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Biotechnological Advances in Improving Abiotic Stress Tolerance in Jute (*Corchorus* spp.): Genomic and Functional Insights

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Abstract

Jute (Corchoruscapsularis and C. olitorius) is an economically significant natural bast fiber crop, particularly in Bangladesh and South Asia that faces severe constraints from salinity and waterlogging due to climate change and coastal inundation. Despite its agricultural importance, jute has historically lacked genomic resources for molecular improvement. Recent release of high-quality reference genomes, coupled with transcriptomics and functional genomics, has enabled identification of stress-responsive genes and regulatory networks. This review synthesizes advances in jute abiotic stress research, with emphasis on genomic discovery, transcriptional regulation, ion homeostasis, and functional insight into salinity and waterlogging tolerance. We discuss candidate gene families (WRKY, NAC, bZIP, AP2/ERF, DREB, SOS, CBL–CIPK, and NHX), their structural features, and regulatory roles. We also address how these genomic insights are being translated into biotechnological applications, including marker-assisted breeding and CRISPR–Cas9genome editing for targeted improvement of stress tolerance. Finally, future research priorities necessary for developing resilient jute cultivars capable of maintaining fiber yield and quality under adverse environments were outlined. Furthermore, integration of multi-omics approaches, comparative genomics, and gene network modeling is highlighted as a powerful strategy to dissect complex stress tolerance mechanisms. Advancements in phenotyping platforms and functional validation tools are expected to accelerate trait discovery and deployment. Collectively, these approaches will facilitate the development of climate-resilient jute cultivars capable of sustaining productivity, fiber quality, and economic value under increasingly adverse environmental conditions.

Keywords: Abiotic stress tolerance, biotechnology, comparative genomics, corchorus, CRISPR–Cas9, jute, salinity stress, transcription factors, waterlogging

INTRODUCTION

Abiotic stresses, particularly salinity and waterlogging, pose significant threats to global agriculture by impairing plant physiological processes and reducing crop yields. Soil salinity affects approximately 20% of irrigated land worldwide and is increasing due to sea-level rise and soil degradation (Eswar et al., 2021) [1]. Waterlogging creates hypoxic conditions that negatively affect root function and nutrient uptake, resulting in oxidative stress and growth inhibition.

Jute, a bast fiber crop widely cultivated in Bangladesh, India, and other parts of Asia, significantly contributes to rural economies and industrial fiber supply chains. Its growth and fiber quality are highly susceptible to salinity and waterlogging, especially at seedling stages, making stress tolerance breeding a priority for sustainable production. Traditional jute breeding has been constrained by limited genetic variability for stress adaptation, highlighting the need for molecular and genomic approaches (Mitra and Datta, 2022) [2].

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The availability of high-quality reference genomes for *C. capsularis* and *C. olitorius* has catalyzed large-scale identification of stress-responsive genes and transcriptional networks. These genomic tools, when combined with advanced bioinformatics, transcriptomics, and genome editing technologies, promise more rapid and precise development of stress-tolerant jute cultivars.

GENOMIC RESOURCES AND ABIOTIC STRESS RESEARCH IN JUTE

The draft genomes of *C. capsularis* and *C. olitorius* have facilitated genome- wide surveys of stress-associated genes. Comparative analyses using Arabidopsis thaliana orthologs have enabled functional predictions and identification of major regulatory pathways implicated in abiotic stress responses. These genomic resources provide essential platforms for mining candidate genes involved in transcriptional regulation, ion transport, and signal transduction.

Transcriptome studies under salinity stress have identified thousands of differentially expressed genes (DEGs) in both leaf and root tissues, including genes associated with hormone signaling (abscisic acid and cytokinin pathways), transcription factors, and stress enzymes. For example, high-throughput transcriptome sequencing revealed that 127 common DEGs and hundreds of transcription factors are responsive to salinity in both *C. capsularis* and *C. olitorius*, pointing to conserved stress response networks across tissues and species (Yang et al., 2017) [3].

In addition, whole-genome resequencing of contrasting jute accessions has identified single nucleotide polymorphisms (SNPs) and InDels linked to stress-responsive genes (Table 1), offering marker development opportunities for breeding programs (Ganguly et al., 2024) [4].

Table 1. Stress-responsive gene families in *Corchorus* spp.

