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Unraveling the Genetic Basis of Abiotic Stress Tolerance in Crop Plants

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ABSTRACT

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This study probes into unravelling the genetic basis of abiotic stress tolerance in crop plants, addressing critical gaps in knowledge and contributing to sustainable agricultural practices. Employing a mixed-method approach, the research integrated genomic, transcriptomic, proteomic, and metabolomic analyses to characterize stress-tolerant crop varieties comprehensively. The experimental setup involved controlled stress induction (drought, extreme temperatures) on selected varieties, enabling the collection of morphological, physiological, and molecular data. Results revealed distinctive morphological responses, with cassava exhibiting superior growth in height, leaf area, and root length under abiotic stress. Physiological analyses indicated cassava's heightened resilience, showcasing higher chlorophyll content, stomatal conductance, and lower osmotic potential. Transcriptomic profiling highlighted cassava's elevated expression of stress-responsive genes, while proteomic analysis showcased an increased abundance of stress-responsive proteins. Genomic variations, represented through single nucleotide polymorphisms, were associated with stress tolerance traits, emphasizing the genetic diversity within crop varieties. Comparative stress tolerance indices further underscored cassava's superior performance. Line graphs and bar graphs were the visualization tools used to enhance data interpretation. These findings contribute significantly to the theoretical framework of plant-environment interactions, fostering interdisciplinary collaborations. The study's multidisciplinary nature and innovative methodologies provide a nuanced understanding of stress tolerance mechanisms, bridging existing knowledge gaps. The practical implications include the potential development of stress-tolerant crop varieties, crucial for ensuring global food security amid environmental challenges. Overall, this research advances our understanding of crop resilience and lays the groundwork for future agricultural innovations.

Keywords:

Abiotic stress, Cassava, Crop plants, Genomics, Proteomics.

1.0 INTRODUCTION

In the realm of Agricultural Sciences, the ability to ensure food security in the face of unpredictable environmental changes stands paramount. Abiotic stresses, including drought, extreme temperatures, and nutrient deficiencies, have emerged as critical challenges, jeopardizing global crop yields and exacerbating food insecurity concerns [1],[2]. Understanding the intricate genetic mechanisms that confer abiotic stress tolerance in crop plants is not merely an academic pursuit but a pressing necessity in our rapidly changing climate scenario. The importance of delving into the genetic fundamentals of stress tolerance becomes evident when one considers the global population's growing demand for food, the waning availability of arable land, and the

rising frequency of extreme weather events[3],[4]. Moreover, while conventional breeding strategies have achieved commendable progress in enhancing crop resilience, there remains a significant gap in our knowledge concerning the nuanced genetic factors that can provide sustainable and durable stress tolerance.

The significance of this investigation extends beyond immediate agricultural concerns. At a practical level, uncovering the genetic determinants of abiotic stress tolerance can dictate the development of innovative biotechnological interventions, such as gene editing and molecular breeding, tailored to enhance crop resilience [5],[6]. Such advancements hold the promise of creating stress-tolerant crop varieties that can thrive in adverse environmental conditions, thereby safeguarding yields and ensuring food security for vulnerable populations.

Theoretical advancements in this domain promise to reshape our knowledge of plant biology, stress responses, and evolutionary adaptations. By elucidating the complex genetic networks and molecular pathways that coordinate stress tolerance, researchers can unravel fundamental principles governing plant-environment interactions [7], [8]. This understanding not only enriches our theoretical frameworks but also paves the way for interdisciplinary collaborations, fostering synergies between genetics, physiology, ecology, and computational experts.

Furthermore, addressing the genetic basis of abiotic stress tolerance in crop plants fills a conspicuous gap in the existing literature. While numerous studies have explored the physiological and morphological responses of plants to environmental stresses, there remains a paucity of comprehensive genetic studies that integrate multi-omics (combination and analyses of data from various *omics* disciplines, such as genomics, transcriptomics, proteomics, metabolomics, etc., to gain a comprehensive understanding of biological systems) data to provide holistic insights [9],[10]. This investigation, therefore, aspires to bridge this knowledge gap, offering a clear understanding that transcends reductionist approaches and embraces the complexity inherent in plant stress responses.

The literature surrounding abiotic stress tolerance in plants is complete with studies delineating physiological, morphological, and biochemical responses to environmental stresses. Numerous investigations have elucidated the intricate signaling pathways, stress-responsive genes, and adaptive mechanisms that enable plants to withstand adverse conditions [11], [12]. Additionally, advancements in high-throughput sequencing technologies have facilitated genome-wide analyses, revealing genomic variations and gene expression profiles associated with stress tolerance traits. However, a noticeable gap persists in the integration and broad analysis of multi-omics data to unravel the complex genetic networks governing stress resilience. While individual studies have provided invaluable insights into specific aspects of plant stress responses, there remains a paucity of holistic approaches that synthesize genomic, transcriptomic, proteomic, and metabolomic data [13], [14],[15]. This fragmented landscape hampers our ability to understand the full complexity of stress tolerance mechanisms and limits the translational potential of research findings into tangible agricultural applications.

