



Genome-Wide Analysis of *WRKY* Genes and Their Response to Salt Stress in the Wild Progenitor of Asian Cultivated Rice, *Oryza rufipogon*

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Specialty section:

This article was submitted to
Evolutionary and Population Genetics,
a section of the journal
Frontiers in Genetics

Received: 13 June 2019

Accepted: 24 March 2020

Published: 08 May 2020

Citation:

Nan H, Li W, Lin Y-I and Gao L-z
(2020) Genome-Wide Analysis
of *WRKY* Genes and Their Response
to Salt Stress in the Wild Progenitor
of Asian Cultivated Rice, *Oryza*
rufipogon. *Front. Genet.* 11:359.
doi: 10.3389/fgene.2020.00359

The *WRKY* gene family is widespread in plants, which plays key roles in plant development and stress response. Although *WRKY* transcription factors have been widely characterized in many plants, a genome-wide analysis of the *WRKY* gene family is lacking in *Oryza rufipogon*. In this study, we identified 101 *O. rufipogon* *WRKY* (*OrWRKY*) transcription factors, which were further classified into eight subgroups. Phylogenetic analysis showed that *OrWRKY* transcription factors were supported by highly conserved motifs and gene structures. Chromosomal distribution of *OrWRKYs* indicated that most genes were dispersed on all 12 chromosomes, especially enriched on Chromosome 1. Syntenic analysis revealed that 69 (68.3%) genes were derived from either segmental (49) or tandem duplication events (20), suggesting a pivotal role of segmental duplications. We totally characterized 39 orthologous gene pairs between *Oryza sativa* ssp. *japonica* *WRKY* (*OsjWRKY*) and *OrWRKY* genes. We performed quantitative real-time polymerase chain reaction (qRT-PCR) experiments to validate tissue-specific and differential expression of the *OrWRKYs* and responsive expression of the *OrWRKYs* in response to salt stresses in leaves and roots. This study provides a new insight on the evolution of the *WRKY* gene family in *O. rufipogon* and will help further functional characterization of candidate genes toward wild rice germplasm exploration for rice genetic improvement programs.

Keywords: *WRKY* transcription factor, wild rice, *Oryza rufipogon*, expression divergence, whole genome duplication, salt stress

INTRODUCTION

Among the genus *Oryza* comprising 23 species and nine recognized genome types (Vaughan et al., 2003), common wild rice, *Oryza rufipogon* Griff., is, besides the assumed annual wild progenitor *Oryza nivara*, another presumed perennial wild progenitor of Asian cultivated rice, *Oryza sativa* (Oka, 1988; Khush, 1997; Cheng et al., 2003; Fuller et al., 2010; Huang X. et al., 2012), which feeds half of the human population in the world. As a result of the domestication under intensive human cultivation, *O. sativa* has undergone considerable phenotypic and physiological changes, leading to an extensive loss of genetic diversity through successive bottlenecks and artificial selection for

agronomic traits compared to its wild progenitors (Kovach et al., 2007; Xu et al., 2012). *Oryza rufipogon* spans a broad geographical range of global pantropical regions (Morishima and Barbier, 1990) and, for example, extensively grows in diverse natural habitats in South China (Gao et al., 1996; Gao, 2004). As a promising donor for genetic improvement of cultivated rice, many of alien genes associated with morphological traits, quality traits, abiotic stress- and disease resistance-related traits have successfully been introduced through introgression lines from *O. rufipogon*, which has helped expand the rice gene pool important to the generation of environmentally resilient and high-yielding varieties (Brar and Ramos, 2008).

Salt stress is one of the most devastating abiotic stresses in rice, and the salt-affected soils currently account for about 20% of the total paddy rice planting area (Zhou Y. et al., 2016). More seriously, the increased salinization of arable land is expected to have devastating global impacts, resulting in 30% land loss within the next 25 years and up to 50% by the year 2050 (Wang et al., 2003). In recent years, lots of studies have shown valuable insight into the molecular and cellular mechanisms by which rice responds to and tolerate salinity (Schmidt et al., 2013; Zhu et al., 2015). However, the regulatory mechanisms involved in coordinating salt stress tolerance and plant growth are not fully understood. Plants have developed a series of complex, effective systems to keep themselves from numerous adverse environmental fluctuations during growth. And studies have shown that these coping mechanisms mainly function *via* specific transcriptional activation or inhibition of transcription-related genes. Transcription factors play an essential role in this process by binding to specific DNA regions (Singh et al., 2002).

The *WRKY* transcription factors family, one of the largest families in higher plants, plays an essential role in plant development and stress processes. Since the first *WRKY* gene (*SPF1*) was identified and cloned in potato (Huang S. et al., 2012), a large number of *WRKY* genes in other plants were increasingly reported through genome-wide analyses (Zhang and Wang, 2005; Bi et al., 2016; Zhou H. et al., 2016). *WRKY* proteins, which can identify and bind to W-box *cis*-regulatory elements, are about 60 amino acids in length and contain one or two highly conserved WRKYGQK motifs and a typical zinc-finger structure (Eulgem et al., 2000). Besides the conserved sequences of a WRKYGQK motif, some variants including WRKYGEK, WKKYGQK, and WRKYDHK can also be found in plants. And the zinc-finger motif is either Cx4-5Cx22-23HxH (C₂H₂) or Cx7Cx23HxC (C₂HC) (Tang et al., 2013; Guo et al., 2014). Previous studies suggested that the *WRKY* gene family could be divided into three subgroups based on the number of *WRKY* domains and the type of zinc-finger motif. Group I contains two *WRKY* domains and one zinc-finger structure, which can be classified into Ia and Ib subgroups based on the variants in zinc-finger motifs. Ia harbors two *WRKY* domains and C₂H₂ structure, while Ib has two *WRKY* domains and C₂HC motif (Xu et al., 2016). Group II has one *WRKY* domain and a C₂H₂ (Cx4-5Cx22-23HxH) type of zinc-finger structure. On the basis of variants in zinc-finger motif, Group II can also be further divided into five subgroups, including II-a, II-b, II-c, II-d, and II-e. Proteins from Group

III have only one *WRKY* domain but with a C₂HC motif (Eulgem et al., 2000).

