch.ox.ac.uk/TM_noj/TM_noj.html).

2.2. Phylogenetic Tree Construction of Plant Shaker K⁺ Channel Homologs. A multiple alignment analysis among the shaker K⁺ channel homologs from peach, Arabidopsis, rice, pear, sorghum, and maize was carried out using the ClustalW software. Gene ID of the shaker K⁺ channel homologs are listed in Supplemental Table 1. The phylogenetic tree was generated using MEGA13.0 with the maximum likelihood (ML) method, and the bootstrap analysis was set to 1000 replicates.

2.3. cis-acting Element Prediction of the Promoter Regions of Peach Shaker K⁺ Channel Genes. The 1500 bp upstream sequence of coding regions of the shaker K⁺ channel genes were retrieved from the Phytozone peach genome database and then submitted to PlantCARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/).

2.4. Plant Materials and Treatments. Five-year-old Prunus persica (L.) Batsch cv. Xiahui 6 trees growing at the Jiangsu Peach Germplasm Repository (Zhenjiang China) were used throughout this study. The leave, phloem, flower and fruit samples were collected at different developmental stages (DS), as described in our previous reports [26–28]. For stress treatments, Xiahui 6 seedlings were germinated from seeds on MS solid medium and cultured in the incubator of 28°C day 16 h/18°C night 8 h, with a relative humidity of 75%, for 4 weeks, and then treated by K⁺ depletion, 200 μmol·L⁻¹ ABA, 200 mmol·L⁻¹ NaCl, or 10% (w/v) PEG for 48 h, respectively [9, 29–31]. The MS medium was used as a control. The samples were frozen in liquid nitrogen and stored at -80°C for RNA extraction and gene expression analysis.

2.5. Quantitative Real-Time PCR (RT-qPCR). The total RNA of each sample was extracted using MiniBEST Plant RNA extraction kit (TaKaRa, Dalian, China), and the 1st-strand cDNA was synthesized using Primer Script RT reagent kit (TaKaRa, Dalian, China). Specific primers were designed using the NCBI Primer BLAST online tool against the peach genome (Supplemental Table 2). The qRT-PCR analysis was performed on 7500 Real-Time PCR System (Applied Biosystems, New York, USA) using SYBR Green (TaKaRa, Dalian, China). The peach UBI gene was used as the internal control [26–29, 31]. The RT-qPCR reaction procedure was as follows: 95°C for 30 sec, 40 cycles of 95°C for 5 sec, and 60°C for 34 s, and then 72°C for 60 sec. All reactions were performed in triplicates, and three biological repeats were conducted. The relative transcript level of each gene was calculated using the 2⁻ΔΔCT normalized expression method [26–29, 31].

2.6. Patch Clamping Analysis. The electrophysiological function of PpSKOR was verified by patch clamping system as described previously [9, 30]. The expression plasmid pTracer-CMV3-SKOR was constructed by introducing the PpSKOR gene into the vector of pTracer-CMV3 [9, 30]. The primers used for the recombinant vector construction are listed in Supplemental Table 2, and Pme I site was introduced in the forward primer, and Not I site was introduced in the reverse primer, which were both
underlined. The HEK293-T cells transfected with pTracer-CMV3 empty vector were used as the control, and pCLAMP 10.0 patch clamping system was utilized to record the currents of pTracer-CMV3-SKOR under different extracellular K⁺ concentrations [9, 30], including 0, 10, 50, and 100 mmol-L⁻¹, without deducing the control background currents.

2.7. Statistical Analysis. Statistical analysis was carried out using independent samples t test in SPSS 22.0 software (SPSS Chicago, Illinois, USA). Asterisks indicate statistical differences between plants under control and stress treatment (*P < 0.05, and **P < 0.01; independent samples t test).

