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**Research Article**

# Genome-wide Characterization of Far-Red Impaired Response 1 (*FAR1*) Transcription Factor Gene Family in Wild Rice *Oryza brachyantha*

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## ABSTRACT

The wild rice variety, *Oryza brachyantha*, is categorized as having the F genome type and is a member of the primitive *Oryza* lineage. The *O. brachyantha* is particularly noteworthy because of its genetic variability and applications in rice breeding, especially for increasing traits like disease resistance and tolerance to abiotic stimuli. Bisexual spikelets, two almost completely developed sterile lemmas, acuminate entire lemmas that are occasionally setiform, herbaceous to crustaceous leaves, and herbaceous margins are the characteristics of *Oryza* species. The *FAR1* gene family is a crucial part of the far-red light signal pathway regulated by phyA. With estimated sizes ranging from 531 to 851 amino acids, these proteins have commonalities in amino acid composition between 12.0% and 82.4% over their whole lengths. The light signaling pathways that impact photomorphogenesis and the general development of plants are influenced by the *FAR1* gene family. In the present study, 32 genes encoding potential *FAR1* TFs were found in the *O. brachyantha* genome. We retrieved these genes based on the presence of the *FAR1* domain in the protein sequence. The map chart indicates that chromosomes 1 and 8 have one gene on them. Similarly, seven genes are present on both chromosomes 2 and 3. There are four genes on chromosomes 4 and 7. Two genes are present on Chromosome 6. Chromosomes 11 and 12 contain two genes. Using the Molecular Evolutionary Genetics Analysis (MEGA 11) program, a phylogenetic analysis was carried out which divided 32 *FAR1* genes into 3 clades. The location and pattern of intron-exon distribution within the genomic regions of the *FAR1* gene served as evidence for the expansion and its evolutionary connection with its progenitors. *O. brachyantha FAR1* genes showed variation in the number of introns ranging from 2 to 10. The motif analysis of *FAR1* genes demonstrated the conservation of different motifs among the members of the same clades. Synteny analysis between *O. brachyantha* and Arabidopsis showed conservation and evolutionary relationships of the 5 *O. brachyantha FAR1* genes in *Arabidopsis*. This study provides the basic characterization of *FAR1* genes in *O. brachyantha* and their relationship with the Arabidopsis genes.

**Keywords:** Genome-wide analysis, *FAR1* family, *Oryza brachyantha*, Phylogenetics, Motifs

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## INTRODUCTION

The primary features of Oryza species include bisexual spikelets, two sterile lemmas that are more or less fully formed, acuminate whole lemmas that are occasionally setiform, herbaceous to crustaceous leaves, and herbaceous margins. (Smith and Dilday, 2002). There are twenty-four species in the genus *Oryza*; among them, two are cultivated (2n = 24) and the other twenty-two are wild (2n = 24 or 48) and distributed widely around the globe. *O. brachyantha*, the wild rice variety, belongs to the primitive lineage of *Oryza* and is classified as the F genome type. Compared to the genomes of rice or other Oryza species, it has a distinct collection of repetitive sequences (Chen *et al.*, 2013). This grass grows in tufts and is an annual species.

The genome of *O. brachyantha* was recently sequenced and studied (Chen *et al.*, 2013). It contains unique genes for stress tolerance and disease resistance that are absent from other closely related species and has the most conserved genome (Liu *et al.*, 2016). Because of its genetic variation and potential applications in rice breeding, particularly for improving qualities like disease resistance and tolerance to abiotic stressors, the *O. brachyantha* species is particularly interesting (Ricachenevsky *et al.*, 2018). Originally discovered in *Arabidopsis*, *FAR1* (Far-Red Impaired Response 1) gene family is an essential component of the far-red light signal pathway mediated by *phyA*. The members of this gene family are crucial and positive regulators in the *phyA* pathway, where they may interact directly with the promoters of *FHY1* and *FHL* (Lu *et al.*, 2022). These proteins share 12.0% to 82.4% amino acid similarities throughout their whole lengths, with projected sizes ranging from 531 to 851 amino acids (Lin and Wang, 2004).

The light signalling pathways that impact photomorphogenesis and the general development of plants are influenced by the *FAR1* gene family. In reaction to far-red light, *FAR1* proteins work as transcription factors and their interaction with phytochrome A (*phyA*) and control gene expression (Lin and Wang, 2004; Lu and Jiang, 2022). Many members of the *FAR1* gene family have been found in *O. brachyantha* through recent genomic investigations, which have provided insight into their potential roles in light-mediated developmental processes. Improved growth and development of rice cultivars and productivity under changing light circumstances can be facilitated by this information, which is essential for understanding the evolution of light signaling pathways in rice species (Chen *et al.*, 2013; Zhang *et al.*, 2024). The whole genome sequencing of *O. brachyantha* has opened the door to identify stress tolerance- and disease resistance-related genes absent in other closely related species (Chen *et al.*, 2013). The overall understanding of the *FAR1* gene family in *O. brachyantha* advances knowledge regarding the mechanisms regulating plant development and light signaling (Tang *et al.*, 2024). Knowledge of the roles of these genes could help enhance our understanding of how the various rice cultivars can acclimate to different light environments to optimize growth and productivity.

