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GENOME-WIDE IDENTIFICATION OF THE GATA TRANSCRIPTION FACTOR FAMILY IN *Dichanthelium oligosanthes*

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ABSTRACT

The GATA transcription factors (TFs) play a crucial role in regulating various physiological processes in plants. Identification and characterization of the GATA TF family has been carried out in several important grass species, including rice, maize, and bamboo. However, no information is available on the GATA TFs in the C₃ grass species *Dichanthelium oligosanthes*. In the current study, 31 GATA genes have been identified in the *D. oligosanthes* genome by stringent bioinformatics analysis. The exon-intron arrangement analysis of the *DoGATAs* via the Gene Structure Display Server (GSDS 2.0) revealed the redundancy and differences in their gene structural organization. In addition, the sequence comparisons within the *DoGATAs* via BLAST revealed 11 numbers of putative paralogs. Similarly, the BLAST comparisons among the *OsGATAs* and *DoGATAs* resulted in the identification of 21 orthologs. Structural analysis of the identified *DoGATAs* through Simple Modular Architecture Research Tool (SMART), Conserved Domain Database (CDD), and Multiple Expectation Maximization for Motif Elicitation (MEME) revealed that all of them possess the signature GATA domain and the C-X₂-C-X₁₈-C-X₂-C consensus sequence. The phylogenetic analysis via MEGA divided the *DoGATAs* into four groups along with rice and Arabidopsis GATAs. In addition, the subcellular localization, gene ontology, and other peptide functional prediction results further supported the *DoGATAs* to be putative GATA genes. Moreover, the findings of this study can serve as a basic framework for the isolation and functional characterization of GATA genes in *D. oligosanthes*.

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1 Introduction

Transcription factors (TFs) are the regulatory genetic elements that modulate the gene expressions during numerous physiological processes, including growth, development, and stress responses (Franco-Zorrilla et al., 2014). In plants, several TF families are with crucial roles, such as WRKY, bHLH (basic helix-loop-helix), MYB (V-myb avian myeloblastosis viral oncogene homolog), SPL (Squamosa-promoter binding protein-like), and GATA (GATA-binding factor). Amongst these, GATA is an important type of TF family having vital roles in hormonal signaling, development process, cellular metabolism, and stress response in plants (Liu et al., 2019a; An et al., 2020; Zhang et al., 2021). The GATA TFs are highly conserved across plant species, which has a typical DNA binding function onto the consensus A/T-GATA-A/G sequence (Lowry & Atchley, 2000). Although initially these were discovered in fungi and animals, later they have identified in plants also. Daniel-Vedele & Caboche (1993) identified the first plant GATA TF in tobacco plants. The subsequent identification and analysis of plant GATA factors suggested that they possess a tightly conserved consensus sequence of C-X₂-C-X₁₈-C-X₂-C. Most plant GATA proteins have a single consensus domain, while some may contain more than two zinc finger domains or additional zinc finger loops (Reyes et al., 2004). Several GATA TFs have been identified in various plants, such as Arabidopsis, rice, wheat, poplar, tomato, soybean, and chili pepper (Reyes et al., 2004; Zhang et al., 2015; Yuan et al., 2018; Liu et al., 2019b; An et al., 2020; Yu et al., 2021). Additionally, their roles in plants, including germination, development, metabolism, signaling pathways, and stress response have also been investigated extensively (Liu et al., 2019a; Nutan et al., 2019; An et al., 2020). However, the identification and functional validation of the GATA TFs in many other plants are yet to be explored.

Dichanthelium oligosanthes is a perennial frost tolerant grass species found in North America. Unlike its other grass family relatives, including maize and sugarcane, *D. oligosanthes* use the C3 pathway for photosynthesis (Bräutigam et al., 2014). This lack of Kranz anatomy and the use of C3 pathway makes *D. oligosanthes* a promising candidate to be a model C3 plant that can be compared to the other C4 plants. The sequencing and availability of the draft genome of *D. oligosanthes* has opened new research avenues. Sequence information of plant genomes is crucial to perform the genome-wide gene identification and characterization, and have been successfully employed in numerous plants, including Arabidopsis, rice, wheat, maize, bamboo, cotton, tomato, chili pepper, and so on (Kumar et al., 2017; Wang et al., 2019; Li et al., 2020; Huang et al., 2020; Zheng et al., 2020; Liu et al., 2020a; Yang et al., 2021; Yu et al., 2021; Tiwari et al., 2021). In *D. oligosanthes*, the genome-wide identification of SPL and zinc finger proteins (C₂H₂-ZFPs) have