WRKY transcription factors are involved in morphology forming processes, such as seed development, germination, and flower induction. For example, *ScWRKY1*, isolated from *Solanum chacoense*, was related to seed development and highly expressed in fertilized ovules at late torpedo-staged embryos (Eulgem et al., 1999). In *Arabidopsis*, the mutant with *AtWRKY39* knockdown had less germination compared with wild-type plants (Li et al., 2010). A total of 18 *DIWRKY* genes in longan showed a specific expression during three stages of flower induction, indicating that these genes may be involved in the flower induction and the genetic control of the perpetual flowering trait (Jue et al., 2018). Except for plant development, *WRKY* genes also play important roles in biotic and abiotic stress responses including fungal-induced defense programs and responses to heat/cold, drought, and salt stresses (Raineri et al., 2015; Yang et al., 2018; Jimmy and Babu, 2019). As one of the most important functions, the *WRKY* gene family seems to regulate the response to salt stress. For example, *ZmWRKY33* was induced by salt treatments and overexpressed in *Arabidopsis*, which was more salt tolerant than the wild type (Li et al., 2013). *GarWRKY17* and *GarWRKY104* overexpression plants in *Arabidopsis* showed enhanced salt tolerance during different developmental stages (Fan et al., 2015). Besides, the transgenic *Nicotiana tabacum* seedlings expressing *VvWRKY2* from grapevine exhibited strong resistance to salt treatments (Mzid et al., 2018).

Due to diverse and important functions of *WRKY* genes in various physiological and developmental processes, many *WRKY* genes have been functionally studied in rice (Xie et al., 2005; Wu et al., 2009; Xu et al., 2016). However, little is known about *WRKY* TFs and their responses to salt stresses in *O. rufipogon*. In this study, we comprehensively characterized the *WRKY* gene family with an emphasis on genome-wide identification of salt-responsive members of the *WRKY* family in *O. rufipogon*. The results of this study enhance our understanding of the *OrWRKY* gene family, which will facilitate the genetic improvement of salt stress tolerance in rice.

MATERIALS AND METHODS

Identification of Putative *OrWRKY* Genes

The genome sequences of *O. rufipogon*, which was sampled in Yuanjiang, Yunnan Province, China, were generated by our lab (Li et al., 2020), and the HMM file (PF03106) of *WRKY* domain was obtained from the Pfam database¹. To comprehensively identify the *OrWRKYs*, HMMER 3.0 software² was used to search against the rice protein sequences with default parameters. The incorrect and redundant predicted sequences were manually removed, and then all putative *OrWRKY* genes were further verified using Pfam database³. The molecular weight (MW) and isoelectric point (PI) were evaluated using

¹<http://pfam.xfam.org/>

²<http://hmmer.janelia.org/>

³<http://plantfdb.cbi.pku.edu.cn/>

ExPASy-ProtParam online software⁴. Meanwhile, the protein sequences of *O. sativa* ssp. *japonica* cv. *Nipponbare* and *O. sativa* ssp. *indica* were downloaded from Phytozome⁵ and plantfdb (see text footnote 3), respectively. We employed the same method as described above to identify the candidate *WRKY* genes. The deduced *WRKY* genes of *O. nivara* were named as *OnWRKY1* to *OnWRKY125* according to Xu et al. (2016). The sequences of *Arabidopsis* *WRKY* genes were downloaded from TAIR⁶. To name the *WRKY* genes of *O. rufipogon* and *O. sativa* ssp. *indica* (*OsiWRKY*), we employed the same method (McCouch, 2008; Group, 2012). The proteins of all candidate *OrWRKY* and *OsiWRKY* genes were aligned against the *OsjWRKY* proteins via BLASTP program with *E* value $1e^{-13}$ and then named the *OrWRKY* and *OsiWRKY* genes according to their homology to *O. sativa* ssp. *japonica* cv. *Nipponbare*.

Classification of *OrWRKY* Genes

Based on the number of *WRKY* domains and the type of zinc-finger motif, the *WRKY* genes can be classified into three groups (Xie et al., 2005; Ross et al., 2007). Group I contains two *WRKY* domains and can be divided into two subgroups. Ia has two *WRKY* domains with C2H2 zinc-finger motifs, while Ib owns C2HC structures. Group II contains one *WRKY* domain with a C2H2 zinc-finger motif. Based on a specific sequence variation in zinc-finger motifs, Group II can be further divided into five subgroups. Subgroup II-a contains CX5CPVKKK(L/V)Q structure, II-b CX5CPVRKQVQ, II-c CX4C, II-d CX5CPARKHVE, and II-e CX5CPARK(Q/M)V(E/D). Group III has one *WRKY* domain with a C2HC zinc-finger motif. The *WRKY*s with incomplete domain are assigned to Group IV.

Sequence Alignment and Phylogenetic Analysis

Multiple sequence alignment of the *WRKY* domains and full-length proteins was performed by CLUSTAL (Larkin et al., 2007). The phylogenetic tree was constructed with MEGA5.0 using a neighbor-joining (NJ) method (Tamura et al., 2011). The bootstrap values were calculated for 1,000 iterations.

Characterization of the Structure and Motif of *OrWRKY*s

The available information of exons and introns was retrieved from the *O. rufipogon* genome sequences and then visualized by the GSDS (version 2.0)⁷ online program with coding sequences and genomic sequences. The motifs of each deduced *OrWRKY* protein were analyzed by MEME suit software (version 4.12.0)⁸ (Bailey et al., 2009) with parameters as follows: maximum number of motifs, 10. The upstream 1.5-Kb sequences of *WRKY*

genes were extracted with an in-house Perl script to determine the *cis*-elements by using the PlantCARE database⁹.

Determination of Chromosomal Distribution, Gene Duplication, and Synteny

The chromosomal distribution of *OrWRKY* genes was determined from the annotation file (GFF3) of *O. rufipogon*. The synteny and segmental and tandem duplications were analyzed using a previously reported method (Tang et al., 2013) and visualized (including gene positions) using the Circos v0.69 (Krzywinski et al., 2009). To date *OrWRKY* genes derived from duplication events, *Ka* and *Ks* values were estimated using the maximum likelihood method implemented in codeml program (Yang, 2007). The divergence time (*T*) was estimated as $T = Ks/2r \times 10^{-6}$ MYA (million years ago) according to the approximate substitution rate $r = 6.5 \times 10^{-9}$ (Yu et al., 2005). And the branch-site model A in EasyCodeML v1.21 (Gao et al., 2019) was used to further assess positive selection in *OrWRKY* genes.