Furthermore, phylogenetic analysis of the *FAR1* gene family members can reveal the phylogenetic relatedness between *Oryza* species and show how these genes have evolved and/or adapted to different environments (Zhou *et al.*, 2024). This could also help in breeding programs that sought to enhance the quality of rice varieties through the employment of genetic variation. Furthermore, the possible identification of new conserved sequences in the genome of *O. brachyantha* may shed light on the process that determines the specificities of the wild rice genome compared to cultivated rice species. This could improve our knowledge of genetic conservation and variation in the Genus. In this paper, we analyzed the *FAR1* gene family from the genome of *O. brachyantha* by using different bioinformatic tools.

## MATERIALS AND METHODS

### Sequence Retrieval and Database Search

PlantTFDB (plant transcription factor database) was used to obtain all of the *O. brachyantha's* protein sequences, isoelectric points (PI), and Molecular weight (Jin *et al.*, 2016). Chromosome counts, protein sizes, gene accession numbers, and genomic data were retrieved from Phytozome (phytozome-next.jgi.doe.gov). The retrieved sequence data of *O. brachyantha FAR1* gene family was validated by the National Center for Biotechnology (NCBI) (https://ncbi.nlm.nih.gov/) by using the Basic Local Alignment Search Tool (BLASTP).

### Location of Introns and Exons, Chromosome Mapping and Conserved Protein Motifs Analysis

The locations of the *FAR1* family genes in *O. brachyantha* were acquired from the NCBI, and Map Chart software (v.2.32) was utilized to map these genes on the chromosomes (Voorrips, 2002). GSDS (Gene Structure Display Server) (https://gsds.gao-lab.org/) was used to determine the distribution of introns and exons in *FAR1* genes of *O. brachyantha* and *A. thaliana*. To find common protein motifs inside the *FAR1* proteins of *O. brachyantha* and *A. thaliana*, MEME (Multiple Em for Motif Elicitation; v5.03) was employed (Bailey *et al.*, 2009). The default parameters, which included limiting motif occurrence to either 0 or 1 per sequence, optimizing motif width to be between 10 and 55 residues, setting the motif count to 50, and choosing a minimum of 5 sites for a motif, were used in the study.

### Phylogenetic and Conserved Domain Analyses of *FAR1* proteins from *O. brachyantha* in comparison with *A thaliana*

A phylogenetic tree was created using the putative *FAR1* transcription factor (TF) protein sequences from *O. brachyantha* and *A. thaliana*. The default parameters for ClustalW (Gibson and Higgins, 2003) were used to align all protein sequences (the gap opening penalties were set to 10.00 for both pairwise and multiple alignments). But in the pairwise alignment and the multiple alignment, the gap extension penalty was 0.10 and 0.20, respectively. 30% delay

divergence cutoff and the elimination of the negative matrix were employed (Mun *et al.*, 2012). Using the aligned amino acid sequences and the Neighbor Joining (NJ) method with the bootstrap approach (with 1000 bootstrap replications), a phylogenetic tree was built using MEGA v. 11 (Tamura *et al.*, 2011). For this purpose, the Poisson model was used with partial deletions and 95% site coverage limit (Tamura *et al.*, 2021). To comprehend the evolutionary connection between the same gene family of various species, a single tree was created using the non-redundant 32 genes of *O. brachyantha* compared to *A thaliana* using 22 amino acid sequences of the *FAR1* family from PlantTFDB. In iTOL (https://itol.embl.de/tree/), more changes and visualizations were made (Letunic and Bork, 2021).

**Comparative Synteny Gene Analysis of *O. brachyantha* and *A thaliana***

To find evolutionary relationships and similarities between *O. brachyantha* and *A. thaliana*, a synteny analysis was conducted using the Circoletto (Darzentas, 2010) web server (http://tools.bat.infspire.org/circoletto/).

## RESULTS

**Identification and Distribution of *FAR1* TFs Encoding Genes**

From the *O. brachyantha* genome, 32 *FAR1* genes encoding putative *FAR1* TFs were identified. We then looked for major domains in the encoding proteins that were specific to *FAR1* in the retrieved genes. For this reason, the basic requirement for a gene to be included in the *FAR1* family was determined to be the presence of the entire *FAR1* domain. Different properties of 32 *FAR1* genes from *O. brachyantha* are given in Table 1.

