



Genetic Basis and Identification of Candidate Genes for Drought Tolerance in *Oryza sativa* L. by DNA Molecular-assisted Selection

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ABSTRACT

Background: Drought stress represents a major obstacle to ensuring worldwide agricultural output and food availability. As a primary dietary staple, rice is highly vulnerable to insufficient water, suffering significant productivity declines under drought pressure. Gaining insight into plant mechanisms of coping with drought is essential for creating future cultivars adapted to limited water access.

Methods: This investigation focuses on large-scale discovery and assessment of ten drought-resilient genes in *Oryza sativa* L. Information on these genes was gathered from publicly accessible platforms, including the National Center for Biotechnology Information (NCBI) and examined through bioinformatics approaches such as the basic local alignment search tool (BLAST) searches and protein interaction mapping.

Result: Findings confirmed the presence of ten genes actively engaged in modulating drought-associated biological responses. Additional transcription factors were pinpointed, highlighting their critical role in amplifying adaptation to water deficit. The research highlights the utility of computational genomics for rapidly identifying candidate drought-resilient genes, thus presenting a framework for targeted breeding strategies aimed at producing rice varieties better adapted to climate variability and water limitation.

Key words: Gene transcripts, Genomic regions, NCBI, Phylogenetic, Plant, Proteins, Tolerance genes.

INTRODUCTION

Oryza sativa L. (rice) is recognised as the most vital staple in the developing world (Mandal *et al.* 2019) and source of dietary fibre, minerals, vitamins, proteins and carbohydrates (Olivya *et al.*, 2025), though its overall productivity and yield reliability remain highly vulnerable to environmental stresses (Chengqi *et al.*, 2024). Feeding more than half of humanity, rice is indispensable, yet its production is drastically reduced under drought conditions. While traditional landraces display wide-ranging morphological, physiological and molecular traits that confer resilience to water scarcity, many modern high-yielding cultivars show pronounced sensitivity to drought stress (Yadav *et al.*, 2023). Drought represents one of the most critical environmental challenges, with nearly 50% of global rice output estimated to be directly affected by insufficient water availability (Sircar and Parekh, 2019). Furthermore, drought prompts the build-up of osmo-protective compounds such as proline, sugars, polyamines and antioxidants, while also modifying gene expression patterns, particularly those of transcription factors and stress-related proteins, ultimately diminishing crop productivity. To withstand such effects, rice plants employ strategies including drought avoidance, drought escape and drought tolerance-mechanisms aimed at mitigating damage caused by water stress (Kumar *et al.*, 2022).

The ongoing shifts in climate are intensifying land degradation, advancing desert expansion and increasing soil salinity-processes which are severely diminishing cultivable areas and agricultural productivity. This issue is especially urgent given the steadily rising global population (González, 2023).

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Abiotic stresses like salinity, drought and temperature are expected to get worse because of climate change. This will have a negative impact on crop plants, especially rice plants and lower their output (Mohapatra and Saho, 2025). Among abiotic stressors, drought ranks as a major constraint on crop yields across the globe and its severity is escalating with changing climate patterns. At any point in a plant's life cycle, drought exerts harmful and yield-suppressing effects, ultimately threatening survival. Like other environmental challenges, exposure to water deficit provokes a cascade of molecular, physiological and biochemical adjustments that attempt to counteract drought pressure (Oguz *et al.*, 2022). Droughts have become more common because of global warming and big changes in the climate (Xu *et al.*, 2025)

Plants have gradually developed a broad spectrum of defensive strategies for mitigating the damage caused by

biotic and abiotic constraints (Alhasnawi, 2019). Of these, drought stands out as the most destructive abiotic factor, generating severe reductions in productivity worldwide. Water deficit induces osmotic stress, which lowers chlorophyll and relative water levels while increasing osmolyte build-up, epicuticular wax deposition, antioxidant enzyme function, reactive oxygen species formation, secondary metabolite accumulation, lipid membrane oxidation and abscisic acid activity (Ahmad *et al.*, 2022).

It must be emphasised that these adaptive strategies enabling plants to withstand drought stress are controlled by numerous genes. Thus, pinpointing the specific genes which improve drought resilience is essential for maintaining yield stability within global crop production systems (Hura *et al.*, 2022).