2.0 DEFINITION AND SIGNIFICANCE OF PREVIOUS STUDIES

Previous studies in the field have predominantly focused on opening up individual components of the stress response machinery, ranging from the identification of stress-responsive genes and transcription factors to the characterization of metabolic pathways and hormone signaling cascades [16], [17]. These foundational studies have established the groundwork for understanding the molecular basis of stress tolerance and have crystallized

into the development of stress-tolerant crop varieties through conventional breeding and genetic engineering approaches. In summary, while previous studies have made significant contributions to the field by elucidating various features of abiotic stress tolerance, there exists a compelling need for integrative research endeavors that go beyond disciplinary boundaries and embrace the complexity of plant stress responses. This study endeavors to address this gap by adopting a multi-omics approach, thereby providing a comprehensive understanding of the genetic basis of stress tolerance in crop plants and facilitating the development of resilient agricultural systems.

2.1 Theoretical Framework

The theoretical framework guiding this study is anchored in the principles of systems biology, genomics, and molecular genetics. Systems biology provides a holistic perspective, emphasizing the interconnectedness of biological systems and the emergent properties that arise from complex interactions among genes, proteins, metabolites, and environmental factors [18],[19]. By integrating multi-omics data, this framework enables a comprehensive review of the genetic networks and regulatory pathways that govern abiotic stress tolerance in crop plants. Furthermore, the application of genomic tools and molecular techniques facilitates the identification of critical genetic determinants, enabling a nuanced understanding of adaptive mechanisms and their evolutionary implications.

2.2 Purpose Statement

The primary purpose of this study was to review the genetic determinants and molecular mechanisms that trigger abiotic stress tolerance in crop plants, thereby addressing critical knowledge gaps and advancing our understanding of plant-environment interactions. By integrating multi-omics approaches, this study aims to uncover novel genetic markers and regulatory networks associated with stress resilience, paving the way for targeted biotechnological interventions and sustainable agricultural practices.

2.2.1 Objectives of the Study

The primary objective of this study is to review the genetic basis of abiotic stress tolerance in crop plants through an integrative multi-omics approach. Specifically, the study aims to:

- i. Elucidate the morphological parameters of selected crop varieties under abiotic stress conditions.
- ii. Determine the physiological responses of crop varieties to drought stress.
- iii. Investigate the transcriptomic responses of crop plants to environmental stresses, elucidating the regulatory networks and gene expression profiles that underlie stress tolerance mechanisms.
- iv. Analyze the proteomic and metabolomic changes associated with stress responses, identifying essential

proteins, metabolites, and metabolic pathways that contribute to stress resilience.

- v. Integrate multi-omics data to construct comprehensive genetic networks and regulatory models that encapsulate the complexity of abiotic stress tolerance mechanisms in crop plants.

By achieving these objectives, this study aspires to advance our theoretical understanding of plant-environment interactions, foster interdisciplinary collaborations, and contribute substantively to the development of sustainable agricultural practices aimed at enhancing global food security.

In summary, the exploration of the genetic basis of abiotic stress tolerance in crop plants is a pivotal research avenue with profound implications for agriculture, food security, and scientific understanding. By elucidating the molecular mechanisms that underlie stress resilience, this investigation endeavors to contribute substantively to the broader field of study, fostering innovations, advancing theoretical frameworks, and addressing critical gaps in the literature.

3.0 MATERIALS AND METHODS

3.1 Description of the General Research Strategy

The central research strategy employed in this study was anchored in an integrated approach, encompassing both quantitative and qualitative methodologies. This integrative strategy enabled a comprehensive analysis of the genetic basis of abiotic stress tolerance in crop plants, facilitating the synthesis of empirical data, experimental insights, and theoretical frameworks. By combining genomic analyses, transcriptomic profiling, proteomic evaluations, and targeted genetic manipulations, this research strategy endeavors to unravel the multifaceted genetic networks and regulatory mechanisms underlying stress resilience.

The experimental setup comprised a diverse collection of crop plant varieties, specifically selected based on their documented variations in stress tolerance traits. Seeds of these varieties (Cassava, Water Yam, Yellow Yam, Beans and Maize) were germinated under controlled environmental conditions to ensure uniform growth conditions. Subsequently, seedlings were subjected to simulated abiotic stresses, including drought and extreme temperature regimes, in specialized growth chambers equipped with precise environmental control systems. Concurrently, a reference set of plants was maintained under optimal growth conditions to serve as controls for comparative analyses. Measurements were conducted at multiple hierarchical levels, encompassing morphological, physiological, and molecular parameters. Morphological evaluations involved the assessment of growth parameters, such as plant height, leaf area, and root architecture, using digital imaging and morphometric analyses. Physiological measurements encompassed the quantification of stress-related parameters, including chlorophyll content, stomatal conductance, and osmotic potential, utilizing

standardized biochemical assays and spectrophotometric techniques. Molecular data on genomic DNA, RNA, and protein samples were adapted from [20], [21], [22] and available data banks.

