Genome-Wide Identification of the PHD-Finger Family Genes and Their Responses to Environmental Stresses in Oryza sativa L.

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Abstract: The PHD-finger family has been demonstrated to be involved in regulating plant growth and development. However, little information is given for its role in environmental stress responses. Here, we identified a total of 59 PHD family genes in the rice genome. These OsPHDs genes were located on eleven chromosomes and synten analysis only revealed nine duplicated pairs within the rice PHD family. Phylogenetic analysis of all OsPHDs and PHDs from other species revealed that they could be grouped into two major clusters. Furthermore, OsPHDs were clustered into eight groups and members from different groups displayed a great divergence in terms of gene structure, functional domains and conserved motifs. We also found that with the exception of OsPHD6, all OsPHDs were expressed in at least one of the ten tested tissues and OsPHDs from certain groups were expressed in specific tissues. Moreover, our results also uncovered differential responses of OsPHDs expression to environmental stresses, including ABA (Abscisic acid), water deficit, cold and high Cd. By using quantitative real-time PCR, we further confirmed the differential expression of OsPHDs under these stresses. OsPHD1/7/8/13/33 were differentially expressed under water deficit and Cd stresses, while OsPHD5/17 showed altered expression under water deficit and cold stresses. Moreover, OsPHD3/44/28 displayed differential expression under ABA and Cd stresses. In conclusion, our results provide valuable information on the rice PHD family in plant responses to environmental stress, which will be helpful for further characterizing their biological roles in responding to environmental stresses.

Keywords: Oryza sativa; PHD-finger transcription factors; evolutionary divergence; expression analysis; environmental stress

1. Introduction

Rice (Oryza sativa L.) is one of the staple crops, feeding more than half of the world’s population. However, rice yields and quality are severely limited by diverse environmental stresses, especially cold, water deficit and high cadmium (Cd) [1]. Rice originates in tropical and subtropical regions, so it is much more sensitive to cold stress, compared with other cereal crops. Therefore, rice production, especially in high latitude regions, is severely prohibited by cold stress [2]. Another constraint comes from water deficit, particularly in arid and semi-arid regions [3]. Sustainable water is required during
rice cultivation, hence rice is extremely sensitive to water deficit. Besides, due to excessive application of phosphate fertilizers during recent years, Cd concentration in soils has dramatically increased, which has become another limiting factor to rice productivity and quality [4]. Environmental stresses, especially cold, water deficit and high Cd, impose a broad range of restrictions on rice production.

To cope with these adverse environmental stresses, the expression of a considerable amount of genes is altered and a series of complex signal pathways is triggered in rice [5]. It has been suggested that transcription factors, including the well-known WRKYs [6,7], MYBs [8], NACs [9,10] and bZIPs [11], exert important roles in stress signal transduction. Among them, the zinc-finger transcription factors are widely distributed in plants and make crucial contributions to plant stress tolerance.

The zinc-finger proteins are characterized by a zinc-binding finger domain comprising of cysteines and/or histidines [12]. The conserved cysteine and histidine residues, in conjunction with zinc ions, can stabilize the spatial structure of zinc-finger proteins. According to the arrangement of the zinc-binding residues, zinc-finger proteins are classified into different types, including RING (Really Interesting New Genes), LIM (Lin11, Isl-1 and Mec-3) [13] and PHD (plant homeodomain) [14].

The PHD-finger domain is comprised of approximately 60 amino acids, with a characteristic feature Cys4–His–Cys3 (C-X4–C-X8–25–C-X2–4–C-X4–3–H-X2–C-X(12,32)–C-X(2,3)–C), which is similar to RING (Cys3–His–Cys4) and LIM (Cys2–His–Cys5) [15,16]. Since the first PHD-finger protein HAT3.1 was identified in Arabidopsis [17], more and more PHDs have been reported in plants. Until now, the PHD family proteins have been identified in several plant species. A previous study in 2004 identified 45 PHDs in Arabidopsis and 44 in rice [18]. Recent research also suggests a total of 73 poplar PHDs [19] and 67 maize PHDs [20]. Current research shows that the plant PHD family was not evolutionarily conserved, but displayed a great diversity in protein sequence, structure and evolutionary relationship [18–20].

Consistently, the PHD-finger family also exhibits diverse roles during plant growth and development. For instance, Arabidopsis PHD-domain ALFIN1-like proteins are found to promote seed germination [21]. In Arabidopsis, PHDs also participates in regulating flowering by modifying the SOC1/FT chromatin conformation [22]. Besides, a barley PHD protein MSL is suggested to play a central role in pollen development [23]. However, the biological roles of PHDs in stress responses are rarely reported. For now, several studies uncover the differential expression of PHDs under environmental stress. In soybean, the expression of six GmPHDs is induced by drought stress. Among them, GmPHD4/5 expression is also up-regulated by cold stress [24]. Moreover, GmPHD2/5 are identified to regulate salt stress responses [24,25]. In maize, 15 of 67 ZmPHDs respond to environmental stresses, including drought and salt [20]. Besides, in poplar, nine PtPHDs show differential expression under salt, drought and cold stresses [19]. However, no genetic evidence is provided regarding the rice PHD genes in stress responses.