For these reasons, it is imperative to investigate the molecular genetic framework underlying drought resistance in rice through advanced bioinformatics methods. The stress-responsive genes are classified as genes encoding proteins engaged in osmolyte biosynthesis (proline, mannitol, glycine betaine, trehalose, *etc.*), protective proteins (heat shock proteins and late embryogenesis abundant proteins, *etc.*), transcription factors (WRKY, DREB, ERF, MYC, MYB, bZIP, NAC, GRAS, *etc.*), antioxidant enzymes (superoxide dismutase, ascorbate peroxidase, catalase, glutathione S-transferases, glutathione reductase, *etc.*) and phytohormones (auxin, abscisic acid, jasmonic acid, ethylene, *etc.*) (Srivastava *et al.*, 2022). Genetic diversity is important for breeding projects that want to create new types of rice (Kumar *et al.*, 2025). The different genotypes' genetic diversity is an important tool for breeding programs because it helps create new farming systems and increase output diversity (Rai *et al.*, 2025).

Advances in transcriptome profiling, along with improved computational resources, have enabled bioinformatics-driven identification of rice genes potentially linked to drought resistance by comparison with previously characterised drought-associated genes. Using a sub-network extraction algorithm combined with gene co-expression data, we constructed an integrated interaction network encompassing both well-identified drought-responsive rice genes and putative ones (Gao *et al.*, 2020).

In the present work, a variety of computational platforms and omics-based approaches were employed to explore molecular factors and biological pathways that underlie drought tolerance in rice. The primary aim was to analyse and contrast drought-resilient genes across diverse rice cultivars through bioinformatics pipelines in order to pinpoint critical genetic determinants contributing to drought adaptation. These findings are expected to provide a valuable resource for gene discovery relevant to drought tolerance. Moreover, this analytical framework can clarify functional interconnections among genes involved in the multifaceted drought stress response in rice, while also serving as a comparative reference point for extending similar investigations in other agriculturally important crop species.

MATERIALS AND METHODS

Data collection

The research was conducted at Department of Biology, College of Education for Pure Sciences, Al-Muthanna University in 2025 to identify genes associated with drought tolerance in *Oryza sativa* L. using different drought-responsive genes from the National Center for Biotechnology Information (NCBI) database. The study included molecular responses using indicators and genes related to drought stress.

Known drought-responsive genes contributing to tolerance in rice, specifically *Oryza sativa* L., were identified and retrieved from the National Center for Biotechnology Information (NCBI) database. The collected data were then used to compile essential details regarding these rice genes, while homology-based comparisons allowed assessment of their chromosomal distribution across ten gene symbols.

Utilising these data, we have summarised the generic information regarding the genes in *Oryza sativa* L. and on the basis of the homology information, we have compared the location of the ten gene symbols for drought tolerance, including LOC4323843, LOC4337576, LOC4343219, LOC4347708, LOC4346460, LOC4345942, LOC4327045, LOC4325652, LOC4334350 and LOC4326935. Ten genomic context datasets and sequences remain distinct from specific genome assemblies. Both messenger ribonucleic acid (mRNA) and protein sequences are widely applied in computational studies to derive evolutionary insights into drought tolerance in *Oryza sativa* L.

Sequence alignment

Sequence comparisons of analysed clones with drought-related candidate genes in *Oryza sativa* L. were carried out through multiple sequence alignment using NCBI resources. The NCBI platform provides the basic local alignment search tool (BLAST) utilities that enable gene sequence queries, serving as a key bioinformatics method for assessing protein similarities. This approach highlights conserved domains and sequence variations, thereby offering insights into evolutionary linkages as well as functional stability among proteins implicated in drought tolerance mechanisms.

Phylogenetic analysis

Phylogenetic relationships were inferred using the distance-matrix neighbour-joining approach. Gene sequences associated with drought tolerance in *Oryza sativa* L. were first aligned and evolutionary trees were then generated through molecular evolutionary genetics analysis (MEGA) software (Version 11.013, 1993-2025) to examine divergence and conservation patterns among drought-responsive genes.

In addition, homologs of experimentally verified salinity tolerance genes were identified. Corresponding nucleotide sequences were retrieved either from GenBank or directly

from contributing authors, followed by BLAST analysis to detect homologous counterparts. This process enabled recognition of related sequences, expanding the genetic framework for understanding stress adaptation mechanisms in rice.

RESULTS AND DISCUSSION

Bioinformatics analysis was employed to identify drought-resilient genes, focusing on a selected group of ten gene symbols in *Oryza sativa* L. The findings summarised in Table 1 highlight several rice genes critically associated with tolerance to water deficit. The table lists 10 specific genes demonstrated to play significant roles in mediating the plant's adaptive responses to drought-induced stress. The identified gene symbols include LOC4323843, LOC4337576, LOC4343219, LOC4347708, LOC4346460, LOC4345942, LOC4327045, LOC4325652, LOC4334350 and LOC4326935. All identified genes were classified as protein-coding and verified under the Reference Sequence (RefSeq) database's categories (validated or model), ensuring the accuracy of their reference sequence information.