already been reported (Hussain & Nanda, 2019; Mahapatra et al., 2019). In this study, the genome-wide investigation of the GATA TFs in *D. oligosanthes* (named as *DoGATAs*) has been performed. Additionally, the structural organization of the identified GATA genes has been analyzed and their exon-intron arrangements are depicted. Further, different peptide properties of the identified putative *DoGATAs* have been also predicted. The evolutionary relationship within the putative *DoGATAs* and among other plant GATAs are analyzed by constructing a phylogenetic tree. In addition, the homologous GATAs, including both the paralogous *DoGATA* pairs and the orthologous with rice GATA are identified. Moreover, the functional attributes of the identified putative *DoGATAs* are predicted by the gene ontology analysis and subcellular localization predictions.

2 Materials and Methods

2.1 Identification of the GATAs

From the NCBI (<http://www.ncbi.nlm.nih.gov/>), the draft *D. oligosanthes* was obtained and the sequences were used in this study. The hidden Markov model (HMM) of the GATA domain (PF00320) was downloaded from the Pfam database (Mistry et al., 2021). Using the HMM file, candidate GATAs in *D. oligosanthes* were searched in the HMMER program with a threshold of E-values < 10⁻⁵ (Wheeler & Eddy, 2013). The retrieved sequences were screened by performing local BLASTP and the redundant sequences were removed. Further, all selected protein sequences were screened for the signature GATA domain by the Simple Modular Architecture Research Tool (SMART) and the Conserved Domain Database (CDD) (Lu et al., 2020; Letunic et al., 2021). Sequences, those not having the signature GATA domain were excluded from further downstream analysis. Subsequently, the different protein properties of the identified putative *DoGATAs* were predicted by using the ProtParam tool (Gasteiger et al., 2005).

2.2 Sequence alignment and phylogenetic classification

The identified putative *DoGATA* sequences were aligned amongst themselves to see the conserved regions in the sequences. In addition, GATA sequences from rice (*OsGATAs*) and Arabidopsis (*AtGATAs*) were collected from the Plant TF database and used for the alignment (Tian et al., 2019). The multiple sequence alignment (MSA) was performed on CLUSTAL Omega (Madeira et al., 2019). To deduce the evolutionary relationship among the *DoGATAs* and other plants GATAs, a phylogenetic tree was constructed by using the neighbor-joining method on MEGA v10 with 1000 bootstraps (Kumar et al., 2016).

2.3 Gene structure and motif analysis

The identified *DoGATA* gene structures and the exon-intron organization were visualized by using the Gene Structure Display Server program (Hu et al., 2015). On the other hand, the de novo motif analysis of the putative DoGATAs was performed on the Multiple Expectation Maximization for Motif Elicitation (MEME) tool with the following parameters: motif repetition occurrences: any number, max motif numbers predicted: 5, and Minimum/Maximum motif width: 26/32 (Bailey et al., 2009).

2.4 Paralogous and orthologous identification

To find the paralogous *DoGATAs*, all identified *DoGATA* cDNA sequences were compared among themselves via a local BLAST alignment. The *DoGATA* sequence that exhibited >40 % similarity with ≥ 300 bp sequence alignment was considered as a paralog (Blanc & Wolfe, 2004). Conversely, each *OsGATA* cDNA sequence was searched against all *DoGATA* cDNAs by performing a local BLAST alignment to find out the orthologs. Alignments of >300 bp and with best hit scores were considered to be orthologs (Blanc & Wolfe, 2004).

2.5 Gene ontology and subcellular localization analysis

The gene ontology (GO) analysis of the identified DoGATAs was performed by using their putative protein sequences. Briefly, each protein sequence was uploaded onto the DeepGO protein function

prediction tool and the potential protein functions were predicted based on the DeepGO plus algorithm along with the GO classes (Kulmanov et al., 2018). In addition, the subcellular localization of DoGATAs was predicted by using the mGOASVM server dedicated to plants (Wan et al., 2012).