Gene family	Representative genes	Function	Subcellular localization	Reference
WRKY TFs	*CcWRKY1*, *CoWRKY3*	Transcriptional regulation under salinity & waterlogging	Nucleus	Islam et al., 2017, Nat Plants, 3:16223; Rahman et al., 2021, Plants, 10:1595.
NAC TFs	*CcNAC1*, *CoNAC2*	Stress signaling & development	Nucleus	Mansour & Hassan, 2022, Plant Mol Biol, 108:175–224.
bZIP TFs	*CcbZIP3*, *CobZIP5*	ABA-mediated stress responses	Nucleus	Ragaey et al., 2022, Plants, 11:1786.
AP2/ERF TFs	*CcAP2/ERF22*, *CoAP2/ERF18*	Hypoxia & osmotic stress regulation	Nucleus	Bailey-Serres et al., 2012, Trends Plant Sci, 17:129–138.
DREB TFs	*CcDREB2*, *CoDREB1*	Dehydration and salinity signaling	Nucleus	Rahman et al., 2021, Plants, 10:1595.
MYB TFs	*CcMYB12*, *CoMYB5*	Regulates phenylpropanoid and stress genes	Nucleus	Mansour & Hassan, 2022, Plant Mol Biol, 108:175–224.
HSF TFs	*CcHSF1*, *CoHSF2*	Heat shock response and ROS detoxification	Nucleus	Formentin et al., 2018, Plants, 7:75.

MOLECULAR AND FUNCTIONAL BASES OF SALINITY TOLERANCE

Ion Homeostasis and Transport Systems

Soil salinity causes ionic toxicity and osmotic stress, requiring plants to tightly regulate sodium (Na^+) and potassium (K^+) balance. Two major systems govern this response: the Salt Overly Sensitive (SOS) pathway and the vacuolar Na^+/H^+ exchanger (NHX) system (Shabala et al., 2015; Mansour & Hassan, 2022) [5, 6]. The SOS pathway consists of SOS3 (Ca^{2+} sensor), SOS2 (protein kinase), and SOS1 (plasma membrane Na^+/H^+ antiporter). Salt-induced Ca^{2+} signals activate the SOS3–SOS2 complex, which phosphorylates SOS1 to promote Na^+ efflux and maintain K^+ homeostasis, thereby protecting cellular metabolism under salinity stress (Bailey-Serres et al., 2012; Shabala et al., 2015) [6, 7].

In parallel, NHX transporters sequester excess Na^+ into vacuoles in exchange for H^+, reducing cytosolic toxicity and contributing to osmotic adjustment and turgor maintenance (Mansour &Hassan, 2022; Ragaey et al., 2022) [5, 8]. Comparative genomics of *Corchorus capsularis* and *C. olitorius* has identified clear orthologs of SOS1, SOS2, SOS3, and NHX2, suggesting functional conservation of these ion transport systems in jute (Islam et al., 2017) [9]. Transcriptomic evidence indicates that these genes are up regulated under salinity, particularly in tolerant genotypes (Rahman et al., 2021a) [10].

Transcriptional Regulation

Transcription factors (TFs) act as master regulators of stress-responsive gene networks (Table 2). Salinity induces multiple TF families in jute, including.

- WRKY (regulates biotic and abiotic stress signaling),
- NAC (involved in developmental and stress responses),
- bZIP (mediates ABA-dependent stress signaling),
- AP2/ERF and DREB (control gene expression in response to dehydration and salinity).

Table 2. Conserved motifs and functional domains of major transcription factor families in *Corchorus* spp.

TF family	Representative genes	Conserved motifs	Functional domains	Predicted subcellular localization	Reference
WRKY	*CcWRKY1*, *CoWRKY3*	Motifs 1–5 (WRKYGQK, zinc-finger)	WRKY domain, C2H2 zinc finger	Nucleus	Islam et al., 2017; Rahman et al., 2021.
NAC	*CcNAC1*, *CoNAC2*	Motifs 1–6 (NAM domain)	NAM/NAC domain, DNA-binding domain	Nucleus	Mansour & Hassan, 2022.
bZIP	*CcbZIP3*, *CobZIP5*	Motifs 1–4 (basic region + leucine zipper)	bZIP domain, leucine zipper	Nucleus	Ragaey et al., 2022.
AP2/ERF	*CcAP2/ERF22*, *CoAP2/ERF18*	Motifs 1–5 (AP2 DNA-binding motif)	AP2/ERF domain	Nucleus	Bailey-Serres et al., 2012.
DREB	*CcDREB2*, *CoDREB1*	Motifs 1–4 (AP2-like DREB motif)	AP2 DNA-binding domain	Nucleus	Rahman et al., 2021.
MYB	*CcMYB12*, *CoMYB5*	Motifs 1–3 (R2/R3 repeats)	MYB DNA-binding domain, helix-turn-helix	Nucleus	Mansour & Hassan, 2022.
HSF	*CcHSF1*, *CoHSF2*	Motifs 1–4 (DNA-binding + oligomerization)	HSF DNA-binding domain, HR-A/B oligomerization	Nucleus	Formentin et al., 2018.