Each gene occupies a unique chromosomal position and is annotated with an individual locus tag, such as OSNPB_010971100 for LOC4323843, OSNPB_050107900 for LOC4337576, OSNPB_070476900 for LOC4343219, OSNPB_090537700 for LOC4347708, OSNPB_090133600 for LOC4346460, OSNPB_080499800 for LOC4345942, OSNPB_010785700 for LOC4327045, OSNPB_010184900 for LOC4325652, OSNPB_030786400 for LOC4334350 and OSNPB_010702500 for LOC4326935. All analysed genes originate from the *Oryza sativa* Japonica group and each is associated with several alternative designations recorded across scientific references and databases, such as DI19-5, OsDi19-5, OsJ_004810 and P0518C01.8 for LOC4323843; DI1, DI19-6, OsDi19-6 and

OsJ_016081 for LOC4337576; cdsp32, OsCDSP32 and OsJ_24223 for LOC4343219; PAP2 for LOC4346460; OJ1118_A06.9 for LOC4345942; R1G1A, bip104, SSRP1-A and OsJ_00664 for LOC4325652; and rDRP1 and rab25 for LOC4326935; signifying the terminological variations in gene naming for drought tolerance (Table 1).

The genomic context analysis of Chromosome 1 - NC_089035.1, Chromosome 5 - NC_089039.1, Chromosome 7 - NC_089041.1, Chromosome 9 - NC_089043.1, Chromosome 9 - NC_089043.1, Chromosome 8 - NC_089042.1, Chromosome 1 - NC_089035.1, Chromosome 1 - NC_089035.1, Chromosome 3 - NC_089037.1, and Chromosome 1 - NC_089035.1 indicated a high density of drought-responsive loci distributed along proximal as well as distal regions. Multiple candidate genes were identified, notably including transcription factor family members, which show strong associations with tolerance to abiotic stresses (Fig 1A-1J).

The observed clustering of stress-responsive genes within syntenic chromosomal regions indicates the presence of potential regulatory hubs supporting adaptive functions. Furthermore, conserved promoter motifs and cis regulatory sequences were identified upstream of these candidate loci, underscoring their likely involvement in transcriptional control during water-deficit stress. Collectively, chromosome 1 emerges as a pivotal genomic region governing several drought-resilience pathways in rice.

Ten rice genes encoding proteins implicated in drought stress resistance were further characterised by mapping gene identifiers to corresponding symbols and compiling details regarding their gene sequences and protein products. Transcript sizes ranged from 994 nucleotides in LOC4323843 to 2529 nucleotides in LOC4325652. At the protein level, polypeptide lengths spanned from 202 amino acids (LOC4323843) to 641

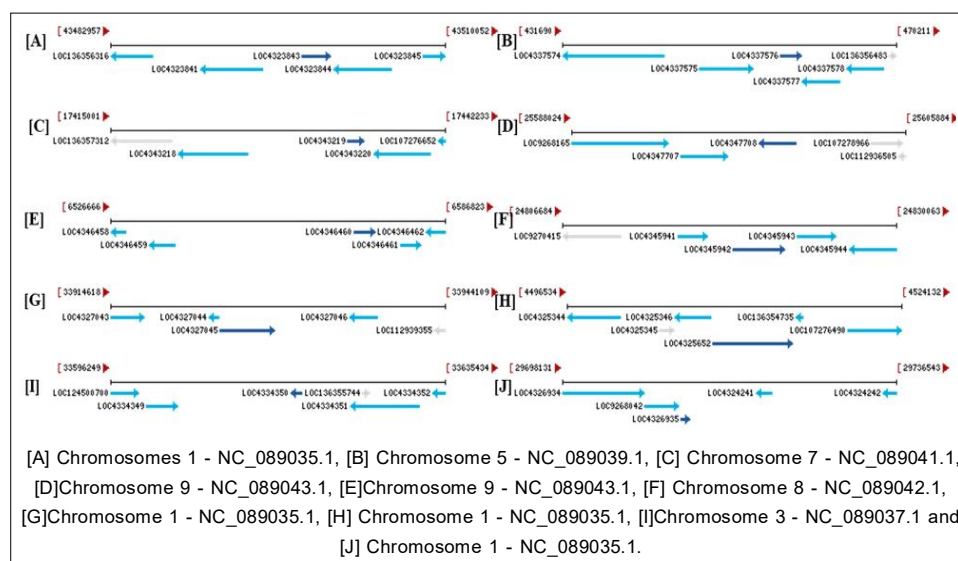


Fig 1: Genomic context sections of the chromosomes.