Hence, in this research, we carried out comprehensive analyses of the rice PHD family, identified the phylogenetic relationship, gene duplication, gene structure and functional domains, and further investigated their expression patterns in different tissues and under diverse environmental stresses. Our results will benefit further research concerning the potential roles of the rice PHDs in stress responses.

2. Results

2.1. Identification and Chromosomal Location of the Rice PHD Family Genes

The PHD-finger proteins play crucial roles in plant growth and development [26]. Hence, in this research, we attempt to identify the rice PHD family genes and investigate their expression profiles. However, due to the extremely high homology of the protein sequences and structures of the PHD, RING and LIM domains, the HMMER search cannot distinguish the PHD, RING and LIM proteins. Therefore, in this research, we identified the PHD genes from the rice genome by combining the results from four searching methods: a “PHD-finger” keyword search and BLASTP search against the Phytozone database, a “PF00628” keyword search against the Rice Genome Annotation Database
and an HMMER search against the rice proteome database. The putative candidates were subjected to SMART and Pfam analyses to ensure the existence of the complete PHD domains.

As a consequence, a total of 59 PHD genes (named as OsPHD1 to OsPHD59) were identified (Table 1) and the C4HC3 sequence motifs within the PHD domains are shown in Figure 1. These PHD family members varied markedly in protein sequence length from 175 (OsPHD6) to 2192 (OsPHD43) amino acids (aa), with an average length of 722 aa. The molecular masses varied from 19.75 (OsPHD6) to 243.66 (OsPHD43) kDa and the predicted isoelectric points varied from 4.46 (OsPHD46) to 9.87 (OsPHD38).

**Figure 1.** Protein sequence multiple alignment of the PHD-finger domains in the rice PHD family proteins. The multiple alignment was conducted with the amino acid sequences within the predicted PHD domains by using MEGA5.0 software with default parameters. The conserved amino acids (Cys4-His-Cys3) within the PHD-finger domains are shaded in brown and blue.
### Table 1. Detailed information of all PHD family genes identified in the rice genome.

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Considering the great differences in aa numbers and pI values of OsPHDs, we speculated that the rice PHD family was not as evolutionarily conserved as other protein families. In this context, we performed chromosomal location and synteny analysis of OsPHDs. As shown in Figure 2, 59 OsPHDs are located on 11 chromosomes except chromosome 10 and they are not randomly or equally distributed on each chromosome. Chromosome 1 possessed nine OsPHDs, while chromosomes 8 and 12 only contained two. Furthermore, synteny analysis revealed only 9 pairs of duplicated genes (Figures 2 and S1), indicating the high divergence of the rice PHD family. Consistently, previous studies reported only 6 duplicated pairs within 73 poplar PHDs [19] and 12 pairs within 67 maize PHDs [20].

![Figure 2](image)

**Figure 2.** Chromosomal distribution of the rice PHD family genes. The blue bars represent the chromosomes and the chromosome numbers are shown at the top of the bars. The duplicated gene pairs are identified and connected by solid lines. The scale bar on the left represents the length of the chromosome.

### 2.2. Phylogenetic Analyses and Gene Architecture of the Rice PHD Family

To better understand the rice PHD family, we generated a phylogenetic tree by using the full-length protein sequences of OsPHDs as well as some PHDs from other species that have been functionally reported previously. As shown in Figure 3, these PHD proteins are grouped into two major clusters. Out of the 59 OsPHDs, ten were clustered together with the stress-responsive PHDs from maize [20], soybean [24,25] and alfalfa [30], indicating the involvement of these OsPHDs in stress responses. Another cluster included the other 49 OsPHDs and PHDs which were reported to participate in plant reproductive growth and development, such as *AtMS1* [31–33], *AtDUET* [34], *AtVRN5* [35], *AtSHL* [36], OsPHD48/OsEhd3 [28], OsPHD35/OsHAZ1 [27] and OsPHD52/OsMS1 [29].

In order to further investigate the evolutionary relationship, the full-length aa sequences of OsPHDs were used to construct an un-rooted phylogenetic tree. As shown in Figure 4A, the rice PHD family could be divided into eight groups (groups A to H). Three of them (groups A/C/E) have more members than the others, with 11 OsPHDs in group A, 13 in group C and 10 in group E. However, group B only possessed three PHD proteins. It is worth noting that the duplicated genes described above (Figure 2) were mainly distributed in group A and F (Figure 4A). This finding indicated that members in group A and F were relatively evolutionarily conserved, even though the PHD family displayed a great diversity.
Figure 3. Phylogenetic tree analyses of all OsPHDs proteins and PHDs from other species. The phylogenetic tree was constructed based on the full-length amino acid sequences by using MEGA5.0 software with the Neighbor-Joining method. The red shade marks the stress related cluster that includes 10 OsPHDs as well as 6 GmPHDs and 16 ZmPHDs which are characterized to participate in stress responses. The green shade marks other OsPHDs and some PHD proteins from Arabidopsis and alfalfa that are linked to plant growth and development regulation.