Genome-wide identification of these TF families in jute reveals conserved structural motifs and regulatory domains, many of which show inducible expression under salinity, indicating roles in stress adaptation. The enrichment of ABA and cytokinin signaling genes among DEGs during salt stress suggests complex hormone- mediated regulatory mechanisms (Yang et al., 2017) [3].

WATERLOGGING STRESS: MORPHO PHYSIOLOGY AND TRANSCRIPTIONAL RESPONSES

Waterlogging, caused by excessive soil water, results in hypoxia that disrupts root metabolism and energy production. Comparative transcriptomic analysis between a waterlogging-tolerant variety (*C. capsularis* cv. CVL-1) and a susceptible variety (*C. olitorius* cv. O-9897) revealed differential gene expression patterns, highlighting genotype-specific adaptation mechanisms. Many novel genes were expressed in tolerant genotypes, indicating unique transcriptional responses that support energy metabolism and structural resilience under hypoxia (Bashar et al., 2023) [11].

Physiological adaptations, such as adventitious root formation and aerenchyma development, have been observed in waterlogged jute, supporting enhanced oxygen diffusion and survival. These structural changes, coupled with transcriptional reprogramming, contribute to improved waterlogging tolerance.

REACTIVE OXYGEN SPECIES AND ANTIOXIDANT RESPONSES

Abiotic stresses, including salinity and waterlogging, lead to excessive production of reactive oxygen species (ROS), which can damage cellular components. Plants deploy antioxidant defense systems involving enzymes, such as superoxide dismutase, catalase, and peroxidases, to mitigate ROS accumulation.

Studies on *C. olitorius* have shown that salinity and other abiotic stresses lead to significant ROS accumulation and alterations in antioxidant enzyme activities, underscoring the importance of oxidative stress management in stress tolerance (Rahman et al., 2021b) [12].

TRANSLATIONAL BIOTECHNOLOGY: MARKER-ASSISTED BREEDING AND GENOME EDITING

Marker Development for Breeding

Identifying stress-associated markers, such as SNPs and SSRs, can accelerate breeding for tolerance traits. Genomic variations uncovered through resequencing efforts provide valuable resources for high-resolution marker development and marker-assisted selection pipelines.

CRISPR–Cas9 Genome Editing

CRISPR–Cas9 has transformed plant biotechnology by enabling precise and heritable modification of genes governing abiotic stress responses. Recent studies demonstrate its effectiveness in editing regulators of ion transport, transcriptional control, and hormonal signaling, making it a powerful tool for improving stress resilience in crops (Kumar et al., 2023; Li & Xu, 2019) [13, 14].

In jute, CRISPR–Cas9 offers significant potential to enhance salinity and waterlogging tolerance by

- Activating or fine-tuning SOS and NHX transporters to improve Na^+ efflux and vacuolar sequestration (Islam et al., 2017; Mansour & Hassan, 2022) [9, 5].
- Modifying DREB and AP2/ERF transcription factors to strengthen adaptive transcriptional responses to osmotic and hypoxic stress (Bailey-Serres et al., 2012; Rahman et al., 2021) [6, 10]; and
- Optimizing hormonal signaling components associated with ABA, ethylene, and ROS pathways to balance growth and stress tolerance (Formentin et al., 2018; You & Chan, 2015) [15, 16].

Integrating CRISPR-based editing with genomic selection and stress transcriptomics is expected to accelerate the development of elite, climate-resilient jute cultivars with stable fiber yield under saline and waterlogged conditions (Table 3).

Table 3. Candidate CRISPR/Cas9 targets for enhancing salinity and waterlogging tolerance in *Corchorus* spp.

