Open Access

Phytopathogenomics and Disease Control., *2024, 3(2)201-211*
ISSN (Online):2957-5842; ISSN (Print):2957-5834
DOI https://doi.org/10.22194/Pdc/3.1033
https://societyfia.org/journal/PDC

Society for Innovative Agriculture

Genome-Wide Analysis of the DNA-Binding One Zinc Finger (Dof) Family in Vigna Species: Unveiling Insights into Transcriptional Regulation

Zakia Habib* and Siddra Ijaz

Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture, Faisalabad-38040, Pakistan.
*Corresponding author's e-mail: zakianoor92@gmail.com

The Dof (DNA-Binding One Zinc Finger) transcription factor family is unique to plants and performs various functions associated with activities unique to plants, including defense mechanisms, light and phytohormone responses, and seed development and germination. Though genome-wide studies have been carried out for this family in many species, but there is scarce information about Dof genes in *Vigna* species. In the current study, 79 non-redundant Dof proteins including 35 of them were found in V. angularis, 33 in *V. radiata*, and 11 in *V. unguiculata*. Furthermore, a comparative study was conducted on 33 non-redundant Dof proteins found in Arabidopsis thaliana. All of the identified Dof proteins in the Vigna species were found in the nucleus, according to predicted subcellular localization, which is consistent with the Dof proteins' known function as transcription factors. Moreover. All three Vigna species have several Dof proteins with predicted nuclear localization signals, suggesting a possible function for these proteins in nuclear transport and localization. Most Dof proteins were shown to have no introns by gene structure analysis; however, a small number of genes have one or two introns. The motif distribution analysis revealed motifs that were preserved over various clusters, with certain motifs being more common in particular clusters. A phylogenetic tree was constructed to assess the evolutionary hierarchy between the Dof proteins of Arabidopsis thaliana and Vigna species that revealed four major clusters, with cluster I having the greatest number of Dof proteins. These results could contribute to a better understanding of and roles of Dof genes in *Vigna* species.

Keywords: Genome-wide analysis, *Vigna* species, transcription factor, DNA binding one zinc finger (DOF), Plant genetics, Gene expression.

INTRODUCTION

Beans or pulses are considered the source of human and animal diets having high nutritional value including high protein, carbohydrates, vitamins, minerals, and health-benefiting fatty acids. Moreover, Pulse flour is an excellent candidate for blending due to the high quantities of lysine present in pulse protein and the high amount of folate it contains. Pulses also include a variety of antioxidants that improve health, such as phenolic chemicals and carotenoids. There is a notable concentration of antioxidants (phenolic acid, polyphenols, flavonoids, and tannins) in pulses. Beans belong to the *Vigna* genus which has flowering plants in the *Fabaceae* family (Hall *et al*., 2017).

The genus *Vigna* consists of approximately 200 species having pantropical distribution, native to tropical regions worldwide (Habib, 2023; Siddiq and Uebersax, 2022). Several species including mung bean (*Vigna radiata*), cowpea (*Vigna* unguiculata), mat bean (*Vigna* aconitifolia), urd bean (*Vigna* mungo), rice bean (*Vigna* umbellate), and adzuki bean (*Vigna angularis*) of *Vigna* genus are considered potential food crops for millions of people in developing countries and these *Vigna* species exhibited considerable economic importance in recent decades (Harouna *et al.*, 2018). However, these valuable *Vigna* species are vulnerable to many environmental stresses as well as biological stresses. Environmental stress includes extreme temperature (cold or heat), drought, salinity, water-loggings, and oxidative stresses (Harouna, 2020). Biological factors involve many living organisms like bacteria, fungi, parasites, and insects that cause particular diseases in beans (HanumanthaRao *et al.*, 2016).

Genes that respond to these stresses have a vital role in plant physiology (Tutlani *et al*., 2022). However, these genes are controlled by several transcription factors that regulate their functioning in particular stressed environments. Transcription

Habib, Z. and S. Ijaz. 2024. Genome-Wide Analysis of The Dna-Binding One Zinc Finger (Dof) Family In Vigna Species: Unveiling Insights Into Transcriptional Regulation. Phytopathogenomics and Disease Control 3: 201-211.
[Received 28 Feb 2024; Accepted 14 Apr 2024; Published 18 Jun 2024]

factors (TFs) are the specific proteins that control RNA polymerase activity either by triggering or hindering (Srivastava *et al.*, 2018). These factors attach to the regulatory sequences within the promoter part of the target gene and regulate its expression. These regulatory sequences can act as either repressors or enhancers. A transcriptional factor of plants consists of DNA-binding domain (DBS) that binds to a particular sequence of a target gene, activation domain (AD) that have the binding regions for transcription co-regulators, an oligomerization site, and signal sensing domain (SSD) that can sense any external signal (a signal that can interrupt gene expression) (Wang *et al.*, 2021).

TFs are also classified based on different families such as eukaryotic-specific bZIP, MYB or bHLH factors, and kingdom specific NAC, WRKY, DOF, and DREB factors (Gupta *et al.*, 2015). The concept of the functional and structural relationship between the TFs and the target gene will be helpful in understanding the molecular analysis of the target gene expression. In plants, these transcriptional factors control the gene expression under different environmental and biotic stresses (Weidemüller *et al.*, 2021). Among these, DNA-binding with one zinc finger (DOF) is particularly linked to all plant species and plays its part in gene regulation. The DOF family is considered as one of the highly effective TF-family in plant crops that regulates their normal growth, differentiation, and developmental processes. These factors also control ongoing biological processes like photosynthesis, transpiration, accumulation (seed storage), transportation, germination, flowering duration, light-based gene expression, dormancy, phytohormonal response, and a lot of others that are specifically associated with the plants (Zou and Sun, 2023). DOF genes are extensively distributed throughout the plant genome (Gupta *et al.*, 2015).

The DOF transcriptional factors in *Vigna* species play a vital part in development, growth as well as in conferring resilience to different environmental and biological stresses. A number of DOF transcriptional factors have been reported in *Vigna* species such as WRKY, MYB, and PHD (Li *et al.*, 2023), AP2/ERF (Chen *et al.*, 2022) in mungbean and bZIP in adzuki bean (Yin *et al.*, 2022). Furthermore, the discovery and characterization of DOF genes in *Vigna* species have been made easier by the availability of innovative genomic resources such whole-genome sequencing and high-throughput transcriptome data. By combining these genetic resources with functional investigations, such as functional validation experiments and gene expression profiles, we may improve our comprehension of the biological relevance of the DOF family in *Vigna* species (Chen *et al.*, 2022). The objective of this research study if the genome-wide investigation of DNA binding with one zinc finger (DOF) family in *Vigna* species to thoroughly explore and comprehend the genetic architecture, distribution, and functional functions of DOF family members throughout the genome of *Vigna* species and the role of transcription factors in plant physiology.

MATERIALS AND METHODS

The DNA-binding one zinc finger (DOF) is an important transcriptional factor present specifically in plants. These DOF factors play vital role in plant-linked cellular functions such as plant growth, differentiation, development as well as their response during biotic and abiotic stresses. Although genome wide analysis of Dof protein family has been explored in many crop species but in case of *Vigna* species, no relevant study has been emerged yet. The present study was conducted to identify the Dof genes, their location on chromosomes, intron-exon architecture and motif distribution as well as comparative evolutionary relationship of non-redundant Dof proteins among *Vigna* species in reference to *Arabidopsis* using computational biology.

***Sequence retrieval*:** A database specify to plant transcription factors, known as PlantTFDB (Plant Transcription Factor database) version 5.0 (http://planttfdb.gao-lab.org/) was used for obtaining DOF proteins sequences and CDS in three *Vigna* species (*Vigna angularis*, *Vigna radiata* and *Vigna unguiculata*) and *Arabidopsis thaliana*. However, genomic sequences of Dof protein of three *Vigna* species and Arabidopsis were searched from NCBI (National Center for Biotechnology Information) (https://www.ncbi.nlm.nih.gov/) database.

