International
Journal of Agriculture Innovations
and Cutting-Edge Research

Genome-Wide Identification, Structural Characterization and Phylogenetic Analysis of Dof (DNA-Binding with one finger) Transcription Factor in Lima Bean (Phaseolus lunatus L.)

Arif Ullah[1], Zamarud Shah[2](Corresponding Author)**, Raham Sher Khan[3], Osaid Kamran Marwat[4], Kaleem Ullah[5]**

[1] PhD Student, Department of Biotechnology, University of Science and Technology Bannu, Pakistan, Email: au254837@gmail.com
[2] Assistant Professor, Department of Biotechnology, Abdul Wali Khan University, Mardan, Pakistan, Email: zamarud@awkum.edu.pk
[3] Professor, Department of Biotechnology, Abdul Wali Khan University Mardan, Pakistan, Email: rahamsher@awkum.edu.pk
[4] M. Phil Student, School of Interdisciplinary Engineering and Sciences, National University of Science and Technology, Islamabad, Pakistan, Email: usaidkmarwat@gmail.com
[5] BS Student, Department of Biotechnology, Abdul Wali Khan University Mardan, Pakistan, Email: kaleemullah31220@gmail.com

Abstract

Dofs are plant-specific transcription factors involved in diverse functions, including growth, development, hormonal and Abiotic stress response regulation. Although genome-wide analysis of Dof genes has been performed in many species, these genes have yet to be analyzed in lima bean. The current study was aimed at exploring and characterizing the Dof gene family across the genome of the lima bean. Forty PlDof genes in the genome of lima bean were detected during the present study, and named as PlDof1-PlDof40 based on their location on the chromosome in the ascending order. PlDof12 was recorded as the largest gene with 1560 bp CDS, 519 amino acid protein length (PL) and 57.126 kDa protein molecular weight (PMW), while PlDof-23 was found as the smallest one with only 522 CDS, 173 PI and 19.75 kDa PMW, respectively. Nucleus was predicted as a major residence for all 40 PlDof proteins. Isoelectric points and GRAVY were found in the range of 5.35 to 8.91 and -0.269 to -0.746, respectively. The varying number of exons reveals that deletions/additions have occurred during evolution, resulting in variation in motif number. Motif1was conserved in all PlDof genes. The phylogenetic tree reveals that paralogs contributed 33% to the PlDof gene family expansion. Ka/Ks ratios of paralogs reveal that they were all under purifying selection. The promoter region has environmental, developmental, light and hormone-responsive elements that might contribute to the diverse function of PlDof. This study provides a basis for the functional validity of PlDof genes.

Keywords: Lima bean, Dof, genome-wide analysis, evolutionary analysis, transcription factor

DOI:	https://zenodo.org/records/15656357
Journal Link:	https://jai.bwo-researches.com/index.php/jwr/index
Paper Link:	https://jai.bwo-researches.com/index.php/jwr/article/view/117
Publication Process	Received: 30 Mar 2025/ Revised: 15 Jul 2025/ Accepted: 23 Jul 2025/ Published: 27 Jul 2025
ISSN:	Online [3007-0929], Print [3007-0910]
Copyright:	© 2025 by the first author. This article is an open-access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).
Indexing:	Academia.edu DRJI doi zenodo Google Scholar INDEX COPERNICUS INTERNATIONAL
Publisher:	BWO Research International (15162394 Canada Inc.) https://www.bwo-researches.com

Introduction

Dof genes encode 200-400 amino acid-long transcription factors with 2 distinct ends. The N-terminal end with 52 52-amino-acid conserved domain and a variable domain occupying the C-terminal end (Yang *et al.*, 2017). Specific cis-acting element (AAAG or CTTT) in upstream regions of target genes is recognized by the highly conserved N-terminal domain (Plesch *et al.*, 2001; Yanagisawa, 2004). The C-terminal domain is less conserved and mainly concerned with the regulation of diverse genes at the transcriptional level (Gupta *et al.*, 2015). Thus, the cross-talk of DNA binding N-terminal and variable C-terminal ends with cis-acting elements and other proteins helps in regulating the genes of interest (Noguero *et al.*, 2013).

