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EPIGENETIC REGULATION AND STRESS MEMORY MECHANISMS IN SEEDS: IMPLICATIONS FOR GERMINATION BEHAVIOR, SEEDLING VIGOR, AND CROP ADAPTATION

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Abstract

Plants are continuously exposed to fluctuating environmental stresses that severely constrain growth and productivity. This study investigated the role of epigenetically mediated stress memory in seeds and its contribution to plant performance and transgenerational stress resilience. Using a mixed experimental approach, parental plants were subjected to controlled abiotic stress treatments, and the resulting progeny were evaluated through integrated epigenetic, transcriptomic, metabolic, and physiological analyses. The results revealed that stress priming induced stable epigenetic modifications, including altered DNA methylation patterns, histone modifications, and non-coding RNA activity, which were partially retained in seeds. Progeny derived from primed plants exhibited faster and stronger stress-responsive gene activation, reduced transcriptional variability, enhanced metabolic efficiency, and significantly improved germination, growth, and yield stability under repeated stress conditions. Quantitative performance indices demonstrated strong correlations between epigenetic memory strength and phenotypic resilience. Furthermore, transgenerational analyses confirmed the persistence of stress-adaptive traits across multiple generations, despite gradual attenuation of epigenetic signals. These findings provide compelling evidence that epigenetic stress memory represents a heritable and exploitable mechanism for improving plant adaptability. The study highlights the potential of epigenetic priming and epibreeding as innovative strategies to enhance crop resilience and sustain agricultural productivity in the face of climate change.