***Conserved Domain/ motif analysis*:** Online web servers were used to identify conserved Dof domains among collected Dof protein sequences. Retrieved sequences of Dof proteins were subjected to ScanProsite tool (https://prosite.expasy.org/scanprosite/) and *Batch* Web-CD search tool (https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi) for identification of Dofdomains. While the conserved motifs within these retrieved protein sequences were identifiedusing MEME (Multiple Expression motifs for Motif Elicitation) search tool (http://meme-suite.org/tools/meme). In MEME, maximum number of motif was set at 15 while the remaining parameters were at their default setting.

***Physicochemical properties*:** Online protein servers, ProtParam (https://web.expasy.org/protparam/) and PlantTFDB v5.0 were used for collecting information about amino acid composition, isoelectric point (*pI*), molecular weight, molecular formula, instability index (II), aliphatic index and grand averageof hydropathicity (GRAVY) of Dof proteins along with chromosomal location of the DOF genes of *Vigna* species.

***Protein subcellular localization*:** The prediction of subcellular localization of DOF protein of three *Vigna* species was performed using CELLO v.2.5 (http://cello.life.nctu.edu.tw/). This online server provides

location of Dof proteins within cell based on SVMs (support vector machines) classification system.

***Nuclear localization signals (NLS)*:** NLStradamus (http://www.moseslab.csb.utoronto.ca/NLStradamus/) was used for predicting NLS regions in investigated Dof proteins of *Vigna* species. This NLS signal prediction was based on hidden markov model.

***Gene Structure analysis*:** In gene structure display analysis, gene sequences were retrieved from their respectiveselected Dof proteins. The genes structure with intron-exon architecture of retrieved DOF genes was explored through Gene structure display server 2.0 (GDS) (http://gsds.cbi.pku.edu.cn/).

***Phylogenetic analysis*:** The amino acid sequences of Dof proteins from three *Vigna* species in reference to Arabidopsis Dof proteins were aligned using CLUSTALW program (https://www.genome.jp/tools-bin/clustalw). The Phylogenetic trees were generated using Molecular Evolutionary Genetics Analysis v. 7.0 (MEGA7) software package (Kumar et al., 2016) under neighbor-joining algorithm.

RESULTS

The genome wide analysis is the characterization of genes linked to particular cellular activities in plant species. Although genome wide analysis of Dof family has been explored in many crop species in the case of *Vigna* species, no relevant study has emerged yet. The present study was conducted to identify the Dof genes, their location on chromosomes, intron-exon architecture, and motif distribution as well as the comparative evolutionary relationship of non-redundant Dof proteins among *Vigna* species and Arabidopsis using computational biology. So, this research study was aimed "In silico Genome-wide probing and analysis of DOF family in *Vigna* species (*Vigna radiata*, *Vigna angularis*, *Vigna* unguiculata) for the characterization and function prediction".

***Genome wide identification of Vigna Dof proteins*:** In genome wide analysis, a total of 79 non redundant Dof proteins in *Vigna* species (35 in *Vigna angularis*, 33 in *Vigna radiata* and 11 in *Vigna ungucuilata*) and 33 non redundant Dof proteins in Arabidopsis thaliana were identified from Plant Transcription Factor Database (PlantTFDB) and National Center for Biotechnology Information (NCBI).

Conserved Domain/ motif analysis: The conserved Dof domains were confirmed in 79 non-redundant Dof proteins of three *Vigna* species in BatchCD search and ScanProsite. Moreover, fifteen (15) conserved motifs with different architecture were identified in three *Vigna* species using MEME search tool (Table 1, Figure 1, 2 & 3).

***Physicochemical properties of DOF proteins*:** The physicochemical properties of DOF proteins of three *Vigna* species have been explored. In V. *angularis* Dofs, serine (Ser) was found as a highly abundant amino acid followed by leucine (Leu), glycine (Gly) and arginine (Arg). In V. *angularis*, the length of amino acids for Dof proteins varied from 129 for VangDOF_24 to 516 for VangDOF_16. The average length of amino acids was 310. The maximum molecular weight (MW) for Dof proteins in VangDOF_16 was 56843.80 Da and the minimum molecular weight in VangDOF_24 was 14311.07 Da. The average MW for Dof proteins was 33917.82 Da. The theoretical isoelectric point (pH value where net charge on protein is zero) ranged from

Table 1. Conserved motif in identified Dof proteins of *Vigna* species, predicted by MEME suit.

Motif #	Protein motif of *V. angularis*	Protein motif of *V. radiata*	Protein motif of *V. ungucuilata*
1	PPPEQALKCPRCBSTNTKFYYNNYSLSQPRH FCKNCR RYWTKGGALRNV	PKPDEALKCPRCDSTNTKFCY YNNYSLSQPRHFCKNCRRYW	CPRCDSTNTKFCYYNNYSLSQPRHFCKS CRRYWTKGGTLRNVP VGGGCRK
2	PVGGGCRKNKR	TKGGTLRNVPVGGGCRKNKRSSSSSSS	VPKTLRIDDPNEAAKSSIWTTLGIKNEVM
3	NGCVLVPKTLRIDDPNEAAKSSIWTTLGIKNE	REGCVLVPKTLRIDDPNEAAKSSIWTT LGIKNE	GLSSKQVSNRGLDWGQTLLQAQNLELPK PTPMRKQQQQTQ
4	KNRVVEASPVLQANPAALSRSLNFHESS	EKNRVVEASPVLQANPAALSRSLNFHESS	NDRLDFGDGSFZQDYYDVGSDDLJVNPQI
5	KDPAIKLFGRTIPLP	KDPAIKLFGRTIPLP	MHHSSTNPGFLDSLRSGFLGTQSNVQNLY YGYGNGDMGEVD
6	CSGPNSPTLGKHSRDGBIAKE	PSSSTSSSPCSGPNSPTLGKHSRDGBIAK	KRPKIDQPSVAQMVSVEIQPGNHQPFKNV QENNDFVGSFGA
7	FGSDTPLCESMASVLNLAEK	LTFGPDTPLCESMASVLNLAEK	VERKPRPEPDQALK
8	LASSIESLSSINQDLHWKLQQQRLATLFG	NDRLDFGDGSFZQDYYDVGSDDLJVNPQI	RDPAIKLFGKTIPF
9	VPWPYPWNPTG	IRPGSMADRARLAKI	MDNLNVFANEDNQVNDVKPPP
10	SHYRHITISEALQPA	VSQTASVKMEE	RVLWGFPWQM
11	NDRLDFGDGSFZQDYYDV GSDDLJVNPQI	VPWPYPWN	MDGELRTRVTVPPLAVDDHKP TPSSLYQSLCLPQQNPTSTKVSE GKDFGI
12	KIDQPSVAQMVSVEIQPGN HQPFKNVQENNDFVGSFG ASSS	DHHHHHLM	ETSPVLQANPAALSRSINFHEQ M
13	IRPGSMADRARLANI	RHFCKTCRRYW	RAGSMAERARLANIPLPEAAL
14	VSQTASVKMEEN	RVLFPFEDLK	DLTALKKPDKIJP
15	WHAATASHGGFRHDFPVKRLRCYSDGQSC	QMVSVEIQPGNHQPFKNVQENNDFVGSF	DHHHHHLH

Table 2. Physicochemical properties of identified *Vigna angularis* Dof proteins andchromosomal location of respected gene.