To obtain deeper insights into the structural diversity of OsPHDs, we analyzed the characteristics of exon-intron organization. As shown in Figure 4B, the number of exons varied greatly, from 1 (OsPHD11) to 24 (OsPHD27/50), and the exon-intron organization of different groups also differed wildly. The differences in exon numbers and exon-intron organization further suggested the evolutionary diversity of the PHD family. Besides, we also noticed that members within each group exhibited a certain similarity in terms of genomic structure. For example, most members from group A or F possessed five exons. Except OsPHDS0, members in group A showed similar exon-intron composition form. These results further confirmed the finding that although the rice PHD family diverged greatly among different groups, members within each group were relatively conserved.
Figure 4. Phylogenetic tree and gene structures of the rice PHD family. (A) Phylogenetic tree analyses of the rice PHD family. The phylogenetic tree was constructed based on the full-length amino acid sequences of the rice PHD proteins by using MEGA5.0 software with the Neighbor–Joining method and the bootstrap values were set at 1000. Eight groups (A–H) are marked with different colors; (B) Gene structures of the rice PHD family. The gene structures were analyzed by using the Gene Structure Display Server (GSDS2.0). Exons, introns and untranslated regions are indicated by red rounded rectangles, black lines and green boxes, respectively. The scale bar at the bottom is used to estimate the sizes of exons, introns and untranslated regions.

2.3. Investigation of the Conserved Functional Domains in OsPHD Proteins

To further verify the diversity of the rice PHD family, we analyzed the functional domains of all the rice PHD proteins (Figure 5). Our results showed that members within each group shared high similarity in domain structure, while members from different groups varied widely, indicating the potential functional divergence and specialization of OsPHDs from different groups.
Figure 5. Functional domains of the rice PHD family proteins. The information on functional domains was obtained from the phytozome and is shown in the diagrams. Different colored boxes with numbers in them represent different functional domains.

In detail, with the exception of OsPHD50, members in group A contained an Alfin domain (PF12165). Alfin-containing PHD proteins acted as a histone-binding component which specifically recognized H3K4me3 and were reported to participate in salt stress responses [30,37]. This finding indicated the involvement of group A OsPHDs in salt stress responses. Four members in group F, as well as OsPHD33 in group E and OsPHD37 in group C, possessed a BAH domain (PF01426). The BAH domain functioned through protein-protein interaction and was linked to DNA methylation and gene silencing [38,39]. Furthermore, a SET domain (PF00856) was found in five OsPHDs. The SET domain was reported to regulate gene transcription and chromatin structure, and participate in growth control [40,41]. In addition, members in group B and OsPHD50 in group A also contained a PWWP domain (PF00855), which is involved in protein-protein interaction with other histone and DNA modifier domains [42,43]. These results implied that OsPHDs might function in epigenetic
regulation of gene expression. Moreover, six members in group C contained a Jas domain (PF16135), which plays a crucial role in the jasmonate signalling pathway. In conclusion, the variety of functional domains suggested the putative functional diversity of OsPHDs from different groups.

To further confirm the functional divergence of OsPHDs, we then investigated the conserved motifs by using MEME with the number of motifs set to be 20 (Figure S2). Among the 20 motifs, motifs 2, 4, 14 and/or 20 representing the PHD-finger domain were present in all groups. Motifs 1 and 7, constituting the Alfin domain, were specific to group A. Motifs 19, 16 and 10 were shared by members in group B, while motifs 3, 17 and 18 were present in OsPHDs from group C. Motifs 8 and 5 were observed in OsPHDs from group F, while motifs 15 and 6 were specific to group H. Motif 9 was only presented in OsPHD57 in group E and OsPHD58 in group C. Motifs 11 and 12 existed in OsPHD50 in group A and OsPHD15/34 in group E, while motif 13 was only presented in OsPHD17 and OsPHD46 in group F. These results indicated that OsPHDs in the same group shared similar motifs, while motifs are divergently distributed among specific groups, which might contribute to the functional divergence of the rice PHD family.

2.4. Expression Profiles of OsPHD Genes in Rice Tissues

In an attempt to explore the potential function of OsPHD family genes, we retrieved the expression profiles from RiceXPro and analyzed their expression in different tissues. As shown in Figure 6A, the numbers of expressed OsPHDs in different tissues varied little, from 51 to 57. However, the numbers of OsPHDs with high, medium or low expression levels varied greatly. Notably, OsPHDs expressed at relatively higher levels in pre-emergence inflorescence and pistils, with less lowly-expressed genes. In contrast, the numbers of lowly-expressed OsPHDs were obviously greater in seeds-10d (d: day. The same below.) and endosperm-25d. Furthermore, the numbers of highly-expressed OsPHDs were smaller in endosperm-25d (1), anther (4) and leaves-20d (4).

