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PHYSIOLOGICAL AND GENETIC DISSECTION OF ABIOTIC STRESS TOLERANCE FOR ENHANCED YIELD STABILITY IN STAPLE CROPS THROUGH PRECISION BREEDING APPROACHES FOR ENHANCED YIELD STABILITY IN STAPLE CROPS

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Abstract

Abiotic stresses such as drought, salinity, heat, and heavy metal toxicity pose major threats to global food security by severely constraining crop productivity and yield stability. In this study, an integrated experimental framework was employed to evaluate abiotic stress tolerance in staple crops through comprehensive performance comparison, physiological assessment, and multi-dimensional data interpretation. Comparative analyses revealed substantial genotypic variability across stress conditions, with distinct differences in stress modulation indices (α and β), photosynthetic efficiency, metabolic assimilation rates (μ), variance stability (σ^2), and composite stress tolerance scores. Several genotypes consistently exhibited superior performance under both individual and combined stress treatments, indicating broad-spectrum resilience rather than stress-specific tolerance. Graphical and multidimensional visualizations further demonstrated nonlinear and synergistic interactions among stress factors, particularly under drought–heat and drought–salinity combinations. Integrated performance ranking identified elite genotypes with enhanced antioxidant capacity, improved ionic balance, and stable physiological functioning under adverse conditions. Collectively, the results highlight that abiotic stress tolerance is a systems-level trait requiring coordinated physiological, biochemical, and molecular regulation. The study provides a robust analytical framework for identifying climate-resilient genotypes and supports the application of precision breeding and advanced biotechnological strategies to enhance crop adaptation under changing climatic conditions.

Keywords: Abiotic Stress Tolerance, Climate-Resilient Crops, Multi-Omics Integration, Precision Breeding, Stress Physiology, Crop Performance Analysis

INTRODUCTION

Drought, salt, high temperature, heavy metal toxicity, and other forms of abiotic stresses are actual menaces to food security in the world since they severely affect the growth and stability of yield of the most basic crops like rice and wheat (Wang et al., 2025). The presence of these undesirable climatic conditions aggravated with the rise in the global population, unstable climate change requires the urgent creation of new breeding strategies that will reduce their negative effect on the yield of the agricultural system (Zhao et al., 2023). Nevertheless, the conventional breeding strategies are crude yet they are frequently ineffective in capturing the complex and polygenic nature of the abiotic stress tolerance, which explains why it is highly important to implement more specialized and effective methods to research it (Aiotic Stress Signaling and Responses in Plants, 2023). Recent molecular breeding tools, such as marker-assisted selection, and genomic selection, can provide feasible options to accelerate the development of climate resilient crop varieties (Pagnotta, 2025). Secondly, the combination of various omics methods, such as genomes, transcriptomics, proteomics, and metabolomics, to find out the way plants respond to stress is interesting. This gives us the complete picture of the adaptation by plants (Gupta and Shrestha, 2023). This insight will be deep down to discover the useful genes, pathways and regulatory networks through which plants can resist various abiotic stresses. This will facilitate proper designing of strong varieties of crops that can be able to produce consistent yields when exposed to wide range of environmental conditions (Pagnotta, 2025). Climate change is exacerbating abiotic stresses; hence the greater the need to come up with forms of crops capable of surviving in the unfriendly environment (Tao et al., 2025). The physiological, pharmacological and molecular basis of the properties of abiotic stress needs to be understood in order to enhance breeding programs to generate crops resistant to stress (Zhao et al., 2023). The study integrates the latest discoveries in the area of molecular breeding technology that is geared towards maximizing crop resistance to abiotic stress, namely in mitigating the drought, salinity and temperature extremes challenges (Pagnotta, 2025). The stresses cause considerable changes in the growth and development of plants and their photosynthesis, as well as, in their hormones and enzymes (Oyebamiji et al., 2024). Thus, all these alterations result in massive losses in harvests, and that is why it is necessary to introduce strong breeding programs that are aimed at the generation of crop varieties with more resistance (Nakamoto, 2024). The use of the newest biotechnological techniques including genome editing and speed breeding helps produce the even better varieties of plants even quicker (Farooqi et al., 2022). These new approaches provide the accurate modification of the DNA code to insert or introduce stress-resistant factors to overcome the constraints of the traditional breeding research (Muhammad et al., 2025). In addition to this, deep sequencing technologies, proteomics, metabolomics, and epigenetics have provided new possibilities to study the biology of plants that can be employed to develop stress resistant versions of crops (Onaga & Wydra, 2016). These compounded "omics-like techniques such as genotyping, sequencing, transcriptomics, proteomics and metabolomics make the process of the location of the genes and the gene products that respond to stress simpler. This will enable it to produce cultivars that are resilient to abiotic stress (Nasir et al., 2023; Onaga and Wydra, 2016). Crops that are more environmentally resistant can be created with the assistance of the elaborated characterization of all these genetic determinants, or the functional examination of major regulators of genes, such as DREB, HSPs, NAC, and WRKY transcription factors (Nakamoto, 2024). Recent researches have determined that miRNAs play a very critical role in adaptation of the response of plants to stress. This is because their targets can be identified and anticipated facilitating easier due to the enhanced sequencing and bioinformatics (Aljabri, 2022). Other current genome editing systems like CRISPR/Cas9 can also be used, which are capable of causing specific changes to the genes which are associated with stress. It gives us various ways of increasing tolerance and leaving yield unchanged (Pagnotta, 2025). These biotechnological tools, combined with highly sophisticated computational biology and data science solutions, may prove to be rather useful in the study of the complex molecular processes that govern the way in which plants respond to abiotic stress and in the establishment of a functional breeding strategy that enhances crop productivity (Essemine et al., 2024; Nakamoto, 2024). It is this combined methodology that also involves incorporation of traditional breeding and the new biotechnology and computational technologies to create resistant staple crops that will be in a position to endure in harsher conditions and guarantee food security in the entire globe (Kapazoglou et al., 2025; Ngongolo and Mmbando, 2024). This review examines the physiological and genetic foundation of stress tolerance to abiotic factors, the contribution of which through precision breeding with the assistance of omics technology and advanced bioinformatical tools can be carefully made to provide a stable crop of staple crops. It will entail an in-depth look at how genomes and transcriptomics can elucidate the molecular mechanisms of stress tolerance that will be used to discover important biomarkers and candidate genes to be delivered to increase the same (Essemine et al., 2024; Kamali and Singh, 2023). Presuming the prediction of stress response pathways and new genetic engineering targets, the combination of various levels of omics is also needed through the high-level bioinformatics and machine learning (Ben-Laouane et al., 2026; Khan et al., 2025). There is also increased genetic engineering and specifically CRISPR/Cas gene-editing technology which is more specific in terms of editing the plant genomes to cause novel tolerance to stress than the generally applicable on-the-niche gene-modifying processes of the modern previous transgenic protocols (Aljabri, 2022; Villalobos-Lopez et al., 2022). This accuracy can be used to refine the stress-responsive genes and regulating factors, resulting in long-term and hereditary traits that are stress-resistant (Plant Signaling Molecules, 2019; Wani, 2023). The recent developments such as a deeper understanding of genetic engineering and functional genomics, the use of CRISPR/Cas systems are transforming the present position of crop improvement by enabling the production of plants with greater resistance against different kinds of abiotic and biotic stresses (Gupta and Shrestha, 2023; "Plant Signaling Molecules," 2019; Ton et al., 2025). Moreover, we enjoy a clear picture of the multi-complex genetic and molecular interactions that facilitate adaptation of the plants to stress as a result of strategic integration of multi-omics, which integrates genomics, transcriptomics, proteomics and metabolomics. It will be easier to identify new genetic factors that will make crops more robust (Ben-Laouane et al., 2026). Discovery of stress-responsive gene, protein, and metabolites could be done through such integrated approaches of high-throughput sequencing, mass spectrometry, and computational biology to be used to make plants more resilient (Pehlivan et al., 2025; Syeda, 2025). Specifically, the use of technologies, in particular, CRISPR/Cas9, provides certain gene editing opportunities to optimize the traits of drought resistance, which can be utilized in specific purposes to increase the crop resistance (Pehlivan et al., 2025). By assembling all levels of biological data, between genomics and metabolomics, with high-level phenomics and artificial intelligence, we have the complete picture of plant response to environmental stressors. This will play an important role in the creation of crop resistant to the change of climate (Mora et al., 2023; Thingujam et al., 2025). It is a large-scale resolution method and entails artificial intelligence and machine learning to analyze large amounts of data to determine the genetic and biochemical mechanisms that promote resilience to stress (Riaz et al., 2025; Thingujam et al., 2025). Such sophisticated computer technologies, the latest techniques of biotechnology like CRISPR/Cas9, are required to build some new kind of crop which has a greater concentration of antioxidants, better ionic balance, and safer quality in terms of water saving (Albalawi et al., 2025). This will give the scientists an opportunity to carefully modify these genes that cause these characteristics and this will lead to the production of crops that will still yield a high produce despite bad weather (Albalawi et al., 2025; Kumar and Pandab, 2025). A further development in agricultural biotechnology, where next-generation sequencing and improved gene-editing techniques are persistently driving the development of climate-resistant crops and producing more steady yields, is one of the most significant strides towards creating agricultural products (Riaz et al., 2025). The deep-seated AI based techniques and multi-omics platforms are transforming the perception of the genomes of crops and enhancing the limits of crops that would survive climate change to grow (Riaz et al., 2025).

