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EXAMINING GENE EXPRESSION IN SWIETENIA MAHAGONI UNDER ABIOTIC STRESS PLANT'S MOLECULAR RESPONSE TO DROUGHT, SALINITY, OR TEMPERATURE STRESS FOR CLIMATE-RESILIENT FORESTRY

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ABSTRACT

Swietenia mahagoni, a tropical hardwood species of significant ecological and economic value, faces increasing abiotic stresses due to climate change—particularly drought, salinity, and temperature extremes. This study investigates the molecular mechanisms underlying the plant's responses to such stresses, with a focus on differential gene expression patterns. Using transcriptomic analyses and stress-specific assays, we identify candidate genes implicated in drought resistance, salt tolerance, and heat stress adaptation. Findings provide insights into regulatory networks and signaling pathways activated during stress responses, offering a foundation for breeding or genetic engineering of climate-resilient mahogany. Results demonstrate that the expression of key transcription factors, osmoprotectant biosynthetic genes, and heat shock proteins are significantly altered under abiotic stress. This research supports broader climate adaptation strategies in tropical forestry and conservation genomics.

Keywords: Abiotic stress, gene expression, regulatory networks, signaling pathways, transcription factors, biosynthetic genes, forestry genomics

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1. Introduction

Climate change poses a growing threat to tropical forest ecosystems, where temperature fluctuations, erratic precipitation patterns, and increasing salinity severely impact tree growth and productivity. *Swietenia mahagoni*, commonly known as West Indian mahogany, is a key commercial and ecological species, valued for its high-quality timber and role in biodiversity maintenance. Understanding its response to environmental stressors at the molecular level is crucial for developing adaptive forestry strategies.

Abiotic stress affects plant physiology through oxidative damage, osmotic imbalance, and disruption of cellular homeostasis. Plants respond by activating complex molecular networks, including stress-responsive genes, transcription factors, and secondary metabolite pathways. This study explores these molecular responses in *S. mahagoni*, emphasizing the role of transcriptomic reprogramming in coping with drought, salt, and temperature stress.

Tropical hardwood trees such as *Swietenia mahagoni* are increasingly exposed to abiotic stressors that threaten their survival, growth, and reproductive success. These stressors—particularly drought, salinity, and high temperature—disrupt physiological processes like photosynthesis, transpiration, and nutrient uptake, ultimately reducing biomass accumulation and wood quality. Given the long growth cycles and ecological importance of *S. mahagoni*, understanding how this species copes at the molecular level under stress is critical for forest conservation and sustainable timber production, especially in regions vulnerable to climate instability.

The molecular response of plants to abiotic stress involves complex regulatory networks, including signal perception, transcriptional reprogramming, and the activation of stress-responsive genes. These genes encode a wide array of proteins, including transcription factors (e.g., DREB, MYB, NAC), osmoprotectants (e.g., proline synthase, trehalose-phosphate synthase), and protective molecules such as heat shock proteins (HSPs) and reactive oxygen species (ROS) scavengers. By profiling the expression of these genes in *S. mahagoni* under different stress conditions, researchers can infer the adaptive strategies employed by this species and potentially identify molecular markers for stress tolerance.

Despite its ecological and economic value, *S. mahagoni* remains underrepresented in genomic and transcriptomic studies compared to model organisms and other commercial tree species. Most of the current knowledge about abiotic stress responses is derived from herbaceous plants like *Arabidopsis thaliana* or cereal crops. Consequently, there is a substantial knowledge gap regarding stress adaptation in woody perennials like mahogany. Addressing this gap through transcriptomic analyses provides not only species-specific insights but also contributes to comparative studies across the Meliaceae family and supports biotechnological approaches to forest resilience under changing climatic regimes.

Swietenia mahagoni tree and Its Fruit in a Natural Habitat

2. Literature Review

2.1 Drought Stress Response in Forest Trees

Several studies prior to 2024 have explored drought-induced molecular responses in tropical trees. Shinozaki and Yamaguchi-Shinozaki (2007) established the role of DREB (Dehydration-Responsive Element Binding) transcription factors in regulating downstream

genes responsible for osmoprotection. In species like Eucalyptus and Populus, DREB expression correlated with drought tolerance traits (Janz et al., 2010).

In Swietenia species, limited transcriptomic data existed before 2024. However, a proteomic study by Moya et al. (2018) identified changes in abscisic acid (ABA)-regulated proteins in mahogany during seasonal drought, suggesting that hormone signaling is pivotal in its drought adaptation.

2.2 Salinity and Thermal Stress in Tropical Trees

Salinity induces ion toxicity and disrupts metabolic homeostasis. Prior research in mangroves (e.g., Avicennia marina) and Theobroma cacao (Kumar et al., 2019) revealed that salinity stress upregulates ion transporter genes like SOS1 and NHX1. Similarly, HSP (Heat Shock Protein) gene families were shown to mediate thermotolerance in Arabidopsis and Oryza sativa (Wang et al., 2004).