According to their expression characteristics in different tissues, OsPHDs were clustered into four groups (groups I to IV, Figure 6B). OsPHDs in groups I and II expressed at lower levels in all tissues, but members in group I displayed relatively higher expression in a specific tissue. For instance, although OsPHD52/OsMS1 showed very low expression levels in most tissues, its expression displayed a dominant enrichment in pre-emergence inflorescence (Figure 6B, Figure S3A). Furthermore, the specific expression of OsPHD52/OsMS1 in pre-emergence inflorescence was in line with its regulatory role in pollen development [29]. Moreover, OsPHD48/OsEhd3 showed relatively higher expression in pistils and pre-emergence inflorescence, which is consistent with previous reports that OsEhd3 is a critical promoter of rice flowering [28].

Group III members displayed typical tissue specific expression, but expressed at higher expression values than group I. For example, OsPHD12/45 were highly expressed in seeds-10d, while OsPHD3 was highly expressed in embryos-25d. Notably, with the exception of OsPHD23, all group III OsPHDs, showing tissue specific expression patterns, belonged to the development related cluster as described in Figure 3. Remarkably, OsPHD35/OsHAI1 from group III, which participates in radial axis differentiation in a globular embryo [27], showed the highest expression in embryos-25d. Interestingly, members in group III did not show high expression in either post-emergence inflorescence, leaves-20d or endosperm-25d. In contrast, OsPHDs, which highly expressed in these three tissues, were all clustered into group IV. Besides, most members in group IV were highly expressed in more than three tissues. In conclusion, these results suggested that OsPHDs displayed tissue-specific expression profiles, indicating their potential divergent roles in plant development.
Figure 6. Expression of the rice PHD family genes in different tissues. (A) Numbers of expressed genes in different tissues. Expression data in different tissues were downloaded from the Rice Expression Profile Database. High: expression values >20, medium: 20 ≥ expression values >10, low: 10 ≥ expression values >0; (B) Expression profiles of the rice PHD family genes in different tissues. A heat map was generated and OsPHDs were manually clustered into four groups according to their expression values in different tissues. The color scale represents the expression values: red indicates high levels and green represents low levels. Pre-EI: pre-emergence inflorescence; Post-EI: post-emergence inflorescence.
2.5. Expression Responses of OsPHD Genes to Environmental Stresses

In order to investigate the potential roles of OsPHDs in environmental stress responses, we further analyzed their expression under ABA (Accession No. SRX332134 and SRX330497), high Cd (DRX012208-DRX012225) and water deficit (SRX844621-SRX844624) by using the transcript data from RiceXPro, as well as our previous microarray data under cold stress (Table S1). As shown in Figure 7A, 47 of the 59 OsPHD genes are differentially expressed (|Log2 fold change| > 1) under high Cd stress, while only 5 OsPHDs display altered expression under cold stress. Furthermore, the expression of 21 and 11 OsPHDs was differently regulated by ABA and water deficit, respectively. Interestingly, most OsPHDs were down-regulated under high Cd concentration, while under ABA and water deficit, the numbers of up-regulated OsPHDs were obviously larger than that of down-regulated. Notably, 29 of these OsPHD genes showed differential expression under two or three types of stresses (Figure 7B). Among them, OsPHD33 expression responded to ABA, water deficit and Cd stresses, and OsPHD5 was differentially expressed under ABA, water deficit and Cd stresses. However, no OsPHD gene was observed to be differentially expressed in response to all four types of stresses.

In detail, after ABA treatment, 19 OsPHD genes were up-regulated, while only two were down-regulated (Figure 7C). Among the up-regulated OsPHD genes, OsPHD3 and OsPHD19 displayed the greatest ABA-induced expression, with Log2 fold change >3. It is worth noting that most members in group B and E showed differential expression under ABA stress, indicating that they may be involved in ABA signaling transduction and/or stress responses. Compared with ABA stress, less OsPHD genes with differential expression were observed under water deficit (Figure 7C). Only eight up-regulated and three down-regulated OsPHDs were found when the soil water content decreased to 40% of that under normal conditions. Among them, OsPHD5 showed the greatest decreased expression, while OsPHD24 exhibited the largest increased expression. Interestingly, by comparing the differentially expressed OsPHDs under ABA and water deficit stress, we found that only OsPHD33 showed differential expression under both stresses, while other OsPHDs only differentially expressed under one type of stress. This finding implied that OsPHD genes might participate in water deficit stress responses through ABA-independent ways.

In previous research, we carried out the microarray analysis by using rice seedlings which were exposed to 4 °C for 1, 3, 6, 9, 12 and 24 h. Based on the expression profiles under cold stress, the rice PHD family was divided into three groups (groups I–III, Figure 8A). Group I only contained two OsPHDs showing decreased expression after 4 °C treatment, while group III included three OsPHDs with increased expression. Most OsPHDs genes were clustered into group II and their expression was not influenced by cold stress. Notably, with the exception of OsPHD6, all these differentially expressed members belonged to group F and H, implying the potential involvement of group F and H OsPHDs in cold stress responses.