Table 1: A gene symbol provides information about gene description, locus tag, gene type, RefSeq status and organism in *Oryza sativa* L. for improved drought tolerance.

Gene symbol	Gene description	Locus tag	Gene type	RefSeq status	Organism	Also known as
LOC 4323843	Protein dehydration-induced homolog 5-like	OSNPB_010971100	Protein coding	Validated	<i>Oryza sativa</i> japonica group	DI19-5; OsDI19-5; OsJ_004810; P0518C01.8
LOC 4337576	Protein dehydration- induced homolog 6-like	OSNPB_050107900	Protein coding	Validated	<i>Oryza sativa</i> japonica group	DI1; DI19-6; OsDI19-6; OsJ_016081
LOC 4343219	Thioredoxin-like protein CDSP32, chloroplastic	OSNPB_070476900	Protein coding	Validated	<i>Oryza sativa</i> japonica group	cdsp32; OsCDSP32; OsJ_24223
LOC 4347708	Ribonuclease 3	OSNPB_090537700	Protein coding	Model	<i>Oryza sativa</i> japonica group	-
LOC 4346460	probable plastid-lipid-associated protein 2, chloroplastic	OSNPB_090133600	Protein coding	Validated	<i>Oryza sativa</i> japonica group	PAP2
LOC 4345942	Pentatricopeptide repeat-containing protein At1g80150, mitochondrial	OSNPB_080499800	Protein coding	Model	<i>Oryza sativa</i> japonica group	OJ1118_A06.9
LOC 4327045	Small ribosomal subunit protein mS78 (rPPR3a)	OSNPB_010785700	Protein coding	Model	<i>Oryza sativa</i> japonica group	-
LOC 4325652	FACT complex subunit SSRP1-A-like	OSNPB_010184900	Protein coding	Validated	<i>Oryza sativa</i> japonica group	R1G1A; bip104; SSRP1-A; OsJ_00664
LOC 4334350	Zinc finger protein GIS3	OSNPB_030786400	Protein coding	Model	<i>Oryza sativa</i> japonica group	-
LOC 4326935	Dehydrin Rab25-like	OSNPB_010702500	Protein coding	Validated	<i>Oryza sativa</i> japonica group	rDRP1; rab25

amino acids (LOC4325652). These variations demonstrate extensive structural and functional diversity among drought-associated genes and their encoded proteins, with findings summarised in Table 2.

The genomic context analysis of genomic sequences LOC4323843, LOC4337576, LOC4343219, LOC4347708, LOC4346460, LOC4345942, LOC4327045, LOC4325652, LOC4334350 and LOC4326935 revealed that these loci are positioned within drought-responsive regions and encode transcripts containing predicted regulatory and functional domains linked to stress adaptation. The constructed gene models display distinct exon–intron structures, generating transcripts that are translated into proteins carrying conserved motifs associated with abiotic stress signalling pathways. Functional annotation further indicates that these products may operate as transcriptional regulators or stress-responsive proteins, thereby contributing to cellular stability under conditions of water scarcity. Additionally, surrounding genomic regions harbour other stress-related genes, indicating potential co-regulation or coordinated expression patterns during drought exposure (Fig 2A-2J).

The examined gene data were cross-referenced with standard databases to retrieve complete mRNA and protein sequences, along with source sequence details and UniProt accession numbers. Analyses demonstrated that each gene possesses dual identifiers corresponding to both its mRNA transcript and encoded protein, such as NP_001359124.1, NP_001406959.1, P_001409084.1, P_015651317.1, NP_001390665.1, XP_015648389.1, XP_015622164.1, NP_001388399.1, XP_015628802.1 and NP_001393222.1. This highlights the reliability of molecular characterisation for these genes within genomic repositories (Table 3).

The results in Table 4 and Table 5 depict that the source sequence for every gene is also documented, for instance, AK069516 and AU057067 for LOC4323843; AP014961, AY335486 and EG709698 for LOC4337576; AU172639, CB653462, CI167083, CI286584 and CI688566 for LOC4343219; A0A0P0XPV8, A2Z3I6, A3C107, Q69JX7 and Q940D3 for LOC4347708; CA754409, CB678401 and CI199149 for LOC4346460; AB117991, AK068832 and AK068959 for LOC4325652; and AY333185 for LOC4326935. The UniProt Knowledgebase's (UniProtKB) TrEMBL database also contains corresponding entries, which are automatically generated protein sequences, thereby broadening the scope of the analysis and facilitating monitoring of predicted protein models. Such integration improves the dependability of datasets used in functional annotation and diagnostic assessments of genes. Moreover, these findings represent a critical step in clarifying links between nucleotide sequence and protein architecture, ultimately supporting the development of computational diagnostic tools for drought stress resilience.