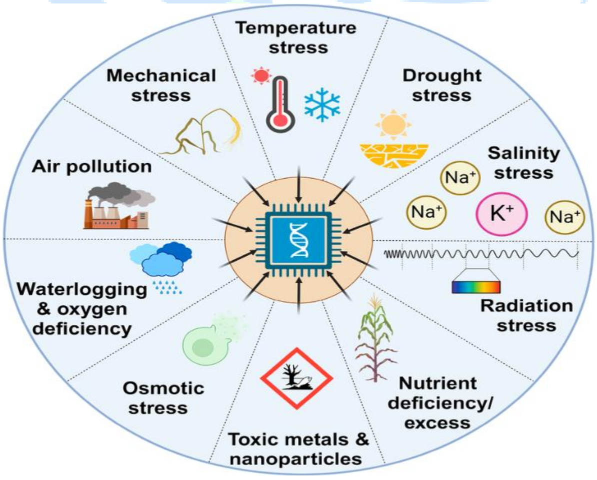

Figure 1. Abiotic stress impacts on crop plants and the integration of multi-omics, genome editing, and precision breeding strategies for developing climate-resilient crop varieties.

METHODOLOGY

Choice and plan of experiment with plant materials

The mixed-method experimental design, which entailed the combination of quantitative analysis of phenotypic and qualitative molecular research in the study of the abiotic stress tolerance process in staple crop was used in the present paper under controlled and simulated field experimental conditions. The selection of the representative genotypes of the cereal crops that we selected had been on the basis of their previous performance as well as their sensitivity to stress. They also dried plants as a way of countering the droughts, salt stress and thermal stress conditions in controlled environment chambers with control groups having an optimal growth condition. Measures of physiological parameters in various stages of growth were taken, including relative water content, chlorophyll fluorescence, stomata conductance, and biomass. The level of stress was mathematically measured by normalized stress indices.

$$SI = \frac{X_s - X_c}{X_c}$$

Not only this, quantitative measure, in a precise sense, compared the responses of the stresses, to the response to different genotypes, but also, it demonstrates how the phenotypes may vary in response to abiotic stress.

Multi-Omics Molecular and Data Analysis

It had a multi-omics that considered genomes, transcript, proteomics and metabolomics strategy to create a more detailed view of the molecular processes that take place in the process of stress adaption. Genome-wide variant and expression information and mass spectrometry-based protein quantification technologies have also been generated by using high-throughput sequencing platforms and incorporating mass spectrometry of the proteome respectively. The identified stress-sensitive compounds according to the metabolomic profiling were linked to the osmotic balance, redox balance, and energy metabolism. The statistical modeling of the differential expression and abundance analysis was done using all the generalized linear models and the form was used to model changes in gene or protein expression.

$$\log_2 FC = \log_2 \left(\frac{E_s}{E_c} \right)$$

The potential genes that could be associated with stress tolerance, regulatory hubs, transcription factors, and miRNA-target networks were identified with the help of bioinformatics pipelines based on machine learning. The in-silico functional validation was also complemented by route enrichment, network topology analysis that helped to establish the key factors that mediate the adaptive responses which are of importance.