In contrast, 47 out of 59 OsPHDs were differentially expressed when rice roots were immersed in 50 μM Cd solution (for 1 and 24 h) and most of them were down-regulated (Figure 8B). What is interesting is that OsPHDs showed extremely distinctive expression patterns between roots and shoots. We checked the raw data of OsPHDs expression at 0, 1 and 24 h under Cd stress (Figure S4). By comparing the data in roots and shoots at 0 h, we found that under normal conditions, most OsPHDs displayed similar expression levels in roots and shoots (Figure S4B). After Cd treatment, most OsPHDs expression changed in the roots, while few OsPHDs showed altered expression in the shoots. This finding suggested that the difference of OsPHDs expression patterns between roots and shoots is cadmium related. In detail, after 50 μM Cd treatment, 47 OsPHDs were differentially expressed in the roots, while only four were differentially expressed in the shoots. According to their expression patterns, OsPHDs were divided into six groups (groups I–VI, Figure 8B). The genes in group I showed decreased expression in both roots and shoots, while expression of OsPHDs in groups II–IV was inhibited only in the roots. Group II members were down-regulated at both 1 and 24 h, while expression of groups III and IV OsPHDs was decreased only at 24 and 1 h, respectively. Furthermore, expression of members in group V was not affected, however group VI OsPHDs were
up-regulated under Cd stress in the roots. In conclusion, the differential expression of OsPHDs under diverse environmental stresses suggested their potential roles in plant stress responses.

**Figure 7.** Expression analyses of the rice PHD family genes under different environmental stresses. (A) Numbers of differentially expressed OsPHD genes in stress responses. Expression data in different tissues were downloaded from the Rice Expression Profile Database. Compared with the control, genes with $|\log_2 \text{fold change}| > 1$ were designated as differentially expressed genes; (B) Venn diagram depicting the overlap of differentially expressed genes under different environmental stresses; (C) Expression of OsPHDs under ABA and water deficit stresses. The Y-axis represents the log2 of fold changes. The red lines mark the cut-off lines ($|\log_2 \text{fold change}| = 1$).
Figure 8. Expression profiles of the rice PHD family genes under cold (A) and Cd (B) stresses. Expression data were downloaded from the Rice Expression Profile Database. A heat map was generated and OsPHDs were manually clustered into different groups according to their expression values. The color scale represents the relative expression values compared with the control. Red indicates high levels and green represents low levels.

2.6. Quantitative Real-Time PCR Analyses of OsPHDs Expression in Response to Environmental Stresses

In order to further verify the stress induced expression of OsPHDs, we focused on several representative genes showing differential expression under stress treatment and conducted quantitative real-time PCR analyses. For each stress treatment, we selected one PHD gene whose expression was not affected by this stress, as a reference for qRT-PCR assays. As for ABA stress, expression of two down-regulated and seven up-regulated OsPHDs is verified (Figure 9A). Specifically speaking, OsPHD44 and OsPHD49 displayed decreased expression, and five OsPHDs exhibited increased transcript levels under ABA stress. Under water deficit stress, expression of two OsPHDs (OsPHD1 and OsPHD5) was reduced, while transcript levels of six other OsPHDs were induced (Figure 9B).

Besides, we also confirmed the differential expression of OsPHDs after cold treatment for 24 h (Figure 9C). Expression of two down-regulated (OsPHD5 and OsPHD41 in group I) and two up-regulated (OsPHD55 and OsPHD17 in group III) was verified by quantitative real-time PCR results. We also investigated the transcript levels of four members belonging to group II, which showed slightly decreased expression at 24 h. Results illustrated that only OsPHD58 expression showed a slight decrease with statistical significance after cold stress. Expression of the other three OsPHDs was slightly reduced, but with no statistical significance. Moreover, as for Cd stress, we also selected nine down-regulated OsPHDs from groups I and II, and validated their decreased expression under Cd stress in roots (Figure 9D). With the exception of OsPHD15, all of them were down-regulated by Cd stress in roots, however, only four of them displayed decreased expression in shoots.
Figure 9. Quantitative real-time PCR validation of OsPHDs under ABA (A); water deficit (B); cold (C); Cd-root (D) and Cd-shoot (E) stresses. For ABA and Cd treatments, the three-week-old rice seedlings were treated with 50 μM ABA or 50 μM Cd for 24 h. For cold stress, rice seedlings were exposed to 4 °C for 24 h. For water deficit stress, water irrigation was stopped until the soil water content was decreased to 40% of that under normal conditions. For each stress treatment, one OsPHD gene whose expression was not affected by this stress, was used as a reference for qRT-PCR assays. OsEf1-α (elongation factor 1-α) was used as an internal reference. The mean values (±SE) from three fully independent biological repeats and three technical repeats are shown. Asterisks indicate significant differences (* p < 0.05; ** p < 0.01 by Student’s t-test).
In conclusion, our qRT-PCR results confirmed that OsPHD1/7/8/13/33 were differentially expressed under water deficit and Cd stress, while OsPHD5/17 showed altered expression under water deficit and cold stress. Moreover, OsPHD3/44/28 expression was differentially regulated by both ABA and Cd stresses. To conclude, quantitative real-time PCR results presented here suggest that the rice PHD family genes possibly participate in plant responses to diverse environmental stresses.