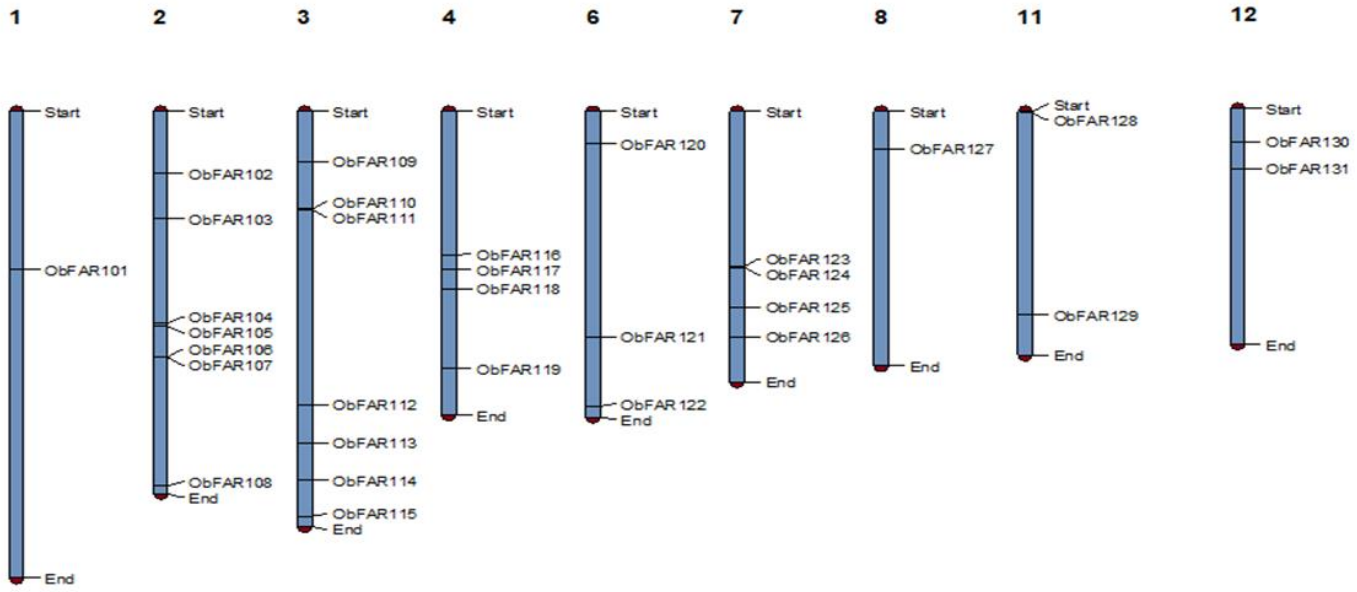


Figure 1. The positioning of 31 *FAR1* genes across 9 chromosomes *O. brachyantha*. These maps were developed using MapChart.

**Genomic Localization and Mapping of *FAR1* Genes Using Map Chart**

This chromosomal data regarding the length of the chromosomes and positions of the genes were used for the localization of genes on the corresponding chromosomes using MapChart (Figure 1). According to the results from gene localization of chromosomes, chromosome 1 contains only a single gene. Similarly, 7 genes were present on both chromosomes 2 and 3. Chromosome 4 also has four genes. Likewise, Chromosome 6 contains two genes. Chromosome 7 contains four genes. Chromosome 8 contains one gene. Chromosome 11 includes two genes. Chromosome 12 contains two genes. One gene is present with the scaffold. However, chromosomes 5, 9, and 10 do not contain any of the *FAR1* genes.

**Phylogenetic Tree Analysis of *FAR1* Genes in *O. brachyantha***

The resulting alignment was then utilized to generate a phylogenetic tree using the neighbor-joining method with 1000 bootstrap replicates. This was accomplished using the Molecular Evolutionary Genetics Analysis (MEGA 11) tool. The phylogenetic tree is divided into three Clades: 1, 2, and 3. Clade 1 is divided into 6 sub-branches, clade 2 is divided into 8 sub-branches, and clade 3 is divided into 5 sub-branches (Figure 2). Clade 1 contains 11 *FAR1* genes,

whereas clade 2 exhibits 8 members of this gene family. However, on the other hand, clade 3 displays 13 *FAR1* transcription factors.

Table 1. Detailed properties of identified *FAR1* genes in *O. brachyantha*.