Identification of Orthologous *WRKY* Genes Between *O. rufipogon* and *O. sativa* ssp. *japonica*

In order to identify the putative orthologous *WRKY* genes between *O. rufipogon* and *O. sativa* ssp. *japonica*, a reciprocal best hit (RBH) method was employed (Xia et al., 2014). Briefly speaking, each sequence from *OrWRKY* was initially searched against all sequences from *OsjWRKY*s using Blast, and each sequence of *OsjWRKY* was in turn searched against all sequences from *OrWRKY*s. We selected pairs of gene sequences that were the best hits for each other as putative orthologs. Due to the limitation of RBH method, potential paralogs may not be completely excluded from the ortholog dataset. To remove the possible paralogs, we first searched all pairs of gene sequences against all plant protein sequences available in GeneBank and selected only pairs of gene sequences unambiguously mapped to the same protein with an *E*-value $< 1e^{-13}$ as orthologous genes. The CDS sequences of each orthologous gene were employed to calculate the synonymous (*Ks*) and non-synonymous (*Ka*) substitution rate by codeml program (Yang, 2007) using the maximum likelihood method. To validate whether the orthologous *WRKY* genes between *O. rufipogon* and *O. sativa* ssp. *japonica* have undergone positive selection, we used the branch-site model A in EasyCodeML v1.21 (Gao et al., 2019).

Quantitative Real-Time PCR Experimental Validation

The *O. rufipogon* plants were grown in the greenhouse at 28°C to collect expression profiles of *WRKY* genes under salt treatments. They were transferred into containers filled with 200 mM NaCl solution. Then, the leaves and roots were harvested at 0, 1, 2, 4, and 8 h after treatments and immediately frozen in liquid nitrogen until used. Three seedlings were

⁴<http://web.expasy.org/protparam/>

⁵<https://phytozome.jgi.doe.gov/pz/portal.html#>

⁶<https://www.arabidopsis.org/>

⁷<http://gsds.cbi.pku.edu.cn>

⁸<http://meme-suite.org/tools/meme>

⁹<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>

sampled for each treatment with the three biological replicates. Total RNA was extracted with Trizol reagent (Invitrogen) and treated with RNase-free DNase I (Boehringer Mannheim). And then, the cDNA was synthesized by reverse transcription of 1.0 µg total RNA using MMLV reverse transcriptase (Toyobo) according to manufacturer's instructions. Gene-specific primers of *OrWRKY* genes were designed using Primer Premier 5.0 software (**Supplementary Table S1**). The designed quantitative real-time polymerase chain reaction (qRT-PCR) primer pairs were first verified using BLAST *On Line* at NCBI, and a dissociation curve was then analyzed after the PCR reaction to confirm their specificity. RT-PCR was performed with a multicolor RT-PCR detection system (Bio-Rad). Each reaction contained 10 µl SYBR, 1.0 µl samples, and 0.8 µl of each primer pair in a final volume of 20 µl. The RT-PCR cycle was as follows: 95°C for 30 s; 40 cycles of 95°C for 5 s, and 60°C for 30 s. The *Actin* gene was selected as an internal standard for normalization, and three technical replicates were conducted for each sample. The $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001) was performed to analyze RT-PCR data, and we used 0 h as an untreated control (expression = 1.0) to calculate the fold change in the expression level of the relevant genes.

Statistic Analysis

All data were expressed as the mean \pm SD after normalization. The Fisher's least significant difference (LSD) analysis at $P = 0.05$ level was performed by SPSS software (version 18.0).

RESULTS

Identification of *OrWRKY* Genes

The PF03106 file and HMMER 3.0 software were used to comprehensively identify the *OrWRKY* genes. We totally detected 101 non-redundant deduced *OrWRKY* gene members, which were further named as *OrWRKY1* to *OrWRKY121* according to names of their *OsjWRKY* orthologs (**Supplementary Table S2**). Among them, WRKYGQK domain was a highly conserved motif, while other members also contained WRKYGKK, WRKYGEK, WSKYEQK, WRMCGQK, WRMCGQN, WRMCGQS, WRMTGQS, and WIKYGQK domains. In addition, three genes, *OrWRKY87.2*, *OrWRKY96.2*, and *OrWRKY105*, were found to lose the WRKYGQK domain, and the four genes (*OrWRKY27*, *OrWRKY39*, *OrWRKY49*, and *OrWRKY116*) were found to lose zinc-finger motif. The lengths of the *OrWRKY* proteins spanned from 97 to 1,209 amino acids,

and the detailed information about each *OrWRKY* gene was shown in **Supplementary Table S2**.

Classification of the *OrWRKY* Genes

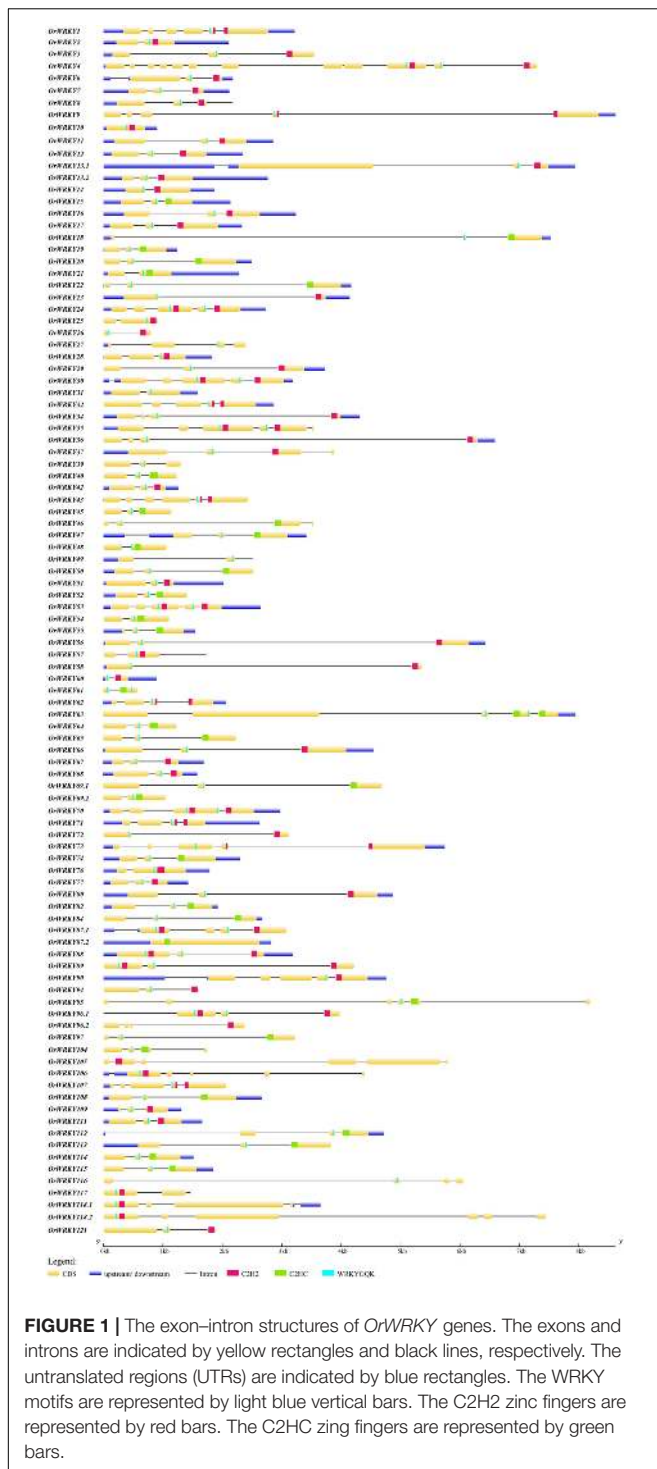
All of the putative *WRKY* genes could be divided into four groups (i.e., I, II, III, and IV). **Table 1** presented a summary of classification for the *WRKY* gene family from this wild rice genome. Groups I, II, III, and IV had 12, 52, 30, and 7 members, respectively. Group II comprised of five subgroups, and each of subgroup II-a, II-b, II-c, II-d, and II-e contained 4, 6, 24, 6, and 12 members, respectively. In addition, based on the phylogenetic relationships of both *WRKY* domains and full-proteins (**Supplementary Figures S1, S2**), all the seven members (*OrWRKY27*, *OrWRKY39*, *OrWRKY49*, *OrWRKY87.2*, *OrWRKY96.2*, *OrWRKY105*, and *OrWRKY116*) in Group IV could be classified into the other subgroups (Groups II-b, II-e/II-c, II-c, II-c, Ia, II-c, and III, respectively). Detailed information about the classification of *OrWRKY* genes and the *WRKY* domains could be found in **Supplementary Table S2** and **Supplementary Figure S3**.