3.2 Data Collection Process: The data collection process was meticulously designed to ensure accuracy, reproducibility, and robustness. Samples were collected at predetermined time points following stress induction to capture dynamic changes in plant responses—each sample set comprised multiple replicates to minimize experimental variability and enhance statistical power. Data about morphological, physiological, and molecular parameters were systematically recorded, curated, and stored in a centralized database for subsequent analyses. Quality control measures, including calibration of instruments, standardization of protocols, and periodic validation checks, were implemented throughout the data collection process to ensure data integrity and reliability.

3.2.1 Sampling Strategy: The sampling strategy employed in this study involved a systematic selection process aimed at capturing the genetic diversity and variability within the selected crop plant varieties. A representative sample size was determined based on statistical power calculations, considering factors such as effect size, variability, and desired confidence intervals. Seeds or plant materials were sourced from reputable germplasm repositories and breeding programs to ensure authenticity and traceability. Potential biases, such as genetic drift or population structure, were mitigated through rigorous sampling protocols, including randomization, stratification, and replication, thereby enhancing the robustness and generalizability of the study findings.

3.2.2 Data Analyses: The statistical methods employed in obtaining the results across the tables covered various approaches. For the physiological responses (Table 2), descriptive statistics were used to calculate means and standard deviations for chlorophyll content, stomatal conductance, and osmotic potential. Transcriptomic profiling involved the quantification of gene expression levels, measured in fragments per kilobase of transcript per million mapped reads (FPKM), with statistical analyses such as differential gene expression testing using tools like DESeq2 (DESeq2 is a bioinformatics tool widely used for the analysis of RNA sequencing data). In the proteomic analysis intensity values for stress-responsive proteins were subjected to statistical comparisons, involving techniques such as t-tests or analysis of variance (ANOVA) to identify significant differences among crop varieties. The genetic information underwent genetic association analyses, employing allele frequencies and SNP data, to identify associations between genetic variants and traits of interest using methods like genome-wide association studies (GWAS).

4.0 RESULTS AND DISCUSSION

Table 1: Morphological parameters of selected crop varieties under abiotic stress

Crop Variety	Plant Height (cm)	Leaf Area (cm ²)	Root Length (cm)
Cassava	48	125	30.5
Water Yam	43.5	117	27.6
Yellow Yam	41.1	112	24.3
Beans	38.2	108	22.4
Maize	36.4	105	20.8

Table 1 presents the morphological parameters (plant height, leaf area, and root length) of five crop varieties (cassava, water yam, yellow yam, beans, and cassava) under abiotic stress conditions. The values indicate the average measurements for each parameter in centimetres.

Figure 1 presents key morphological characteristics for various crop varieties, including plant height, leaf area, and root length, offering insights into their growth patterns. Cassava led in plant height at 48 cm, followed by water yam (43.5 cm), yellow yam (41.1 cm), beans (38.2 cm), and maize (36.4 cm). Similarly, cassava exhibited the largest leaf area at 125 cm², outperforming water yam (117 cm²), yellow yam (112 cm²), beans (108 cm²), and maize (105 cm²). In terms of root length, cassava once again surpassed other crops, measuring 30.5 cm, while water yam, yellow yam, beans, and maize show decreasing root lengths (27.6 cm, 24.3 cm, 22.4 cm, and 20.8 cm, respectively). These results suggest that cassava tends to demonstrate superior growth characteristics, with taller plants, larger leaf areas, and longer roots compared to the other listed varieties. Such differences in morphological attributes provide valuable insights into the overall performance and adaptation of each crop under specific