The Dof gene family has been explored in diverse plant species with a vital role in plant growth (Fornara *et al.*, 2009), stresses (Cai *et al.*, 2016) and light signal transduction (Kondhare *et al.*, 2019). The AtDofs help in the healing of mechanical injury and promote callogenesis in Arabidopsis thaliana by enhancing the growth (Zhang *et al.*, 2022). The inhibition of SIDof1, via RNAi approach, delayed the production of lycopene, resulting in late maturity of Solanum lycopersicum (Wang *et al.*, 2021). Similarly, PavDof6 and PavDof2/15 are involved in switching on and off of cell wall modifying genes, respectively, eventually leading to early maturity and delayed softening of cherry fruit (Zhai *et al.*, 2022). AdDof3 bind to cis-acting elements and activates the AdBAM3L gene and hence promoting kiwifruit maturity (Zhang *et al.*, 2018). Likewise, the role of AdDof4 in inhibiting fatty acid desaturase gene (AdFAD1) was unlocked while evaluating the response of ethylene(to volatile compounds) in kiwifruit (Zhang *et al.*, 2020). Hardness provides a barrier for the protection of fruits against insects, which is attributed to the deposition of lignin and cellulose in the plant cell wall (Zhao and Dixon, 2011). Dof factors regulate these polymers by playing a vital role in carbon metabolism (Kasirajan *et al.*, 2018). VDof1 and VDof2 target different genes at various stages and facilitate differentiation of vascular tissues in Arabidopsis thaliana (Ramachandran *et al.*, 2020).

Recent research has demonstrated the role of Dof genes in combating the ill-effects of high/low temperature, salinity and drought stress. Over-expression of SLDOF25/26 in Arabidopsis elevates its resistance to water deficiency and salinity (Park et al., 2003). Transforming upland cotton with DOF1 changes oil composition in seeds and enhances resistance to cold and salt stresses (Su *et al.*, 2017). SoDof15 and SoDof3 up-regulated against drought and heat stress, respectively (Yu *et al.*, 2021).

Among the bean crops, lima bean is the second largest one, both with respect to area under cultivation and consumption (López-Alcocer *et al.*, 2016). Lima bean originated from the USA, but over time its cultivation gained speed and has grown in many regions all across the globe (Baudoin *et al.*, 2006; Martínez-Castillo *et al.*, 2014). Lima bean is a rich source of proteins, fibres, vitamins and minerals (Jin *et al.*, 2014). The fat-free proteins make this crop superior to other legume crops (Adebo *et al.*, 2023). Lima bean has shown enhanced tolerance to abiotic stresses (Nascimento *et al.*, 2017) and exhibited vigorous growth to plant growth-promoting hormones (Sá *et al.*, 2023). Thus, the current study was carried out on the assumption of lima bean as a rich source of Dof genes.

Materials and Methods

Identification of Dof genes across the lima bean genome

DOF sequence of *Arabidopsis thaliana* (NP_201099.1) was isolated from NCBI (https://www.ncbi.nlm.nih.gov/) and inserted in Motif finder (https://www.genome.jp/tools/motif/) for detecting zf-Dof domain. AtDOF domain was blasted against Lima bean genome using Phytozome v.13 (https://phytozome-next.jgi.doe.gov. (Goodstein *et al.*, 2012) for extracting PlDof transcripts. Short sequences, with no more use in the onward process, were deleted.

Physical characterization and predicting the location of PlDofs proteins

Molecular weight, protein length and CDS of PlDofs were taken from Phytozome. Similarly, other features of PlDof proteins, including PI and GRAVY, were obtained from Expasy Protparam (https://web.expasy.org/protparam, Gasteiger *et al.*, 2003). PlDof protein sequences were inserted into Wolf Psort for predicting their sub-cellular location. Wolf Psort-based generated data was used for making a heatmap through TBtool.v1.09854

Conserved domain and interspecific phylogeny of PlDof Proteins

Two files, including renamed protein and hit data files, mandatory for finding conserved domains, were obtained from TBtool.v1.09854 (Chen *et al.*, 2018) and conserved domain database (Marchler-Bauer *et al.*, 2015), respectively. The files were subjected to TBtool v1.09854 for generating domain architecture (Chen *et al.*, 2018). *PlDof* sequences were inserted in MEGA 11 (Kumar *et al.*, 2016) for exploring phylogeny between lima bean and Arabidopsis thaliana based on maximum likelihood (ML, 1,000 bootstrap replicates). Two leaf (Dof) from the same plant and originating from the most recent common ancestor (node)in the phylogenetic tree were termed as paralogs, while those belonging to different plants were named as orthologs.

Conserved motif and structure of PlDof genes

Conserved motifs were visualized in PlDof proteins using Multiple Em for Motif Elicitation (http://memesuite.org). CDS and genomic sequences of *PlDof* genes were extracted from Pytozome and subjected to Gene Structure Display Server 2.0 (http://gsds.gao-lab.org/) (Hu *et al.*, 2015) for visualizing the gene's structure.