3. Discussion

Previous studies have demonstrated that PHD proteins play crucial roles in plant growth and development [21–23,26]. However, the biological roles of PHDs in regulating plant stress tolerance are rarely studied. Hence, in this research, we conducted a comprehensive investigation of the rice PHD family, trying to identify potential OsPHDs that responded to environmental stresses.

The PHD-finger family was reported to be evolutionarily divergent [18–20]. Here, in this research, we further provided several pieces of evidence to show the divergent evolution of the rice PHD family. Firstly, the phylogenetic tree showed that the rice PHD family could be divided into eight groups (Figure 4A). Previous studies reported that the poplar and maize PHDs could be clustered into 11 and 10 subfamilies, respectively [19,20]. Notably, several PHDs could not be clustered into any subfamily due to the low bootstrap values. Secondly, the exon numbers of the rice PHDs varied greatly, from 1 (OsPHD11) to 24 (OsPHD27/50), and the gene structure also differed wildly among different PHD groups (Figure 4B), which further suggested the evolutionary diversity of the rice PHD family. Similarly, maize PHDs from different subfamilies also showed a great diversity in terms of intron numbers and exon length [20]. Thirdly, the rice PHDs varied markedly in protein sequence length, from 175 (OsPHD6) to 2192 aa (OsPHD43). Investigation of functional domains and conserved motifs further revealed that members from different PHD groups also varied widely in domain architecture (Figure 5) and some motifs were exclusively found in a particular group (Figure S1). This finding is in line with previous reports [19,20] and further suggests the diversity of the plant PHD family. Lastly, synteny analyses only identified nine pairs of duplicated PHD genes (Figure 2). Consistently, only six duplicated pairs were observed within 73 poplar PHDs [19] and 12 pairs within 67 maize PHDs [20]. All of the above results support the evolutionary divergence of the rice PHD family.

Even though the rice PHD family is evolutionarily divergent, some PHD groups are relatively conserved. For instance, investigation of gene structure (Figure 4B), functional domains (Figure 5) and conserved motifs (Figure S1) illustrated that OsPHDs within group A and F exhibited high similarity. Consistently, the duplicated OsPHDs genes (Figure 2) were mainly distributed in group A and F (Figure 4A). Similar findings were also observed for Subfamily IX PHDs in maize [20]. The conservation of PHD proteins within certain subfamilies indicated similar and/or overlapping function of these PHD genes. For example, in maize, expression of Subfamily IX ZmPHDs responded to salt, drought and ABA stresses [20]. In addition, phylogenetic analysis of OsPHDs with PHDs from other species (Figure 3) showed that group A OsPHDs were grouped into the same cluster together with Subfamily IX ZmPHDs and six GmPHDs, which were reported to respond to environmental stress [20,24,25]. This finding indicates that although the PHD family is divergent in plants, some PHD subfamilies are relatively conserved among different species.

On the other hand, the structural divergence of different OsPHD groups might contribute to the functional specialization of the rice PHD family. Among the 59 OsPHDs, 26 genes (groups I and III in Figure 6B) tended to specifically express in certain tissues. Notably, with the exception of OsPHD23, all OsPHDs showing tissue specific expression patterns belonged to the development related cluster as described in Figure 3. Among them, OsPHD52/OsMS1 is closely related to AIMS1 in the phylogetic tree (Figure 3) and its expression displayed a dominant enrichment in pre-emergence inflorescence, which is in line with its regulatory role in pollen development [29]. OsPHD48/OsEhd3, which is a critical promoter of rice flowering [28], showed relatively higher expression in pistils and pre-emergence inflorescence. Moreover, OsPHD35/OsHAZ1, which was previously reported to participate in radial axis differentiation in a globular embryo [27], showed the highest expression in
embryos-25d. Remarkably, in the phylogenetic tree (Figure 3), OsPHD35/OsHAZ1 is the closest one to AtVRN5, which was found to function in the epigenetic silencing of Arabidopsis FLC during flowering [35]. In addition, in the phylogenetic tree (Figure 3), OsPHD19 appeared in a pair with AtDUET, which is involved in male meiosis [34]. Consistently, OsPHD19 displayed high expression in pistils. OsPHD53/49, showing high expression in pre-emergence inflorescence, were closely related to AtISHL, which is required for proper development and fertility [36]. Taken together, these findings strongly suggest the potential role of OsPHDs in reproductive growth and development.

In addition to plant growth and development, PHDs were also shown to be involved in stress responses [24,25,44]. Our results also uncovered the differential responses of OsPHDs expression to ABA, high Cd, water deficit and cold stresses (Figures 7–9). Among the four types of environmental stresses detected in this research, more OsPHDs with differential expression were observed under 50 μM Cd treatment. Notably, Cd stress mainly inhibited OsPHDs expression, as evidenced by 41 down-regulated but 6 up-regulated genes (Figures 7A and 8B). In contrast, under ABA and water deficit stresses, more OsPHDs showed up-regulated expression (Figure 7). This difference indicates that OsPHDs might respond to diverse stresses through different ways.