| TF No. | Genes Names | Chr. No. | Start | End | Protein Size (aa) | Stat Domain | End Domain | PI | Wt (Da) |
|---|---|---|---|---|---|---|---|---|---|
| OB0054G10020.1 | ObFAR101 | 1 | 17657645 | 17664419 | 857 | 94 | 175 | 6.4328 | 97457.2 |
| OB0054G10030.1 | ObFAR102 | 2 | 17667623 | 17672186 | 817 | 54 | 137 | 8.9992 | 92587.8 |
| OB01G18260.1 | ObFAR103 | 2 | 26903404 | 26905813 | 751 | 59 | 153 | 9.102 | 86700.6 |
| OB01G25460.1 | ObFAR104 | 2 | 11387394 | 11392539 | 383 | 307 | 359 | 4.333 | 42918.2 |
| OB02G17140.1 | ObFAR105 | 2 | 4436705 | 4439890 | 1110 | 491 | 577 | 8.3727 | 127828 |
| OB02G21030.1 | ObFAR106 | 2 | 7714652 | 7719393 | 1232 | 341 | 423 | 7.0637 | 141709 |
| OB02G27370.1 | ObFAR107 | 2 | 15187805 | 15196118 | 795 | 64 | 153 | 7.2341 | 90600 |
| OB02G27690.1 | ObFAR108 | 2 | 15449937 | 15454757 | 727 | 105 | 191 | 6.6088 | 82504.9 |
| OB02G44380.1 | ObFAR109 | 2 | 26903404 | 26905813 | 772 | 80 | 174 | 8.9584 | 89065.2 |
| OB03G16050.1 | ObFAR110 | 3 | 3567396 | 3571425 | 693 | 1 | 24 | 8.4544 | 79394.1 |
| OB03G21170.1 | ObFAR111 | 3 | 7018237 | 7021552 | 1058 | 176 | 282 | 6.6223 | 120515 |
| OB03G21220.1 | ObFAR112 | 3 | 7040569 | 7045811 | 705 | 70 | 160 | 6.7899 | 78442.3 |
| OB03G35710.1 | ObFAR113 | 3 | 21057199 | 21063478 | 1068 | 78 | 179 | 5.8117 | 116667 |
| OB03G39100.1 | ObFAR114 | 3 | 23810571 | 23810571 | 785 | 67 | 154 | 6.6693 | 90805.2 |
| OB03G43000.1 | ObFAR115 | 3 | 26529179 | 26535288 | 1144 | 54 | 130 | 7.8659 | 129919 |
| OB03G47710.1 | ObFAR116 | 3 | 29112240 | 29116276 | 785 | 40 | 124 | 6.1716 | 89429.9 |
| OB04G19620.1 | ObFAR117 | 4 | 10305282 | 10309843 | 779 | 13 | 101 | 7.2947 | 89139 |
| OB04G20960.1 | ObFAR118 | 4 | 11288110 | 11291143 | 769 | 148 | 244 | 6.9998 | 87362.9 |
| OB04G23370.1 | ObFAR119 | 4 | 12731904 | 12736554 | 803 | 54 | 139 | 9.2496 | 91703.1 |
| OB04G32220.1 | ObFAR120 | 4 | 18460706 | 18465057 | 839 | 83 | 166 | 7.8079 | 96148.5 |
| OB06G14070.1 | ObFAR121 | 6 | 2319157 | 2325052 | 779 | 54 | 140 | 6.9746 | 88790.5 |
| OB06G27780.1 | ObFAR122 | 6 | 16191720 | 16194945 | 671 | 82 | 173 | 7.0236 | 76870.5 |
| OB06G34800.1 | ObFAR123 | 6 | 21172530 | 21174529 | 685 | 52 | 150 | 8.6609 | 77109.1 |
| OB07G20960.1 | ObFAR124 | 7 | 11144995 | 11149223 | 642 | 12 | 111 | 7.8098 | 72376.1 |
| OB07G21030.1 | ObFAR125 | 7 | 11199462 | 11204118 | 944 | 93 | 179 | 6.8375 | 107141 |
| OB07G24510.1 | ObFAR126 | 7 | 14074624 | 14079018 | 1694 | 370 | 469 | 7.5643 | 189420 |
| OB07G27730.1 | ObFAR127 | 7 | 16213929 | 16217988 | 714 | 48 | 84 | 7.7991 | 81531.8 |
| OB08G14200.1 | ObFAR128 | 8 | 2685072 | 2691824 | 842 | 90 | 178 | 7.3542 | 95697.1 |
| OB10G13790.1 | ObFAR129 | 11 | 14635899 | 14637532 | 338 | 31 | 81 | 9.2853 | 40438.2 |
| OB12G10090.1 | ObFAR130 | 11 | 99812 | 102886 | 524 | 30 | 121 | 7.9493 | 61478.3 |
| OB12G13670.1 | ObFAR131 | 12 | 2362179 | 2366497 | 818 | 97 | 183 | 5.015 | 93735.7 |
| OB12G16010.1 | ObFAR132 | 12 | 4284530 | 4288790 | 692 | 86 | 175 | 6.3749 | 78682.3 |

**Unveiling the *FAR1* Gene Family Classification, Gene Structure and Conserved Domain Investigations**

Further information on the development of the *FAR1* gene family in wild rice was obtained by determining the gene structure, or the intron/exon distribution pattern, of 32 *FAR1* genes. A gene family's expansion trend and evolutionary link to its forebears are supported by the location and intron-exon distribution pattern of the gene's genomic region. The variety of rice *FAR1* genes was evident in the range of intron counts, which ranged from two to ten. A largely conserved gene organization has been found among the groupings of phylogenetic trees, despite the variations in the size of their genomic areas.