A phylogenetic tree was generated using alignment scores for NC_089035.1, NC_089039.1, NC_089041.1,

Table 2: List of gene transcripts and proteins in *Oryza sativa* L. for improved drought tolerance.

Gene ID	Symbol	Transcript	Length (nt)	Protein	Length (aa)	Protein name
4323843	LOC4323843	NM_001372195.1	994	NP_001359124.1	202	Protein dehydration - induced 19 homolog 5
4337576	LOC4337576	NM_001420030.1	1007	NP_001406959.1	208	protein dehydration - induced 19 homolog 6
4343219	LOC4343219	NM_001422155.1	1413	NP_001409084.1	301	Thioredoxin-like protein CDSF32, chloroplastic
4347708	LOC4347708	XM_015795831.3	1090	XP_015651317.1	252	Ribonuclease 3
4346460	LOC4346460	NM_001403736.1	1345	NP_001390665.1	319	Probable plastid-lipid-associated protein 2, chloroplastic
4345942	LOC4345942	XM_015792903.3	2358	XP_015648389.1	443	Pentatricopeptide repeat-containing protein
4327045	LOC4327045	XM_015766678.3	1632	XP_015622164.1	434	At1g80150, mitochondrial
4325652	LOC4325652	NM_001401470.1	2529	NP_001388399.1	641	Small ribosomal subunit protein mS78 (rPPR3a)
4334350	LOC4334350	XM_015773316.3	1267	XP_015628802.1	301	fACT complex subunit SSRP1-A
4326935	LOC4326935	NM_001406293.1	1015	NP_001393222.1	228	Zinc finger protein GIS3
						Dehydrin Rab25

NC_089043.1, NC_089043.1, NC_089042.1, NC_089035.1, NC_089035.1, NC_089037.1 and NC_089035.1, revealing a close evolutionary association between the genomic sequences. The clustering arrangement demonstrates strong sequence conservation, indicating probable functional similarity and shared evolutionary origins. Branch length measurements displayed limited divergence, reinforcing the hypothesis that these loci trace back to a common ancestral gene. Furthermore, the grouping of these sequences within the same phylogenetic clade emphasises their likely contribution to preserving conserved biological roles, potentially linked to mechanisms of drought tolerance. This conserved evolutionary signature offers additional support for the functional relevance of these genomic loci in *Oryza sativa* L. (Fig 3A-3J).

Plants adapt to environmental challenges by modulating their physiological processes and developmental programs through genome-wide changes in gene expression. Epigenetic regulators, including deoxyribonucleic acid (DNA) methylation and demethylation, are thought to exert critical influence in this process (Wang *et al.*, 2011). The degree of drought tolerance exhibited by any plant species is largely determined by the presence and efficiency of genetic mechanisms underlying adaptation (Kim *et al.* 2020). Bioinformatics-based platforms and analytical tools are highly valuable for evaluating plant responses to abiotic stressors (Neelapu and Chaitanya, 2024).

High-throughput technologies, such as RNA sequencing (RNA-seq), enable detailed profiling of differential gene expression, offering insights into genes central to stress resilience. The integration of bioinformatics, genomics and next-generation sequencing provides a deeper understanding of molecular pathways responsible for tolerance to diverse stress conditions. Such knowledge can be strategically applied to accelerate the breeding of stress-resilient crops and to enhance both yield performance and crop quality (Mu *et al.*, 2022).

This research applied an integrative bioinformatics framework to uncover multiple drought-associated candidate genes, including regulatory transcription factors and functional enzymes, using publicly accessible rice transcriptome datasets. The outcomes support the prevailing model in which drought resilience arises from a complex genetic network controlling traits such as stomatal regulation, deep root systems and cellular equilibrium (Kumar *et al.*, 2015). The capacity to interrogate multi-omics datasets computationally facilitates systematic dissection of this multifactorial trait.