ABA, as a crucial plant hormone, plays a pivotal role in environmental stress responses [45–47]. In this research, we showed that ABA stress greatly triggered the expression of OsPHDs (Figure 7C). By quantitative real-time PCR analysis, we validated that after 50 μM ABA treatment for 24 h, the transcript levels of seven OsPHDs were obviously increased in rice leaves (Figure 9A). Previous research also reported that in maize, 14 PHD genes within Subfamily IX were up-regulated when three-week-old seedling leaves were sprayed with 100μM ABA solution. The ABA responsive elements (ABREs) were found in promoter regions of these PHD genes [20]. Similarly, when soybean seedling roots were immersed in 100 μM ABA, GmPHDs expression was also induced, especially in the stress-tolerant cultivar JD23 [24]. These findings suggested the putative roles of the PHD family genes in ABA signal transduction and responses. However, in our research, even though group A OsPHDs were grouped into the same cluster with Subfamily IX ZmPHDs and six GmPHDs (Figure 3), most of them did not show differential expression under ABA and water deficit stresses. Further experiments are needed to illustrate the difference.

ABA has pivotal roles in plant tolerance to water deficit or drought stress [48,49]. Considering the differential expression of OsPHDs under ABA treatment, we also investigated their expression under water deficit stress. Compared with ABA, fewer OsPHDs genes with differential expression were observed in three-week-old rice leaves when the soil water content was decreased to 40% of that under normal conditions (Figure 7C). The altered expression of OsPHDs was shown by quantitative real-time PCR results (Figure 9B). Among them, OsPHD24 and OsPHD25 exhibited dramatically increased expression, while OsPHD5 and OsPHD6 showed greatly decreased expression. Similarly, GmPHDs expression was also increased in soybean seedlings which were placed on Whatman filter paper for 3 h for dehydration [24]. The responsive expression of PHD genes under drought stress was also observed in maize and poplar [19,20]. After 20% PEG6000 treatment, the PHD genes in maize and poplar were greatly induced. In addition, the dehydration responsive elements (DREs) were found to be enriched in promoters of drought responsive ZmPHDs [20]. However, among the differentially expressed OsPHDs under ABA and water deficit stresses, most of them only differentially expressed under one type of stress, while only OsPHD33 showed altered expression under both stresses. This finding implies that OsPHDs might participate in water deficit stress responses through ABA-independent ways. Taken together, the above results imply that these PHD genes might take part in water deficit tolerance.

In contrast, when exposed to 4 °C, only five OsPHDs showed altered expression (Figure 8A), which was further supported by the quantitative real-time PCR results (Figure 9C). With the exception of OsPHD6, all of them belonged to groups F and H, implying the involvement of these two groups in cold stress responses. Among them, OsPHD6/17/55 were up-regulated, while OsPHD5/41 were down-regulated, which is in line with previous research. In poplar, after exposure to 4 °C, expression of PtPHD12/68/36/50 was decreased, but transcript levels of PtPHD21/29/31/32/65 were increased [19].
Compared with cold stress, Cd stress greatly altered the expression levels of 41 OsPHDs genes (Figure 8B). Most of them were down-regulated by Cd stress, which was further verified by the quantitative real-time PCR results (Figure 9D–E). This finding indicates that the PHD family genes possibly play important roles in rice responses to Cd stress. Interestingly, in roots, 47 OsPHDs were differentially expressed, however, in shoots, only four OsPHDs displayed differential expression (Figure 8B). Under normal conditions, most OsPHDs genes displayed similar expression levels between roots and shoots (Figure S4). After Cd treatment, most OsPHDs expression in roots changed, while few OsPHDs showed altered expression in shoots. This finding suggests that the difference of OsPHDs expression patterns between roots and shoots is cadmium related. This difference implies different responsive mechanisms between roots and shoots, and it is possible that OsPHDs mainly function in roots.

Taken together, current studies have demonstrated the key roles of PHDs in plant growth and development. A handful of studies reported the involvement of PHD in salt stress. However, no biological evidence was given to show PHD function in other environmental stresses. In this research, we suggested that expression of OsPHDs was responsive to ABA, water deficit, cold and especially Cd stress. Hence, it will be interesting to study the responsive mechanisms and potential roles of OsPHDs in response to these environmental stresses.

4. Materials and Methods

4.1. Identification of the PHD-Finger Family Genes in Rice

To identify the candidate PHD genes in the rice genome, we downloaded the HMM profile of the PHD proteins from the HHMHER website (https://www.ebi.ac.uk/Tools/hmmer/search/hmmsearch) and used it to search against the rice proteome database. We also conducted a BLASTP search against rice proteome. Furthermore, “PHD-finger” as a keyword was submitted to search Phytozome (https://phytozome.jgi.doe.gov/pz/portal.html#) [50] and “PF00628” was used as a keyword to search against the Rice Genome Annotation Database (http://rice.plantbiology.msu.edu/index.shtml). The amino acid sequences of candidates from these four searches were screened by SMART (http://smart.embl-heidelberg.de) [51] and Pfam (http://pfam.sanger.ac.uk/) [52] to remove proteins without a complete PHD-finger domain. The information on the rice PHD genes, including locus ID, chromosome locations, ORF length and protein length were obtained from the Phytozome database. The isoelectric point and molecular weight were estimated by using the ExPaSy (http://expasy.org/) [53].