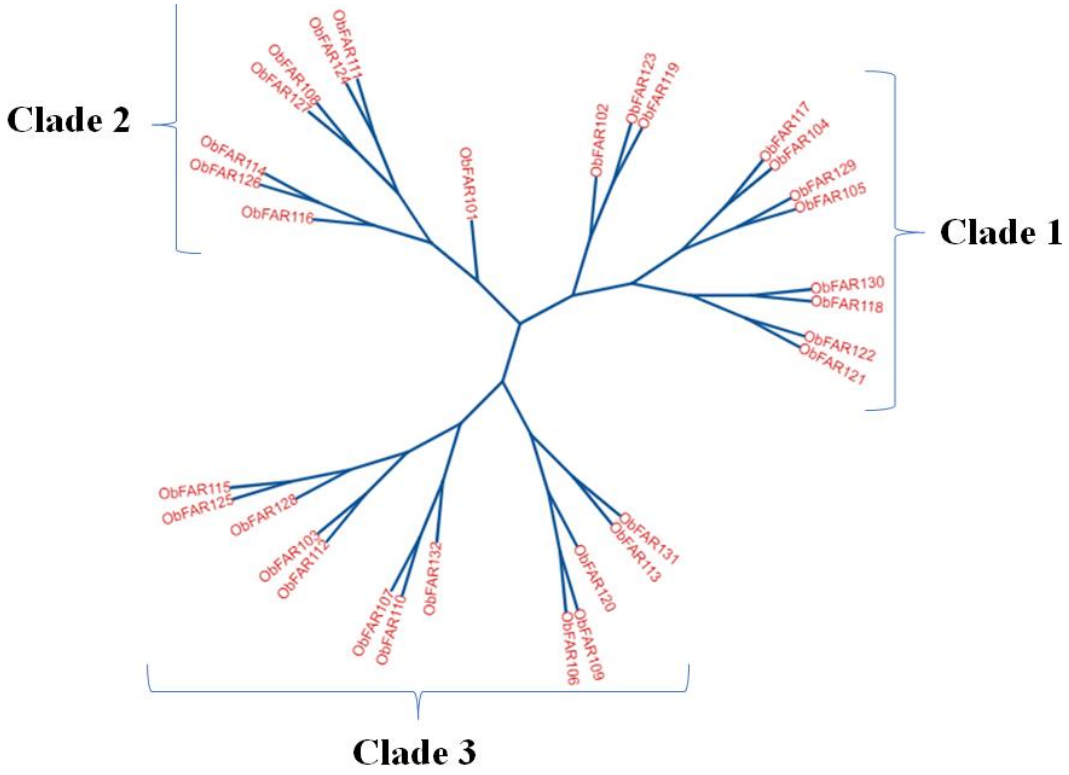


Figure 2. Phylogenetic tree of *Oryza brachyantha FAR1* transcription factors, illustrating the evolutionary relationships among the gene family members. The tree highlights clustering patterns, reflecting the genetic divergence and potential functional similarities within subgroups of *FAR1* proteins.

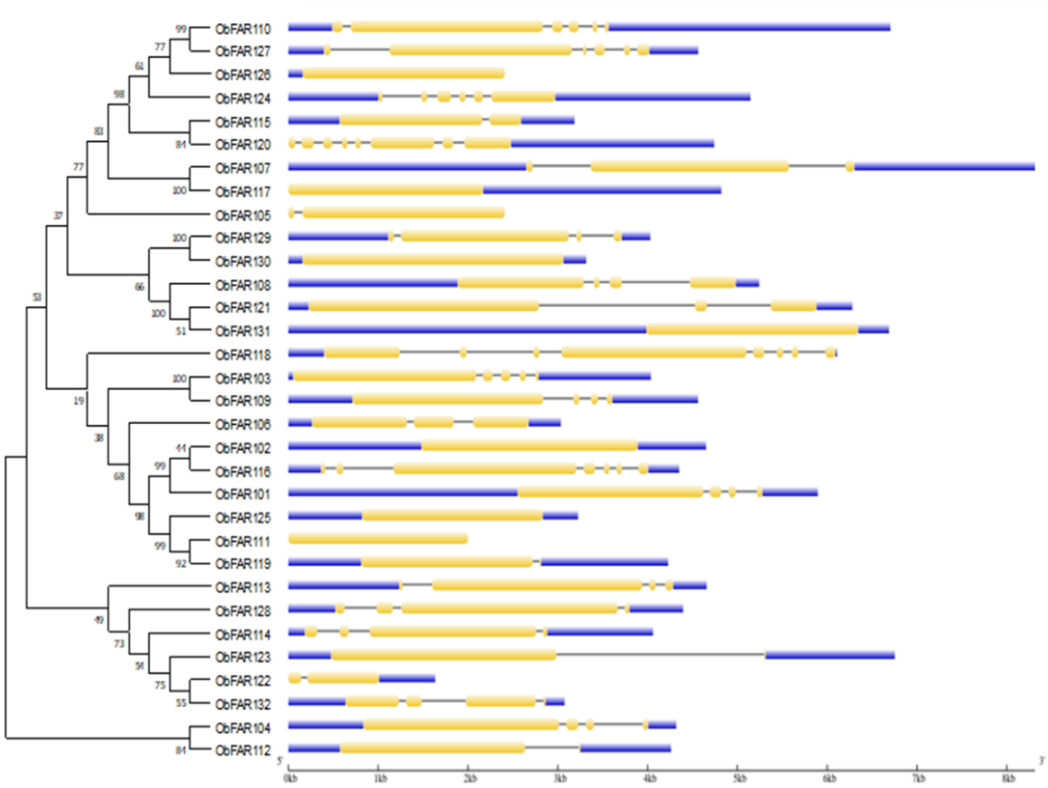


Figure 3. Phylogenetic tree-based clustering and structural organization of *FAR1* transcription factors in *Oryza brachyantha*. Introns are shown as a grey line, while exons are shown as yellow boxes. The blue boxes represent the untranslated region (UTR).