Sr.	Sequence code	AA	MW (Da)	*pI*	Molecular formula	II	Aliphatic index	GRAVY	Chromosome
1	VangDOF_1	277	30182.79	9.63	$C_{1304}H_{2031}N_{397}O_{402}S_{15}$	61.11	57.40	-0.619	6
2	VangDOF_2	235	25806.56	4.90	$C_{1096}H_{1694}N_{318}O_{367}S_{19}$	52.75	56.89	-0.676	6
3	VangDOF_3	272	29604.28	9.78	$C_{1285}H_{2005}N_{391}O_{389}S_{14}$	60.71	58.12	-0.591	7
4	VangDOF_4	341	36776.47	8.68	$C_{1593}H_{2428}N_{468}O_{512}S_{14}$	54.16	46.36	-0.777	10
5	VangDOF_5	205	21999.59	9.02	$C_{954}H_{1481}N_{285}O_{296}S_{10}$	55.42	58.54	-0.612	7
6	VangDOF_6	482	52444.96	7.25	$C_{2261}H_{3521}N_{653}O_{747}S_{20}$	56.79	52.24	-0.792	10
7	VangDOF_7	207	22280.58	8.70	$C_{955}H_{1480}N_{286}O_{312}S_{10}$	58.42	51.40	-0.713	9
8	VangDOF_8	269	29555.42	9.49	$C_{1302}H_{2042}N_{368}O_{397}S_{11}$	51.43	58.44	-0.687	2
9	VangDOF_9	293	31637.13	6.65	$C_{1375}H_{2130}N_{394}O_{442}S_{12}$	53.61	60.65	-0.561	1
10	VangDOF_10	498	54342.74	6.25	$C_{2343}H_{3605}N_{679}O_{774}S_{21}$	59.13	48.27	-0.796	1
11	VangDOF_11	443	48115.01	7.82	$C_{2068}H_{3267}N_{603}O_{665}S_{28}$	44.14	62.98	-0.540	4
12	VangDOF_12	142	16539.59	8.97	$C_{721}H_{1111}N_{221}O_{213}S_{8}$	51.79	45.35	-1.059	1
13	VangDOF_13	300	33431.04	5.49	$C_{1444}H_{2222}N_{414}O_{469}S_{17}$	60.11	60.17	-0.633	2
14	VangDOF_14	335	35757.82	8.72	$C_{1553}H_{2394}N_{448}O_{492}S_{17}$	53.05	54.81	-0.521	9
15	VangDOF_15	271	29296.61	8.46	$C_{1274}H_{1988}N_{358}O_{414}S_{11}$	43.88	59.78	-0.549	1
16	VangDOF_16	516	56843.80	6.77	$C_{2461}H_{3840}N_{688}O_{791}S_{35}$	48.17	59.38	-0.597	11
17	VangDOF_17	278	30885.31	8.58	$C_{1335}H_{2081}N_{385}O_{434}S_{13}$	50.44	54.35	-0.810	5
18	VangDOF_18	304	32793.12	9.04	$C_{1396}H_{2195}N_{423}O_{467}S_{13}$	57.41	56.22	-0.721	5
19	VangDOF_19	306	33198.05	3.09	$C_{1441}H_{2239}N_{409}O_{462}S_{16}$	46.04	67.52	-0.416	5
20	VangDOF_20	179	20284.21	9.43	$C_{878}H_{1395}N_{267}O_{259}S_{14}$	71.40	52.91	-0.733	5
21	VangDOF_21	253	27657.96	8.81	$C_{1213}H_{1857}N_{345}O_{373}S_{13}$	49.63	53.60	-0.729	5
22	VangDOF_22	501	54516.29	5.95	$C_{2365}H_{3684}N_{668}O_{781}S_{17}$	50.61	55.68	-0.830	4
23	VangDOF_23	307	33379.29	9.15	$C_{1447}H_{2238}N_{426}O_{452}S_{17}$	49.28	58.14	-0.570	4
24	VangDOF_24	129	14311.07	9.73	$C_{617}H_{969}N_{191}O_{189}S_{7}$	47.44	49.84	-0.891	4
25	VangDOF_25	271	29450.12	9.52	$C_{1270}H_{2019}N_{385}O_{397}S_{13}$	50.02	62.29	-0.573	4
26	VangDOF_26	225	25209.15	8.64	$C_{1100}H_{1683}N_{315}O_{342}S_{13}$	56.34	48.53	-0.814	8
27	VangDOF_27	322	35302.00	5.74	$C_{1518}H_{2325}N_{439}O_{496}S_{20}$	48.95	57.24	-0.615	8
28	VangDOF_28	338	36876.19	6.62	$C_{1580}H_{2429}N_{461}O_{504}S_{29}$	42.59	52.81	-0.656	2
29	VangDOF_29	400	44327.44	8.75	$C_{1903}H_{3002}N_{572}O_{612}S_{20}$	53.33	52.75	-0.932	2
30	VangDOF_30	475	52615.65	7.21	$C_{2286}H_{3587}N_{655}O_{737}S_{18}$	43.50	62.36	-0.686	1
31	VangDOF_31	232	24392.98	8.72	$C_{1052}H_{1602}N_{314}O_{333}S_{13}$	53.16	45.82	-0.568	1
32	VangDOF_32	278	30206.78	8.77	$C_{1327}H_{2035}N_{381}O_{406}S_{12}$	47.91	65.97	-0.440	1
33	VangDOF_33	294	32193.19	8.51	$C_{1388}H_{2167}N_{405}O_{437}S_{21}$	46.57	64.97	46.57	1
34	VangDOF_34	232	25277.80	6.48	$C_{1108}H_{1658}N_{324}O_{344}S_{8}$	28.21	57.20	-0.594	1
35	VangDOF_35	457	49632.66	8.40	$C_{2170}H_{3387}N_{613}O_{683}S_{20}$	53.26	61.07	-0.613	1

3.09 for VangDOF_19 to 9.78 for VangDOF_3. Most of the VangDOF proteins were in the basic range of pI value with an average of 7.93. The instability index is basically a stability measure of proteins and if the instability index is less than 40 than protein is considered to be stable. The instability index (II) for VangDOF_34 was 28.21, considered stable while the rest of the Dof proteins were unstable. Aliphatic index is the relative volume covered by aliphatic amino acids in the side chain. The aliphatic index ranged from 45.35 for VangDOF_12 to 67.52 for VangDOF_19 with an average of 56.29. GRAVY index measures hydrophathy (hydrophilic-positive GRAVY and hydrophobic-negative GRAVY) value for peptides. The GRAVY value of VangDOFs was in the negative range. In addition, the chromosomal location of the respected Dof gene was also given in Table 2.

In *Vigna radiata* Dofs, serine (Ser) was found a highly abundant amino acid followed by glycine (Gly), lysine (Lys) and thrionine (Thr). In V. *radiata*, the length of amino acids for Dof proteins varied from 156 for VradiDOF_3 to 501 for VradiDOF_11. The average length of amino acids was 308.27. The maximum molecular weight (Da) for Dof proteins in VradiDOF_11 was 54602.38 and the minimum molecular weight (Da) in VradiDOF_3 was 17857.24. The average molecular weight (Da) for Dof protein was 33605.34. The theoretical isoelectric point ranged from 5.62 for VradiDOF_24 to 9.78 for VradiDOF_10. Most of the VradiDOF proteins were in the basic range of pI value with

Table 3. Physicochemical properties of identified *Vigna radiata* Dof proteins andchromosomal location of respected gene.