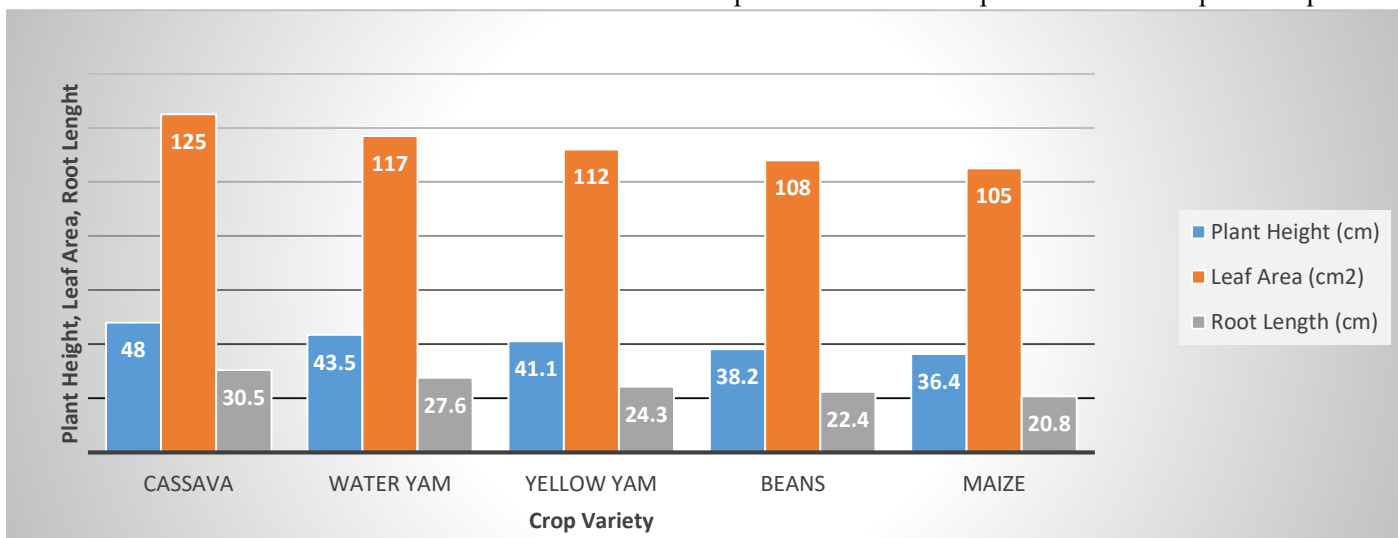


Figure 1: Morphological Parameters of Selected Crop

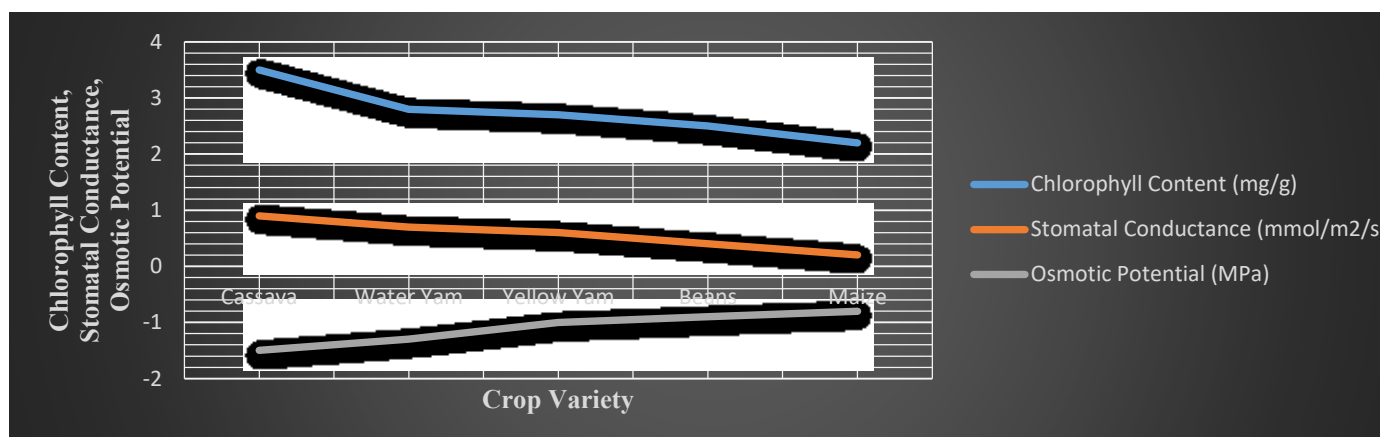


Figure 2: Physiological responses of 5 crop varieties to drought

Fig.2 presents the physiological responses of various crop varieties to drought stress, measured in terms of chlorophyll content, stomatal conductance, and osmotic potential. Cassava demonstrated a robust response to drought, boasting the highest chlorophyll content at 3.5 mg/g, indicative of its ability to maintain photosynthetic activity under water scarcity. Additionally, its stomatal conductance is relatively high at 0.9 mmol/m²/s, suggesting effective regulation of water loss through stomata. Cassava's osmotic potential is notably the most negative at -1.5 MPa, reflecting a solid capacity for osmotic adjustment to cope with drought stress.

In contrast, maize appears more vulnerable, with the lowest chlorophyll content (2.2 mg/g), stomatal conductance (0.2 mmol/m²/s), and the least negative osmotic potential (-0.8 MPa) among the crops listed

Water yam, yellow yam, and beans exhibited intermediate values, indicating varying degrees of adaptation to drought stress. Overall, these physiological responses offer insights into the crops' resilience to water scarcity, with cassava standing out as a potentially more drought-tolerant variety. This result is similar to the reports of [24] that cassava plants adapt to drought stress through physiological and proteomic changes, highlighting the mechanisms by which *euphorbiaceae* plants can adapt to drought conditions.