Mapping and duplication of the PID of genes

The mandatory information required for locating PlDof genes, including chromosome number, position and length of PlDof genes, was extracted from Phytozome. The information was inserted in PhenoGram Plot for mapping PlDof on the chromosomes (http://visualization.ritchielab.psu.edu/phenogram s/plot). The values of non-synonymous (Ka) and synonymous (Ks) substitutions, PIDof paralog pairs, were obtained from TBTool (Chen *et al.*, 2018). The Ka/Ks ratio was analyzed to determine the pattern of duplicated PID of genes.

Promoter Region Analysis

A sequence of 1500bp upstream to the translation initiation site (ATG) was taken from Phytozome of each gene. PlantCARE (https://bioinformatics.psb.ugent.be/webtools/plantcare/html/) was used for exploring *cis*-regulatory elements in *PlDof* genes (Lescot *et al.*, 2002).

Statistical analysis

A factorial complete randomized design (CRD) with 3 replications was used to get valid estimates of treatment effect, having minimum experimental error. Statistical software was used for the analysis of data. ANOVA or the F test was used to determine the level of treatment effect, while the least significant difference (LSD) test was applied to compare means after ANOVA.

Results

Detection of Dof genes across the lima bean genome and physico-chemical characterization of respective proteins

Forty *PlDof* genes across the genome of lima bean were detected during the present study, and named as PlDof1-PlDof40 based on their location on the chromosome in the ascending order. *PlDof12* was recorded as the largest gene with 1560 bp CDS, 519 amino acids protein length (PL) and 57.126 kDa protein molecular weight (PMW), while *PlDof23*was found as the smallest one with only 522 CDS, 173 PI and 19.75 kDa PMW, respectively. Nucleus was predicted as a major residence for all PlDof proteins(Table 1). The predicted sub-cellular location of PlDof proteins has been visualized in Figure 1. Isoelectric points and GRAVY were found in the range of 5.35 to 8.91 and -0.269 to -0.746, respectively (Table 1)

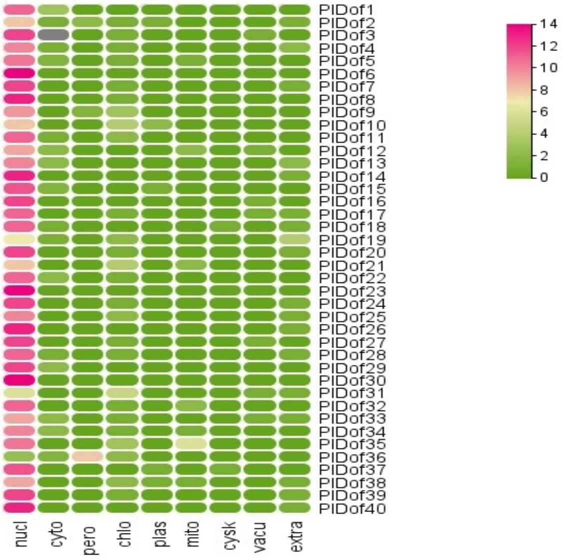


Figure 1. Wolf Psort-based sub-cellular localization of PlDof proteins. Quantitative heat map of the PlDof gene represents sub-cellular localization. The red bar represents a high quantity of proteins, and the green bar represents a low quantity of proteins.

Interspecific Phylogeny of PlDof Proteins

Seventy-six PlDof proteins across two different species, including *Phaseolus lunatus* and Arabidopsis *thaliana,* were clustered into 9sub-groups(A, B1, B2, C1, C2.1, C2.2, C3, D1, and D2). Sub-group A comprise 7 genes, Sub-group-B1 comprises 10 genes and Sub-group-B2 on 10 genes. Sub-group C1 comprise 8 genes, C2.1 have 9 genes, C2.2 have 5 genes, and C3 have 6 genes. Sub-group D1 has 17 genes and D2 have 4 genes. A total of 23 paralogs were found, and out of 23, P. lunatus has the maximum (13) paralogs, while A.thaliana has 10. Two orthologs were reported in Phaseolus lunatus and A.thaliana (Figure 2).