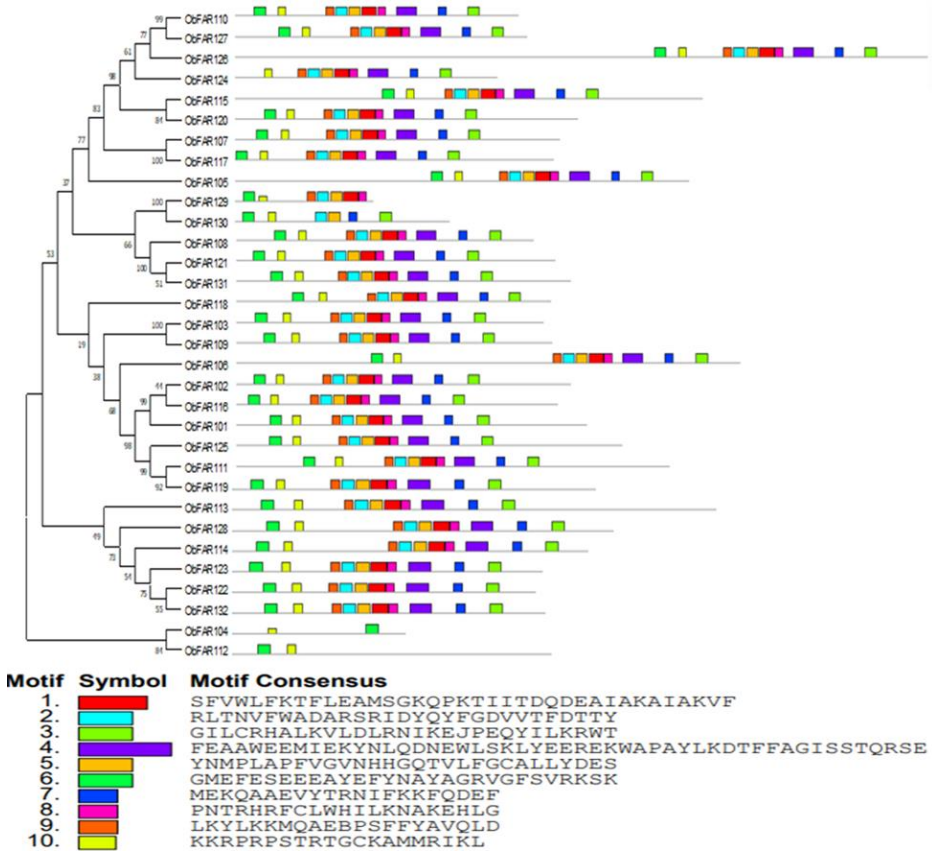


Figure 4. Phylogenetic tree and conserved motif analysis of *Oryza brachyantha FAR1* proteins. Motifs were identified using MEME, with each colored box representing a specific conserved motif. The consensus sequences of the motifs are displayed below the diagram. The clustering of *FAR1* proteins in the phylogenetic tree reflects similarities in motif composition, offering insights into their evolutionary relationships and potential functional roles.

Surprisingly, the intron-exon structure was partially conserved in different clades but did not follow strict conserved patterns. The number of introns ranged from 0 to 7, however, most genes contained 3 introns. The discovery of conserved domains within a gene family also provides information to assist the analysis of their functional conservation and the confirmation of gene duplication events during evolution. This was accomplished by running MEME across the protein sequences of *FAR1* TFs to identify conserved domains (Figure 4). At the bottom of the phylogenetic tree, the categorization of different motifs is shown using different colors. The distinctive *FAR1*-DNA binding domain, which is completely conserved across all 32 *FAR1* protein sequences, is represented by domains 1, 2 and 3 as shown in Figure 4.

**Unveiling of Conserved domains Investigation of *FAR1* proteins**

Investigating the conserved domain of *FAR1* proteins involves examining the sequences and structures preserved across different species or within different members of *FAR1* protein family. *FAR1* protein plays crucial roles in cell cycle regulation, signal transduction and various cellular processes. The image provided in Figure 5 is a domain architecture analysis of various ObFAR proteins. Each horizontal bar represents a different ObFAR protein domain, with colored segments indicating specific conserved domains and their positions within the protein sequences. Conserved domains identified: *FHY3* superfamily (Green). This domain is found in almost all ObFAR proteins. It indicates a broad conservation of function related to transcriptional regulation and possible light signalling pathways. *FAR1* superfamily (Yellow-Green): this domain is another highly conserved feature across the ObFAR proteins, consistent with the role of *FAR1* protein in cell cycle regulation and signal transduction. *FAR1* (Red): specific to same ObFAR proteins, this domain indicates a more specific function or interaction that may be unique to certain members within the *FAR1* protein family. B3-DNA (Teal): present in *ObFAR126*, suggesting a role in DNA binding or regulation, typical for domains that interact with genetic material. ZnF_GATA (pink): Found in *ObFAR115*, Ob*FAR12*7, and a few others, this zinc finger domain is indicative of DNA binding properties, likely involved in transcriptional regulation. ZnF_GATA Superfamily (Gray): Present in *ObFAR108*, similar to ZnF_GATA, further emphasizing the DNA binding and regulatory role. Amelogenin Superfamily (Light Green): Appears in *ObFAR115*

and *ObFAR116*, this domain is typically involved in biomineralization processes, suggesting specialized functions in these proteins. CCT Superfamily (Yellow): Found in *ObFAR106* and *ObFAR119*, these domains are linked to protein folding and chaperone activities indicating roles in maintaining protein structure.