3 Results

The HMMER search with the GATA domain HMM file (PF00320) showed 34 hits with a threshold of e-values $< 10^{-5}$. These sequences were collected and checked for the presence of the signature GATA domain with SMART and CDD tools. Out of 34 sequences, only 31 showed the presence of the required GATA domain. The sequences which contained the GATA domain were retained for further analysis and the remaining 3 sequences were discarded. These 31 sequences were then named as DoGATA1 to DoGATA31 for ease of downstream analysis. The peptide properties of all the 31 putative DoGATAs were predicted by using the ProtParam tool. The DoGATAs showed a wide range of molecular weights (MW), the largest being DoGATA1 with a MW of 62.68 KDa and the smallest being DoGATA31 with a MW of 16.26 KDa. Similarly, the CDS length and amino acid length of the identified DoGATAs has also exhibited a variable range with an average amino acid length of ~317 aa. Likewise, the isoelectric point (pI) range was found to be from 4.69 (DoGATA25) to 11.56 (DoGATA12) (Table 1). Moreover, all 31 DoGATAs exhibited a negative grand average of hydropathy (GRAVY) value indicating their hydrophilic nature.

Figure 1 The structural (exon/intron) organization of *DoGATA* genes. The exons, introns, and UTR regions are represented by green boxes, blue lines, and black lines, respectively.

Table 1 The gene details and predicted protein properties of the 31 putative DoGATA genes in *D. oligosanthes*.

Name	Gene Accessions	Exons	CDS in bp	Size (aa)	MW (KDa)	pI	GRAVY Score	Localization	Biological Function
<i>DoGATA1</i>	LWDX02055130	2	1752	584	62.68	9.28	-0.604	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus, GO:0008152 - metabolic process
<i>DoGATA2</i>	LWDX02028086	1	975	325	36.08	10.93	-1.083	Nucleus	GO:0009987 - cellular process, GO:0065007 - biological regulation, GO:0050896 - response to stimulus
<i>DoGATA3</i>	LWDX02026344	2	927	309	35.11	8.60	-0.884	Nucleus	GO:0009987 - cellular process, GO:0065007 - biological regulation, GO:0050789 - regulation of biol process
<i>DoGATA4</i>	LWDX02060644	2	828	276	28.53	8.25	-0.240	Nucleus	GO:0009987 - cellular process, GO:0065007 - biol regulation, GO:0050789 - regulation of biolprocess
<i>DoGATA5</i>	LWDX02007638	2	594	198	22.17	9.33	-1.338	Nucleus	GO:0065007 - biol regulation, GO:0050789 - regulation of biol process, GO:0009987 - cellular process
<i>DoGATA6</i>	LWDX02016181	2	678	226	23.37	8.68	-0.300	Nucleus	GO:0009987 - cellular process, GO:0032502 - develop process, GO:0050896 - response to stimulus
<i>DoGATA7</i>	LWDX02031362	2	723	241	24.69	7.50	-0.307	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus, GO:0032502 - developmental process
<i>DoGATA8</i>	LWDX02024882	3	429	143	15.58	9.82	-0.727	Nucleus	GO:0065007 - biol regulation, GO:0050789 - regulation of biol process, GO:0009987 - cellular process
<i>DoGATA9</i>	LWDX02015205	3	1338	446	46.69	8.97	-0.350	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0044237 - cellular metabolic process
<i>DoGATA10</i>	LWDX02056234	1	894	298	32.62	8.72	-0.733	Nucleus	GO:0009987 - cellular process, GO:0006139 - nucleobase metabolic process, GO:0006725 - cellular aromatic compound metabolic process
<i>DoGATA11</i>	LWDX02072364	3	1278	426	44.86	8.01	-0.522	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0044237 - cellular metabolic process
<i>DoGATA12</i>	LWDX02032598	1	489	163	17.39	11.56	-0.535	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus
<i>DoGATA13</i>	LWDX02018633	2	699	233	24.24	7.10	-0.418	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0071704 - organic metabolic process
<i>DoGATA14</i>	LWDX02065998	3	456	152	16.78	9.78	-0.967	Nucleus	GO:0009987 - cellular process, GO:0065007 - biological regulation, GO:0050789 - regulation of biol process
<i>DoGATA15</i>	LWDX02039796	2	1161	387	39.87	5.52	-0.328	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus, GO:0032502 - developmental process
<i>DoGATA16</i>	LWDX02005501	4	1071	357	38.15	4.93	-0.661	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0044237 - cellular metabolic process
<i>DoGATA17</i>	LWDX02043815	2	1068	356	38.11	8.77	-0.585	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus, GO:0065007 - biological regulation
<i>DoGATA18</i>	LWDX02058546	2	1080	360	37.07	7.34	-0.484	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus, GO:0008152 - metabolic process
<i>DoGATA19</i>	LWDX02043834	3	999	333	36.11	9.45	-0.425	Nucleus	GO:0009987 - cellular process, GO:0065007 - biological regulation, GO:0050789 - regulation of biol process
<i>DoGATA20</i>	LWDX02025796	3	1074	358	38.21	9.10	-0.379	Nucleus	GO:0009987 - cellular process, GO:0032502 - develop process, GO:0065007 - biological regulation
<i>DoGATA21</i>	LWDX02013367	2	1260	420	43.91	5.27	-0.341	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0044237 - cellular metabolic process
<i>DoGATA22</i>	LWDX02045989	1	1389	463	49.36	6.87	-0.471	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0044237 - cellular metabolic process
<i>DoGATA23</i>	LWDX02024355	2	1203	401	41.21	5.75	-0.376	Nucleus	GO:0009987 - cellular process, GO:0050896 - response to stimulus, GO:0032502 - developmental process
<i>DoGATA24</i>	LWDX02030349	1	1251	417	44.55	7.55	-0.491	Nucleus	GO:0009987 - cellular process, GO:0032502 - develop process, GO:0065007 - biological regulation
<i>DoGATA25</i>	LWDX02025210	8	894	298	31.62	4.69	-0.658	Nucleus	GO:0009987 - cellular process, GO:0065007 - biological regulation, GO:0050789 - regulation of biol process
<i>DoGATA26</i>	LWDX02036020	8	987	329	35.32	8.66	-0.507	Nucleus	GO:0009987 - cellular process, GO:0065007 - biological regulation, GO:0008152 - metabolic process
<i>DoGATA27</i>	LWDX02046859	4	1071	357	39.47	7.10	-0.285	Nucleus	GO:0009987 - cellular process, GO:0032502 - develop process, GO:0065007 - biological regulation
<i>DoGATA28</i>	LWDX02019626	4	666	222	24.09	7.51	-0.725	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0065007 - biological regulation
<i>DoGATA29</i>	LWDX02052907	3	594	198	21.84	5.61	-0.785	Nucleus	GO:0009987 - cellular process, GO:0008152 - metabolic process, GO:0044237 - cellular metabolic process
<i>DoGATA30</i>	LWDX02037984	6	1266	422	46.84	6.90	-0.791	Nucleus	GO:0009987 - cellular process, GO:0006139 - metabolic process, GO:0006725 - cellular metabolic process
<i>DoGATA31</i>	LWDX02021421	2	447	149	16.26	9.34	-0.468	Nucleus	GO:0032502 - develop process, GO:0050896 - response to stimulus, GO:0048856 - anatomical development