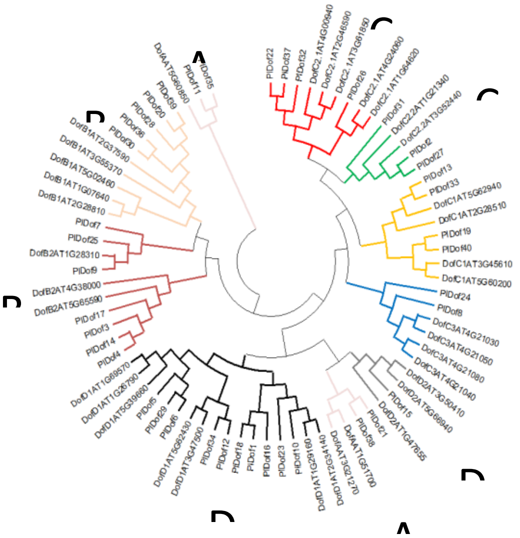


Figure 2. Comparative analysis of PlDof proteins across different plant species. A phylogenetic tree was constructed through MEGA 6.0 using the Maximum Likelihood (ML) method. Different subgroups are highlighted with different colours.

Chromosomal mapping and duplication of *PlDof* genes

Forty *PlDof* genes were unequally distributed on 11 chromosomes. Eight *PlDofs* (maximum) were placed on chromosome number 8, while only 1 *PlDof* (minimum) was found on chromosome number 4 (Figure 3). Segmental duplication was witnessed in all the paralog pairs (Figure 3). The Ka/Ks ratio was less than 1 for 12 paralogs, so they were under purifying selection, while no result was shown for Pl01G0000238000-Pl04G0000060700 paralog (Table 2)

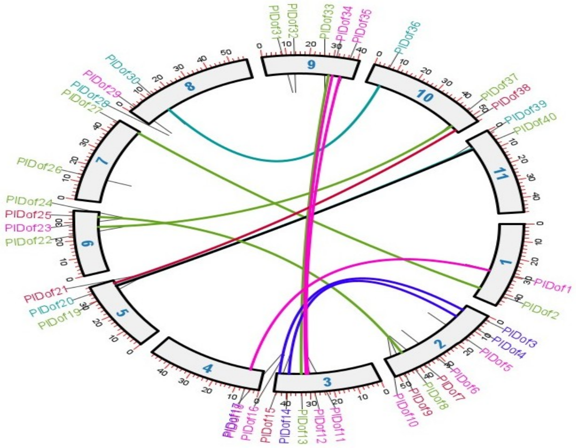
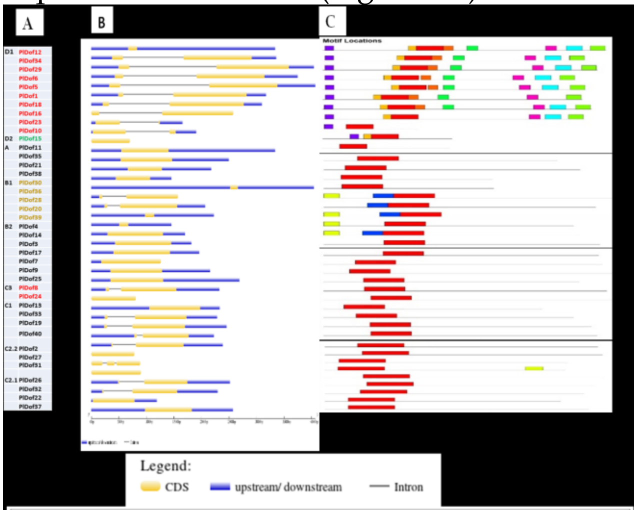


Figure 3. Chromosomal locations and duplication patterns of PlDof genes across the lima bean genome. The chromosome number is mentioned in each bar. Each line connects genes of a paralog pair.

PID of genes, structural motifs, and configuration

PIDof in phylogenetic tree were divided into nine sub-groups, including A, B1, B2, C1, C2.1, C2.2, C3, D1, and D2.The Sub-groups A, B1 and B2have 4, 5 and 7 genes, respectively. Similarly, sub-groups C1, C2.1, C2.2 and C3 comprise 4, 4, 3 and 2 genes, respectively. Ten genes were allocated to sub-group D1 and only 1 gene to D2 (Figure 4A). Each member of subgroups A, C3 and D2 has only 1 exon. The number of exons in members of subgroups B1 and C2.1 range from 1-2, while genes associated with C1 have 2 exons. All genes belonging to B2 have 1 exon, except PlDof25, with 2 exons. Similarly, each gene of subgroup D1 has 2 exons, except PlDof12 with 1 exon. Subgroup C2.2 has the widest range with 1-3 exons (Figure 4B). Maximum motifs (7) were detected in eight members of subgroup D1 with similar order and type, while only 1 motif (minimum) was found in each member of subgroups A, B2, C1, C2.1 and C3. All members belong to subgroup C2.2 have 1 motif except PlDof27, with 2 motifs (1 &10). Subgroup B1 revealed 3 motifs. A conserved motif1 was explored in all PlDofs (Figure 4C).