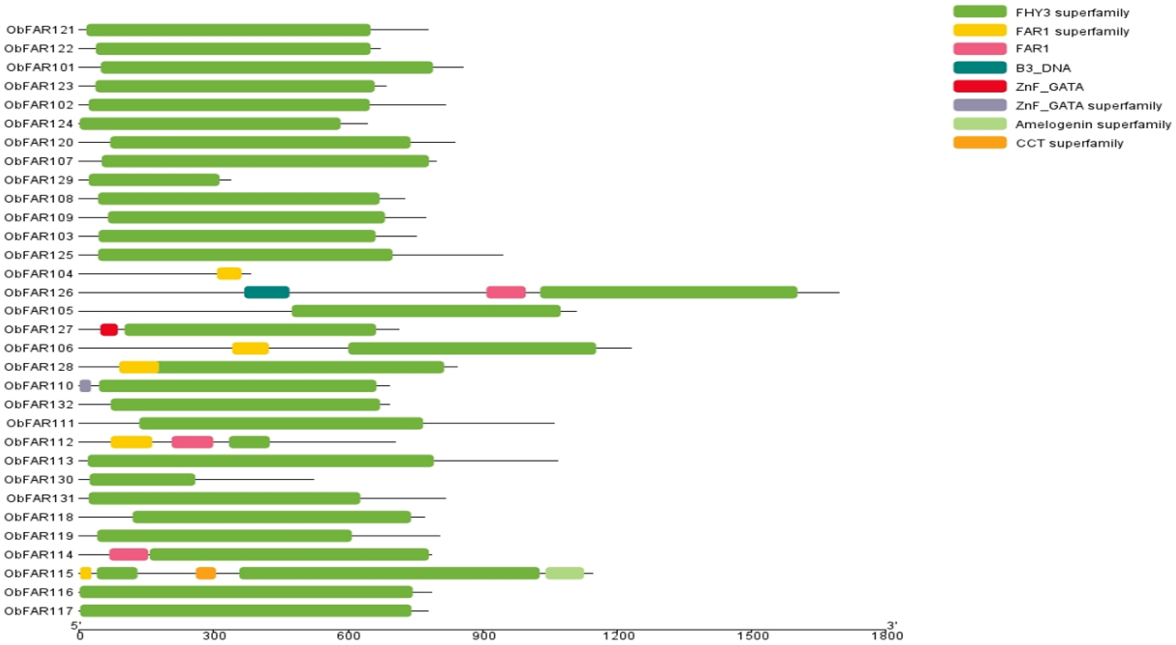


Figure 5. Conserved motif analysis of *FAR1* proteins in *Oryza brachyantha* using TBtools. The diagram shows the distribution and arrangement of conserved motifs within each *FAR1* protein. Each colored box represents a specific motif, with annotations indicating motif superfamilies (e.g., FHY3, *FAR1*, ZnF_GATA, B3_DNA, and CCT). The scale at the bottom represents protein length in amino acids, highlighting structural diversity among *FAR1* family members.

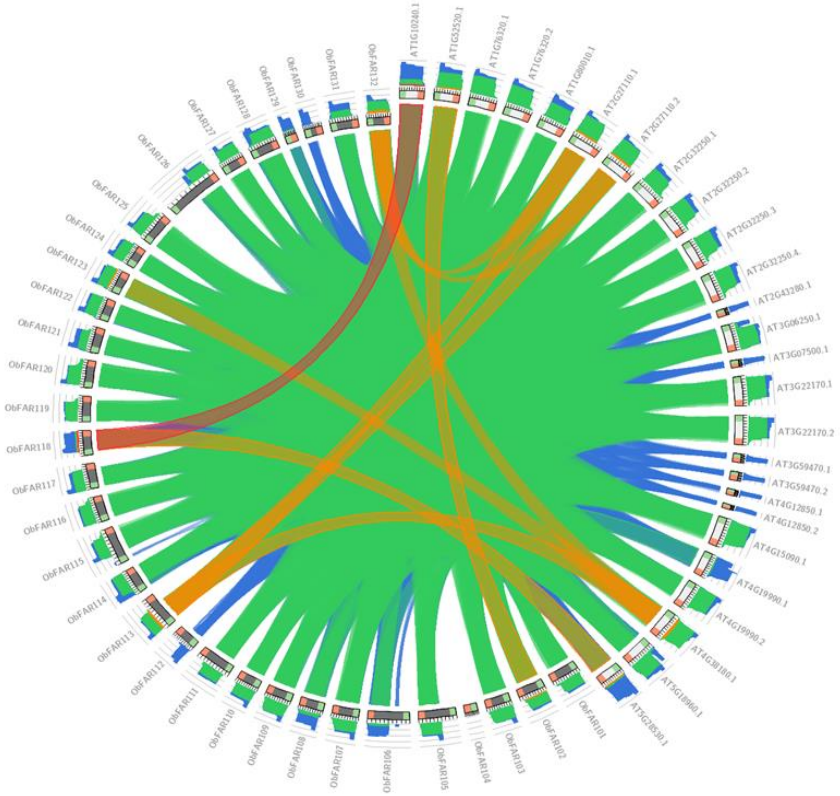

Figure 6. Synteny analysis between *A. thaliana* and *O. brachyantha* genes visualized using a circular diagram. The arcs represent homologous gene pairs, with varying color intensities denoting sequence identity: blue (50%), green (75%), orange (99.9%), and red (100%).

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### *FAR1* Gene Correlation between *A. thaliana* and *O. brachyantha* through Synteny Analysis

A comparative study of the protein sequences from the model plant, *Arabidopsis thaliana,* and wild rice was done by using Circoletto tool which provides information about the evolutionary relationship and conservation of *FAR1* genes presented in both species (Figure 6). After running the protein sequence of both species, each gene shows an evolutionary relation with the other gene of the related species. Genes of the same color are connected through an evolutionary relationship between genes. The query sequence is magnified as a bulging region in the histogram as compared to the subject sequence which shows the evolutionary relation of both species in the *FAR1* gene family. In this analysis, blue, green, orange, and red colors show 50, 75, 99.9, and 100% identity respectively. Five Ob*FAR1* genes showed 99% synteny with six genes of *A. thaliana*. However, *ObFAR118* was 100% syntenic to *At1g10240* showing similar functions of both genes in their respective plant species.