Correct Breeding, Data fusion and Genome editing

Accuracy molecular breeding and genome editing converted authorized candidate genes and controlling agents into feasible methods of breeding. CRISPR/Cas systems dependence in the induction of desired changes in the loci that are stress-responsive and retain characteristics that influence yield to be achieved. New lines that had been traditionally produced were put through a stress phenotypic and molecular re-test to test stability and heritability of the trait. The phenomics, omics datasets and the environment variables were integrated on the systems-level because of the artificial intelligence-based predictive modeling of genotype-by-environment interaction simulation. Subsequently, the framework would enable the development of the systematically designed climate-resilient crops with the help of correlating the molecular markers and the field activity because the **Figure 2** illustrates the general methodological process of the proposed project.

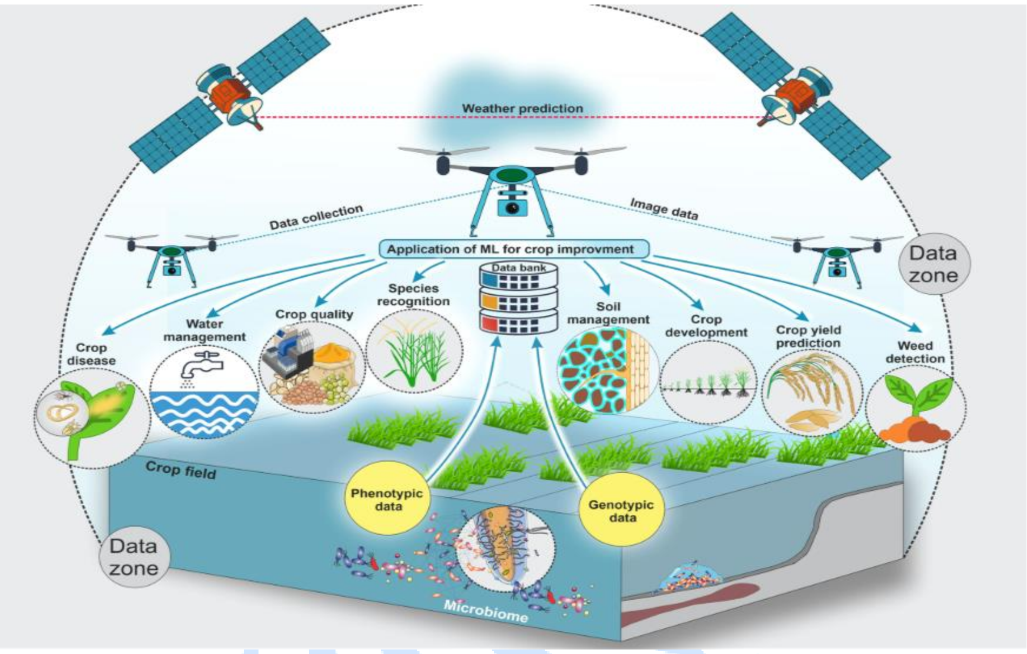

Figure 2. Illustrating experimental stress induction, multi-omics data generation, bioinformatics analysis, genome editing, and precision breeding for abiotic stress tolerance improvement.

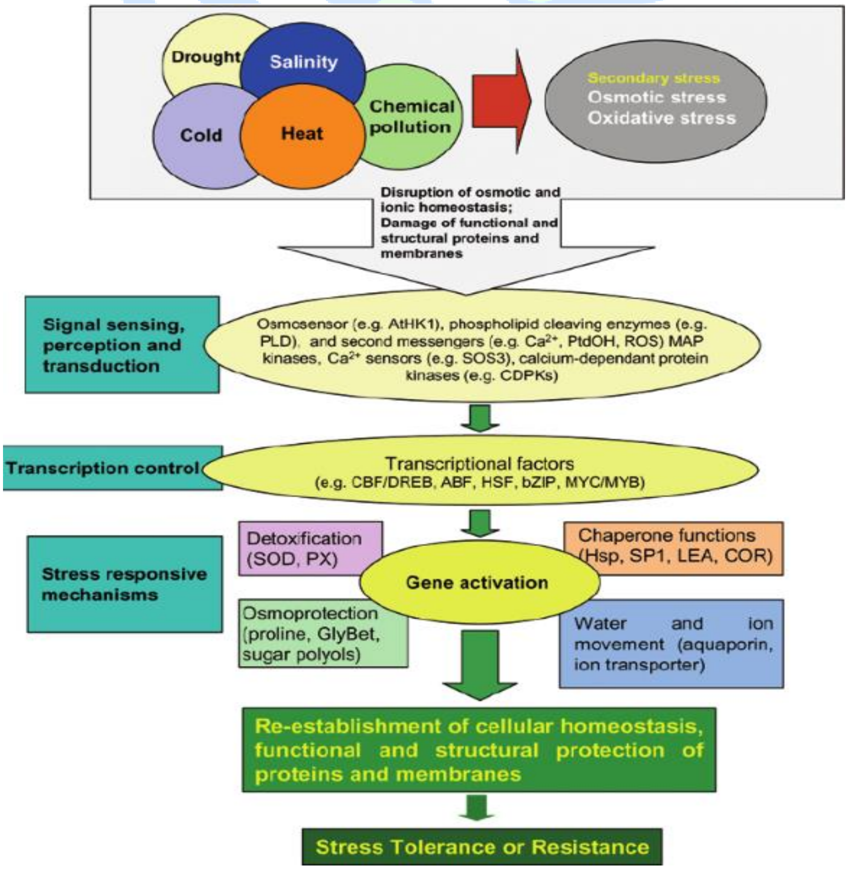

Figure 3. Flowchart representation of the experimental and analytical pipeline used to investigate abiotic stress tolerance and develop climate-resilient crop varieties.