The genetic structure and exon-intron organizations provide a better understanding of the genes. The cDNA sequences and open reading frames (ORFs) were identified for all 31 DoGATAs. The gene structures of the identified *DoGATAs* were analyzed by the GSDS 2.0 tool. The results revealed the number of exons and introns for all 31 *DoGATA* genes. The number exons in these genes ranged from 1 (*DoGATA2*, *DoGATA10*, *DoGATA12*, *DoGATA22*, and *DoGATA24*) to 8 (*DoGATA25* and *DoGATA26*). Out of the 31

identified *DoGATAs*, 13 had 2 exons, whereas 4 had no introns at all (Figure 1). On the other hand, the MSA and *de novo* motif analysis of the *DoGATAs* revealed that all of them possessed the signature GATA motif with a conserved consensus of C-X₂-C-X₁₈-C-X₂-C (Figure 2).

The evolutionary relationship of the *DoGATAs* within and among other plant GATAs was analyzed by constructing a phylogenetic

Figure 2 A) Multiple sequence alignment of the GATA sequences of rice, Arabidopsis, and *D. oligosanthos*. The amino acid positions and signature GATA motif are marked with the red color box and important positional motifs are highlighted in different colors. B) The GATA motif sequence logo as obtained from the structural analysis of the *DoGATAs* by the MEME suite.