Sr.	Sequence code	AA	MW (Da)	*pI*	Molecular formula	II	Aliphatic index	GRAVY	Chromosome
1	VradiDOF_1	479	52095.14	6.57	$C_{2229}H_{3531}N_{657}O_{731}S_{27}$	48.21	61.09	-0.681	4
2	VradiDOF_2	253	27711.09	8.81	$C_{1220}H_{1872}N_{344}O_{373}S_{12}$	49.19	58.04	-0.693	5
3	VradiDOF_3	156	17857.24	9.39	$C_{778}H_{1219}N_{239}O_{228}S_{9}$	41.25	51.92	-0.896	1
4	VradiDOF_4	214	23756.47	6.58	$C_{1024}H_{1606}N_{298}O_{332}S_{11}$	58.59	66.50	-0.581	2
5	VradiDOF_5	465	50749.57	6.52	$C_{2164}H_{3387}N_{627}O_{715}S_{35}$	49.72	51.63	-0.696	11
6	VradiDOF_6	307	33258.13	9.53	$C_{1436}H_{2239}N_{437}O_{447}S_{15}$	61.71	59.12	-0.625	6
7	VradiDOF_7	263	29434.68	6.38	$C_{1283}H_{1934}N_{372}O_{397}S_{16}$	45.47	54.83	-0.666	4
8	VradiDOF_8	359	39463.83	8.47	$C_{1696}H_{2656}N_{506}O_{549}S_{17}$	53.94	49.55	-0.944	2
9	VradiDOF_9	193	20691.92	9.57	$C_{879}H_{1375}N_{275}O_{284}S_{11}$	58.07	47.05	-0.660	4
10	VradiDOF_10	272	29565.29	9.78	$C_{1285}H_{2008}N_{388}O_{389}S_{14}$	63.02	57.76	-0.583	7
11	VradiDOF_11	501	54602.38	5.96	$C_{2362}H_{3682}N_{670}O_{783}S_{19}$	51.45	54.35	-0.849	4
12	VradiDOF_12	334	35775.77	6.50	$C_{1545}H_{2404}N_{452}O_{497}S_{16}$	46.61	63.08	-0.501	4
13	VradiDOF_13	338	36941.33	6.62	$C_{1588}H_{2444}N_{460}O_{504}S_{28}$	43.15	54.85	-0.624	2
14	VradiDOF_14	211	23003.88	9.11	$C_{1006}H_{1558}N_{294}O_{305}S_{11}$	52.52	61.94	-0.542	7
15	VradiDOF_15	473	52403.35	8.34	$C_{2274}H_{3571}N_{657}O_{734}S_{17}$	41.63	61.40	-0.703	1
16	VradiDOF_16	456	49360.73	7.24	$C_{2126}H_{3314}N_{616}O_{697}S_{22}$	60.83	52.48	-0.710	1
17	VradiDOF_17	227	24176.59	9.00	$C_{1033}H_{1586}N_{316}O_{335}S_{12}$	62.93	43.39	-0.707	1
18	VradiDOF_18	288	31246.19	8.48	$C_{1364}H_{2117}N_{389}O_{421}S_{17}$	44.39	65.73	-0.444	1
19	VradiDOF_19	329	35862.16	6.81	$C_{1538}H_{2390}N_{448}O_{492}S_{26}$	50.46	62.19	-0.541	1
20	VradiDOF_20	209	22947.50	8.90	$C_{987}H_{1558}N_{288}O_{325}S_{9}$	47.63	50.43	-0.869	1
21	VradiDOF_21	224	24117.66	9.24	$C_{1036}H_{1605}N_{317}O_{331}S_{10}$	43.77	54.02	-0.779	1
22	VradiDOF_22	455	49462.50	8.43	$C_{2166}H_{3373}N_{611}O_{678}S_{20}$	50.13	58.33	-0.672	1
23	VradiDOF_23	250	27139.87	6.02	$C_{1186}H_{1794}N_{338}O_{379}S_{9}$	38.79	57.36	-0.650	1
24	VradiDOF_24	296	32375.59	5.62	$C_{1386}H_{2124}N_{408}O_{458}S_{17}$	50.99	55.68	-0.686	8
25	VradiDOF_25	216	23858.70	9.25	$C_{1034}H_{1600}N_{304}O_{322}S_{13}$	53.49	46.99	-0.832	8
26	VradiDOF_26	207	22141.38	8.70	$C_{948}H_{1467}N_{283}O_{312}S_{10}$	54.70	49.03	-0.715	9
27	VradiDOF_27	320	34249.29	8.14	$C_{1498}H_{2297}N_{423}O_{467}S_{17}$	52.18	57.66	-0.413	9
28	VradiDOF_28	293	32244.59	9.68	$C_{1423}H_{2240}N_{402}O_{430}S_{12}$	54.13	62.97	-0.612	2

Table 4. Physicochemical properties of identified *Vigna unguculata* Dof proteins.

Sr.	Sequence code	AA	MW (Da)	*pI*	Molecular formula	II	Aliphatic index	GRAVY
1	VunDOF_1	342	37357.79	6.66	$C_{1603}H_{2468}N_{466}O_{510}S_{29}$	46.79	53.65	-0.622
2	VunDOF_2	333	35601.53	8.62	$C_{1527}H_{2398}N_{444}O_{505}S_{17}$	60.71	62.10	-0.509
3	VunDOF_3	273	30354.54	6.88	$C_{1307}H_{1999}N_{377}O_{426}S_{17}$	55.95	50.73	-0.792
4	VunDOF_4	306	33437.91	6.58	$C_{1420}H_{2195}N_{421}O_{473}S_{22}$	55.57	50.03	-0.767
5	VunDOF_5	277	30698.14	8.57	$C_{1328}H_{2076}N_{378}O_{434}S_{13}$	53.75	52.74	-0.806
6	VunDOF_6	245	26600.78	8.89	$C_{1117}H_{1739}N_{341}O_{370}S_{16}$	56.99	46.98	-0.833
7	VunDOF_7	223	24327.53	9.78	$C_{1033}H_{1638}N_{314}O_{333}S_{10}$	75.36	54.62	-0.794
8	VunDOF_8	222	24451.78	9.80	$C_{1053}H_{1700}N_{316}O_{328}S_{13}$	60.67	60.23	-0.766
9	VunDOF_9	208	23040.17	9.82	$C_{1002}H_{1598}N_{296}O_{306}S_{11}$	50.92	55.24	-0.786
10	VunDOF_10	206	22147.67	9.16	$C_{959}H_{1481}N_{289}O_{298}S_{10}$	52.51	53.54	-0.690
11	VunDOF_11	161	16694.84	9.94	$C_{714}H_{1160}N_{214}O_{231}S_{8}$	51.95	57.02	-0.442

an average of 8.02. The instability index forVradiDOF_23 was 38.79 considered as stable while the rest of the Dof proteins were unstable. The aliphatic index ranged from 43.39 for VradiDOF_17 to 66.50 for VradiDOF_4 with an average of 55.80, whereas the average GRAVY value was -0.68. In addition, chromosomal location of the respected Dof gene was also given in Table 3.

In *Vigna ungucuilata* Dofs, serine (Ser) was found as highly abundant amino acid followed by glycine (Gly) and thrionine (Thr). In V. *ungucuilata*, the length of amino acids for Dof proteins was varied from 161 for VunDOF_11 to 342 for VunDOF_1. The average length of amino acids was 254.18. The maximum molecular weight (Da) for Dof proteins in VunDOF_1 was 37357.79 and the minimum molecular weight (Da) in VunDOF_11 was 16694.84. The average molecular weight (Da) for V. *ungucuilata* Dof proteins was 25192.06. Their theoretical pI values were ranged from 6.58 for VunDOF_4 to 9.94 for VunDOF_11. Most of the VunDOF proteins were in basic range of pI value with an average of 8.61. In V. *ungucuilata*, all Dof proteins were unstable with more than 40 instability index. The aliphatic index ranged from 46.98 for VunDOF_6 to 62.10 for VunDOF_2 with an average of 54.26. The average GRAVY value was -0.17 (Table 4).

***Subcellular localization and nuclear localization signal prediction in DOF proteins*:** Subcellular localization is the location of proteins that present in plant cells. In general, all Dof proteins are present in nucleus (Kushwahan *et al*., 2008). Thereby, the subcellular location for Dof proteins of three *Vigna* species has also been predicted. The predicted localization through software program (CELLO 2.5) indicated that all 35 *V. angularis* Dof proteins were found in nucleus with exception of VangDOF_32 which was found both in nucleus and extracellular space. Similarly, subcellular localization predictionof *V. radiata* indicated that all 33 VradiDOF proteins were found in nucleus with exceptionof VradiDOF_3 which was found both in nucleus and extracellular space. While the predicted localization of *V. ungucuilata* indicated that all identified VunDof proteins were found in nucleus. The nuclear localization signal (NLS) is a paticular sequence of amino acids found inproteins. These sequences tag proteins for their transport into the nucleus through specific nuclear channels. These signals consist of positively charged amino acids such as lysine and arginine. NLStradamus predicted the NL sequences in identified DOF proteins of three *Vigna* species. For *V. angularis*, results showed NL sequences in VangDOF_1, VangDOF_DOF3, VangDOF_DOF15, VangDOF_DOF17, VangDOF_DOF20 andVangDOF_DOF23 proteins (Table 5). While, for *V. radiata* the NL sequence were predicted in VradiDOF_6, VradiDOF_10, VradiDOF_12, VradiDOF_20 and VradiDOF_31 proteins (Table 6). Similarly, for *V. ungucuilata* the NL sequence were predicted in VunDOF_5, VunDOF_8 and VunDOF_9 proteins (Table 7).