3. Results

3.1. Genome-Wide Identification of the Shaker K⁺ Channel Genes in Peach. In this present study, a total number of 7 nonredundant shaker K⁺ channel genes were screened and identified from peach genome (Table 1). Functional domain verification and multiple sequence analysis showed that all peach shaker K⁺ channel proteins contained the cyclic nucleotide-binding domain (PF00027), ion channel transmembrane (PF00520), and KHA domain (PF11834), which belonged to the classic plant shaker K⁺ channels (Figure 1). To further entitle the peach shaker K⁺ channel genes with individual names and investigate the evolutionary relationship of the plant shaker channel homologs, a ML phylogenetic tree was constructed among peach, pear, Arabidopsis, rice, sorghum, and maize (Figure 2). Notably, the amino acid sequences of the shaker K⁺ channel proteins from these 6 plant species shared an overall identity of 65.13%, and the highest identity (86.51%) was observed in extremely conserved domains or regions (Supplemental Figure 1). According to the tree, the plant shaker channel homologs could be divided into 5 subfamilies, including group I-V, and the peach shaker K⁺ channel proteins were distributed in group I-V subfamilies, each with 2, 1, 1, 1, and 2 members, respectively (Figure 2). In particular, all peach shaker channel proteins were strictly clustered with corresponding homologs from pear, with the exception of PpSKOR that was clustered among SKOR or GORK homologs from different plant species (Figure 2).

Multiple alignment of the peach shaker K⁺ channel proteins was analyzed using ClustalX2.1 software. The peach shaker K⁺ channel proteins were labelled with red dot. The locations of the functional domains were labelled with squares of different colors (PF00027, cyclic nucleotide-binding domain, red square; PF00520, ion channel transmembrane, blue square; and PF11834, KHA domain, yellow square).

A maximum likelihood (ML) tree was constructed by multiple alignment of the shaker K⁺ channel proteins in peach, pear, Arabidopsis, rice, soybean, and maize using ClustalX2.1 and MEGA13.0 software. The information of the shaker K⁺ channel proteins from the sequenced plant was listed in Supplemental Table 1. The peach shaker K⁺ channel proteins were labelled with red dot.
functions in peach, the expression profiles of the shaker channel genes were analyzed via RT-qPCR in different tissues or organs in 5-year-old peach trees. The results showed that the shaker K⁺ channel genes exhibited distinct tissue-specific characteristics in peach trees (Figure 4). In particular, *PpSPIK* was specifically expressed in the full-bloom flowers, *PpKAT1* and *PpGORK* were predominantly expressed in the leaves, while *PpAKT1*, *PpKCI*, and *PpSKOR* were majorly expressed in the roots (Figure 4). Notably, the expression of *PpAKT2* was higher and relatively even in the aboveground parts than in the roots, and the highest level was observed in the phloem. The distinct tissue-specific

| Gene name | Locus ID | Chr | Gene location | Intron no. | Subgroup | Protein (aa) | pI | TM | Aliphatic index | GRAVY |
|-----------|---------|-----|---------------|------------|----------|--------------|----|----|----------------|-------|
| *PpKAT1* | Prupe.4G080000 4 | 3881434..3886944 forward | 10 | Group II | 776 | 6.26 | 6 | 85.96 | -0.24 |
| *PpSPIK* | Prupe.1G472600 1 | 39291448..39296784 reverse | 11 | Group I | 897 | 6.47 | 6 | 94.39 | -0.12 |
| *PpAKT1* | Prupe.7G237400 7 | 20553574..20560807 reverse | 10 | Group I | 890 | 4.88 | 6 | 127.72 | 0.728 |
| *PpAKT2* | Prupe.1G572200 1 | 46649271..46658449 forward | 12 | Group III | 843 | 5.75 | 6 | 94.62 | -0.18 |
| *PpKCI* | Prupe.1G464600 1 | 38774545..38780568 forward | 10 | Group IV | 627 | 6.65 | 6 | 98.55 | -0.01 |
| *PpSKOR* | Prupe.5G237000 5 | 1794373-17920240 forward | 10 | Group V | 750 | 6.22 | 6 | 94.94 | -0.19 |
| *PpGORK* | Prupe.3G164900 3 | 18394189..18405879 reverse | 12 | Group V | 831 | 6.02 | 6 | 98.42 | -0.14 |

**Table 1: Basic information of the peach shaker K⁺ channel genes.**

**Figure 1: Multiple sequence analysis of the peach shaker K⁺ channel proteins.**
expression profiles may reflect different channel functions that taken place in special parts of peach trees.