A key strength of the approach was the incorporation of co-expression network methodologies, notably weighted gene co-expression network analysis (WGCNA). This enabled identification of complete gene modules strongly associated with drought-related traits, extending beyond traditional differential expression analysis. Central hub genes within these modules, such as protein kinases mediating signalling events, were recognised as high-

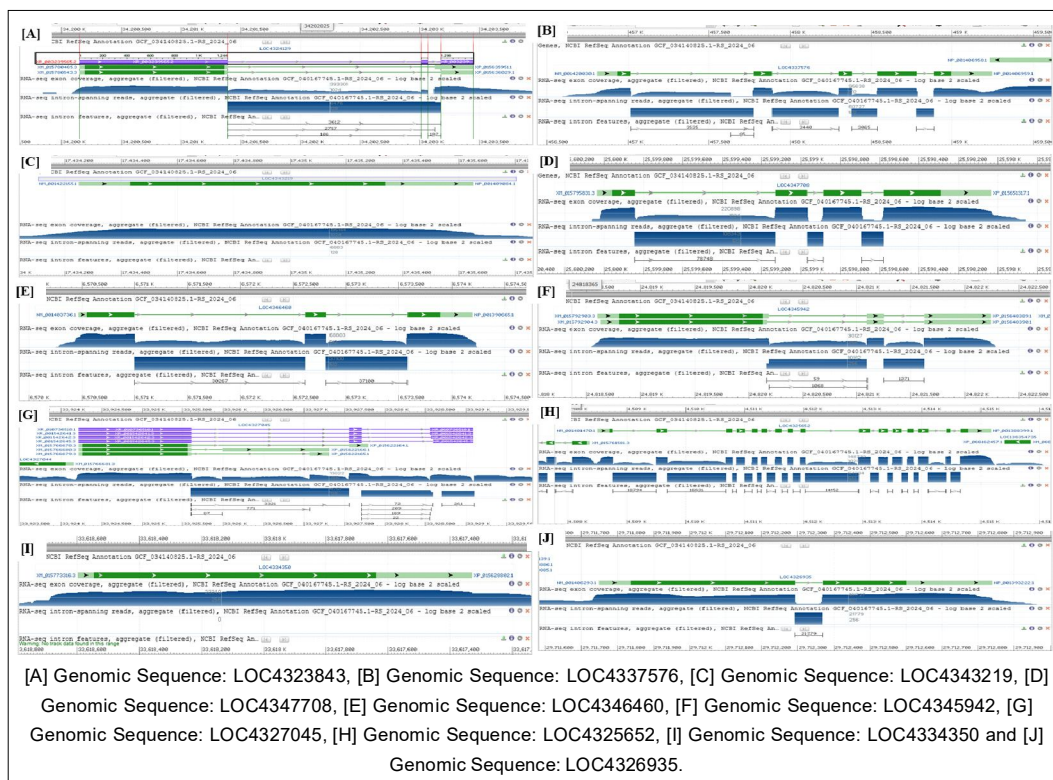


Fig 2: Genomic regions, transcripts and products.

Table 3: These reference sequences exist independently of genome builds mRNA and protein(s).

Gene ID	mRNA and protein	Source sequence (s)	UniProtKB/ swiss-Prot	UniProtKB/ TrEMBL
4323843	NM_001372195.1 → NP_001359124.1 protein dehydration-induced 19 homolog 5	AK069516, AU057067	B7EGH2, Q5JME8	A2WZJ8
4337576	NM_001420030.1 → NP_001406959.1 protein dehydration-induced19 homolog 6	AP014961, AY335486, EG709698	-	A0A0P0WH15
4343219	NM_001422155.1 → P_001409084.1 thioredoxin-like protein CDSP32, chloroplastic	AU172639, CB653462, CI167083, CI286584, CI688566	A0A0N7KNF3, Q84NN4	A2YL83
4347708	XM_015795831.3 → P_015651317.1 ribonuclease 3	A0A0P0XPV8, A2Z316, A3C107, Q69JX7, Q940D3	-	-
4346460	NM_001403736.1 → NP_001390665.1 probable plastid-lipid-associated protein 2, chloroplastic	CA754409, CB678401, CI199149	B7EP08, Q6K439, Q84P91	B8BD60
4345942	XM_015792903.3 → XP_015648389.1 pentatricopeptide repeat-containing protein At1g80150, mitochondrial	-	A0A0P0XHL5, A2YWP3, A3BUI7, Q6ZKM5	-
4327045	XM_015766678.3 → XP_015622164.1 small ribosomal subunit protein mS78 (rPPR3a)	-	-	A0A0P0V920, Q0JIP5, Q8H219, Q8LQM2
4325652	NM_001401470.1 → NP_001388399.1 FACT complex subunit SSRP1-A	AB117991, AK066832, AK068959	Q0JQ27, Q8LKS8, Q9LGR0	A0A0P0W3U8, A0A8J8Y3V7, A3AND9, Q10CE2
4334350	XM_015773316.3 → XP_015628802.1 zinc finger protein GIS3	-	-	-
4326935	NM_001406293.1 → NP_001393222.1 dehydrin Rab25	AY333185	P30287, Q5N9R4, Q7E0Y0	Q0JK19

priority targets due to their potential to orchestrate the expression of numerous downstream genes (Ambrosino *et al.*, 2020).