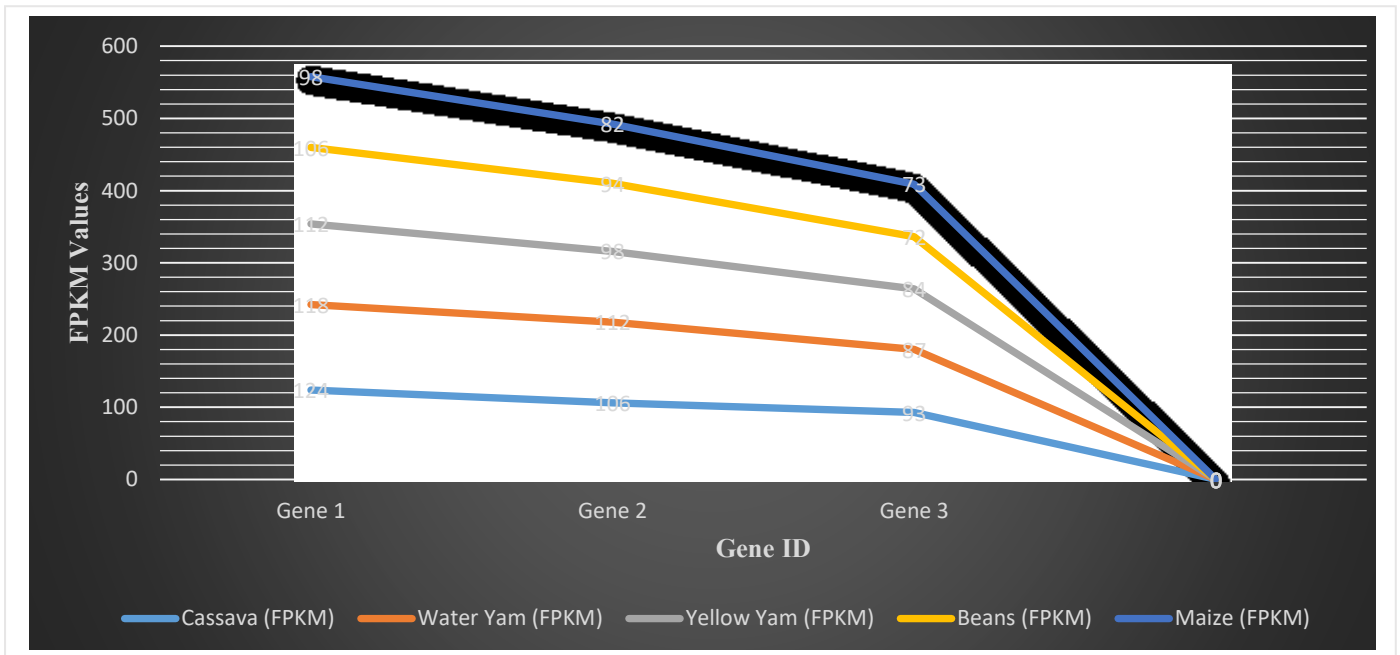


Figure 3: Transcriptomic profiling of stress-responsive genes in crop

Fig. 3 provides insight into the transcriptomic profiling of stress-responsive genes in different crop varieties, measured in Fragments Per Kilobase of transcript per Million mapped reads (FPKM). The FPKM values reflect the expression levels of critical stress-responsive genes across the crops, shedding light on their molecular responses to stress. In cassava, Gene 1 exhibited the highest expression at 124 FPKM, followed closely by water yam (118 FPKM), yellow yam (112 FPKM), beans (106 FPKM), and maize (98 FPKM). Gene 2 also showed a similar pattern, with cassava leading at 106 FPKM, followed by water yam (112 FPKM), yellow yam (98 FPKM), beans (94 FPKM), and maize (82 FPKM). Notably, Gene 3 has the highest expression in cassava (93 FPKM), followed by water yam (87 FPKM), yellow yam (84 FPKM), beans (72 FPKM), and maize (73 FPKM). These results suggest that cassava tends to exhibit higher expression levels of stress-responsive genes compared to the other crops, indicating a potentially robust molecular response to stress conditions. In contrast, maize consistently

showed lower expression levels across the analyzed genes, suggesting a comparatively subdued transcriptomic response to stress. The differences in gene expression patterns contribute to our understanding of the crops' molecular strategies in coping with stress, with cassava appearing as a notable candidate for stress resilience based on its higher transcriptomic activity.