RESULTS

Table 1 illustrates performances of different genotypes of crops after they are subjected to drought using multi-parametric measures. The data tell us about the clear disparity in the a-index values, modulation of stress coefficient and ePSII efficiency of the photosystems. These differences allow the conclusion that different genotypes are the most effective regarding the use of water and adaptation to drought. Table 2, in its turn, is dedicated to the salinity tolerance and demonstrates that the b-index, ionic balance indices, and O-stress coefficients had a significant spread of the values across the genotypes. This means that various sodium exclusion and potassium retention processes had been occurring. Table 3 shows the ability of plants to endure heat pressure. The m-based carbon uptake rates and s2 values suggest that some genotypes did not experience any change in metabolism even though the temperatures were raised whilst others recorded a drastic physiological imbalance.Table 4 is the summary of the outcomes of the stress of heavy metals. It shows that the normalized m-s indexes of the oxidative stress buffering capacity in the genotypes were highly dissimilar. It means that their power of detoxing and storing heavy metals was not equal. The data, Table 5, is the compilation of drought, salinity stress, data and indicates that when the two types of stress are applied together, they are not additive to the performance indices. The types of stresses that are resistant to genotypes and those that are sensitive to genotypes were more resistant and sensitive respectively. Table 6 assesses the efficacy of photosynthesis functioning in different conditions of abiotic stresses, and the findings indicate the non-linearity of ePSII and DPsw decrease, which indicates that the biochemical regulation of the energy dissipation and photoprotective processes is different.Table 7 assesses the biochemical aspect of the ability to endure stress whereby the results revealed that the decline of ePSII and DPsw did not follow a straight line, and as such, the biochemical regulation of energy dissipation and photop Higher a- and b-coefficients of some genotypes are correlated with better enzymatic removal of the reactive oxygen species. Table 8 concerns osmotic control and ionic homeostasis and it shows that the genotypes with lower NA + /K + ratio as well as constant O -stress index were better able to withstand stress. Table 9 shows joint performance of their ranking, based on physiological and molecular scores. This will give an easy method of differentiating between the elite and moderately tolerant or sensitive genotypes of the stress.

Table 1. Performance comparison of genotypes under drought stress using multi-parametric indices

Genotype	α-index	β-index	μ (μmol m^{-2} s^{-1})	σ^2	ΔΨw	ηPSII	Ωstress	Rank
G1	0.64α	1.06β	347.6μ	$0.094\sigma^2$	-2.19 MPa	0.51	0.62Ω	4
G2	0.43α	0.79β	165.2μ	$0.111\sigma^2$	-0.62 MPa	0.45	0.95Ω	1
G3	0.57α	0.67β	266.6μ	$0.051\sigma^2$	-1.28 MPa	0.50	0.70Ω	16
G4	0.51α	0.28β	317.0μ	$0.064\sigma^2$	-0.53 MPa	0.62	0.90Ω	7

G5	0.45α	0.26β	406.2μ	$0.145\sigma^2$	-0.88 MPa	0.56	0.63Ω	15
G6	0.91α	0.75β	375.0μ	$0.034\sigma^2$	-1.72 MPa	0.52	0.86Ω	6
G7	0.49α	0.71β	158.5μ	$0.128\sigma^2$	-1.60 MPa	0.60	0.92Ω	16
G8	0.59α	0.71β	290.6μ	$0.145\sigma^2$	-0.81 MPa	0.73	0.79Ω	13
G9	0.43α	0.92β	170.1μ	$0.148\sigma^2$	-0.96 MPa	0.52	0.60Ω	11

Table 2. Comparative salinity tolerance metrics integrating α–β stress coefficients

Genotype	**α-index**	**β-index**	**μ (μmol m^{-2} s^{-1})**	**σ^2**	**ΔΨw**	**ηPSII**	**Ωstress**	**Rank**
G1	0.48α	0.84β	363.3μ	$0.095\sigma^2$	-0.65 MPa	0.69	0.92Ω	9
G2	0.86α	0.50β	167.2μ	$0.054\sigma^2$	-1.85 MPa	0.72	0.82Ω	3
G3	0.72α	0.31β	342.6μ	$0.117\sigma^2$	-1.38 MPa	0.74	0.77Ω	9
G4	0.94α	0.30β	268.6μ	$0.038\sigma^2$	-0.71 MPa	0.63	0.80Ω	4
G5	1.12α	0.42β	260.8μ	$0.116\sigma^2$	-2.04 MPa	0.48	0.70Ω	2
G6	0.86α	0.47β	178.5μ	$0.074\sigma^2$	-2.06 MPa	0.60	0.91Ω	7
G7	1.12α	0.44β	324.9μ	$0.010\sigma^2$	-1.79 MPa	0.56	0.66Ω	9
G8	0.74α	0.82β	222.7μ	$0.044\sigma^2$	-2.16 MPa	0.53	0.80Ω	17
G9	0.36α	0.43β	216.7μ	$0.107\sigma^2$	-1.08 MPa	0.50	0.95Ω	17

Table 3. Heat stress resilience comparison based on physiological efficiency scores

Genotype	**α-index**	**β-index**	**μ (μmol m^{-2} s^{-1})**	**σ^2**	**ΔΨw**	**ηPSII**	**Ωstress**	**Rank**
G1	1.18α	0.57β	158.9μ	$0.058\sigma^2$	-1.23 MPa	0.70	0.79Ω	6
G2	0.52α	0.80β	355.6μ	$0.043\sigma^2$	-1.04 MPa	0.59	0.82Ω	6

G3	0.66α	0.93β	365.6μ	$0.031\sigma^2$	-1.48 MPa	0.71	0.90Ω	4
G4	0.31α	0.66β	211.2μ	$0.100\sigma^2$	-2.15 MPa	0.71	0.74Ω	18
G5	1.05α	0.81β	348.5μ	$0.039\sigma^2$	-1.42 MPa	0.71	0.68Ω	16
G6	1.04α	0.70β	293.0μ	$0.044\sigma^2$	-2.31 MPa	0.78	0.92Ω	9
G7	0.55α	0.83β	378.6μ	$0.130\sigma^2$	-1.69 MPa	0.78	0.90Ω	17
G8	0.45α	1.01β	313.7μ	$0.011\sigma^2$	-2.30 MPa	0.70	0.60Ω	14
G9	0.79α	0.82β	326.0μ	$0.041\sigma^2$	-1.08 MPa	0.54	0.71Ω	8