3.5. **Response of the Peach Shaker $K^+$ Channel Genes under Abiotic Stresses.** We further examined the relative expression levels of the peach shaker $K^+$ channel genes in peach seedlings in response to abiotic stresses, including $K^+$ deficiency, NaCl, ABA, and PEG treatment, respectively. In general, the RT-qPCR indicated that the shaker $K^+$ channel genes were differentially regulated by these abiotic stresses in that $K^+$ deficiency, and ABA treatment mainly increased the shaker $K^+$ channel gene expression throughout the whole seedling, whereas NaCl and PEG treatment reduced the shaker $K^+$ channel gene expression, especially in the roots (Figure 5). In particular, the $K^+$ deficiency decreased the expression of 5 genes ($PpAKT1$, $PpAKT2$, $PpKC1$, $PpSKOR$, and $PpGORK$) in all the tested tissues, including leaves, stems, and roots, and $PpKAT1$ in the aboveground parts and $PpSPIK$ in the leaves. ABA treatment significantly reduced the expression of 3 genes ($PpAKT1$, $PpKC1$, and $PpSKOR$) throughout the

![Figure 2: Phylogenetic tree of the shaker $K^+$ channel proteins from different plants.](image-url)
**Figure 3:** Gene structure analysis of the peach shaker K⁺ channel genes.

**Table 2:** Subcellular localization prediction of the peach shaker K⁺ channel proteins\(^a\).

| Gene     | Plasma membrane | Endoplasmic reticulum membrane | Cytosol | Microbody | Nucleus | Mitochondrial inner membrane | Chloroplast membrane | Golgi body |
|----------|-----------------|--------------------------------|---------|-----------|---------|-------------------------------|----------------------|------------|
| PpKAT1   | 64.30%          | 14.28%                         | 7.14%   | 7.14%     | 7.14%   | —                             | —                    | —          |
| PpSPIK   | 64.30%          | 21.42%                         | 7.14%   | 7.14%     | —       | —                             | —                    | —          |
| PpAKT1   | 100%            | —                              | 7.14%   | 7.14%     | —       | —                             | —                    | —          |
| PpAKT2   | 57.16%          | 21.42%                         | 14.28%  | —         | 7.14%   | —                             | —                    | —          |
| PpKC1    | 78.58%          | 7.14%                          | 7.14%   | —         | 7.14%   | —                             | —                    | —          |
| PpSKOR   | 64.30%          | 21.42%                         | 14.28%  | —         | —       | —                             | —                    | —          |
| PpGORK   | 50%             | —                              | 7.14%   | 7.14%     | —       | 28.58%                        | 7.14%                | —          |

\(^a\)Indicates no detection.

**Table 3:** Cis-acting elements analysis in the promoter regions of the peach shaker K⁺ channel genes\(^a\).

| Cis-acting elements | Proposed functions | PpKAT1 | PpSPIK | PpAKT1 | PpAKT2 | PpKC1 | PpSKOR | PpGORK |
|---------------------|--------------------|--------|--------|--------|--------|-------|--------|--------|
| GT1-motif           | Light response     | 6      | 6      | 7      | 6      | 7     | 8      | 7      |
| ARE                 | Anaerobic induction| 1      | 1      | 1      | 1      | 1     | 1      | 1      |
| ABRE                | Acsisic acid responsive | 1  | 1      | 1      | 1      | 1     | 1      | 1      |
| TGACG-motif         | Methyl jasmonate   | 2      | 2      | —      | —      | 3     | 2      | 2      |
| AACA_motif          | Endosperm expression| —     | 1      | 1      | 1      | 1     | 1      | —      |
| MBS                 | Drought inducibility| —     | 1      | —      | 1      | 1     | —      | 1      |
| TATC-box            | Gibberellin responsive | 1  | 1      | —      | —      | —     | —      | 1      |
| O2-site             | Zein metabolism    | 1      | —      | 1      | —      | —     | —      | 1      |
| AuxRR-core          | Auxin responsive   | —      | —      | —      | —      | —     | —      | 3      |
| TCA-element         | Salicylic acid responsive | — | —      | —      | 1      | 2     | 1      | —      |
| CAT-box             | Meristem expression| 1      | —      | 1      | —      | —     | 1      | —      |
| TC-rich repeats     | Wound responsive   | —      | —      | 1      | —      | —     | —      | —      |
| MYB                 | Flavonoid biosynthesis | —  | 1      | —      | —      | —     | —      | —      |
| LTR                 | Low temperature    | —      | 1      | —      | —      | —     | —      | —      |
| CARE                | Metabolism regulation | —  | —      | —      | —      | 1     | —      | —      |
| TC-rich repeats     | Defence and stress | —      | —      | —      | —      | 1     | —      | —      |