Exon-Intron Organization of *OrWRKY* Genes

To investigate the evolution of *OrWRKY* genes, the exon/intron boundaries were analyzed. As illustrated in **Figure 1**, exon numbers highly varied among *OrWRKY* genes. The number of exons spanned from 1 to 12, and 52 *OrWRKY* genes (51.4%) contained three exons, accounting for the largest proportion. Fifteen *OrWRKYs* had four exons, and 15 *OrWRKYs* retained two exons, while only one *OrWRKY* gene contained 12 exons. Note that *OrWRKY* genes in the same group seemed to have a similar number of exons. For example, most genes in Groups II-b contained five introns, while most II-d and II-e genes had three introns. And Group III contained 30 members, and 23 genes had three introns. These results showed a strong correlation between exon-intron structure and phylogenetic relationship, additionally supporting the classification of the *OrWRKY* gene family. Based on the position of introns inserted into the conserved *WRKY* structure, they could be divided into two groups (PR and VQR type). The N-terminal domain of Ia *OrWRKYs* all contained a VQR type of intron, while the C-terminal domain had a PR-type intron. On the contrary, the two Ib proteins had a PR-type intron in the N-terminal domain. The PR-type intron was widely distributed among the six other subgroups, the same cases were also found in *Arabidopsis*, grape, and strawberry (Eulgem et al., 2000; Guo et al., 2014; Zhou H. et al., 2016).

TABLE 1 | Number of *WRKY* genes in *Arabidopsis*, cultivated rice, and wild rice.

Species	Ia	Ib	II-a	II-b	II-c	II-d	II-e	III	IV	Total
<i>Arabidopsis</i>	13	–	4	7	18	7	9	14	–	72
<i>O. sativa</i> ssp. <i>japonica</i>	11	2	4	8	23	7	10	31	5	101
<i>O. sativa</i> ssp. <i>Indica</i>	11	3	4	6	29	7	12	31	6	109
<i>O. rufipogon</i>	10	2	4	6	24	6	12	30	7	101
<i>O. nivara</i>	11	2	4	7	22	7	11	28	5	97



Phylogenetic Analysis of WRKY Genes Among *Arabidopsis*, *O. sativa*, *O. nivara*, and *O. rufipogon*

In order to investigate the phylogenetic relationships and evolutionary history of *OrWRKY*s, WRKY domains from the five plant genomes (*Arabidopsis*, *O. sativa* ssp. *japonica*, *O. sativa*