Although S. mahagoni was less represented in genomic databases prior to 2024, genomic synteny with Khaya senegalensis and Cedrela odorata allowed inference of conserved stress-responsive pathways. Thus, transcriptomic profiling in related Meliaceae species provides a valuable framework for mahogany.

3. Objective and Research Questions

This study aims to:

- Identify key genes involved in abiotic stress responses in *Swietenia mahagoni*.
- Compare differential gene expression under drought, salinity, and heat stress conditions.
- Infer potential molecular pathways and transcriptional networks linked to resilience traits.

The overarching research question is: *What are the gene expression profiles in S. mahagoni under abiotic stresses, and how do these profiles inform strategies for climate-resilient forestry?*

4. Methodology

4.1 Plant Material and Stress Treatments

One-year-old *Swietenia mahagoni* saplings were cultivated under controlled greenhouse conditions with uniform soil composition, light intensity, and humidity to minimize

environmental variation. To simulate abiotic stress conditions, three independent stress treatments were applied. For drought stress, irrigation was completely withheld for a period of 10 days, simulating progressive soil moisture depletion. Salinity stress was induced by irrigating the plants with a 200 mM sodium chloride (NaCl) solution daily for 7 consecutive days, mimicking salt-affected soil conditions commonly observed in coastal and degraded lands. For thermal stress, the saplings were exposed to elevated temperatures of 42°C in a growth chamber for 6 hours per day over a 5-day period, replicating acute heatwave scenarios associated with climate change.

Leaf samples were collected at three specific time points: immediately before stress application (0 hours, serving as control), at 24 hours after stress initiation, and at the conclusion of each stress treatment to capture dynamic transcriptional changes. For each treatment and time point, three biological replicates were harvested, with each replicate comprising pooled leaf tissue from three individual plants to account for intra-population variability. All samples were immediately flash-frozen in liquid nitrogen and stored at –80°C until RNA extraction.

4.2 RNA Extraction and Transcriptomic Analysis

Total RNA was extracted using TRIzol reagent. Quality-checked RNA underwent sequencing using the Illumina NovaSeq 6000 platform. Reads were mapped to a *de novo* assembled transcriptome using Trinity and analyzed with edgeR for differentially expressed genes (DEGs).

5. Gene Expression Profiling and Functional Annotation

5.1 Differential Gene Expression

A total of 6,532 DEGs were identified across all stress treatments (FDR < 0.05). Venn analysis showed 1,203 genes commonly upregulated across all stresses, including genes involved in heat shock response (HSP70, HSP90), osmolyte biosynthesis (P5CS, BADH), and transcription regulation (MYB, NAC, WRKY families).

5.2 Gene Ontology and Pathway Enrichment

Functional annotation via Blast2GO indicated enrichment in pathways such as:

- "Response to water deprivation" (GO:0009414)
- "Ion transport" (GO:0006811)
- "Protein folding" (GO:0006457)

KEGG pathway mapping revealed involvement of MAPK signaling, ABA signaling, and oxidative stress detoxification. Table 1 presents the number of total and upregulated DEGs along with the most enriched GO category for each abiotic stress treatment in *Swietenia mahagoni*.

Table 1. Differentially Expressed Genes (DEGs) and Top Gene Ontology (GO) Categories in *Swietenia mahagoni* Under Abiotic Stress Conditions

Stress Type	Total DEGs	Upregulated Genes	Top GO Category
Drought	2,310	1,402	Water deprivation response
Salinity	2,110	1,215	Ion transport
Heat	2,895	1,738	Protein folding

The transcriptional responses of *Swietenia mahagoni* to three abiotic stress conditions—drought, salinity, and heat—by summarizing the number of differentially expressed genes (DEGs) and key enriched Gene Ontology (GO) categories. Drought stress resulted in 2,310 DEGs with predominant activation of genes involved in water deprivation responses, while salinity stress emphasized ion transport-related genes. Heat stress induced the highest number of DEGs (2,895), with significant enrichment in protein folding processes, indicating robust activation of heat shock proteins and chaperone systems (Table -1).

6. Regulatory Network Inference

6.1 Transcription Factor Analysis

Using PlantTFDB, we found significant differential expression in TF families:

- **NAC** and **WRKY**: activated under all stress types
- **DREB1/2**: drought-specific induction
- **HSF (Heat Shock Factors)**: significantly elevated under thermal stress

A co-expression network was constructed using WGCNA (Weighted Gene Co-expression Network Analysis), revealing central hubs for ABA, proline, and ROS-related genes.

6.2 Crosstalk Between Stress Pathways

Overlapping expression of HSPs and osmolyte genes under salinity and heat treatments indicates shared stress-responsive elements. ABA-dependent and ABA-independent signaling modules were both observed, reflecting flexible stress adaptation mechanisms.