## DISCUSSION

*O. brachyantha*, the wild rice species, belongs to the primitive lineage of *Oryza* and is classified as the F genome type. Compared to the genomes of other *Oryza* species, it has a distinct collection of repetitive sequences (Chen *et al.*, 2013). The present study helps understand the structural and evolutionary relationship of *FAR1* TFs in species of *O. brachyantha* and rice in general, and in relation to model plants like *A. thaliana*. This study also provides the localization of the distributions of *FAR1* gene along the chromosome and the evolutionary conservation of domains and gene structures within the *FAR1* gene, which would offer possible approaches to the functional study of monocots and beyond. In the rice genome, 31 *FAR1* genes are identified as localized in various rice chromosomes, but their densities vary considerably: chromosomes 2 and 3 each harbor 7 *FAR1* genes. This distribution pattern is in accordance with the previous studies conducted on rice and other plants where TF families are mostly unevenly distributed over the chromosomes because of duplication events or divergence events at certain points of evolution (Yao *et al.*, 2024). The findings of *FAR1* genes located on scaffolds together with chromosomes imply that these TFs may also located in other regions such as structural and regulatory gene activities that may have different function in rice development and stress responses (Lu *et al.*, 2018; Lu *et al.*, 2022; Roy and Penny, 2007).

The phylogenetic tree based on the neighbor-joining clustering method shows a well-defined grouping pattern for the *FAR1* gene members. This clustering may imply that there are subgroups that exist within the *FAR1* family, that are diverse to perform specific functions (Liu *et al.*, 2021). This phylogenetic analysis demonstrated that Ob*FAR1* genes are divided into three Clades: 1, 2, and 3 where clade 1 is divided into 6 sub-branches (11 *FAR1* genes), clade 2 is divided into 8 sub-branches (8 *FAR1* genes), and clade 3 is divided into 5 sub-branches (13 *FAR1* genes). Recently, in Tea Plants (Camellia sinensis), the family members of the *AtFHY3*/*FAR1* have been clustered into five groups based on phylogenetic analysis: group I consists of *FHY3*, *FAR1*, *FRS1*, *FRS2*, and *FRS4*; group II includes *FRS6* and *FRS8*); group III includes *FRS7* and *FRS12*; group IV includes *FRS3*, *FRS5*, and *FRS9*; and group V includes *FRS10* and *FRS11* (Liu *et al.*, 2021). As noted by other researchers, such a pattern is expected in other plant species, where the diversification of TF families enables the highly differentiated regulation of genes (Yang *et al.*, 2022). A high number of bootstrap values enhances the reliability of the identified clades, proofing the hypothesis about gene duplication in *FAR1* family genes in rice. Similarly, within TF families, researchers have described the same pattern of expansion prominently in *Arabidopsis* for enabling adaptation to a wide range of biotic and abiotic stresses (Khan *et al.*, 2018; Liu *et al.*, 2024). These findings are driven by the variations in exon-intron structures, as observed within *FAR1* genes in the present study, they have introns that vary between 2-7 with general structural diversity. Such differences in gene structures signify the propensity of intron gain or loss in the course of evolution which in turn influences the function and regulatory role of TFs in plants (Roy and Penny, 2007). The conserved *FAR1*- DNA binding domains in all the identified sequences underpin these genes and possess a functional role in transcriptional regulation (Lu *et al.*, 2022). In the same way, conserved motifs preserved in FHY3 and *FAR1* superfamily, other unique motifs, and ZnF_GATA, CCT indicate their specific function in the light signaling pathway, DNA binding, protein stability with conserved role in regulation connected networks as identified earlier by (Chen *et al.*, 2023; Lin and Wang, 2004).

The synteny analysis allowed the evolutionary similarity between *Arabidopsis* and *O. brachyantha*, where several *FAR1* genes are evolutionary conserved among the two species (Lecharny and Aubourg, 2008; Carbonero and Carbajosa, 2003). This conservation suggests that these *FAR1* TFs may control homologous processes, related to light, stress tolerance, and developmental pathways. The homologs of *FAR1* genes are conserved in rice, as well as in *Arabidopsis*, suggesting crucial responsibilities for growth and responsive genic systems of plants under several

stressful conditions hence may be engineered to enhance the resilience of crop plants. Initially discovered to be significant component of phytochrome A (*phyA*)-mediated far-red light signaling in Arabidopsis, the far-red-impaired response 1 (*FAR1*) transcription family is essential for regulating plant growth and development (Lu and Jiang, 2022). In the *phyA* signaling pathway, *FAR1*/*FHY3* were shown to be positive regulatory elements that mainly activated the transcription of light-induced target genes (Tang *et al.*, 2024). In the future, the results presented here will help the researchers to relate computational biology with molecular biology experiments like qPCR and RNA seq to further study the functional analysis of *FAR1* genes in rice and other species.

## CONCLUSION

In conclusion, the present work strengthens the knowledge concerning the *FAR1* gene family in *O. brachyantha* indicates that these genes have significantly diversified in their structure while still having essential conserved domains. Compared with *A. thaliana*, these TFs may be ubiquitously involved in the growth and development of higher plants. Further investigations could be considered for studying functional aspects of these conserved domains under different biotic and abiotic stresses, which might help enhance adaptability in rice and other monocot models.

## AUTHOR CONTRIBUTIONS

All authors contributed equally.

## CONFLICT OF INTEREST

There is no conflict of interest.

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