Table 5. Nuclear localization signal in *Vigna angularis*.

Sr.	Sequence code	NLS signal
1	VangDOF_1	102 - RRNKKNKRSRSK – 113
2	VangDOF_3	91 - RRNKKNKRSRSK – 102
3	VangDOF_15	48 - GGRKNKRVKK – 57
4	VangDOF_17	93 - GGRKNKRAKK – 102
5	VangDOF_20	27 - KGR – 29
6	VangDOF_23	77 - RNKRNKGSGGRSKS – 90

Table 6. Predicted nuclear localization signal (NLS) in *Vigna radiate*.

Sr.	Sequence Code	NLS signals
1	VradiDOF_6	121 - RRNKKNKRSRSK – 132
2	VradiDOF_10	91 - RRNKKNKRSRSK – 102
3	VradiDOF_12	104 - RNKRSKGSGGRSKS – 117
4	VradiDOF_20	99 - GGRKNKRVKK – 108
5	VradiDOF_31	93 - GGRKNKRAKK – 102

Table 7. Predicted nuclear localization signal (NLS) in *Vigna ungucuilata*.

Sr.	Sequence Code	NLS signal
1	VunDOF_5	93 - GGRKNKRAKK – 102
2	VunDOF_8	100 - GGRKNKRVKK – 109
3	VunDOF_9	93 - GGRKNKRAKK – 102

***Comparative phylogenetic analysis, intron-exon architecture and motif distribution*:** In genome wide analysis, a total of 15 conserved motifs were identified using MEME tool and conserved domains were identified using ScanProsite and CD search tool in each *Vigna* species. The pattern of NLS and protein cellular localization was predicted using NLStradamus and CELLO v. 2.5 respectively. A phylogenetic tree was constructed to evaluate the evolutionary relationship among three *Vigna species* in reference to *Arabidopsis thaliana* using their retrieved sequences of Dof proteins using MEGA7 software. This phylogenetic tree was compared to conserved motif distribution in Dof proteins and exon- intron architecture of Dof genes. The comparative study on *V.angularis* and *Arabidopsis* was carried out using their retrieved Dof sequences. The 35 VangDof proteins and 33 AtDof proteins were combined to generate a neighbor joining tree. Their phylogenetic relationship revealed four major clusters (cluster I, II, III, and IV). Among them, the cluster I was comprised of twenty Dof proteins (10 of *V. angularis* and 10 of *Arabidopsis*).

Their gene structure display study revealed all Dof proteins were intronless except VangDOF_11 which had only one intron and VangDOF_29 which had two introns. A maximum number of conserved protein motifs were found in cluster I (motif 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 14 and 15). VangDOF6, 10, 16, and 22 proteins had maximum number of motif (9 motifs) among all other member of this cluster analysis. While, cluster II was the smallest cluster having 6 Dof proteins (4 Dof proteins of *V. angularis* and 2 Dof proteins of *Arabidopsis*). In cluster II, all Dof proteins were intronless except VangDOF_19 which had only one intron. Dof proteins of cluster II had two motifs (motif 1 and 2) while VangDOF_19 and VangDOF_15 had only one motif. Though, cluster III was consisted of 20 Dof proteins (10 of *V. angularis* and 10 of *Arabidopsis*).

Their exon-intron architecture confirmed one (1) intron in VangDOF1, VangDOF23 and, VangDOF34, while two (2) introns in VangDOF25. Motif distribution confirmed motif 1 and motif 2 in all Dof members of this cluster, while motif 14 was also predominant in 9 Dof proteins (Vang_DOF1, 14, 23, 25 and AtDOF1.1, 2.2, 5.1, 3.6, 2.4). In addition, motif 13 was found in VangDOF_1, VangDOF_14, AtDOF2.4, AtDOF3.6, AtDOF5.1 and motif 8 was found in VangDOF_4, AtDOF4.7 and AtDOF5.7. However, Cluster IV was also comprised of 20 Dof proteins (9 of *V. angularis* and11 of *Arabidopsis*). In cluster IV, all Dof proteins were intronless except VangDOF_8, VangDOF_26 and VangDOF_27 that had only one intron. In Cluster IV, motif 1 and motif 2 were found in all Dof proteins. Motif 9 and 10 were only present in 4 Arabidopsis Dof proteins (AtDOF2.1, AtDOF3.2, AtDOF5.3 and AtDOF1.8). Whereas VangDOF_2 andVangDOF_9 were seemed to be distinct one in this

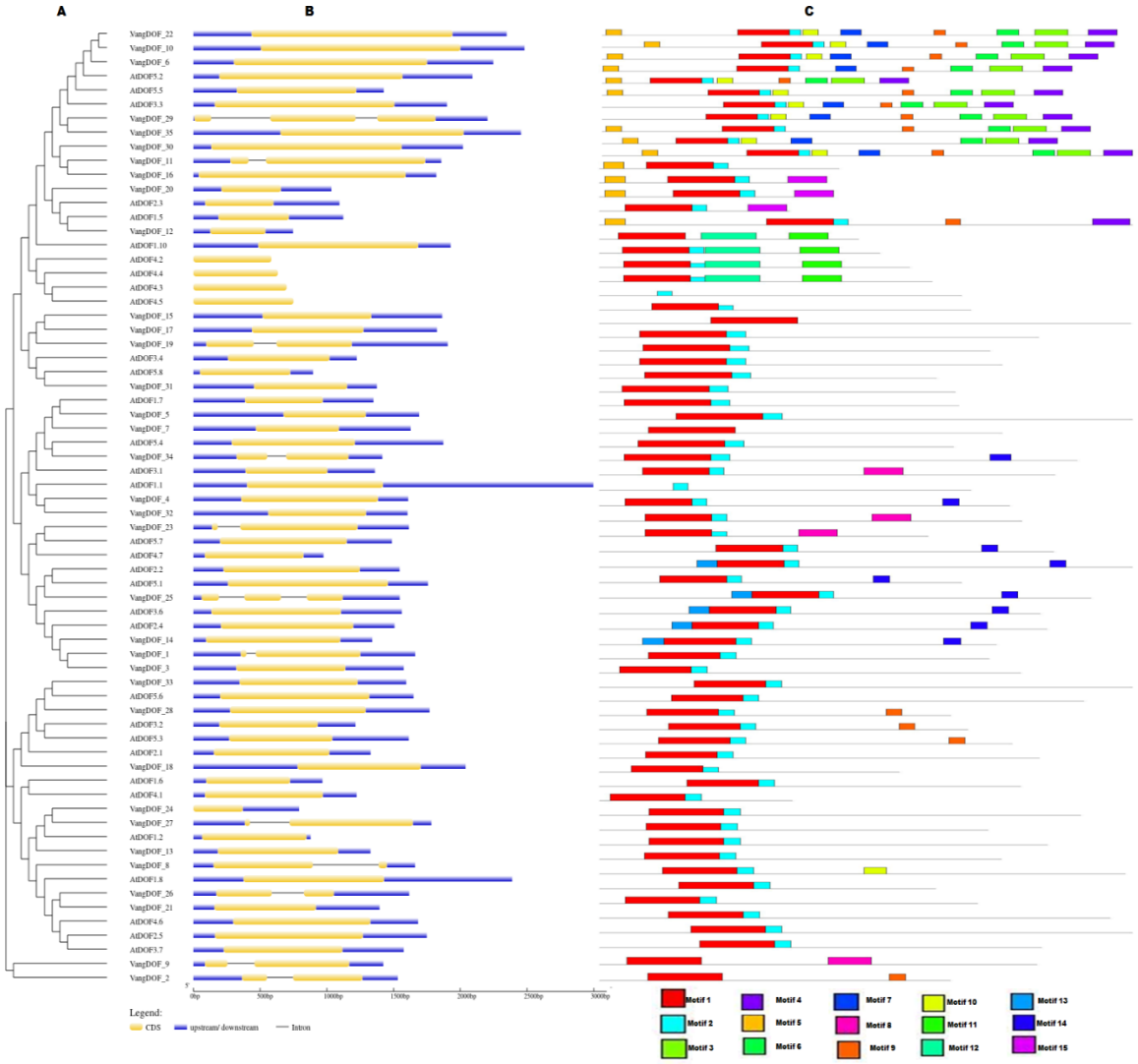

Figure 1. Comparative phylogenetic analysis of *V. angularis* and *Arabidopsis*, gene structure display and conserved motif distribution (A) Phylogenetic tree showed four major Dof clusters. (B) Gene structure analysis indicated that most of the Dof genes from *Vigna* species and *Arabidopsis* were intronless. (C) Several conserved motifs of Dofproteins were shown. These motifs were coded by 15 different colors. Each motif is represented by a specific color.

cluster analysis with larger branch length and consisted of two protein motifs (motif 1 and 8 in VangDOF_2, motif 1 and 9 in VangDOF_9) and also have one intron (Figure 1).