Motif	Symbol	Motif Consensus
1.	🟥	CPRCDSTNTKFCYYNNYSLSQPRHFCKTCRRYWTKGGTLRNVPVGGGCRK
2.	🟦	VLVPKTLRIDDPNEAAKSSIWATLGIKNE
3.	🟩	EKDRVVEASPVLZANPAALSRSLNFHE
4.	🟪	KDPAIKLFGRTIPLPE
5.	🟨	SZDKTLKKPDKILP
6.	🟩	FGPDPPLCDSMASVLNLAEK
8.	🟪	SPSSGPNSPTLGKHSRDGRI
9.	🟧	NKNSASHYRQITVSEALQ

Figure 4. Phylogenetic (A), gene structure (B) and motif analysis (C) of PIDof in lima bean.

Promoter Analysis

From PlantCARE, a total of 838 cis-acting regulatory elements were explored 1500bp upstream region of 40 *PlDof* genes. Cis-regulatory elements were dominated by light-responsive elements(52%), followed by hormone-responsive elements (27%), environmental stress (11%), developmental (8%), and site binding elements (2%)(Figure 5). The detection of a large number of cis-regulatory elements indicates the involvement of *PlDof* genes in functions with a major emphasis on growth and response to environmental stresses.

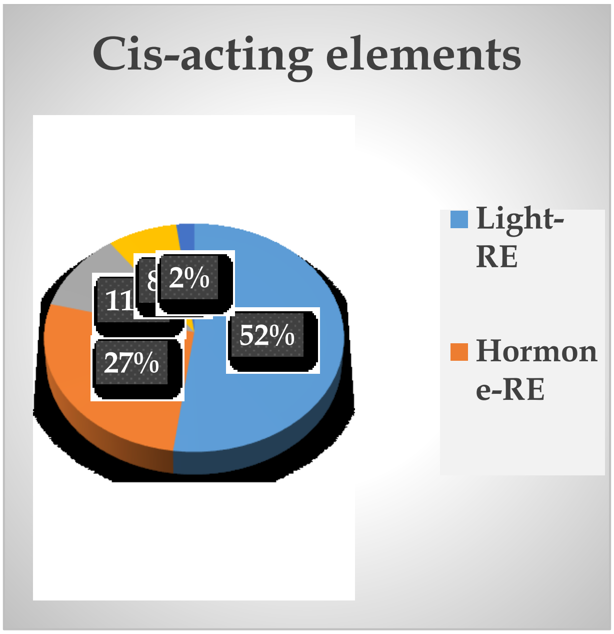


Figure 5: Different cis-regulatory elements (%) in the promoter region of PlDof genes

Discussion

Experimental evidence has unlocked the important role of Dof factors in regulating the expression of various genes major stresses; however, this family has remained unexplored in lima bean. In this study, 40 Dof genes were detected across the genome of lima bean, which is in line with reports of Cao *et al.* (2020) in Medicago sativa. However, the number of Dof detected in the current study is more than 28 reported in Eugenia uniflora (Waschburger *et al.*, 2022), 22 in spinach (Yu *et al.*, 2021) and 16 in tea (Yu *et al.*, 2020), 36 each in watermelon (Zhou *et al.*, 2020) and Areca catechu (Li *et al.*, 2022a), and 20 in Chrysanthemum morifolium (Song *et al.*, 2016). Similarly, the number of Dof explored in the current study is less than 45, as detected in pear (Liu *et al.*, 2020), and 103 in Camelina sativa (Luo *et al.*, 2022). The high number of Dof genes can partially be attributed to the large genome size under study.

The division of the Dof family into nine sub-groups based on their phylogeny with AtDofs was found in agreement with studies of Zhou *et al* (2020) and Li *et al.* (2022) conducted in Tartary buckwheat and watermelon, respectively. These results reflect the conservation of PlDof genes.

Lima bean exhibited some closeness with A. thaliana on account of showing 2 orthologs. The higher number of paralog detected in lima bean (13) than A. thaliana (10) reveal wider expansion of the PlDof family.

Less than 1 of the Ka/Ks ratio, for PlDof paralogs, pointing towards a segmental pattern of duplication. The negative GRAVY value of PlDofs (-0.269 to -0.746) shows its hydrophilic nature and its solubility in water. The results about the Ka/Ks ratio and GRAVY are in agreement with Brian et al.(2021) and Chen *et al.*(2023), respectively. The pI range of PlDofs (5.11-9.77) in the present study strengthened earlier reports of Cai *et al.* (2024) in PsDofs.