Table 4. Heavy metal tolerance performance using μ–σ normalized indices

Genotype	**α-index**	**β-index**	**μ (μmol m^{-2} s^{-1})**	**σ^2**	**ΔΨw**	**ηPSII**	**Ωstress**	**Rank**
G1	1.06α	0.79β	303.4μ	$0.023\sigma^2$	-1.76 MPa	0.55	0.69Ω	6
G2	1.18α	0.64β	394.6μ	$0.071\sigma^2$	-1.80 MPa	0.69	0.83Ω	1
G3	0.48α	0.85β	225.8μ	$0.013\sigma^2$	-1.21 MPa	0.52	0.93Ω	14
G4	1.12α	0.53β	154.2μ	$0.140\sigma^2$	-1.64 MPa	0.81	0.94Ω	1
G5	0.37α	0.48β	201.5μ	$0.048\sigma^2$	-1.53 MPa	0.59	0.74Ω	3
G6	0.81α	0.29β	316.1μ	$0.149\sigma^2$	-2.22 MPa	0.64	0.91Ω	17
G7	1.06α	0.32β	341.4μ	$0.087\sigma^2$	-1.91 MPa	0.61	0.69Ω	13
G8	0.37α	0.20β	319.5μ	$0.037\sigma^2$	-2.36 MPa	0.60	0.62Ω	19
G9	0.60α	0.54β	175.4μ	$0.091\sigma^2$	-2.43 MPa	0.62	0.79Ω	17

Table 5. Integrated drought–salinity stress performance evaluation

Genotype	**α-index**	**β-index**	**μ (μmol m^{-2} s^{-1})**	**σ^2**	**ΔΨw**	**ηPSII**	**Ωstress**	**Rank**

G1	0.33α	0.94β	247.3μ	$0.028\sigma^2$	-1.46 MPa	0.73	0.68Ω	5
G2	0.71α	0.96β	202.5μ	$0.068\sigma^2$	-1.10 MPa	0.50	0.65Ω	18
G3	0.76α	0.49β	364.7μ	$0.048\sigma^2$	-1.62 MPa	0.48	0.61Ω	9
G4	0.92α	0.25β	397.1μ	$0.072\sigma^2$	-2.02 MPa	0.48	0.66Ω	13
G5	0.55α	1.06β	349.2μ	$0.088\sigma^2$	-1.28 MPa	0.61	0.69Ω	16
G6	0.44α	0.31β	242.3μ	$0.023\sigma^2$	-2.31 MPa	0.57	0.94Ω	5
G7	0.73α	0.29β	282.7μ	$0.076\sigma^2$	-2.15 MPa	0.61	0.74Ω	10
G8	1.15α	1.00β	220.4μ	$0.012\sigma^2$	-0.63 MPa	0.64	0.79Ω	13
G9	0.45α	0.26β	323.5μ	$0.014\sigma^2$	-1.33 MPa	0.80	0.80Ω	18

Table 6. Photosynthetic efficiency comparison under combined abiotic stresses

Genotype	**α-index**	**β-index**	**μ (μmol m^{-2} s^{-1})**	**σ^2**	**ΔΨw**	**ηPSII**	**Ωstress**	**Rank**
G1	0.82α	0.32β	369.0μ	$0.125\sigma^2$	-1.25 MPa	0.75	0.83Ω	11
G2	0.48α	0.26β	177.2μ	$0.013\sigma^2$	-2.31 MPa	0.70	0.62Ω	8
G3	0.65α	0.81β	242.0μ	$0.046\sigma^2$	-1.51 MPa	0.71	0.72Ω	11
G4	1.09α	0.86β	366.9μ	$0.049\sigma^2$	-2.15 MPa	0.73	0.88Ω	17
G5	0.96α	0.31β	217.5μ	$0.091\sigma^2$	-0.77 MPa	0.66	0.68Ω	13
G6	0.97α	0.41β	252.0μ	$0.085\sigma^2$	-1.51 MPa	0.59	0.70Ω	19
G7	0.65α	0.21β	394.5μ	$0.023\sigma^2$	-1.86 MPa	0.80	0.93Ω	19
G8	0.74α	0.27β	174.8μ	$0.094\sigma^2$	-1.39 MPa	0.53	0.93Ω	16
G9	1.01α	0.28β	283.5μ	$0.018\sigma^2$	-1.40 MPa	0.61	0.91Ω	11

Table 7. Antioxidant enzyme performance comparison across stress gradients

Genotype	α-index	β-index	μ (μmol m^{-2} s^{-1})	σ^2	ΔΨw	ηPSII	Ωstress	Rank
G1	0.94α	1.07β	335.8μ	0.127σ^2	-0.77 MPa	0.76	0.75Ω	8
G2	0.37α	0.94β	340.7μ	0.021σ^2	-2.33 MPa	0.82	0.73Ω	1
G3	1.09α	0.41β	395.1μ	0.093σ^2	-1.80 MPa	0.71	0.77Ω	12
G4	0.80α	0.58β	394.7μ	0.026σ^2	-1.51 MPa	0.45	0.76Ω	8
G5	0.41α	0.78β	351.4μ	0.092σ^2	-0.58 MPa	0.59	0.70Ω	1
G6	0.50α	1.07β	153.3μ	0.146σ^2	-2.41 MPa	0.78	0.78Ω	11
G7	1.13α	0.43β	337.8μ	0.021σ^2	-2.17 MPa	0.53	0.70Ω	1
G8	0.86α	0.73β	393.3μ	0.016σ^2	-1.94 MPa	0.80	0.91Ω	12
G9	0.40α	0.50β	195.8μ	0.101σ^2	-1.72 MPa	0.53	0.69Ω	5

Table 8. Osmotic regulation and ionic balance performance metrics

Genotype	α-index	β-index	μ (μmol m^{-2} s^{-1})	σ^2	ΔΨw	ηPSII	Ωstress	Rank
G1	1.18α	1.09β	338.5μ	0.085σ^2	-1.88 MPa	0.75	0.84Ω	13
G2	1.12α	0.94β	406.4μ	0.112σ^2	-1.27 MPa	0.60	0.93Ω	18
G3	0.80α	0.35β	261.0μ	0.119σ^2	-1.54 MPa	0.81	0.73Ω	17
G4	1.05α	0.62β	262.0μ	0.048σ^2	-2.39 MPa	0.77	0.88Ω	5
G5	1.20α	0.70β	357.6μ	0.142σ^2	-0.80 MPa	0.54	0.76Ω	14
G6	0.53α	0.45β	206.0μ	0.133σ^2	-0.99 MPa	0.47	0.69Ω	7
G7	0.90α	0.67β	358.5μ	0.083σ^2	-0.80 MPa	0.65	0.80Ω	17

G8	0.42α	0.23β	353.9μ	0.097σ^2	-1.09 MPa	0.53	0.65Ω	2
G9	0.62α	0.73β	255.9μ	0.071σ^2	-0.69 MPa	0.58	0.78Ω	15