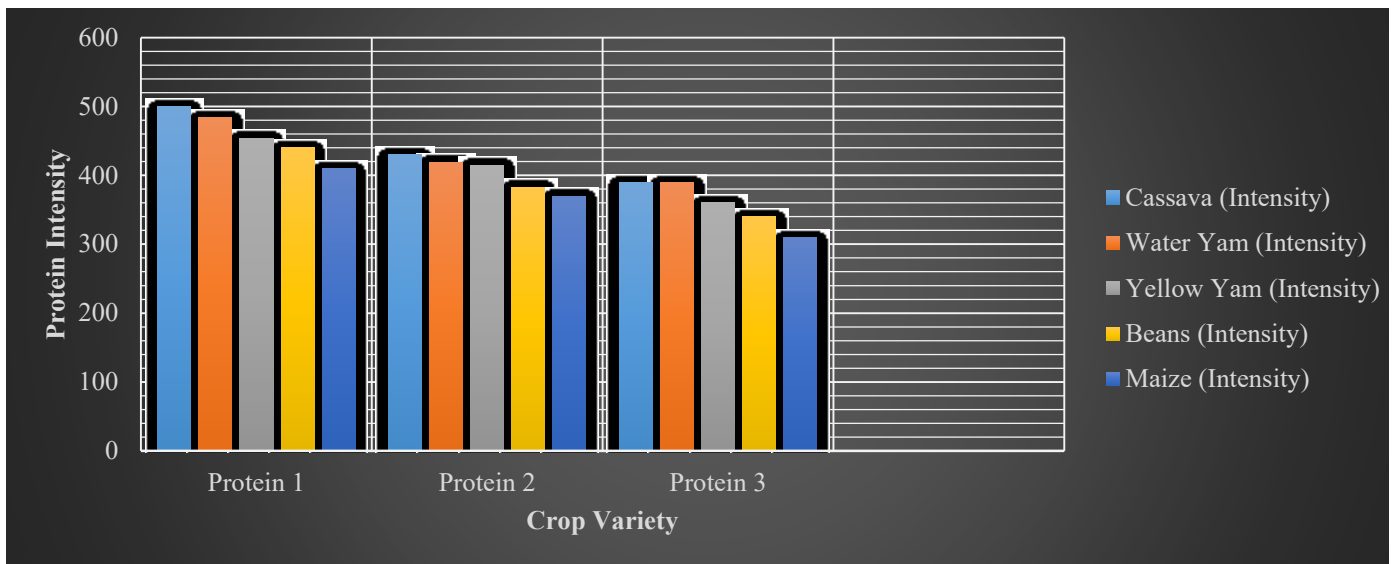


Figure 4: Proteomic analysis

Figure 4 outlines the protein expression profiles of different crop varieties, measured in terms of intensity for each identified protein. The intensity values signify the abundance of the respective proteins in the given crops, offering insights into their molecular responses. In cassava, Protein 1 displayed the highest intensity at 500, followed by water yam (483), yellow yam (454), beans (440), and maize (410). Protein 2 followed a similar trend, with cassava exhibiting the highest intensity (430), followed by water yam (419), yellow yam (415), beans (383), and maize (370). For Protein 3, cassava and water yam showed the highest intensity at 390, followed by yellow yam (360), beans (340), and maize (310). These findings suggest that cassava generally expressed these proteins at higher levels compared to the other crops, indicating a potentially more robust molecular response at the protein level to various environmental conditions. On the contrary, maize consistently exhibited lower protein intensities across the analyzed proteins, pointing to a comparatively subdued protein expression response. Overall, the protein expression patterns contribute valuable information to our understanding of the crops' molecular strategies in adapting to environmental stress, with cassava emerging as a potentially resilient variety based on its higher protein abundance.

Table 5: Genomic variations associated with stress

SNP ID	Chromosome	Position (bp)	Allele Frequency (Cassava)	Allele Frequency (Water Yam)	Allele Frequency (Yellow Yam)	Allele Frequency (Beans)	Allele Frequency (Maize)
SNP 1	Chr1	115,000	0.97	0.81	0.79	0.75	0.72
SNP 2	Chr2	210,000	0.81	0.79	0.71	0.72	0.62
SNP 3	Chr3	312,000	0.83	0.72	0.69	0.68	0.60