The existence of highly conserved Dof domains in PlDof factor, as reflected in the present study, highlights the conservation of Dof transcription factors in plants during the course of evolution. Though a differential distribution of 10 motifs among PlDofs was witnessed, motif 1 was present across all members of the PlDof family. The results about the number of introns in PlDof genes (0-2) were found in agreement with Wu *et al.* (2016), and Kushwaha *et al.* (2011) reported in pepper (0–2) and sorghum (0–2), respectively. These results indicate a relatively stable structure of PlDof genes.

Cis-acting elements associated with hormonal response, plant growth and development, abiotic stresses, particularly light, drought, high and low temperatures, were found abundantly in promoters of PlDof genes. The study of these elements is crucial for understanding the pattern of gene expression in response to the respective stresses or growth attributes. Closely resembling the cis-acting elements have been reported by Liu *et al.* (2020) and Cao *et al.* (2022) in wheat and lotus, respectively.

Conclusions and recommendations

The in silico analysis revealed 40 PlDof genes in lima bean. The protein length, pI, molecular mass, Gene structure and subcellular localization of PlDof protein synchronized with previous reported Dofs.

1. The gene duplication events contributed 33% to the expansion of the PlDof gene family.
2. The ka/ks ratio was less than 1 for all the paralogs, revealing a segmental pattern of duplication.
3. The detection of many cis-acting elements in the upstream region of PIDof uncovered its association with diverse functions.

Functional validity of all PIDof genes, explored in the current study, is recommended.

References

Adebo JA (2023) A review on the potential food application of lima beans (Phaseolus lunatus L.), an underutilized crop. *Appl. Sci. 13*(3), 1996.

Bailey TL, Williams N, Misleh C, Li W (2006) MEME: discovering and analyzing DNA and protein sequence motifs. Nucleic Acids Res. 37, W202–W208

Baudoin, J. P., Rocha, O., Degreef, J., Maquet, A., & Guarino, L. (2006). Phaseolus lunatus L. *Prota. 1.*

Brian L, Warren B, McAtee P, Rodrigues J, Nieuwenhuizen N, Pasha A (2021) A gene expression atlas for kiwifruit (Actinidia chinensis) and network analysis of transcription factors. BMC Plant Biol. 21, 121

Cai X, Zhang C, Shu W, Ye Z, Li H, Zhang Y (2016) The transcription factor Sldof22 involved in ascorbate accumulation and salinity stress in tomato. Biochem. Biophys. Res. Commun. 474, 736–741

Cao B, Cui Y, Lou K, Luo D, Liu Z, Zhou Q (2020) Genome-wide identification and expression analysis of the dof gene family in medicago sativa L. under various abiotic stresses. DNA Cell Biol. 39, 1976–1989

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

Chen G, Xu Y, Gui J, Huang Y, Ma F, Wu W (2023) Characterization of Dof transcription factors and the heat-tolerant function of peDof-11 in passion fruit (Passiflora edulis). Int. J. Mol. Sci. 24, 12091

Corrales AR, Nebauer SG, Carrillo L, Fernández-Nohales P, Marqués J, Renau-Morata B, Granell A, Pollmann S, Vicente-Carbajosa J, Molina RV (2014) Characterization of tomato cycling Dof factors reveals conserved and new functions in the control of flowering time and abiotic stress responses. J. Exp. Bot. 65, 995–1012

Dong C, Hu H, Xie J (2016) Genome-wide analysis of the DNA-binding with one zinc finger (Dof)Transcription factor family in bananas. Genome 59, 1085– 1100

Fornara F, Panigrahi KC, Gissot L, Sauerbrunn N, Rühl M, Jarillo JA, Coupland G (2009) Arabidopsis DOF transcription factors act redundantly to reduce CONSTANS expression and are essential for a photoperiodic flowering response. Dev. Cell *17*(1), 75-86

Gasteiger E, Gattiker A, Hoogland C, Ivanyi I, Appel RD, Bairoch A (2003) ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Res. *31*(13), 3784-3788

Goodstein DM, Shu S, Howson R, Neupane R, Hayes RD, Fazo J, Mitros T, Dirks W, Hellsten U, Putnam N, Rokhsar DS (2012) Phytozome: a comparative platform for green plant genomics. Nucleic Acids Res 40(D1):D1178–D1186

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

Jin Z, Chandrasekaran U, Liu A (2014) Genome-wide analysis of the Dof transcription factors in castor bean (Ricinus communis L.). *Genes & Genomics*, *36*(4), 527-537.