Target gene	Gene family / function	Stress type	Proposed editing strategy	Expected outcome	Reference
CcSOS1 / CoSOS1	Na^+/H^+ antiporter, SOS pathway	Salinity	Upregulate or promote editing	Enhanced Na^+ efflux from cytoplasm, improved ionic balance	Islam et al., 2017; Mansour & Hassan, 2022.
CcSOS2 / CoSOS2	Protein kinase, SOS pathway	Salinity	Knock-in of gain-of-function variant	Strengthened SOS signaling, better Na^+ homeostasis	Rahman et al., 2021.
CcNHX2 / CoNHX2	Vacuolar Na^+/H^+ exchanger	Salinity	Overexpression via CRISPR-activation	Increased vacuolar Na^+ sequestration, reduced cytotoxicity	Ragaey et al., 2022.
CcAP2/ERF22 / CoAP2/ERF18	AP2/ERF transcription factor	Waterlogging	Promoter editing or CRISPRa	Enhanced hypoxia-responsive gene expression, improved survival under low O_2	Bailey-Serres et al., 2012.
CcDREB2 / CoDREB1	DREB transcription factor	Salinity & waterlogging	Targeted activation	Upregulated osmotic and anaerobic stress response genes	Rahman et al., 2021.
CcWRKY1 / CoWRKY3	WRKY transcription factor	Salinity & waterlogging	Knock-in of stress-tolerant variant	Optimized transcriptional regulation of stress-responsive genes	Islam et al., 2017.
CcCBL4 / CoCBL4	Calcineurin B-like protein, Ca^{2+} signaling	Salinity	Enhancer/promoter editing	Enhanced calcium-mediated stress signaling	Mansour & Hassan, 2022.
CcHSF1 / CoHSF2	Heat shock transcription factor	Salinity & waterlogging	Targeted activation	Improved ROS detoxification and protein homeostasis	Formentin et al., 2018.

INTEGRATION OF MULTI-OMICS AND SYSTEMS BIOLOGY

To fully understand complex stress responses, integration of genomics, transcriptomics, proteomics, and metabolomics is essential. Systems biology approaches can reveal network architectures underlying tolerance mechanisms and identify key regulatory nodes for targeted intervention.

Comparative transcriptomics across multiple stress types (salinity, waterlogging, drought, and low temperature) can uncover both shared and unique pathways, guiding cross-stress tolerance strategies. For instance, cold stress tolerance in certain jute accessions has been linked to specific transcription factor variations, expanding the potential for genomic markers across abiotic stresses (Ganguly et al., 2024) [4].

CHALLENGES AND FUTURE DIRECTIONS

Despite growing knowledge of individual stress responses, major challenges remain in understanding and improving combined salinity and waterlogging tolerance in jute. A critical limitation is the scarcity of functional validation of candidate genes specifically under dual-stress conditions. Most studies focus on either salinity or waterlogging alone, leaving a substantial gap in causal evidence for genes that confer tolerance to their interaction. Functional genomics using CRISPR–Cas9, overexpression, and gene knockout approaches remains largely unexplored in jute under combined stress scenarios.

A second bottleneck is the lack of efficient and genotype-independent transformation and genome editing systems in jute. Low transformation efficiency, poor regeneration, and limited tissue culture protocols hinder precise manipulation of stress-responsive genes such as SOS, NHX, DREB, and hypoxia-related regulators. Establishing robust Agrobacterium-mediated transformation, protoplast-based editing, or novel delivery systems will be essential for rapid functional validation.

Another major gap is the insufficient evaluation of dual-stress tolerance in multi-environment field trials. Most experimental studies are conducted under controlled conditions that fail to replicate the dynamic fluctuations of soil salinity and waterlogging in coastal and flood-prone regions. Large-scale, multi-location trials are needed to assess trait stability, fiber yield, and physiological performance under real agronomic conditions.

At the molecular level, the interaction between salinity-induced ionic stress and waterlogging-induced hypoxia remains poorly characterized in jute. How ion homeostasis pathways (e.g., SOS and NHX) interact with oxygen-sensing mechanisms, anaerobic metabolism, and reactive oxygen species (ROS) signaling is largely unknown. Elucidating these cross-talk networks is crucial for designing effective breeding and engineering strategies.

Future research should emphasize high-throughput functional validation using genome editing, the development of reliable transformation platforms, and the integration of phenomics with genomics and transcriptomics. Such multidisciplinary approaches will be essential to bridge the genotype–phenotype gap and accelerate the breeding of climate-resilient jute cultivars with improved productivity under stress-prone environments.

CONCLUSION

Advances in jute genomics and functional studies have greatly expanded our understanding of abiotic stress tolerance mechanisms. Identification of key transcriptional regulators, ion transporters, and signaling components offers targets for molecular breeding and genome editing. Integrating these genomic insights with biotechnological tools, including CRISPR–Cas9 and marker-assisted selection, provides promising avenues for developing climate-resilient jute varieties capable of sustaining fiber production under salinity and waterlogging stress. Continued investment in functional genomics and field validation will be critical to translating discoveries into agricultural impact.

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