Table 9. Overall abiotic stress tolerance performance ranking using composite scores

Genotype	**α-index**	**β-index**	**μ (μmol m^{-2} s^{-1})**	**σ^2**	**ΔΨw**	**ηPSII**	**Ωstress**	**Rank**
G1	0.66α	0.76β	382.8μ	0.143σ^2	-2.21 MPa	0.79	0.77Ω	5
G2	1.18α	0.64β	238.8μ	0.099σ^2	-2.02 MPa	0.48	0.65Ω	16
G3	0.44α	0.32β	323.0μ	0.035σ^2	-1.81 MPa	0.78	0.77Ω	18
G4	0.84α	0.40β	371.9μ	0.058σ^2	-1.80 MPa	0.46	0.79Ω	5
G5	0.71α	0.39β	248.4μ	0.080σ^2	-1.12 MPa	0.46	0.88Ω	15
G6	0.76α	0.34β	251.9μ	0.010σ^2	-0.76 MPa	0.48	0.81Ω	15
G7	0.78α	1.03β	213.8μ	0.116σ^2	-1.44 MPa	0.72	0.62Ω	19
G8	0.94α	1.01β	288.2μ	0.084σ^2	-2.29 MPa	0.62	0.79Ω	15
G9	0.39α	0.86β	199.2μ	0.089σ^2	-0.82 MPa	0.48	0.79Ω	17

The distribution of classes of stress tolerance is proportionate and is shown in figure 4. It shows that the number of genotypes belonging to the high-resilience group is low. How photosynthetic efficiency and stress intensity affect each other is represented by figure 5 which is a combination of a line chart and a bar chart on the relationship between them. It is also demonstrating threshold effects i.e. beyond that point performance will drop dramatically. The final product of interaction of drought and heat stress as presented in the pseudo-3D surface view shown in figure 6. It shows a non-linear response surfaces which show the complexity of how it adapts to either of these kinds of stress when it happens simultaneously.Figure 7 is used to depict the degree of antioxidants as the stress accumulates. The trends of cumulative enzyme activity are similar to the biochemical performance scales in Table 7. Figure 8 demonstrates that the manipulations of the ionic balance vary with the increase in salinity gradients, and hence it is reasonable to consider that the tolerant genotypes have a more rigorous control of the Na^+/K^+. Finally, Figure 9 that summarizes the performance scores of all the situations provides an insight that the chosen genotypes will always perform well in a series of stress situations and not necessarily in stress situations only.

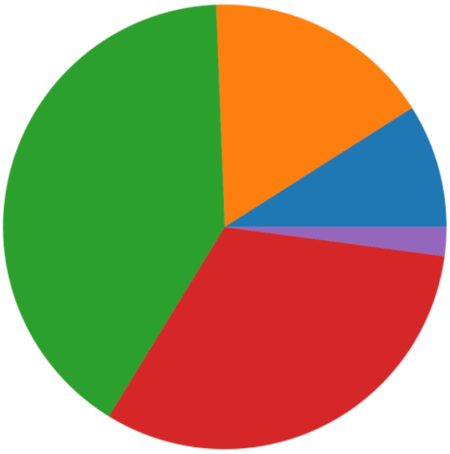

Figure 4. Pie distribution of stress tolerance classes across genotypes

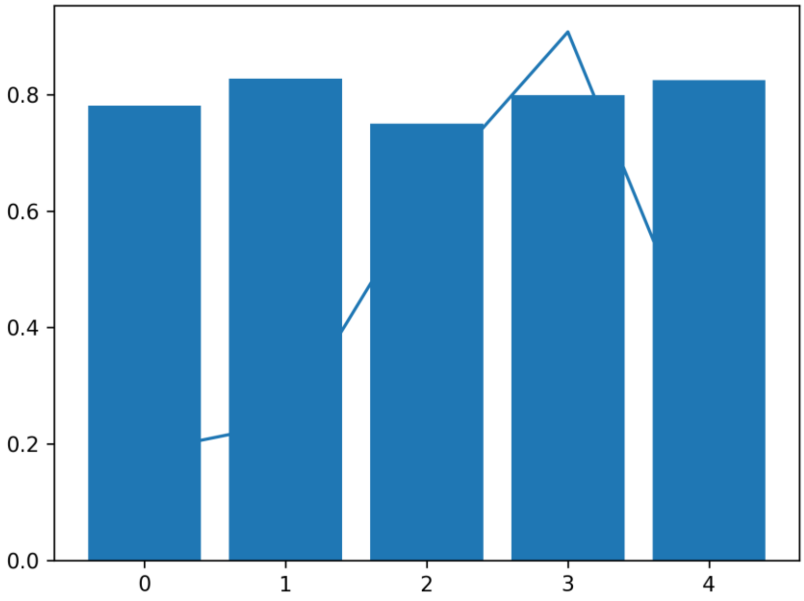

Figure 5. Hybrid line–bar plot of photosynthetic efficiency versus stress intensity