Kang WH, Kim S, Lee HA, Choi D, Yeom SI (2016) Genome-wide analysis of DOF transcription factors reveals functional characteristics during development and response to biotic stresses in pepper. Sci. Rep. 6, 33332

Kasirajan L, Hoang NV, Furtado A, Botha FC, Henry RJ (2018) Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fibre content. Sci. Rep. 8, 11612

Kondhare KR, Vetal PV, Kalsi HS, Banerjee AK (2019) Bel1-like protein (Stbel5) regulates cycling of Factor1 (Stcdf1) through tandem tgac core motifs in potato. J. Plant Physiol. 241, 153014

Kumar S, Stecher G, Tamura K (2016) MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol 33(7):1870–1874

Kushwaha H, Gupta S, Singh VK, Rastogi S, Yadav D (2011) Genome-wide identification of Dof transcription factor gene family in sorghum and its comparative phylogenetic analysis with rice and Arabidopsis. Mol. Biol. Rep. 38, 5037–5053

Lescot M, Déhais P, Thijs G, Marchal K, Moreau Y, Van de Peer Y, Rouzé P, Rombauts S (2002) PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. Nucleic Acids Res 30(1):325–327

Li J, Jia X, Yang Y, Chen Y, Wang L, Liu L (2022a) Genome-wide identification of the dof gene family involved in fruitlet abscission in Areca catechu L. Int. J. Mol. Sci. 23, 11768

Li J, Zhang Y, Xu L, Wang C, Luo Y, Feng S (2022b) Genome-wide identification of DNA binding with one finger (Dof) gene family in tartary buckwheat (Fagopyrum tataricum) and analysis of its expression pattern after exogenous hormone stimulation. Biol. (Basel) 11, 173

Li T, Wang X, Elango D, Zhang W, Li M, Zhang F (2022b) Genome-wide identification, phylogenetic and expression pattern analysis of Dof transcription factors in blueberry (Vaccinium corymbosum L.). PeerJ 10, e14087

Liu W, Ren W, Liu X, He L, Qin C, Wang P, Ma W (2023) Identification and characterization of Dof genes in Cerasus humilis. *Front. Plant. Sci. 14*, 1152685.

Liu X, Liu Z, Hao Z, Chen G, Qi K, Zhang H (2020). Characterization of the Dof family in Pyrus bretschneideri and role of Pbdof9.2 in flowering time regulation. Genomics 112, 712–720

Liu X, Liu Z, Hao Z, Chen G, Qi K, Zhang H (2020) Characterization of the dof family in Pyrus bretschneideri and role of Pbdof9.2 in flowering time regulation. Genomics 112, 712–720

Liu Y, Liu N, Deng X, Liu D, Li M, Cui D (2020) Genome-wide analysis of wheat DNA-binding with one finger (Dof) transcription factor genes: evolutionary characteristics and diverse abiotic stress responses. BMC Genomics 21, 1–18

López-Alcocer JDJ, Lépiz-Ildefonso R, González-Eguiarte DR, Rodríguez-Macías R, López-Alcocer E (2016) Morphological variability of wild Phaseolus lunatus L. from the western region of México. *Rev. Fitotec. Mex 39*(1), 49-58

Luo T, Song Y, Gao H, Wang M, Cui H, Ji, C (2022) Genome-wide identification and functional analysis of the dof transcription factor family in camelina sativa. BMC Genomics 23, 812.

Martínez-Castillo J, Camacho Pérez L, Villanueva Viramontes S, Andueza Noh RH, Chacón Sánchez M I (2014) Genetic structure within the Mesoamerican gene pool of wild Phaseolus lunatus (Fabaceae) from Mexico as revealed by microsatellite markers: implications for conservation and the domestication of the species. Am. J. Bot. *101*(5), 851-864.

Nascimento MDGR, Alves EU, Silva ML, Rodrigues C (2017) Lima bean (Phaseolus lunatus L.) seeds exposed to different salt concentrations and temperatures. *Rev. Caatinga*, *30*, 738-747.

Noguero, M., Atif, R. M., Ochatt, S., and Thompson, R. D. (2013). The role of the DNA-binding one zinc finger (Dof) transcription factor family in plants. Plant Sci. 209, 32–45

Park DH, Lim PO, Kim JS, Cho DS, Hong SH, Nam HG (2003) The Arabidopsis Cog1 gene encodes a Dof domain transcription factor and negatively regulates phytochrome signalin. Plant J. 34, 161–171

Plesch G, Ehrhardt T, Mueller-Roeber B (2001). Involvement of TAAAG elements suggests a role for Dof transcription factors in guard cell-specific gene expression. Plant J. *28*(4), 455-464.