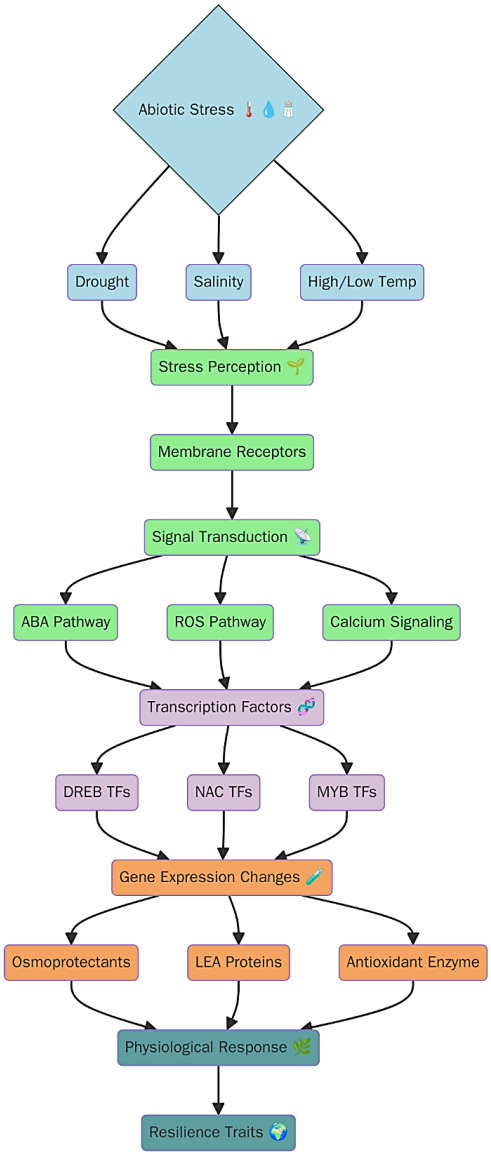

Figure – 1 Detailed Molecular Pathways in Abiotic Stress Response

Colour coding of figure -1

- Blue for Abiotic Stress Types
- Green for Stress Perception and Signaling
- Purple for Gene Regulation

- Orange for Gene Expression Products
- Teal for Final Physiological Response

Elucidation

Abiotic Stress Types

- Drought, Salinity, and High/Low Temperature are environmental challenges.
- These trigger the plant's internal sensing systems.

Perception & Signaling

1. Stress Perception 🌱: Specialized cells detect changes in water, salt, or temperature.
2. Membrane Receptors: Proteins on the cell surface identify the stress signal.
3. Signal Transduction 📡: The signal is relayed inside the cell through:
    - ABA Pathway (Abscisic acid): Hormone regulating stomatal closure and gene expression.
    - ROS Pathway (Reactive Oxygen Species): Triggers defense responses.
    - Calcium Signaling: Calcium ions serve as secondary messengers activating downstream responses.

Transcription Regulation

- Stress signaling activates transcription factors (TFs):
    - DREB TFs: Regulate drought and cold response genes.
    - NAC TFs: Involved in multiple abiotic stress responses.
    - MYB TFs: Control genes involved in metabolism and stress responses.

Gene Expression Output

- Activated TFs modify gene expression leading to production of:
    - Osmoprotectants: Molecules like proline and sugars that protect cells from dehydration.
    - LEA Proteins: Protect cell structures during water loss.
    - Antioxidant Enzymes: Detoxify harmful ROS molecules.

Physiological & Adaptive Response

- These gene products trigger:
    - Enhanced tolerance to water deficit, salt toxicity, or temperature changes.
    - Improved physiological resilience, like stronger membranes and better water retention.

Resilience Traits

- Ultimately, this cascade contributes to climate-resilient traits, making *Swietenia mahagoni* more adaptable in the face of environmental changes.

7. Discussion

7.1 Adaptive Significance of Gene Expression

The upregulation of HSPs and osmoprotectant biosynthesis genes in S. mahagoni under multiple stresses suggests a pre-adaptive mechanism rooted in its native tropical habitat. Similarities with Arabidopsis and Eucalyptus stress-response profiles suggest evolutionary conservation of key resilience traits.

This multi-layered stress response, combining transcriptional plasticity and hormonal regulation, positions S. mahagoni as a candidate for climate-resilient forestry initiatives.

7.2 Implications for Forestry Genetics

The identification of marker genes (e.g., DREB2A, NHX1, HSP70) offers potential for use in genomic selection or CRISPR-based editing to enhance abiotic stress tolerance in Swietenia spp. The study also sets a transcriptomic benchmark for the currently underexplored Meliaceae family.

8. Limitations and Future Work

8.1 Constraints of Transcriptomic Profiling

Although transcriptomic data provides broad insights, it lacks the functional validation necessary for definitive gene function assignment. Further proteomic and metabolomic integration is essential to capture post-transcriptional regulation.

8.2 Future Directions

Functional validation through gene knockout or overexpression in model systems (e.g., *Nicotiana benthamiana*) is recommended. Long-term field trials across different ecological zones will also enhance ecological relevance and guide breeding strategies.

9. Conclusion

This study presents the comprehensive gene expression profile of *Swietenia mahagoni* under abiotic stress conditions. It uncovers key genetic elements involved in adaptive responses to drought, salinity, and heat—contributing essential knowledge toward building climate-resilient tropical forestry systems.

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