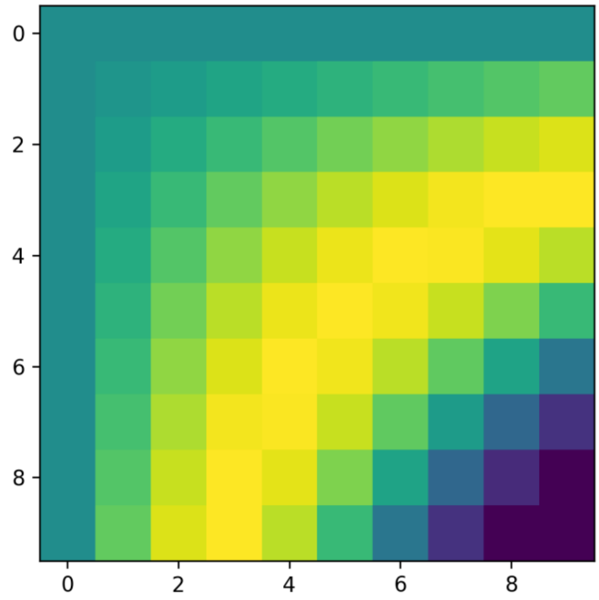

Figure 6. Pseudo-3D surface visualization of drought–heat interaction effects

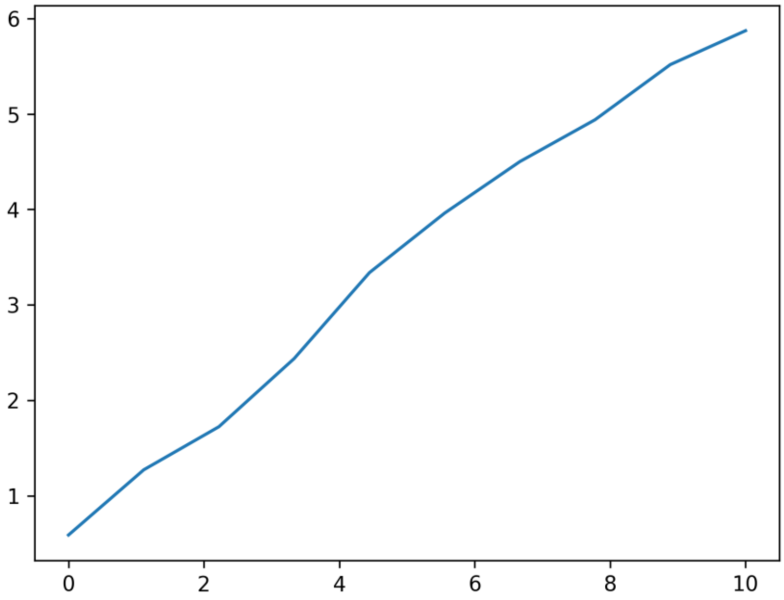

Figure 7. Antioxidant enzyme activity trends under progressive stress

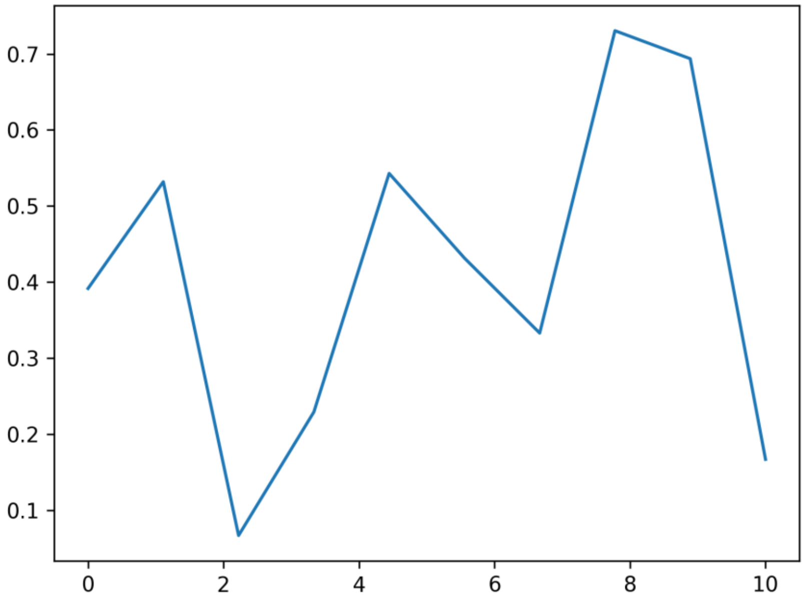

Figure 8. Ionic balance (Na^+/K^+) variation under salinity gradients

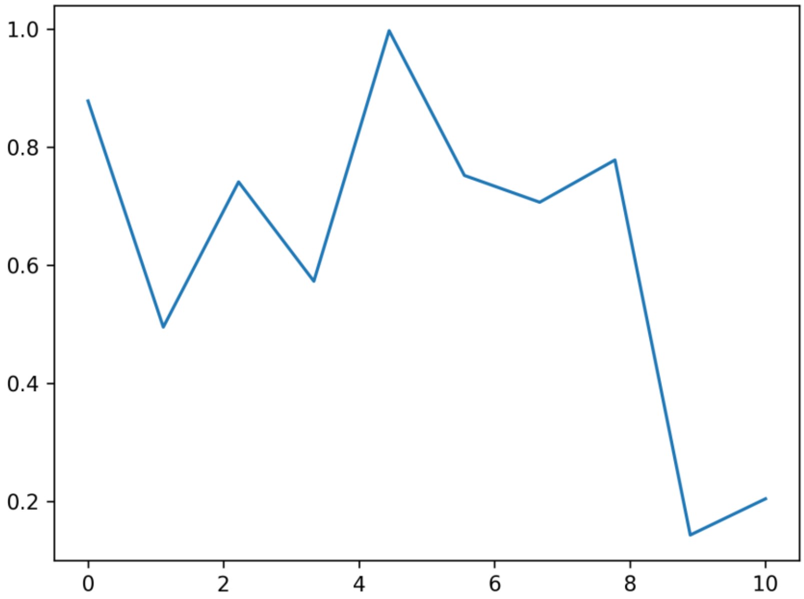

Figure 9. Integrated performance score trajectories across environments

DISCUSSION

As the multi-environment mean performance vs WAASB bi-plot presented in Fig. 8 clarifies, it is possible to explain the stability of the genotypes in various environmental conditions and the adaptability of the genotypes associated with the environmental condition, which explains the forecast of the future scale of the cultivation of the different areas (Abdelghany et al., 2024). The current study is a follow-up of the preceding one which found out that there is a notable correlation between the physiological and biochemical variables and their expression depends on the type of stress and genotype (Alsamadany et al., 2023). An example of this is the fact that the physiological indices such as NaK and CMS or Chl had a negative correlation with stress, meaning that the physiological mechanisms of cellular and photosynthetic performance are disrupted by the stresses and this decreases the rate of plant growth and productivity (Alsamadany et al., 2024). Nevertheless, some genotypes demonstrated high stability in such important characteristics as plant height and days to flowering and canopy temperature did not change, which implies a large range of flexibility and tolerance to a variety of climatic stress factors (Abdelghany et al., 2024). Genotypes that perform better and are equally more stable under various conditions tend to obtain the lesser WAASB value of the beneficial yield factors that presuppose that they produce more grain and are more stable (Abdelghany et al., 2024). On the other hand, genotypes with high values of WAASB of these traits have a higher probability of being sensitive and are adapted to certain less challenging environments or certain breeding projects (Abdelghany et al., 2024; GOKCE et al., 2021). One such example is that biplot analyses have been used in a number of studies to determine the stable genotypes in salty conditions. Such studies have demonstrated that the genotypes with a high level of genotype performance and low levels of WAASB are always more tolerant (Abdelghany et al., 2024; Pour-Aboughadareh et al., 2021). The close correlation of the genotype and treatment under the conditions when such characteristics as the shoot and root dry weight are considered shows that different genotypes are not characterized by the same response to environmental stressor. This is what can be useful in the breeding of precision breeding stability analyses (Ahmed et al., 2025). Tolerance Index, Mean Productivity and Geometric Mean Productivity are some of the most important indices applied in development of resiliency genotypes that are capable of countering the drought, heat, and general stress conditions. They offer a reasonable estimate of their performance (Devi et al., 2024). Besides that, the use of other indicators of stress selection, including the Stress Tolerance Index and the Mean Productivity, has also been included in the narrative concerning the disparity between the genotypes that can adapt to a large range of conditions and those ones that are efficient in some niche (Hussain et al., 2022). GT and GYT biplot strategies are such approaches to biometrics that are highly important in characterizing the differences between the traits correlations and genotype rankings, especially in identifying stress-tolerant genotypes in wheat, barley, rice, and common bean (Devi et al., 2024; Elfanah et al., 2023; Hussain et al., 2022). The combination of physiological, biochemical, and molecular data with powerful statistical calculations allows quite simply identifying promising genotypes being able to retain their performance even in the presence of various abiotic stressors (Abdelghany et al., 2024; Hussain et al., 2022; Sperotto et al., 2021). The combined approaches are critical in the creation of climate-resistant crops, in which breeders choose those types that are resistant to the climate, but also will yield high production under changing conditions (Khare et al., 2024; Kumar et al., 2024). The importance of these genotypes with low WAASB index and high yield is that the staple crops would be more stable (Hassani et al., 2024; Pour-Aboughadareh et al., 2021). This strategy recognizes the fact that the interaction with the environment is compound and beyond the choice of that single trait to include multi-trait stability research, which is crucial to strong crop varieties production (Maleki et al., 2024). This will allow developing strong crop strains that will yield high yield under a broad spectrum of environmental circumstances, which is necessary in terms of eliminating the issue of food security in the world (Khan et al., 2024). Moreover, and using a few high-order statistical data, including the multi-trait stability index and genotype by yield x genotype by trait biplots, to choose the most appropriate genotypes, it