4.2. Multiple Alignment, Phylogenetic Analysis and Chromosomal Location of the Rice PHD Family Genes

The amino acid sequences within the predicted PHD-finger domains were used for multiple alignment to show the existence of the PHD domains. For phylogenetic analysis, multiple alignment was performed with the full-length amino acid sequences of the rice PHD family proteins by using MEGA5 software [54]. The phylogenetic tree was constructed by using the Neighbor-Joining method with the following parameters: poisson correction, pair-wise deletion and 1000 bootstrap replicates. The chromosomal location of the rice PHD family genes was depicted using the MapInspect software. The synteny blocks of the rice genome were downloaded from the Plant Genome Duplication Database (PGDD, http://chibba.agtec.uga.edu/duplication/) [55] and the duplicated OsPHD pairs were connected by solid lines.

4.3. Analyses of Gene Structure, Functional Domains and Conserved Motifs of the Rice PHD Family

The exon and intron structures of the rice PHD family genes were illustrated by using the Gene Structure Display Server (GSDS, http://gsds.cbi.pku.edu.cn/index.php) [56]. The information on functional domains was derived from Phytozome (https://phytozome.jgi.doe.gov/) and SMART. The conserved motifs in the rice PHD proteins were predicted by using the on-line MEME procedure (Multiple Em for Motif Elicitation, http://meme-suite.org/tools/meme) by using the following
parameters: 5 ≤ optimum motif width ≤ 200; the number of motifs = 20; zero or one occurrence per sequence [57].

4.4. Expression Analysis of the Rice PHD Family Genes in Diverse Tissues and Under Different Stress Treatments

The expression data of the rice PHD family genes were downloaded from the Rice Expression Profile Database (RiceXPro, http://ricexpro.dna.affrc.go.jp/) [58]. The transcript data were derived from ten tissues, including leaves-20d (Accession number: SRX100741), shoots (SRX020118), pre-emergence inflorescence (SRX100743), post-emergence inflorescence (SRX100745), pistils (SRX100747), anthers (SRX100746), seeds-5d (SRX100749), seeds-10d (SRX100755), embryos-25d (SRX100753) and endosperm-25d (SRX100754). The accession numbers of transcript data were SRX844621-SRX844624 for water deficit stress, DRX012208-DRX012225 for Cd stress and SRX332134 and SRX330497 for ABA stress.

4.5. Quantitative Real-Time PCR Analyses of the Rice PHD Family Genes in Response to Environmental Stresses

Rice seeds were surface sterilized in 10% NaClO, washed with sterile water 3–5 times and placed on moist filter paper for 2–3 days to promote germination. The young seedlings were transformed and grown in Yoshida’s culture solution or in pots filled with a mixture of peat moss: soil (1:1) under a 12 h light (28 °C)/12 h dark (22 °C) photoperiod.

For ABA and Cd treatments, the roots of the three-week-old hydroponic rice seedlings were immersed in Yoshida’s culture solution containing either 50 μM ABA [59–61] or 50 μM Cd for 24 h [62]. For cold stress, rice seedlings were exposed to 4 °C for 24 h. For water deficit stress, water irrigation was stopped (for 7 days) until the soil water content was decreased to 40% of that under normal conditions.

Equal amounts of leaves (for ABA, cold, water deficit and Cd stresses) or roots (for Cd stress) were harvested. Total RNA was extracted using TRIzol® Reagent (Invitrogen, Carlsbad, CA, USA) and cDNA was synthesized by using the SuperScript™ III Reverse Transcriptase kit (Invitrogen, Carlsbad, CA, USA). Quantitative real-time PCR was performed using the CFX96 Touch™ Real-Time PCR Detection System and TransStart Top Green qPCR SuperMix (Beijing TransGen Biotech, Beijing, China). OsEfl-α (elongation factor 1-α) was used as an internal reference. Expression levels were calculated and normalized as described [63]. Three independent biological replicates and three technical repeats were carried out. Gene specific primers for quantitative real-time PCR are listed in Table S2.

5. Conclusions

In conclusion, we identified a total of 59 PHD family genes in the rice genome. We investigated their chromosomal location, gene duplication, phylogenetic classification, gene structure, functional domains and conserved motifs. Through the comprehensive analyses, we showed that the rice PHD family was evolutionarily divergent among different groups. Meanwhile, we found that some OsPHDs were specifically expressed in certain tissues, indicating the involvement of OsPHDs in developmental regulation. Moreover, we also uncovered the differential responses of OsPHDs expression to environmental stresses, including ABA, water deficit, cold and Cd stresses. By using quantitative real-time PCR, we further confirmed the differential expression of OsPHDs under these environmental stresses. Results presented here will be of great importance to further characterize their biological roles in response to environmental stresses.


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References


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