The comparative study on *V.radiata* and *Arabidopsis* was carried out using their retrieved Dof sequences. The 33 VradiDof proteins and 33 AtDof proteins were combined to generate a neighbor joining tree. Their comparative phylogenetic relationship depicted four major clusters (cluster I, II, III, and IV). Cluster I was comprised of 21 Dof proteins (11 of *V. radiata* and 10 of *Arabidopsis*).

Their gene structure architecture revealed VradiDOF_9 (2 intron, 3 exon), VradiDOF_21 and VradiDOF_29 (1 intron, 2 exon) have introns while all other Dof member of this cluster were comprised of exon region only. Their motif distribution revealed five conserved protein motifs (motif 1, 2, 9, 10, 12 and 13) in the member of this clusters. Among these, motif 1 and 2 were found in all Dof members. Moreover, motif 9 was found in VradiDOF_6, 27, AtDOF2.4, 3.6, 5.1, motif 10 VradiDOF_6, 9, 12, 27, AtDOF1.1, 2.2, 2.4, 3.6, 5.1, motif 12 AtDOF 2.2, 5.1 and motif 13 in VradiDOF_23. While cluster II was comprised of 18 Dof proteins (8 of *V. radiata* and 10 of *Arabidopsis*). Their gene structure display revealed VradiDOF_25 have one intron and two exons, however, all other Dof proteins have exon region only. There were 4 conservedprotein motifs (motif 1, 2, 11, 12 and 14) in these Dof proteins. Moreover, motif 11was

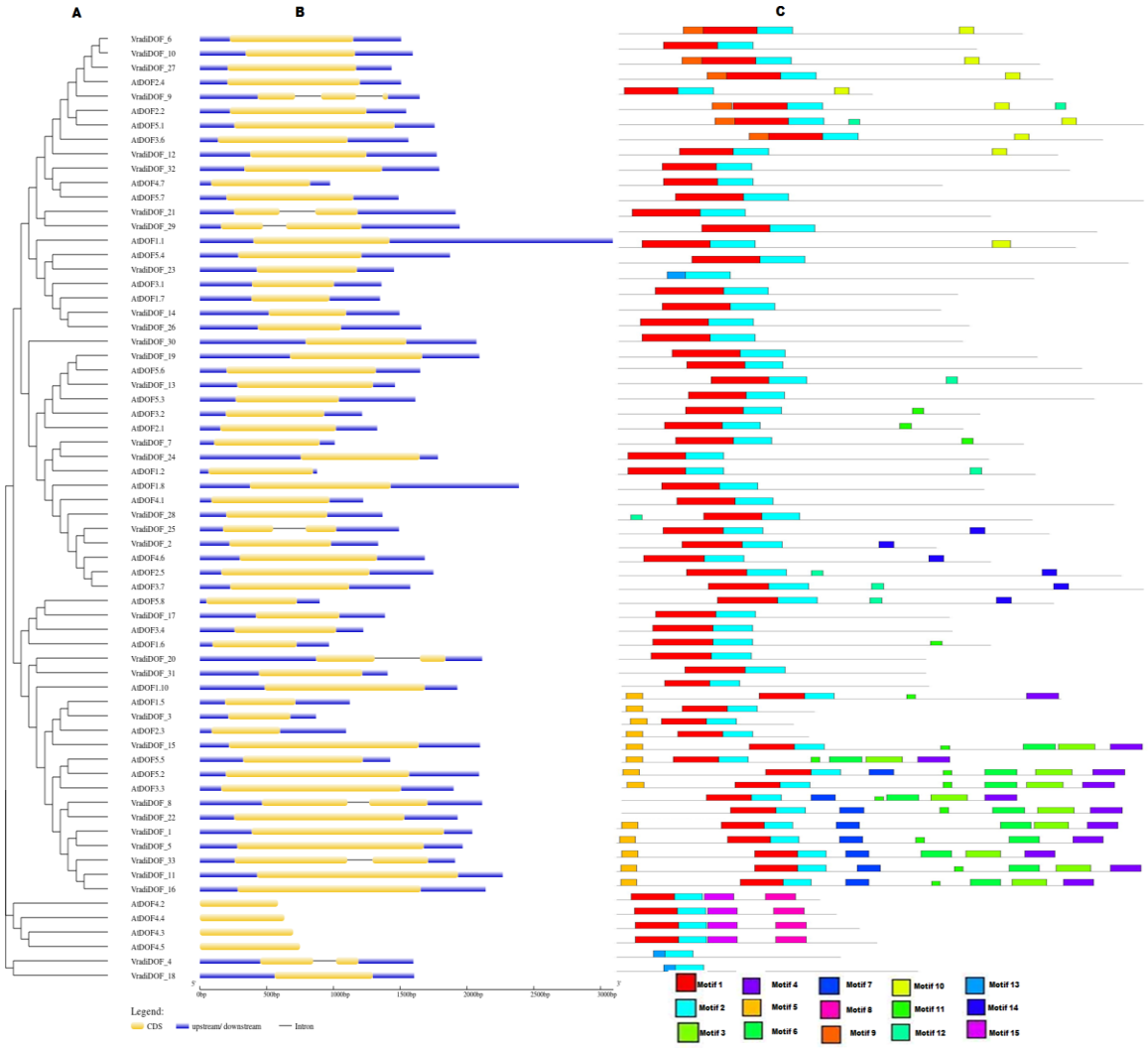

Figure 2. Comparative phylogenetic analysis of *V. radiata* and *Arabidopsis*, gene structure analysis, and motif structure analysis. (A) Phylogenetic tree depicted four Dof clusters. (B) Gene structure analysis indicated that most of the Dof genes from *Vigna* species and *Arabidopsis* were intronless. (C) Several conserved motifs (colored regions) were identified in Dof proteins. Each motif is represented by a specific color.

found in VradiDOF13, 5.3, 3.2, Motif 12 in VradiDOF24, AtDOF2.5, 3.7, 4.1, 4.6, 5.6 and Motif 14 in VradiDOF_2, 25, 28, AtDOF2.5, 3.7, 4.6, whereas cluster III was consisted of 21Dof proteins (12 of *V. radiata* and 9 of *Arabidopsis*).

Their gene structure display study revealed VradiDOF_8, VradiDOF_20 and VradiDOF_33 have two exons and one intron, while remaining Dof proteins were intronless. Motif distribution confirmed the highest number of conserved protein motifs (motif 1, 2, 3, 5, 4, 6, 7, and 11) in cluster III.

Most of theDof proteins had only two motifs (motif 1 & 2), while motif 5 was also predominant in this Dof protein clustering group. Cluster IV was the smallest group having 6 Dof proteins (2 Dofproteins of *V. radiata* and 4 Dof proteins of *Arabidopsis.* However, cluster IV was the smallest cluster with only four Dof proteins of Arabidopsis (AtDOF4.2, AtDOF4.3, AtDOF4.4, and AtDOF4.5). In these clustering proteins, motif1, 2, 8 and 15 were observed. However, in this clustering analysis, VradiDOF_4 and VradiDOF_18 were seemed as distinctand comprised of 2 conserved motifs (motif 2 and 13). The VradiDOF_4 had two exons and one intron, while VradiDOF_18 had only one exon (Figure 2).