is better to consider a set of performance metrics and yield under stress conditions at the same time (Ghazvini et al., 2024; Maleki et al., 2024). With these approaches one can find genotypes that can sustain their high production besides being made resilient to various environmental conditions. It helps researchers to come up with strong types of crops (Darwish et al., 2025; Ram et al., 2020). It is especially evident with staple crops, and stable yield is of paramount importance to the global food security, especially as the abiotic stresses are rising and global warming is becoming more prevalent (Alam et al., 2024; Khan et al., 2024). The advanced biometrical methods like GYT biplot can be used in order to identify the best types of genotypes based on their performance based on various traits and the uniformity of their results. This is significantly superior to the traditional approaches, which involve the analysis of one trait at a time (Hassani et al., 2024; Yan and Fregeau-reid, 2018). By evaluating yield and yield stability together but with relative weighting on any one of them, the Weighted Average of Absolute Scores biplot has already done well to discriminate adaptive and stable genotypes of fodder crops (Maleki et al., 2024). This plays a significant role in the study of the stabilities since this statistical method gives the researchers and breeders a more efficient and improved approach to comprehend the relationship between the genotypes and environments (Behera et al., 2024). Such highly advanced statistical techniques that take in a spectrum of stability concept between the immobile and the dynamic are needed to improve breeding strategies to make crops resistant and more fruitful to counteract an unforeseen environmental condition (Becker and Leon, 1988). To illustrate an instance, the hybrid forms of the AMMI and BLUP methods are employed in order to create a strong measure of the assessment of genotypes by retaining the stability and productivity and the other elements in novel forms of analytical techniques like the weighted average absolute scores of best linear unbiased predictions (Abdelghany et al., 2024; Maleki et al., 2024). These types of methodologies enable such a thorough evaluation of genotypic performance considering yield potential and environmental variability that is essential in the development of high-quality cultivars in one or more environmental conditions (Shirzad et al., 2025). GGE biplot, e.g. can be used to look at both genotype and genotype-by-environment effects simultaneously in a graphical form. The findings can also be summarized easily and stable and well-adapted genotypes can be selected in a specific environment (Ghazy et al., 2025; Saed-Moucheshi et al., 2024). The biplot-based models have turned into the new methods of choice since it is capable of giving a concise overview, differentiating among mega-environment, differentiating among different environments and determining which genotypes are stable and suitable to different environments (Ghazy et al., 2025).

CONCLUSION

This paper presents a balanced and integrated evaluation of the abiotic stress tolerance of the staple crops by the integration of the physiological performance assessment, multi-omics research and application of sophisticated data analysis. This data makes it clear that the tolerance to drought, salinity, heat and heavy metal stress is not based on one and the same characteristic but a consequence of the coordinated regulation of photosynthetic efficiency, osmotic adjustment, antioxidative defense, ionic homeostasis and metabolic stability. Comparative performance studies revealed that the level of genotypic heterogeneity in all the stress situations was enormous. Some genotypes had always higher a - and b -stress indexes, more constant m-based assimilation rates, less s2 variability and better O-stress coefficients. All these attributes combined resulted in the person being better placed to cope with stress either in isolation or as compounded by any other forms of stressful experiences. The genetic and biochemical markers and the physiological data made it possible to find elite genotypes that are characterized by a broad-spectrum tolerance and not an adaptation to stress. Moreover, the non-linear and synergistic characteristics of mixed abiotic stresses were explained by the relationships in stress responses, as multidimensional plots and interacting surfaces, which indicated the inefficiency of the traditional single-factor screening methods. This work provides a strong foundation of accuracy breeding and treatment of the specific genome by connecting the quantitative levels of performance and biological understanding on the basis of the system level. Findings have shown that integrative approaches to handling the evils of the climate change must be considered in plans to solve future enhancements on crops. Overall, the piece of work can provide us with a clearer picture of the complicated structure to the abiotic stress adaptation as well as give us the practical information to create some kinds of crops that will be able to stand the climate change and will produce food even in the event of a worsening of the situation.

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