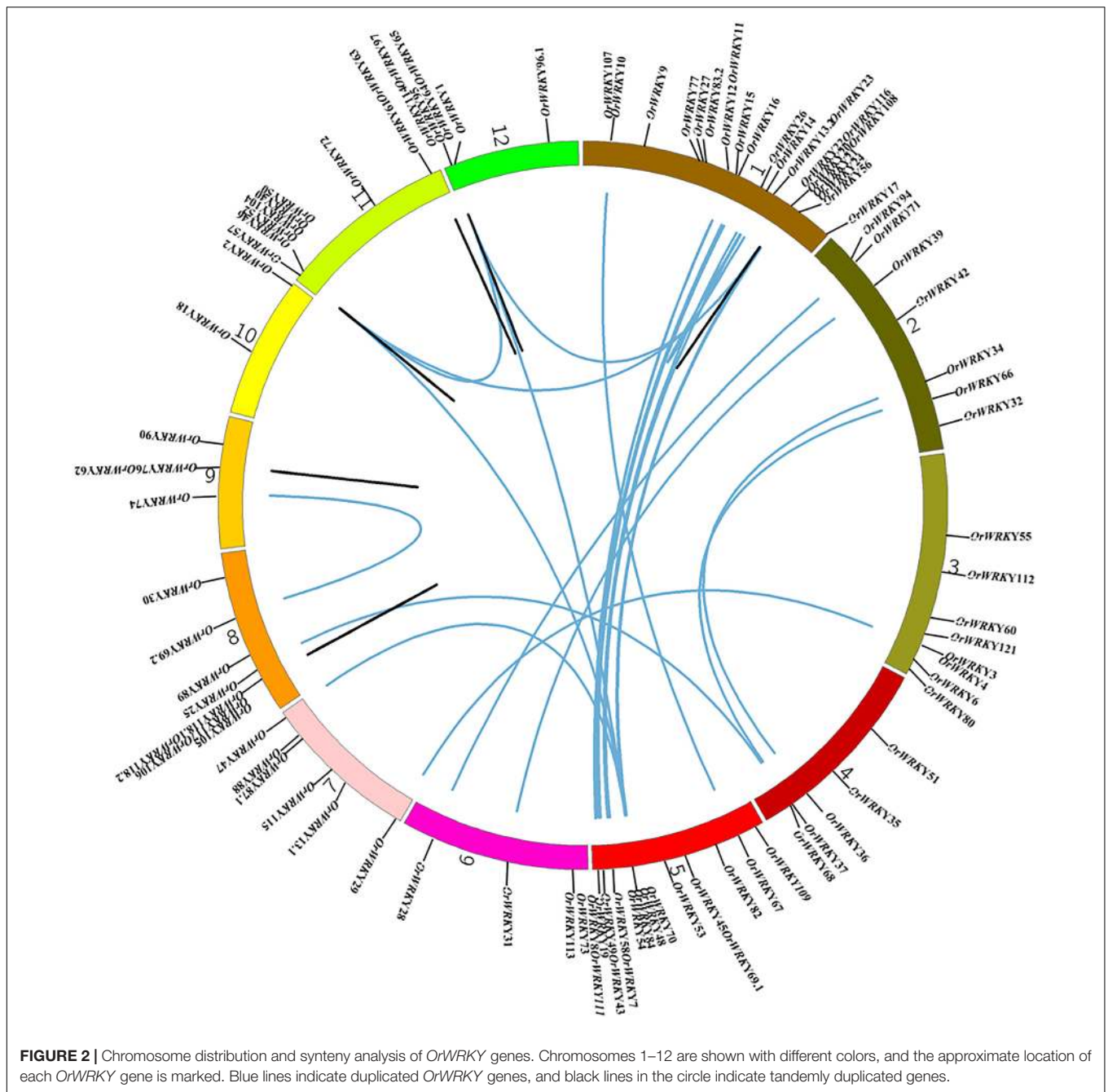
ssp. *indica*, *O. rufipogon*, and *O. nivara*) were combined into the data analysis. The genome data of cultivated rice were retrieved from Phytozome and plantfdb. WRKY genes of *Arabidopsis* were downloaded from TAIR, and WRKY sequences of *O. nivara* were obtained from a previous study (Xu et al., 2016). Sequences with variations in WRKY domains were excluded from the analysis. Finally, an unrooted phylogenetic tree was constructed using the NJ method with MEGA from the 531 conserved WRKY domains from these five genomes. As shown in **Supplementary Figure S4**, all WRKY domains could be divided into eight subgroups. The N-terminal and C-terminal domains of Group Ia were separately clustered in the phylogenetic tree, suggesting that the N-terminal motifs might not be duplicated by the C-terminal motifs. However, both C-terminal and N-terminal motifs of major Ib were clustered with Group III, showing a relatively closed relationship to it. In addition, similar to what was found in other plants, our results further support that II-a and II-b were clustered into a single subgroup and subgroups II-d and II-e were clustered into the other clade.

When the number of WRKY genes was compared with those of *Arabidopsis*, *O. sativa* ssp. *japonica*, *O. sativa* ssp. *indica*, and *O. nivara* (**Table 1**), we observed that the number of Group III in all four rice species genomes greatly increased and they had approximately the same number of WRKY genes. The results indicated that a large-scale expansion of Group III members in rice seemingly occurred before the divergence of the three rice species, evidenced by a number of the rice WRKY domains exclusively clustered together in Group III.

Chromosomal Location, Gene Duplication, and Genomic Synteny of *OrWRKY* Genes

To examine genomic distribution of *OrWRKY* genes, we analyzed their approximate locations on chromosomes. Almost all of the 101 *OrWRKY* genes were mapped on the chromosomes except for *OrWRKY96.2* because of missing gaps in the genome assembly. Among the 12 chromosomes, as shown in **Figure 2**, Chr 1 contained the most number of *OrWRKY* (22, 21.7%) genes, followed by Chr 5 (17, 16.8%), Chr 8 (9, 8.9%), and Chr 11 (9, 8.9%). However, Chr 10 only had two *OrWRKY*s (*OrWRKY2* and *OrWRKY18*).

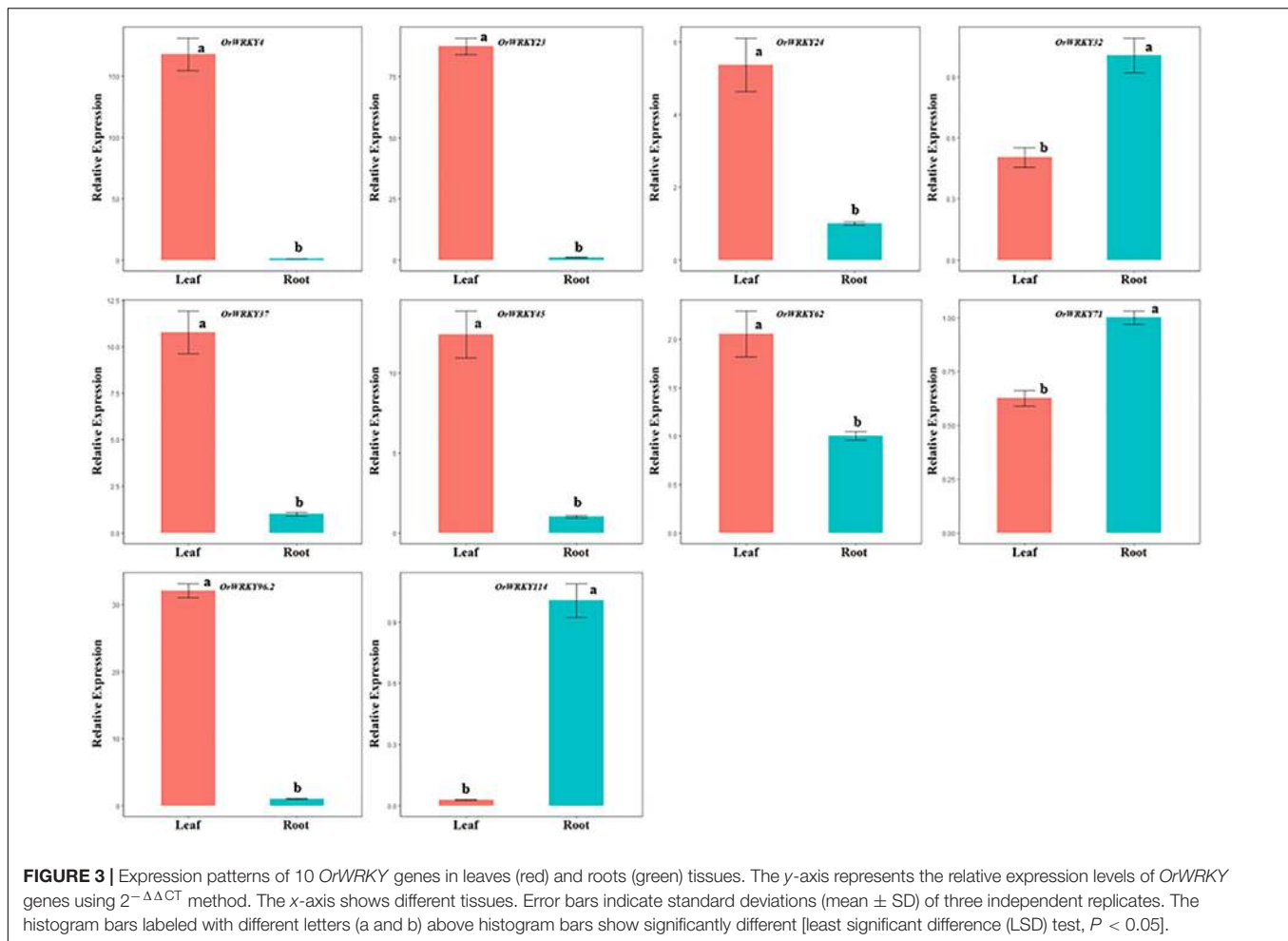
Previous studies suggest that gene duplication events and subsequent positive selection may have played vital roles in gene family expansion and the creation of novel biological functions (Vision et al., 2000; Davidson et al., 2013). In order to investigate the role of gene duplication in the *OrWRKY* gene family, segmental and tandem duplications were detected throughout the *O. rufipogon* genome assembly. Among the 101 *OrWRKY* genes, we found 49 segmentally duplicated genes that formed 29 pairs (**Figure 2** and **Supplementary Table S3**), indicating that segmental duplication events acted as a major force to drive the evolution of the *OrWRKY* gene family. As shown in **Figure 2**, chromosomes 1 and 5 had most of WGD-derived *OrWRKY* duplicated genes, while Chromosome 10 had none of these *OrWRKY* genes. In addition, pairs of *OrWRKY* duplicated genes belonged to the same subgroup, most of which (48.3%;