In addition, exploitation of rice pangenome datasets made it possible to detect allelic diversity among these candidate loci across drought-tolerant and drought-susceptible cultivars. This step is especially important, as it connects genetic polymorphisms with functional adaptation, thereby equipping plant breeders with precise molecular markers for targeted selection (Gao *et al.*, 2019).

Thus, while bioinformatics offers a powerful hypothesis-generating engine, the functional validation of predicted genes remains essential. The candidates identified here should be meticulously tested by utilising clustered regularly interspaced short palindromic repeats (CRISPR)-Cas9 gene editing to generate knockouts and/

or overexpression lines in pertinent genetic backgrounds for substantiating their role in drought resilience by means of exhaustive phenotypic and physiological evaluation (Razaq *et al.*, 2021).

Future studies should aim to integrate additional layers of biological data to enhance prediction accuracy. This encompasses incorporating epigenomic data to capture how DNA methylation and histone modifications control stress memory, as well as metabolomic profiles for linking genetic regulation with physiological outcomes (Zitnik *et al.*, 2019). Moreover, machine learning models trained on multi-omics data from field-grown plants under diverse drought regimes hold strong potential for estimating the most effective gene combinations for breeding (Crossa *et al.*, 2025).

Bioinformatics tools enable the identification of stress-responsive genes, molecular markers and

Table 4: These reference sequences exist independently of genome builds genomic.

Gene ID	Reference	Range
4323843	NC_089035.1 reference ASM3414082v1 primary assembly	43498434 .. 43500801
4337576	NC_089039.1 reference ASM3414082v1 primary assembly	456810 .. 459245
4343219	NC_089041.1 reference ASM3414082v1 primary assembly	17434250 .. 17435651
4347708	NC_089043.1 reference ASM3414082v1 primary assembly	25598035 .. 25600035 complement
4346460	NC_089043.1 reference ASM3414082v1 primary assembly	6570468 .. 6574194
4345942	NC_089042.1 reference ASM3414082v1 primary assembly	24818602 .. 24822236
4327045	NC_089035.1 reference ASM3414082v1 primary assembly	33924214 .. 33929082
4325652	NC_089035.1 reference ASM3414082v1 primary assembly	4508505 .. 4515172
4334350	NC_089037.1 reference ASM3414082v1 primary assembly	33617331 .. 33618597 complement
4326935	NC_089035.1 reference ASM3414082v1 primary assembly	29711748 .. 29712839

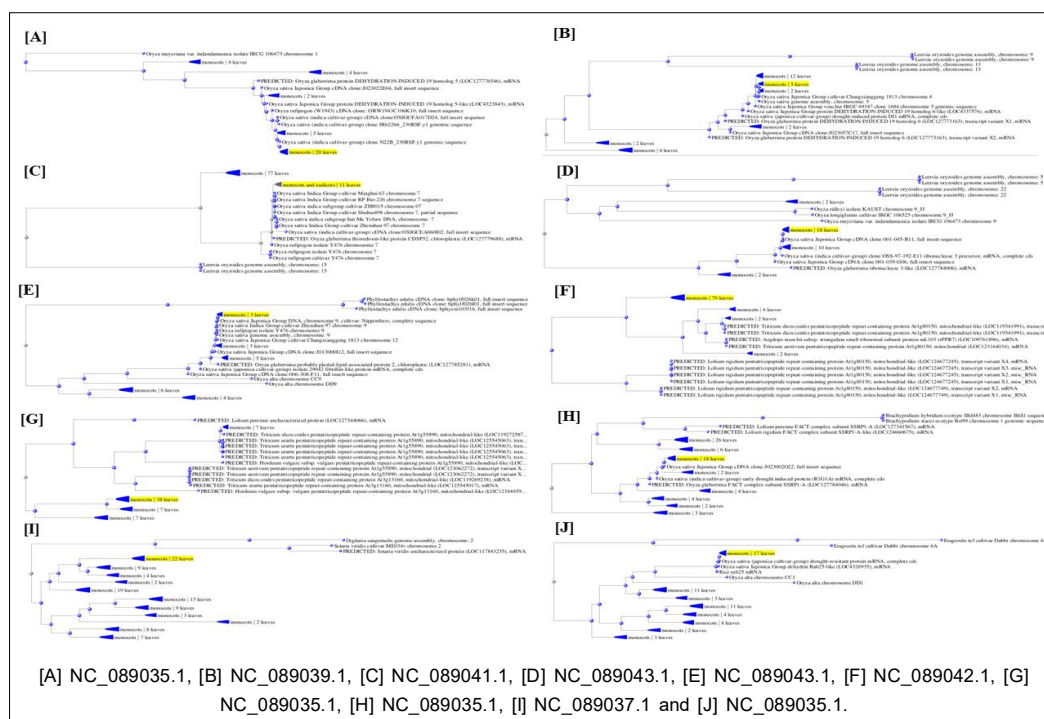


Fig 3: A phylogenetic tree analysis was constructed based on the alignment scores.