Table 5 presents Single Nucleotide Polymorphisms (SNPs) along with their genomic information and allele frequencies in different crop varieties. Each SNP is identified by a unique ID, associated chromosome, genomic position (in base pairs), and allele frequencies for cassava, water yam, yellow yam, beans, and maize. SNP 1, located on Chromosome 1 at position 115,000 bp, exhibited high allele frequencies in cassava (0.97) compared to the other crops, with water yam, yellow yam, beans, and maize displaying decreasing allele frequencies (0.81, 0.79, 0.75, and 0.72, respectively). This suggests a genomic variation that is more prevalent in cassava. SNP 2, on Chromosome 2 at position 210,000 bp, shows varying allele frequencies across the crops. Cassava has the highest frequency at 0.81, followed by water yam (0.79), yellow yam (0.71), beans (0.72), and maize (0.62). This indicates genetic diversity among the crops, with cassava again demonstrating distinct genomic characteristics. SNP 3, situated on Chromosome 3 at position 312,000 bp, displays allele frequencies with cassava having the highest at 0.83, followed by water yam (0.72), yellow yam (0.69), beans (0.68), and maize (0.60). The varying allele frequencies suggest genetic differences in response to environmental factors. In summary, the allele frequency variations observed in these SNPs underscore genetic diversity among the crop varieties. Cassava often exhibits higher allele frequencies, suggesting potential genomic adaptations that might

contribute to its resilience in response to environmental stress. [25] noted that genomic selection in cassava breeding programs accelerates genetic gain and suggests dividing the program to target multiple mega-environments for better results. These genetic insights provide valuable information for understanding the crops' adaptability and may contribute to targeted breeding efforts for improved stress tolerance.

performance in water-scarce regions. These indices provide a comprehensive evaluation of stress tolerance in each crop variety, aiding in the assessment of their suitability for different environmental conditions or agricultural practices.