14/29) were clustered into Group III. Moreover, we identified 11 gene pairs generated from tandem duplication events (Figure 2 and Supplementary Table S4), and more than half of them were clustered into Group III.

To further examine adaptive evolution of *OrWRKY* genes, the *Ka/Ks* (non-synonymous/synonymous) ratios of the duplicated gene pairs were calculated. The *Ka/Ks* ratio is often used to estimate selective pressure acting on protein-coding genes. *Ka/Ks* < 1 shows a sign of purifying (negative) selection, *Ka/Ks* = 1 means neutral evolution, and *Ka/Ks* > 1 suggests adaptive (positive selection) (Hurst, 2002). In this study, we found that most of the segmentally duplicated gene pairs had a

Ka/Ks value < 1 with an average *Ka/Ks* value of 0.9, indicating that the majority of the segmentally duplicated genes underwent negative selection. However, we observed that six pairs of duplicated genes were under positive selection with *Ka/Ks* > 1, and only one pair had *Ka/Ks* > 2 (*OrWRKY16* and *OrWRKY49*). To further validate whether the *OrWRKY* genes have undergone strong selection pressures, we also used the branch-site model [Model A (Model 2, NSites = 2, ncatG = ignored) versus Model null] in EasyCodeML software to detect positive selection sites. We failed to detect any genes under positive selection (Supplementary Table S5). Moreover, the divergence of the duplicated *OrWRKY* genes was also dated using an evolutionary



rate of 6.5×10^{-9} substitutions per site per year. Our results showed that the divergence of segmental duplicated genes spanned from 7.11 to 153.22 million years, and most of the duplicated *WRKY* genes occurred ~ 40 – 70 million years ago.

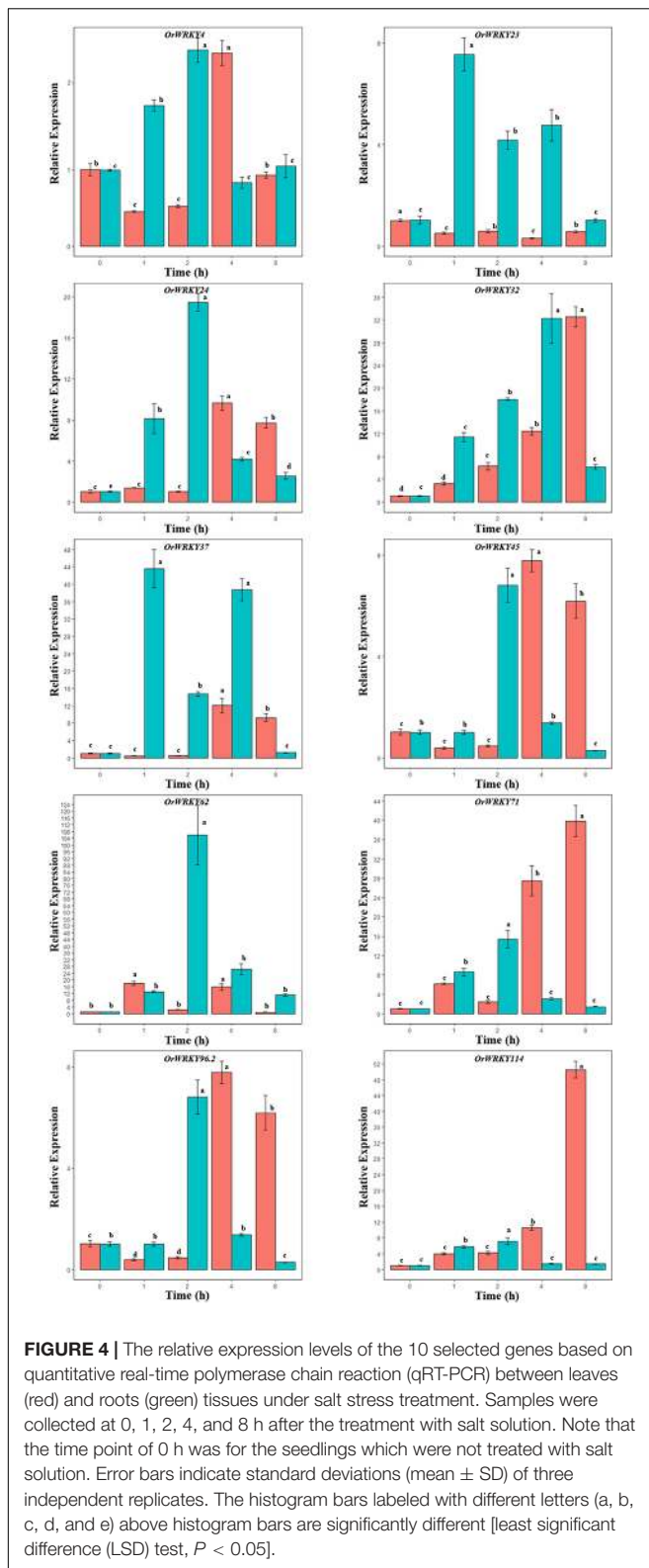
Identification of Orthologous *WRKY* Genes Between *O. rufipogon* and *O. sativa* and Sequence Divergence