The comparative study on *V.ungucuilata* and *Arabidopsis* was carried out using their retrieved Dof sequences. The 11 VunDof proteins and 33 AtDof proteins were combined to generate a neighbor joining tree. Their comparative phylogenetic relationship revealed four major clusters (cluster I, II, III, and IV). Among them, cluster I was comprised of 13 Dof proteins (3 of *V. ungucuilata* and 10 of *Arabidopsis*).

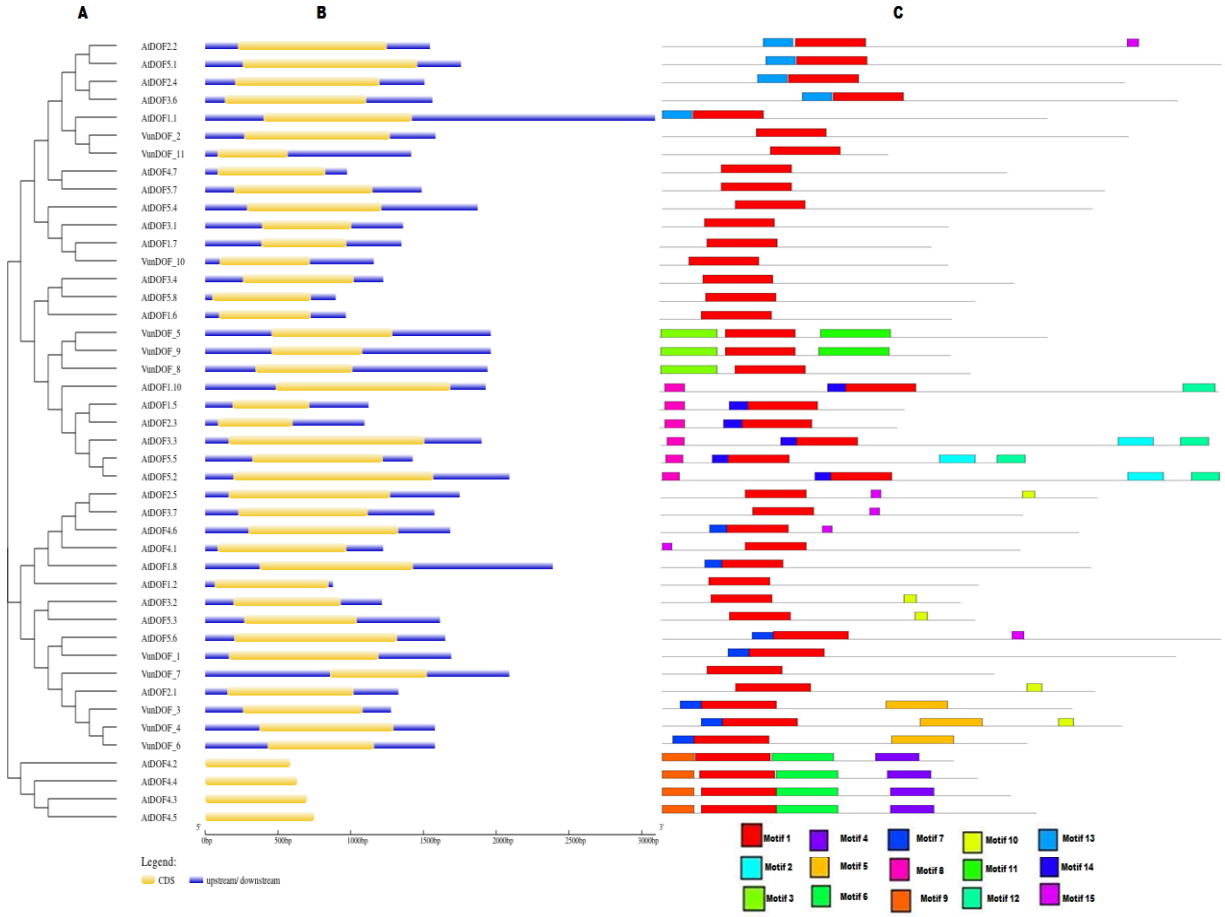

Figure 3. Comparative phylogenetic analysis of *V. ungucuilata* and *Arabidopsis*, gene structure display and conserved motif distribution (A) Phylogenetic tree showed four major Dof clusters. (B) Gene structure analysis indicated that all the Dof genes from *Vigna* species and *Arabidopsis* were intronless. (C) Several conserved motifs of Dof proteins were shown. These motifs were coded by 15 different colors.

Their gene structure display study revealed that all Dof members of cluster I had only exon region. Their motif distribution confirmed the presence of motif 1 in all Dof proteins while AtDOF1.1, AtDOF2.2 AtDOF2.4, AtDOF3.6, and AtDOF5.1 had two motifs (motif 1 & 13). Cluster II was consisted of 12 Dof proteins (3 of *V. ungucuilata* and 9 of *Arabidopsis*). All Dof members of Cluster II had only exon region. Their motif distribution confirmed the presence of 7 motifs (motif 1, 2, 3, 8, 11, 12, and 14). Cluster III was the largest cluster, having 15 Dof proteins (10 of *V. ungucuilata* and 5 of *Arabidopsis*). All Dof members of cluster III had only exon region. There were 5 conserved motifs (motif 1, 5, 7, 10 &15) of DOF protein member ofthis cluster, while motif 1 and 7 are predominant followed by motif 10 and 15. Whereas, cluster IV was the smallest group c 4 consisted of Dof proteins of *Arabidopsis* and having four conserved protein motifs (motif1, 3, 4 and 9). Their gene structure display study revealed that all Dof genes were comprised of just exon regions (Figure 3).

DISCUSSION

Plant-specific transcription factors known as the DNA-binding with one finger (DOF) family are important regulators of many physiological and developmental processes, including as seed maturation, germination, blooming, and responses to environmental stresses (Noguero *et al.*, 2013). The highly conserved DOF domain, which is a single zinc finger motif made up of about 50 amino acids, is what distinguishes the DOF proteins from other DNA-binding proteins. DOF proteins may selectively attach to the cis-regulatory elements found in the promoters of their target genes thanks to this pattern, which modifies the expression of those genes (Waqas *et al.*, 2020).

Genome-wide studies of the DOF family have been carried out in several plant species recently in a bid to clarify their evolutionary background, functional diversity, and regulatory networks. Among these species, the *Vigna* genus which

contains significant leguminous crops including adzuki bean (*Vigna angularis*), cowpea (*Vigna* unguiculata), and mung bean (*Vigna radiata*) has attracted a lot of interest because of its importance in agriculture and nutritional value. Gaining knowledge of the DOF gene range in *Vigna* species might help one better understand the molecular mechanisms governing development, growth, and stress responses in these organisms (Zhang *et al*., 2021).

In current study, a total of 79 non redundant Dof proteins in *Vigna* species(35 in *Vigna angularis*, 33 in *Vigna radiata* and 11 in *Vigna ungucuilata*) and 33 non-redundant Dof proteins in Arabidopsis thaliana were identified these results were consistent with the previous study that found 30 Dof genes in *Oryza sativa* (Khan *et al*., 2021), 43 Dof genes in sweet potato (Zhang *et al*., 2023), and 50 HaDof genes in sunflower (Song *et al*., 2024). Previous studies found the role of Dof genes in response to exogenous hormones in plants and their role in abiotic stress resilience in sunflower seedlings (Song *et al*., 2024). The conserved Dof domains were confirmed in 79 non-redundant Dof proteins of three *Vigna* species in BatchCD search and ScanProsite. Moreover, fifteen (15) conserved motifs with different architecture were identified in three *Vigna* species. Moreover, most of the motifs were shared by all three *Vigna* species.