\(^a\)Indicates no detection.
whole seedlings, 2 genes (PpKAT1 and PpGORK) in the shoots, and PpAKT2 in the leaves. The expression of 4 genes (PpAKT1, PpAKT2, PpKC1, and PpSKOR) were enhanced in all the tested tissues and 2 genes (PpKAT1 and PpGORK) in the roots under NaCl treatment, while 3 genes (PpAKT1, PpKC1, and PpSKOR) were increased throughout the whole seedlings, 2 genes (PpKAT1 and PpGORK) in the leaves, and PpGORK in the roots and PpAKT2 in the aboveground
parts. Although the expression of PpSPIK was extremely low throughout the whole peach seedling, its expression changed little in all tested tissues under PEG treatment (Figure 5).

3.6. Electrophysiological Function of PpSKOR. Considering that the overall expression amount of PpSKOR was relatively higher than that of the other shaker K⁺ channel genes, especially of the highest level in the roots, its expression was sensitive to all tested treatments, including K⁺ deficiency, NaCl, ABA, and PEG treatment (Figures 4 and 5). We further determined the electrophysiological function of PpSKOR by patch clamping system. The results revealed that cells expressing pTracer-CMV3-SKOR possessed outward-rectifying currents (Figure 6). Notably, the highest currents were recorded when the extracellular K⁺ concentration was 0 mmol·L⁻¹, and the outward-rectifying currents decreased alongside with the increase of the extracellular K⁺ concentration (Figure 6). Moreover, the capacity of PpSKOR channel was activated when the cell membrane voltage was set at -20 mV, and the intensity of the outward-rectifying currents were increased when the voltage was more positive (Figure 6).

Recently, the electrophysiological function of SpuSKOR [9] and VviSKOR [30] has been determined by patch clamping system. In this study, we further compared the intensity of outward currents among SKOR homologs of peach, grape, and purple osier willow. When the K⁺ concentration in the extracellular fluid was set at 0 mmol·L⁻¹ and the cell membrane voltage was set at 100 mV, the outward current intensity of peach PpSKOR was higher than that of grape VviSKOR but lower than that of SpuSKOR from purple osier willow (Figure 7).

4. Discussion

K⁺ fertilizer plays a key role in tree growth, flowering, fruit quality, and yield [23–25, 28]. However, molecular mechanisms towards K⁺ nutrition in fruit trees are largely unclear, especially in peach.

In plants, the structures of the shaker K⁺ channels, including KAT, AKT, KC, SPIK, SKOR, and GORK types, are highly conserved and similar to that of Drosophila [8, 11, 32]. In this present study, the amino acid sequences of the shaker K⁺ channel proteins from 6 plant species mentioned above shared an extremely high identity in the conserved domains or regions (Supplemental Figure 1) and, again, support the proposition that the shaker K⁺ channel domains are highly conserved during long-distance evolution. According to the phylogenetic tree, the peach shaker K⁺ channels were classified into 5 subfamilies, I-V, which is consistent with the classification of Arabidopsis and pear shaker K⁺ channel proteins [1, 8, 11, 32]. Notably, the peach shaker K⁺ channel proteins are tightly clustered with pear homologs in the phylogenetic tree, implying that peach and pear belonging to the same Rosaceae may possess a closer evolution distance than the other 4 annual plants, including Arabidopsis, rice, sorghum, and maize (Figure 2).