Table 5: Contextual information includes genomics, genomic assembly and chromosomal location of the genes under study.

Genomic	Assembly	Chromosome	Location
LOC 4323843	ASM3414082v1 (GCF_034140825.1)	1	NC_089035.1 (43498434 .. 43500801)
	IRGSP - 1.0 (GCF_001433935.1)	1	NC_029256.1 (42845769 .. 42848121)
LOC 4337576	ASM3414082v1 (GCF_034140825.1)	5	NC_089039.1 (456810 .. 459245)
	IRGSP - 1.0 (GCF_001433935.1)	5	NC_029260.1 (446328..448730)
LOC 4343219	ASM3414082v1 (GCF_034140825.1)	7	NC_089041.1 (17434250 .. 17435651)
	IRGSP - 1.0 (GCF_001433935.1)	7	NC_029262.1 (17268632 .. 17270110)
LOC 4347708	ASM3414082v1 (GCF_034140825.1)	9	NC_089043.1 (25598035 .. 25600035, complement)
	IRGSP - 1.0 (GCF_001433935.1)	9	NC_029264.1 (21155961 .. 21157951, complement)
LOC 4346460	ASM3414082v1 (GCF_034140825.1)	9	NC_089043.1 (6570468 .. 6574194)
	IRGSP - 1.0 (GCF_001433935.1)	9	NC_029264.1 (2548879..2552766)
LOC 4345942	ASM3414082v1 (GCF_034140825.1)	8	NC_089042.1 (24818602 .. 24822236)
	IRGSP - 1.0 (GCF_001433935.1)	8	NC_029263.1 (24673105 .. 24676744)
LOC 4327045	ASM3414082v1 (GCF_034140825.1)	1	NC_089035.1 (33924214 .. 33929082)
	IRGSP - 1.0 (GCF_001433935.1)	1	NC_029256.1 (33318018..33323754)
LOC 4325652	ASM3414082v1 (GCF_034140825.1)	1	NC_089035.1 (4508505 .. 4515172)
	IRGSP - 1.0 (GCF_001433935.1)	1	NC_029256.1 (4497724 .. 4504386)
LOC 4334350	ASM3414082v1 (GCF_034140825.1)	3	NC_089037.1 (33617331 .. 33618597, complement)
	IRGSP-1.0 (GCF_001433935.1)	3	NC_029258.1 (32645508 .. 32647071, complement)
LOC 4326935	ASM3414082v1 (GCF_034140825.1)	1	NC_089035.1 (29711748 .. 2971)
	IRGSP - 1.0 (GCF_001433935.1)	1	NC_029256.1 (29123529 .. 29124598)

regulatory elements, whereas AI techniques strengthen predictive modelling, inference of gene regulatory networks and actual plant monitoring. Together, these innovations are vital for formulating stress-resilient plant varieties capable of thriving under increasingly extreme environmental conditions caused by global climate change and anthropogenic pressures. Practical applications encompass estimating drought-resistant gene variants, determining salt-tolerant crop cultivars and enabling real-time monitoring of plant health under extreme temperatures by means of AI-driven phenomics platforms (Zhang *et al.*, 2024).

CONCLUSION

In conclusion, this thorough bioinformatics-driven study was successful in identifying a strong and trustworthy group of candidate genes that are essential for giving rice drought tolerance. The study created a comprehensive and potent framework for gene discovery and functional prioritization under water-limited conditions by methodically combining transcriptome profiling, co-expression network analysis and whole-genome-scale techniques. In addition to improving the precision of candidate gene identification, this integrative approach offered a deeper understanding of the intricate biochemical processes and regulatory networks that underlie rice's responses to drought stress. Thorough functional validation employing cutting-edge molecular and physiological assays will be crucial to the successful conversion of these molecular discoveries into useful and

sustainable agricultural uses. To fully utilize the genetic potential identified in this work, it will also be necessary to strategically choose advantageous alleles using marker-assisted selection, genomic selection, or precision genetic engineering techniques. The development of high-yielding, drought-tolerant and climate-resilient rice cultivars is ultimately anticipated to be greatly accelerated by the research's findings, contributing to global food security and strengthening rice production systems' ability to adapt to rising environmental variability and climate change.

Conflict of interest

The authors declare no conflict of interest.

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