Ramachandran V, Tobimatsu Y, Masaomi Y, Sano R, Umezawa T, Demura T (2020) Plant-specific dof transcription factors vascular-related Dof1 and vascular-related Dof2 regulate vascular cell differentiation and lignin biosynthesis in Arabidopsis. Plant Mol. Biol. 104, 263–281

Sá FVS, Oliveira FS, Torres SB, Paiva EP, Nogueira NW, Sarmento ECS, Melo, AS (2021) Hydric and saline stress on Phaseolus lunatus L. seeds.Braz. J. Biol. *82*, e233550.

Song A, Gao T, Li P, Chen S, Guan Z, Wu D (2016) Transcriptome-wide identification and expression profiling of the dof transcription factor gene family in chrysanthemum morifolium. Front. Plant Sci

Su Y, Liang W, Liu Z, Wang Y, Zhao Y, Ijaz B, Hua J (2017) Overexpression of GhDof1 improved salt and cold tolerance and seed oil content in Gossypium hirsutum. *J. Plant. Physiol*. *218*, 222-234.

Tang J, Zhao Y, Qi S, Dai Q, Lin Q, Duan Y (2022) Abscisic acid alleviates chilling injury in cold-stored peach fruit by regulating ethylene and hydrogen peroxide metabolism. Front. Plant Sci. 13

Wang Y, Tang H, Debarry JD, Tan X, Li J, Wang X (2012) Mcscanx: A toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Res. 40, e49

Waschburger EL, Guzman F, Turchetto-Zolet AC (2022) Genome-wide identification and analysis of the dof gene family in Eugenia uniflora L. (Myrtaceae). Genes (Basel) 13, 2235

Wolfe D, Dudek S, Ritchie MD, Pendergrass SA (2013) Visualizing genomic information across chromosomes with PhenoGram. BioData Min 6(1):1–12

Wu Z, Cheng J, Cui J, Xu X, Liang G, Luo X (2016) Genome-wide identification and expression profile of the dof transcription factor gene family in pepper (Capsicum annuum L.). Front. Plant Sci. 7

Yanagisawa, S (2004). Dof domain proteins: Plant-specific transcription factors associated with diverse phenomena unique to plants. Plant Cell Physiol. 45, 386–391

Yang G, Yu L, Wang Y, Wang C, Gao C (2017) The translation initiation factor 1a (Theif1a) from tamarix hispida is regulated by a Dof transcription factor and increased abiotic stress tolerance. Front. Plant Sci. 8

Yu H, Ma Y, Lu Y, Yue J, Ming R (2021) Expression profiling of the dof gene family under abiotic stresses in spinach. Sci. Rep. 11, 14429

Yu Q, Li C, Zhang J, Tian Y, Wang H, Zhang Y (2020) Genome-wide identification and expression analysis of the dof gene family under drought stress in tea (Camellia sinensis). PeerJ 8, e9269

Zhai Z, Xiao Y, Wang Y, Sun Y, Peng X, Feng C (2022) Abscisic acid-responsive transcription factors Pavdof2/6/15 mediate fruit softening in sweet cherry. Plant Physiol. 190, 2501–2508

Zhang A, Matsuoka K, Kareem A, Robert M, Roszak P, Blob B (2022) Cell-wall damage activates Dof transcription factors to promote wound healing and tissue regeneration in Arabidopsis thaliana. Curr. Biol. 32, 1883–1894, e1887

Zhang A, Wang W, Tong Y, Li M, Grierson D, Ferguson I (2018) Transcriptome analysis identifies a zinc finger protein regulating starch degradation in kiwifruit. Plant Physiol. 178, 850–863

Zhang A, Zhang Q, Li J, Gong H, Fan X, Yang Y (2020) Transcriptome Co-expression network analysis identifies key genes and regulators of ripening kiwifruit ester biosynthesis. BMC Plant Biol. 20, 103

Zhao Q, Dixon RA (2011) Transcriptional networks for lignin biosynthesis: More complex than we thought? Trends Plant Sci. 16, 227–233

Zhou Y, Cheng Y, Wan C, Li J, Yang Y, Chen J (2020) Genome-wide characterization and expression analysis of the dof gene family related to abiotic stress in watermelon. PeerJ 8, e8358