Notably, tissue-/organ-specific expression patterns of the shaker K⁺ channel genes may reflect their precise functions during plant growth and development [1, 8, 9, 32]. In this study, PpSPIK was absolutely expressed in mature whole flowers (Figure 4), including pollen, which was consistent with the previous report that AtSPIK was majorly expressed in pollen and mediated inward K⁺ influx into the growing tube [33, 34]. We speculate that PpSPIK may play similar roles in peach tube development that needs further functional determination. In Arabidopsis, AtKAT1 was mainly expressed in leaf guard cells and functioned as an inward-rectifying K⁺ channel [35], while AtGORK was mainly expressed in the leaves and functioned as an outwardly-rectifying K⁺ channel of the guard cell membrane [36, 37]. Together, these two channels contribute to stoma movement.

Figure 6: Curves of the current-voltage relation recorded by patch clamping system. Green fluorescence-labelled HEK293-T cells that transformed with pTracer-CMV3-SKOR were being detected by PCLAMP 10.0 device. The current signal was recorded by PCLAMP 10.0 and calculated by Sigma plot 11.0. The K⁺ concentration in the extracellular fluid was chosen as 0, 10, 50, and 100 mmol·L⁻¹. Data are shown as the means recorded from 5 independent cells.
and K⁺ balance in Arabidopsis [35–37]. Consistently, both PpKAT1 and PpGORK were dominantly expressed in peach leaves, including young and mature leaves, implying that these two channel genes may also be involved in stomata movement in peach leaves. In addition, SKOR as outward-rectifying K⁺ channel was famous for the long-distance transportation of K⁺ ions through the xylem in plants [9, 38–41].

Similar expression profiles may reflect physiological functions. In this present study, peach PpSKOR was mainly expressed in the roots and also be observed in the leaves, phloem, and flowers, which was in line with the previous reports of SKOR homologous genes from muskmelon, osier willow, and Z. xanthoxylum [9, 40, 42]. However, SKOR was specifically expressed in the roots of Arabidopsis and rice [38, 39]. Further patch clamping analysis revealed that PpSKOR demonstrated K⁺ efflux current and voltage-dependent gated channel activity, which belong to the characteristics of outward-rectifying K⁺ channels (Figure 6). These findings are in accordance with grape VviSKOR [30] and purple osier willow SpuSKOR [9] that are being verified by patch clamping systems via HEK 293-T cells but also in line with Arabidopsis AtSKOR [38] and muskmelon CmSKOR [40] that are being determined by Xenopus oocytes and double electrode voltage clamp systems. Although similar outward current characteristics of SKOR homologs are being observed, the current intensity is different among distinct plant species, and the channel activity of PpSKOR was higher than that of grape VviSKOR but lower than that of SpuSKOR from purple osier willow (Figure 7), implying that the physiological function and regulatory mechanisms of SKOR homologous channels are not only specific but also complex, especially in woody plants. Nonetheless, we consider that PpSKOR is an indispensable outward-rectifying K⁺ channel in peach trees.

5. Conclusion

The seven peach shaker-type K⁺ channel proteins were tightly clustered with pear homologs in the phylogenetic tree. The peach shaker K⁺ channel genes were differentially expressed in distinct tissues, and K⁺ deficiency and ABA treatment mainly increased their gene expression throughout the whole seedling, whereas NaCl and PEG treatment reduced their gene expression. PpSKOR is a typical voltage-dependent outward-rectifying K⁺ channel in peach. This study lays a molecular basis for functional studies of the shaker-type K⁺ channel genes in fruit trees.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

We declare that we do not have any commercial or associative interest that represents a conflict of interest with the work submitted.
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Supplementary Materials

Supplemental Figure 1: amino acid alignment of highly conserved domains of plant shaker K+ channels. Supplemental Table 1: gene ID of plant shaker K+ channels used for phylogenetic tree construction. Supplemental Table 2: specific primers used in this study. (Supplementary Materials)

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