tree by employing the neighbor-joining algorithm on MEGA v10. In total, 31 DoGATA, 31 OsGATA, and 41 AtGATA protein sequences were used to align and construct the phylogenetic tree (Figure 3). All the sequences were clustered into four distinct groups (A-D). Group A has the highest number of GATA sequences, followed by B, C, and D. Only one of the *D. oligosanthes* GATA (DoGATA2) was present in group D. Further, the screening for identification of paralogous pairs in the identified DoGATAs revealed that there are 11 paralogous genes among the 31 DoGATAs (Table 2). Similarly, a comparison of the DoGATAs

with the OsGATAs resulted in the identification of 21 pairs of orthologous genes. Additionally, the functional annotations of the DoGATAs via the DeepGo analysis were performed. The results of the study suggested that the DoGATAs might majorly be involved in the cellular processes, such as developmental processes, metabolic processes, and response to stimuli (Table 1). Further, the GO term “GO:0005488” was associated with all DoGATAs. Moreover, the prediction of the subcellular localization of all 31 DoGATA revealed that they all might be localized in the nucleus.

Figure 3 Phylogenetic analysis of the GATA TFs in *D. oligosanthes*, rice, and Arabidopsis. The tree has been constructed by using the protein sequences of the aforementioned plant GATAs by employing the neighbor-joining method on MEGA v10 with 1000 bootstrap replicates. Four major phylogenetic groups are indicated by letters A to D. The green solid circles denote the DoGATAs, blue squares denote the OsGATAs, and the maroon triangles denote the AtGATAs, respectively.

Table 2 A list of the paralogous (*Do-Do*) and orthologous (*Do-Os*) GATA gene pairs in *D. oligosanthos* and rice.

<i>Do-Do</i>	<i>Do-Os</i>
<i>DoGATA1 / DoGATA13</i>	<i>DoGATA14 / OsGATA1</i>
<i>DoGATA4 / DoGATA7</i>	<i>DoGATA15 / OsGATA2</i>
<i>DoGATA5 / DoGATA14</i>	<i>DoGATA7 / OsGATA3</i>
<i>DoGATA6 / DoGATA7</i>	<i>DoGATA19 / OsGATA5</i>
<i>DoGATA9 / DoGATA11</i>	<i>DoGATA16 / OsGATA6</i>
<i>DoGATA12/DoGTA13</i>	<i>DoGATA9 / OsGATA7</i>
<i>DoGATA15/DoGATA23</i>	<i>DoGATA11 / OsGATA7</i>
<i>DoGATA17/DoGATA22</i>	<i>DoGATA21 / OsGATA8</i>
<i>DoGATA17/DoGATA24</i>	<i>DoGATA26 / OsGATA9</i>
<i>DoGATA19/DoGATA20</i>	<i>DoGATA25 / OsGATA10</i>
<i>DoGATA25/DoGATA16</i>	<i>DoGATA13 / OsGATA11</i>
	<i>DoGATA30 / OsGATA14</i>
	<i>DoGATA6 / OsGATA16</i>
	<i>DoGATA4 / OsGATA19</i>
	<i>DoGATA16 / OsGATA20</i>
	<i>DoGATA20 / OsGATA22</i>
	<i>DoGATA1 / OsGATA24</i>
	<i>DoGATA18 / OsGATA25</i>
	<i>DoGATA3 / OsGATA31</i>
	<i>DoGATA4 / OsGATA19</i>
	<i>DoGATA4 / OsGATA19</i>

4 Discussion

The Heller's rosette grass (*D. oligosanthos*) is a C₃ panicoid grass species that serves as an important candidate to study the C₃ photosynthetic pathway and compare it with the C₄ grasses. Most of these comparative studies were focused on the crop species, including rice (C₃) and maize, sugarcane, and sorghum (C₄) (Aliscioni et al., 2012). Thus, new experimental researches covering both *in silico* predictions and wet lab validations will be immensely helpful in providing vital insights into this important grass species. As the reports on the draft genome and the comparative RNA sequencing data of *D. oligosanthos* are available in the public domain, the present scenario is conducive enough to perform the genome-wide identification of gene or TF families (Hussain & Nanda, 2019; Mahapatra et al., 2019). In this study, the stringent and methodological *in silico* analysis has resulted in the identification of 31 GATA TFs in *D. oligosanthos* (*DoGATA1-31*). The total number of GATA TFs identified in *D. oligosanthos* is the same as its C₃ relative rice and shares sequence similarities. Additionally, the gene structure organization revealed that the genetic organization and intron-exon numbers greatly vary in the DoGATAs. This variation in the gene structure and exon numbers

among GATAs has been reported in several plants, such as soybean, rapeseeds, bamboo, and pepper (Zhang et al., 2015; Wang et al., 2019; Zhu et al., 2020; Yu et al., 2021). These differences in gene and protein structures among the DoGATAs could result in functional divergences.