Subcellular localization is the location of proteins that are present in plant cells. In general, all Dof proteins are present in the nucleus (Kushwaha *et al*., 2008; Gupta *et al*., 2015; Jiang *et al*., 2020). Thereby, the subcellular location for Dof proteins of three *Vigna* species has also been predicted. The predicted localization indicated that Dof proteins were found in nucleus except VangDOF_32 and VradiDOF_3 which were found both in the nucleus and extracellular space. These results were validated by previous studies where most of the Dof proteins were found in the nucleus where they play key roles (Lohani *et al*., 2021; Cao *et al*., 2022). The nuclear localization signal (NLS) is a particular sequence of amino acids found inproteins. These sequences tag proteins for their transport into the nucleus through specific nuclear channels. These signals consist of positively charged amino acids such as lysine and arginine. NLStradamus predicted the NL sequences in identified DOF proteins of three*Vigna* species. These signals are considered as highly conserved and in directing the localization of the proteins in cell (Alghanem *et al*., 2023). Moreover, a maximum likelihood-based phylogenetic tree was generated to assess the evolutionary hierarchy of the identified Dof genes.

***Conclusion*:** The objective of this investigation was to discover and characterize the DOF transcription factor, as well as to ascertain the genomic organization, evaluate the evolutionary connections among them, and clarify any possible regulatory roles in Vigna species. To better understand plant biology and possibly contribute to the development of improved crop varieties with desired traits, researchers hope to gain insight into the molecular mechanisms underlying the various biological processes, such as growth, development, stress responses, and metabolism that are regulated by members of the DOF family.

***Funding*:** N/A

***Conflict of Interest*:** We clarify that the submitted manuscript is our original research work and has not been published previously. Additionally, there is no competing interest.

Ethical statement: This article does not contain any research with human participants or animal performed by any of the authors.

***Availability of data and material*:** We declare that the submitted research article is our own work which has not been published before and is not currently considered for elsewhere publication.

***Acknowledgement*:** This research work was conducted and supported by the Molecular Biology of Plant Disease Resistance Laboratory, Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture, Faisalabad.

***Code availability*:** N/A

***Consent for publication*:** All authors have given the consent to publish this manuscript in Phytopathogenomics and Disease Control (PDC).

REFERENCES

Alghanem, S.M.S., G.S.H. Alnusairi, M.A. Alkhateeb, K.M. Alwutayd, A. Alaklabi, B.M. Alharbi, D.A. Albalawi, D. Alshehri, N.A. Al-Harbi and S.M. Al-Qahtani. 2023. Genome-wide identification and characterization of the dof gene family in mango (Mangifera indica L.). Genetic Resources and Crop Evolution 1-17.

Cao, X., W. Wan, H. Mao, D. Yin, X. Deng, H. Yan and L. Ren. 2022. Genome-wide identification and expression analysis of dof transcription factors in lotus (Nelumbo nucifera gaertn.). Plants 11:2057-2072.

Chen, H., L. Hu, L. Wang, S. Wang and X. Cheng. 2022. Genome-wide identification and expression profiles of AP2/ERF transcription factor family in mung bean (Vigna radiata L.). Journal of Applied Genetics 63:22-236.

Gupta, S., N. Malviya, H. Kushwaha, J. Nasim, N.C. Bisht, V.K. Singh and D. Yadav. 2015. Insights into structural and functional diversity of Dof (DNA binding with one finger) transcription factor. Planta 241:549-562.

Habib, Z. n.d. DNA-binding One Zinc Finger (DOF) transcription factors in Vigna species: A review. Phytopathogenomics and Disease Control 1: 37-54.

Hall, C., C. Hillen and J. Garden Robinson. 2017.

Composition, nutritional value, and health benefits of pulses. Cereal Chemistry 94:11-31.

HanumanthaRao, B., R.M. Nair and H. Nayyar. 2016. Salinity and high temperature tolerance in mungbean [Vigna radiata (L.) Wilczek] from a physiological perspective. Frontiers in Plant Science 7:186318-186338.

Harouna, D.V. 2020. Biotic and Abiotic Stress Responses of Domesticated Vigna Legumes: A Comprehensive Review. Microbial Mitigation of Stress Response of Food Legumes 31:11-23.

Harouna, D.V., P.B. Venkataramana, P.A. Ndakidemi and A.O. Matemu. 2018. Under-exploited wild Vigna species potentials in human and animal nutrition: A review. Global Food Security 18:1-11.

Jiang, W., Y. Geng, Y. Liu, S. Chen, S. Cao, W. Li, H. Chen, D. Ma and J. Yin. 2020. Genome-wide identification and characterization of SRO gene family in wheat: Molecular evolution and expression profiles during different stresses. Plant Physiology and Biochemistry 154:590-611.

Khan, I., S. Khan, Y. Zhang and J. Zhou. 2021. Genome-wide analysis and functional characterization of the Dof transcription factor family in rice (Oryza sativa L.). Planta 253:1-14.

Kushwaha, H., N. Gupta, V.K. Singh, A. Kumar and D. Yadav. 2008. In silico analysis of PCR amplified DOF (DNA binding with one finger) transcription factor domain and cloned genes from cereals and millets. Online Journal of Bioinformatics 9:130-143.

Li, S., J. Liu, C. Xue, Y. Lin, Q. Yan, J. Chen, R. Wu, X. Chen and X. Yuan. 2023. Identification and Functional Characterization of WRKY, PHD and MYB Three Salt Stress Responsive Gene Families in Mungbean (Vigna radiata L.). Genes (Basel) 14:463-480.

Lohani, N., S. Babaei, M.B. Singh and P.L. Bhalla. 2021. Genome-wide in silico identification and comparative analysis of Dof gene family in Brassica napus. Plants 10:709-721.

Noguero, M., R.M. Atif, S. Ochatt and R.D. Thompson. 2013. The role of the DNA-binding One Zinc Finger (DOF) transcription factor family in plants. Plant Science 209:32-45.

Siddiq, M. and M.A. Uebersax. 2022. Dry beans and pulses: production, processing, and nutrition. John Wiley and Sons.

Song, H., X. Ji, M. Wang, J. Li, X. Wang, L. Meng, P. Wei, H. Xu, T. Niu and A. Liu. 2024. Genome-wide identification and expression analysis of Dof gene family reveal their involvement in hormone response and abiotic stresses in sunflower (Helianthus annuus L.). Gene 910:148336-148349.

Srivastava, R., S. Kumar, Y. Kobayashi, K. Kusunoki, P. Tripathi, Y. Kobayashi, H. Koyama and L. Sahoo. 2018. Comparative genome-wide analysis of WRKY transcription factors in two Asian legume crops: Adzuki bean and Mung bean. Scientific Reports 8:16971-16989.

Tutlani, A., P.J. Banshidhar and H.S. Janeja. 2022. Abiotic and biotic stresses and their effect on Vigna radiata L. The Pharma Innovation Journal 11:230-237.

Wang, X., Y. Niu and Y. Zheng. 2021. Multiple functions of MYB transcription factors in abiotic stress responses. International Journal of Molecular Sciences 22:6125-6139.

Waqas, M., L. Shahid, K. Shoukat, U. Aslam, F. Azeem and R.M. Atif. 2020. Role of DNA-binding with one finger (Dof) transcription factors for abiotic stress tolerance in plants. Transcription factors for abiotic stress tolerance in plants 1-14

Weidemüller, P., M. Kholmatov, E. Petsalaki and J.B. Zaugg. 2021. Transcription factors: Bridge between cell signaling and gene regulation. Proteomics 21:2000034-2000048.

Yin, Z., X. Meng and Q. Wang. 2022. The bZIP transcription factor family in adzuki bean (Vigna Angularis): genome-wide identification, evolution, and expression under abiotic stress during the Bud stage. Frontiers in Genetics 13:847612-847623.

Zhang, C., T. Dong, J. Yu, H. Hong, S. Liu, F. Guo, H. Ma, J. Zhang, M. Zhu and X. Meng. 2023. Genome-wide survey and expression analysis of Dof transcription factor family in sweetpotato shed light on their promising functions in stress tolerance. Frontiers in Plant Science 14:1140727-1140742.

Zhang, W.H., J.D. Du, D.M. He, X.R. Gu, Y. Huang and F.S. Guo. 2021. Bioinformatics analysis of Dof family genes and expressions analysis under salt stress in Vignia radiata.

Zou, X. and H. Sun. 2023. DOF transcription factors: Specific regulators of plant biological processes. Frontiers in Plant Science 14:1044918-1044934.