To identify orthologous genes between *O. rufipogon* and *O. sativa*, an RBH method was used with further relatively strict filters. We totally found 39 putative orthologous *WRKY* genes with an average length of 442 bp and an average sequence similarity of 98.02%. To examine the molecular evolution of orthologous *WRKY* genes, K_s and K_a of each orthologous gene pair were also evaluated (Supplementary Table S6). Of the 39 orthologous gene pairs, the majority of the orthologous gene pairs (84.6%; 33/39) had ratios of $K_a/K_s < 1$, indicating that they underwent purifying selection. However, we also found six orthologous *WRKY* genes with ratios of $K_a/K_s > 1$, indicating that they may be under positive evolution. Moreover, we used branch-site model A in EasyCodeML to further confirm whether the *WRKY* genes were under positive selection. Our results showed that these genes had no sign of positive selection (Supplementary Table S7).

Expression Profiles of *OrWRKY* Genes

The *OrWRKY* genes could be classified into seven major subgroups (I, II-a–II-d, and III), and thus, a total of 10 *WRKY* genes were randomly selected to represent all these subgroups to exhibit their expression profiling in *O. rufipogon*. The expression patterns of these 10 *OrWRKY* genes were examined in two tissues (leaves and roots) through qRT-PCR. As shown in Figure 3, these *OrWRKY* genes exhibited distinct expression patterns, many of which were differentially expressed between the two tissues. *OrWRKY4*, *OrWRKY23*, *OrWRKY24*, *OrWRKY37*, *OrWRKY45*, *OrWRKY62*, and *OrWRKY96.2* were expressed in leaves and roots, which were relatively highly expressed in leaves but lowly expressed in roots. In contrast, *OrWRKY32*, *OrWRKY71*, and *OrWRKY114* were relatively highly expressed in roots but lowly expressed in leaves. We found that *OrWRKY* genes belonging to different subgroups showed a distinct expression pattern, such as *OrWRKY62* (II-a) and *OrWRKY71* (II-a) as well as *OrWRKY45* (III) and *OrWRKY114* (III).

Previous studies reported that *WRKY* genes were involved in salt stress (Liu et al., 2014; Fan et al., 2015). To investigate expression patterns of *OrWRKY* genes under salt stress, the *O. rufipogon* seedlings were grown in 200 mM NaCl solution. Expression patterns of the 10 selected *OrWRKY* genes from



all subgroups were examined under salt stresses. As shown in **Figure 4**, these selected *OrWRKY* genes that were sensitive to salt stresses, each of which exhibited different expression

profiling in the two tissues after treatments. Some *OrWRKY* genes in roots seemed more sensitive to salt stresses. For example, expression levels of *OrWRKY23* in roots initially increased, reached the maximum level after 1 h and then decreased. However, *OrWRKY23* was not sensitive to salt treatment in leaves. Some genes in leaves seemed to be more sensitive to salt stress. The expression level of *OrWRKY114* in leaves was evidently upregulated by about 50-fold after 8 h, whereas the expression level of *OrWRKY114* in roots increased only by almost seven times at 2 h. These genes showed a different expression profiling under salt stress, suggesting that the *OrWRKY* genes might respond to salt stress through different genetic networks between leaves and roots. Gene expression divergence was also examined by comparing expression levels of *OrWRKY* duplicated genes. Our results showed that the *OrWRKY* genes functionally exhibited similar responses to salt stress but presented differential expression. For example, *OrWRKY62* (II-a) in roots showed relatively sensitive response to salt stress and increased by almost 105 times after 2 h, whereas *OrWRKY62* increased by almost 17 times in leaves after 1 h. However, *OrWRKY71* (II-a) in leaves seemed to be more sensitive to salt stress and raised 39 times after 8 h.

DISCUSSION

In this study, we identified a total of 101 *WRKY* genes from the *O. rufipogon* genome, which could be divided into three groups. In this study, almost all of the *OrWRKY* genes shared the highly conserved WRKYGQK domain. However, we also found some variants, such as WRKYGEK, WRKYGKK, WRMCGQK, and WRMCGQS motifs. Such slight variations in this region had also been reported in other plants. For example, the five unusual VvWRKY domains changed in grape (Guo et al., 2014), and 15 OnWRKY domains varied in *O. nivara* (Xu et al., 2016). Previous studies demonstrated that WRKYGQK domain can bind to w-box *cis*-elements with a C/TTGACC/T core sequence to activate downstream genes (Eulgem et al., 2000). The variation of the WRKYGQK domain could affect the specificity of DNA binding, and the *WRKY* genes lost the motif may bind to other specific sequences (Ciolkowski et al., 2008). In *Arabidopsis*, AtWRKY59 protein, containing a WRKYGKK motif, could not recognize and bound to TTGAC (W-box) (Dong et al., 2003). Moreover, NtWRKY12 with a WRKYGKK domain in tobacco could not recognize the w-box motif, but it may bind to wk-box element (van Verk et al., 2008). Further efforts are required to experimentally validate the function and binding specificities of the 22 proteins with motif variance. In addition, compared with *O. rufipogon* (101 *OrWRKYs*; genome size 439 Mb), a comparable number of *WRKYs* was identified in *O. sativa* (101; genome size 389 Mb) and *O. nivara* (97; genome size 448 Mb), although the number of *WRKYs* was fewer in carrot (67; genome size 473 Mb) and tea tree (56; genome size between 2.9 and 3.1 Gb) and more in *Brassica oleracea* (148; genome size 630 Mb) (International Rice Genome Sequencing Project, 2005; Zuccolo et al., 2007; Yao et al., 2015; Iorizzo et al., 2016; Xia et al., 2017; Nan and Gao, 2019;

Wang et al., 2019). These results indicate that the number of *WRKY* genes may not be associated with the genome size and phylogenetically closed plants may harbor comparable numbers of *WRKY* genes.