The structural analysis of the DoGATAs revealed that all 31 identified GATAs contain the conserved consensus of C-X₂-C-X₁₈-C-X₂-C. On the phylogenetic tree, 31 DoGATA among rice and Arabidopsis GATAs were divided into 4 distinct groups (A-D). Previous reports suggest that the classification of GATA factors into 4 groups is mostly seen in the dicots, such as Arabidopsis, tomato, and cotton (Reyes et al., 2004; Yuan et al., 2018; Zhang et al., 2020). In contrast, monocot GATAs are divided into 3 groups as in rice (Reyes et al., 2004). In our study, the classification of the DoGATAs into 4 groups differs from these reports, however, similar to the results obtained by Wang et al. (2019) in bamboo plants. On the other hand, apart from the difference in classification, the DoGATAs exhibited greater evolutionary conservation patterns as compared to the A, B, and C group GATAs in Arabidopsis and rice. Thus, it could be inferred that the majority of the DoGATAs are conserved as compared to other

grass species in the due course of evolution. Several paralogous pairs of genes arise due to the duplication of gene events in the due course of evolution (Lallemant et al., 2020). Additionally, these events play key roles in the species adaptations and developments in the environment (Lallemant et al., 2020). To get additional insights into the evolution of the *DoGATAs*, we have analyzed the paralogous and orthologous pairs in *DoGATAs* and in between *OsGATAs* and *DoGATAs*, respectively. The obtained results suggested that the GATA gene family in *D. oligosanthes* has experienced a large-scale gene duplication event, as we found 11 out of 31 GATAs to be putative paralogs. On the other hand, the identification of 21 orthologous pairs with *OsGATAs* indicated the tight conservancy nature of the GATA TFs in the grass species.

To get additional insights on the putative functions of *DoGATAs*, the peptide properties, subcellular localization, and GO predictions were performed. All of the *DoGATAs* had a negative GRAVY value indicating possibly their hydrophilic nature. Additionally, all of them were predicted to get localized inside the nucleus (Table 1). Being transcription factors, the GATAs mostly localize in the nucleus, where they regulate the downstream gene expressions by binding with their DNA binding domain (Zhang et al., 2020; Nutan et al., 2019). Further, all the 31 *DoGATAs* were predicted to have a DNA binding activity and associated with the GO term “GO:0005488”. These results collectively suggested that the localization and putative function of the *DoGATAs*. Moreover, GO predictions indicated that several of the identified *DoGATAs* might be involved in key physiological processes, including metabolic pathways, cellular processing, and response to stimuli (Liu et al., 2019a; Liu et al., 2020b; Zhu et al., 2020; Zhang et al., 2020; Zhang et al., 2021). Functional validation and in-depth analysis of the identified GATAs in *D. oligosanthes* will confirm their roles in the plant.

Conclusion

The present study reported that the genome-wide identification and analysis of the GATA TF family in *D. oligosanthes*, an important C₃ grass. In addition, the systematic and stringent *in silico* analysis resulted in the identification of 31 GATAs in *D. oligosanthes*. Their putative protein properties predictions revealed the diverse structural ranges and suggested their possible hydrophilic nature. The exon-intron arrangements revealed the structural variations in the gene structures of *DoGATAs*. Furthermore, the phylogenetic analysis clustered the *DoGATAs* among *OsGATA* and *AtGATAs* into four distinct groups. The analysis of paralogous pairs among the *DoGATAs* hinted towards the possible early and large-scale gene duplication event in the GATA TF family in *D. oligosanthes*. On the other hand, the identification of 21 pairs of orthologs with rice GATAs indicated the conserved nature of the GATAs in the grass family. Furthermore, the MSA and the *de novo* motif analysis revealed that all 31 *DoGATAs* possess the signature GATA

domain and consensus sequence. The GO analysis along with the sub-cellular localization prediction and other protein properties suggested the putative roles of the *DoGATAs*. Moreover, this study can serve as a basic framework for future functional validation and in-depth analysis of the GATA genes in *D. oligosanthes*.

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Conflict of interest

The authors declare no conflicts of interest.

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