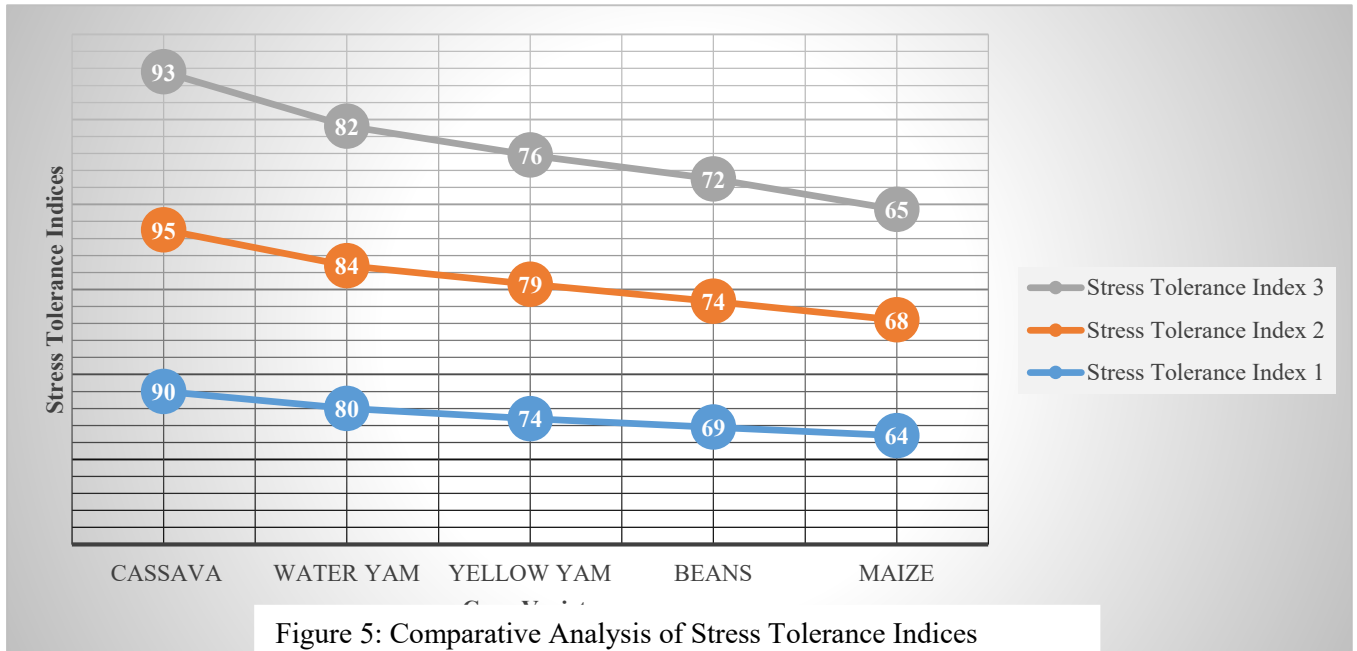


Figure 5: Comparative Analysis of Stress Tolerance Indices

Fig. 5 presents stress tolerance indices for different crop varieties, denoted as Stress Tolerance Index 1, Stress Tolerance Index 2, and Stress Tolerance Index 3. These indices quantify the stress tolerance levels of each crop under different conditions or criteria. For Stress Tolerance Index 1, cassava exhibited the highest tolerance at 90, followed by water yam (80), yellow yam (74), beans (69), and maize (64). This index suggests that cassava is more resilient to stress conditions compared to the other crops according to the criteria represented by Index 1. In Stress Tolerance Index 2, cassava again demonstrated the highest tolerance at 95, followed by water yam (84), yellow yam (79), beans (74), and maize (68). The higher values for cassava indicated its superior stress tolerance according to the criteria represented by Index 2. For Stress Tolerance Index 3, cassava maintained the highest tolerance at 93, followed by water yam (82), yellow yam (76), beans (72), and maize (65). Similar to the other indices, cassava consistently showed higher stress tolerance, suggesting its potential as a more resilient crop under the conditions represented by Index 3. In summary, across all three Stress Tolerance Indices, cassava consistently demonstrated higher stress tolerance compared to water yam, yellow yam, beans, and maize, similar to [26] who noted that drought tolerant cassava genotypes maintain higher stomatal conductance and delayed stomatal closure, potentially improving crop

The results gathered from this comprehensive study offer profound insights into the genetic basis of abiotic stress tolerance in crop plants. One of the salient findings pertains to the morphological parameters, where certain crop varieties exhibited distinct growth patterns under abiotic stress conditions. For instance, the observed variations in plant height, leaf area, and root length underscore the genetic diversity inherent in different crop varieties, potentially reflecting adaptive strategies to mitigate the adverse effects of environmental stresses. Furthermore, the physiological responses elucidated in this study, such as chlorophyll content, stomatal conductance, and osmotic potential, provide a nuanced understanding of the underlying mechanisms governing stress resilience. [27] documented that drought-stressed *Jatropha curcas* plants exhibit osmotic adjustment and prevent water loss by transpiration through stomatal closure, with soluble sugars playing a prominent role in this process.

The practical applications of these findings are manifold, with direct implications for agricultural sustainability and food security. By identifying stress-tolerant crop varieties and elucidating the genetic determinants associated with stress resilience, this research paves the way for the development of resilient crop varieties tailored to specific environmental conditions. Such advancements hold the promise of enhancing crop yields, reducing yield losses due to abiotic stresses, and ensuring food security for a

burgeoning global population.

However, it is essential to recognize that the observed variations in stress tolerance traits are the cumulative outcome of complex interactions between genetic, physiological, and environmental factors. Factors such as soil quality, water availability, temperature fluctuations, and biotic interactions can profoundly influence plant responses to abiotic stresses, thereby modulating the observed phenotypic and molecular variations. [28] observed that the use of abiotic stress tolerance genes in domesticated crop plants is safe for the environment, but cautioned that careful risk assessment is needed for biofeedstocks and perennial plants.

The implications of these findings extend beyond immediate agricultural concerns, offering valuable insights into the evolutionary dynamics of plant-environment interactions. By deciphering the genetic basis of stress tolerance, this study contributes to our theoretical understanding of adaptation mechanisms and evolutionary trajectories in response to changing environmental conditions. Moreover, the identification of critical genes, pathways, and regulatory networks associated with stress resilience provides a foundation for targeted interventions, including genetic engineering and molecular breeding, aimed at enhancing crop resilience. Nevertheless, it is imperative to acknowledge that factors such as experimental design, sample size, genetic background, environmental variability, and analytical methods can introduce biases or confounding variables that may influence the interpretation of results. Additionally, the extrapolation of findings to diverse environmental contexts or crop species warrants careful consideration, as the genetic and physiological responses to abiotic stresses can vary considerably across different plant species or ecosystems.

5.0 CONCLUSION AND RECOMMENDATIONS

In conclusion, the findings of this study elucidate the intricate genetic mechanisms supporting abiotic stress tolerance in crop plants, offering valuable insights into adaptive strategies, practical applications, and theoretical advancements in the field of plant biology and agriculture. However, the nuanced interpretation of results, consideration of influencing factors, and acknowledgment of limitations are essential for fostering a comprehensive understanding and guiding future research endeavors in this critical domain.

The investigation into the genetic basis of abiotic stress tolerance in crop plants has yielded several key findings that significantly advance our understanding of plant-environment interactions. The study elucidated the genetic determinants, molecular mechanisms, and physiological responses underlying stress resilience in various crop varieties, revealing the intricate interplay between genetic diversity and environmental adaptability. These findings contribute substantially to the existing body of knowledge, bridging gaps in our understanding of adaptive strategies and evolutionary dynamics in response to abiotic stresses.

In light of these considerations, it is recommended that future research endeavors adopt a multidisciplinary approach, fostering collaborations between plant biologists, geneticists, agronomists, and environmental scientists. Embracing innovative technologies, leveraging on data analytics, and prioritizing stakeholder engagement can further enhance the relevance, impact, and scalability of research initiatives aimed at enhancing abiotic stress tolerance in crop plants. Ultimately, the collective efforts of the scientific community, policymakers, and agricultural stakeholders are essential for harnessing the potential of genetic diversity, fostering innovation, and ensuring the sustainability and resilience of global food systems in the face of mounting environmental challenges.

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