Phylogenetic analysis suggested that *OrWRKYs* could be classified into three major groups in accordance with the classification of *WRKYs* in *Arabidopsis*, grape, carrot, tea tree, and cabbage (Wu et al., 2005; Guo et al., 2014; Yao et al., 2015; Nan and Gao, 2019; Wang et al., 2019). Several hypotheses have been proposed to explain how the *WRKY* genes evolved in plants. In wild rice *O. nivara*, Xu et al. (2016) suggested that ancient II-c *WRKY* genes were the ancestors of all *WRKY* genes. Our study further supports that the ancient Group II-c was the progenitor of *WRKY* genes in *O. rufipogon*. Moreover, we found that *OrWRKY* genes in the same group seemed to have similar conserved motifs and exon–intron structures. This phenomenon was also observed in apple (Lui et al., 2017), kiwifruit (Jing and Liu, 2018), and *Salix suchowensis* (Bi et al., 2016). All these results indicated that the *WRKY* genes, to a certain extent, were functionally conserved among higher plants.

Gene duplication events, regarded as the major evolutionary force in higher plants, play a crucial role in gene family expansion. The origin of new genes in plants during evolution is mainly caused by gene duplication (Ohno, 1970). Almost 80% of *WRKY* genes in cultivated rice (*O. sativa* ssp. *japonica*) were located in duplicated regions, and it was gene duplication events that lead to generating new genes (Ramamoorthy et al., 2008). In this study, we found that *OrWRKY* genes were derived from either segmental or tandem duplications, indicating that high segmental but low tandem duplications resulted in *OrWRKY* genes, consistent with wheat (Ning et al., 2017), peanut (Song et al., 2016b), grapevine (Wang et al., 2014), and soybean (Song et al., 2016a). Thus, we can infer that compared to tandem duplication events, segmental duplication events have mainly contributed to the expansion of *OrWRKY* genes.

Soil salinity is one of major abiotic stresses to limit plant growth and development. Enhancement of grain yield stability under salt stress would be of great importance. *WRKY* genes participate in the control of a wide variety of biological processes, some of which are associated with salt stress. For example, the overexpression of one *WRKY* gene, *GmWRKY54*, could improve salt stress tolerance in soybean (Zhou et al., 2008). In *Arabidopsis*, the expression of *AtWRKY25* and *AtWRKY33* was dramatically induced by sodium chloride (NaCl) treatment (Li et al., 2011). Our results showed that the expression of 10 selected *OrWRKY* genes was upregulated or downregulated by NaCl in either of these two tissues, suggesting that they might be related to salt responses. Previous study showed that there were two kinds of *OsWRKY45* genes. Under salt treatment, the expression of *OsWRKY45-1* was first induced and then suppressed, whereas the expression of *OsWRKY45-2* was first suppressed, then induced, and later suppressed, indicating their different functions under salt stress (Tao et al.,

2011). In this study, the expression pattern *OrWRKY45* was first suppressed, then induced, and later suppressed, suggesting that it might have the same functions with *OsWRKY45-2*. It was reported that the G-box, ABRE, and CRE are the major *cis*-acting elements for salt-responsive gene expression (Narusaka et al., 2003; Ahmad et al., 2015). Our study showed that nine of the 10 sampled *OrWRKY* genes had G-boxes, and half of them had ABREs. Additionally, we found that the same gene exhibited a distinct expression trend between leaves and roots under salt stresses, suggesting that it might respond to abiotic stresses through different genetic networks.

CONCLUSION

In this study, 101 *OrWRKY* genes were comprehensively identified in the *O. rufipogon* genome assembly. Phylogenetic analysis suggested that *OrWRKY* transcription factors were conserved, supported by the identification of highly conserved motifs and gene structures. Genomic synteny analysis suggested that segmental duplications may have played a major role in the *OrWRKY* gene family evolution, and most duplicated *WRKY* genes underwent purifying selection. We showed tissue-specific expression of the *OrWRKYs* and their differential expression in response to salt stresses, implying the existence of a complicated molecular regulatory network response to salt stresses in *O. rufipogon*. We obtain novel insights into the evolutionary and functional divergence of the *WRKY* gene family, which will greatly help functional genomic studies of candidate *WRKY* genes in *O. rufipogon* for the purpose of rice genetic improvement.

DATA AVAILABILITY STATEMENT

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation, to any qualified researcher.

AUTHOR CONTRIBUTIONS

HN, WL, and YL performed the data analysis and experiments. HN drafted the manuscript. LG served as the principal investigator, facilitated the project, and revised the manuscript.

FUNDING

This study was supported by the Project of Innovation Team of Yunnan Province to LG.

ACKNOWLEDGMENTS

We appreciate the reviewers for their comments on this manuscript.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fgene.2020.00359/full#supplementary-material>

FIGURE S1 | Phylogenetic analysis of the WRKY domains of *OrWRKY* genes. The phylogenetic tree was constructed using Neighbor-Joining method based on WRKY domains. Reliability of the predicted trees was tested using bootstrapping with 1,000 replicates.

FIGURE S2 | Phylogenetic analysis of WRKY proteins in the *O. rufipogon*. The phylogenetic tree was constructed using Neighbor-Joining method based on WRKY full-length proteins. Reliability of the predicted trees was tested using bootstrapping with 1,000 replicates.

FIGURE S3 | Multiple sequence alignment of domains among the *OrWRKY* proteins. The sequences were aligned using Clustal W. Dashes indicate gaps, and

'N' and 'C' mean the N-terminal and C-terminal WRKY domains of a specific WRKY protein.

FIGURE S4 | Phylogenetic analysis of the WRKY genes in *Arabidopsis*, *O. sativa* ssp. *japonica*, *O. sativa* ssp. *indica*, *O. rufipogon*, and *O. nivara*. The phylogenetic tree was constructed using Neighbor-Joining method based on 531 WRKY domain sequences. Reliability of the predicted tree was tested using bootstrapping with 1,000 replicates.

TABLE S1 | Primer pairs of the 10 *OrWRKY* genes identified in this study.

TABLE S2 | *OrWRKY* genes identified in *Oryza rufipogon* and their orthologs in *Oryza sativa* ssp. *japonica*.

TABLE S3 | *Ka/Ks* calculation and divergence times of the duplicated *OrWRKY* gene pairs in syntenic blocks.

TABLE S4 | Tandem duplicated gene pairs identified in *O. rufipogon*.

TABLE S5 | The detection of positive selection by the likelihood method with branch-site model for *OrWRKY* genes.

TABLE S6 | Orthologous WRKY genes between *O. rufipogon* and *O. sativa* ssp. *japonica*.

TABLE S7 | Detection of positive selection by the likelihood method with branch-site model for *OrWRKY* genes between *O. rufipogon* and *O. sativa*.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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