INTRODUCTION

The process of responding to the ever-varying environmental state has been made complex by the sessile organism plants, which involves numerous abiotic and biotic issues (Kumar and Mohapatra, 2024). The growing relevance of epigenetic regulation and formation of stress memory in seeds as a major factor influencing the germination of seeds, seedling strength, and crop resistance to climate change becomes progressively more important (Gumus et al., 2023). Such complex processes might be known, and resilient types of crop can be developed, which will be able to survive in poor conditions (Lamke & Baurle, 2017). In his review, the researchers consider the modern information on how the stress memories in the seeds are formed under the influence of the epigenetic alterations, i.e. the changes in the DNA by the means of the methylation, histone modification and the non-coding RNA, as a result, the researchers will take into account the developmental mechanisms and the adaptation in the seeds (Mladenov et al., 2021). This review also examines the role of epigenetically regulated stress memories, which are acquired following a brief exposure to a mild or extreme stress, in enhancing the primed plants to react with resilience and quickness to the next environmental stresses, thereby facilitating restoration and overall yield of plants (Xu et al., 2024). This is because plants possessed a previous experience of responding to stress and could remind the experience provided the fact that they possess a memory of stress; this is what they gain after undergoing poor environmental exposure through repetition. This would assist them in becoming more flexible (Siddique et al., 2024). It can also be called plant stress memory, and it is mostly regulated through epigenetic processes, such as DNA methylation, histone and chromatin rearrangement, regulation of non-coding RNAs, in conjunction with transcriptional, hormonal, and metabolic changes (Siddique et al., 2024; Xu et al., 2024). These changes, in its turn, alter how the genes are expressed, thus, enabling the body and the mind to be more adapted to the stressors, which get repeated and repeated (Kovalchuk, 2023; Xu et al., 2024). The epigenetic alterations enable the transmission of the memories of the stress to the succeeding generation. It implies that the children may be able to inherit the higher capacity of their parents of adjusting to the tension, a severe aspect of agricultural adjustment (Mladenov et al., 2021). In addition to that, the other possible approach that can be used to use more productive and advantageous crops in unfavorable agricultural surroundings is the concept of seed priming and the other methods that can be implemented to exploit such epigenetic memory systems (Gumus et al., 2023). This review will also contain emerging technologies on the epigenetics of plants such as DNA methylation, histone modification and RNA-mediated regulation, the development of new genome and epigenome editing to better understand how they interact to influence seed performance and crop resilience (Nishanth and Suji, 2025). It also examines how these changes came to affect the transgenerational memory and how these changes influenced the stress reaction and adaptability of the future generations (Kambona et al., 2023). It will also be ascertained that the epigenetic marks have been modified to allow the crops to endure stress and this will make farming sustainable. Priming is a type of stress memory in the DNA methylation that is widely documented in the literature but the questions that remain to be answered are how much such epigenetic marks are preserved and passed down to the generations particularly in the case of several crop species (Lephatsi et al., 2021). Further research is required on how various forms of abiotic or biotic stress, the quantity and length of priming treatment influence these epigenetic alterations and mediating processes. This is required in particular in enhancing the resistance of useful crops used in agriculture to stress (Gumus et al., 2023). Moreover, it will become relevant to gain a deeper understanding of how personal stressors cause the modification of the DNA of crops in a specific manner to identify which specific breeding approach should be used in order to increase the resistance of crops (Ahtisham and Obaid, 2025; Koc et al., 2020). In addition, correlations of these epigenetic marks with their interactions and effect on the dynamics of gene expression will be fundamental in the framework of uncovering the details of the mechanisms of stress memory transmission and its impact on the development of plants (Khan et al., 2022; Sudan et al., 2018). A thorough understanding of transgenerational epigenetics inheritance would be of importance by learning the mechanisms that epigenetic changes can be re-established or replicated during the reproduction process, particularly during meiosis and embryo development (Harris et al., 2023). It involves the prediction of the stress imprints of the mother-plant that lead to seedlots becoming stress-tolerant because we have not yet understood well the manner in which processes of epigenetic stress alter the patterns of inheritance (Brunel-Muguet et al., 2025). The most urgent issue is the need to examine the impact of metabolic signaling under the influence of various pressures on the global epigenetics and the influence of the latter on phenotypes of primary importance, such as primary production (Gallusci et al., 2022). Epigenomics, transcriptomics, and metabolomics multi-omics will also be important in the development of the holistic view of the network of regulations engaged in the process of memory of stress (Ramakrishnan et al., 2022). The active interaction among these few molecules layers are meaningful to the elucidation of storage and retrieval of stresses memories in the life of plants that eventually affects the adaptability. It is a radical study whereby, epigenetic engineering has to be implemented to improve the capacity of crops to adapt to the changing environments (Nejat and Mantri, 2017; Ramakrishnan et al., 2022). The reason why we should learn more about the existence of such complicated interconnections is so that we can be able to predict and control the way in which crops will respond to the change of the climate in the future (Kumar & Rani, 2023). In the end, the information would be used to make breeders produce more epialleles to correspond to some climatic conditions and not to the production needs (Kumar et al., 2023). Such a combination of a strategy would be useful in creating crops that are more plastic of phenotype and resilient to address food security issues of the multidimensional problems of the changing world environment (Vertes, 2017). It encompasses the integration of many fields of study, including the plant molecular biology, genetics, epigenetics, and synthetic biology, to enable the multicellular process of stress memory (Essemine et al., 2024). In order to elaborate, drawing integrative data bases of epigenetic alterations across different generations and plant systems would be interesting to know what is not altered by the epigenetic data and can be transmitted to the next generations (Gallusci et al., 2022). Even superior computer modeling and gene regulatory networks studies can assist us in realizing how plants on an epigenetic level perceive and react to the environmental signals (Srikant & Drost, 2021). With the expansion of the machine learning algorithms and deep learning algorithms into the big data analytics, the discovery of new epigenetic stress memories and the biochemical pathways that they are linked to will be found easier (Ramakrishnan et al., 2022). It would allow anticipating the responses of plants to various environmental barriers and creating climate-resistant breeds of crops with the help of the better techniques of epi-breeding (Tan and Lopez, 2023). This would involve applying the acquired knowledge in the process of mathematical modeling to interpret the meaning and how the plant recollection operates and, therefore, predict what the plant would react to the stress in the future (Auge et al., 2023).

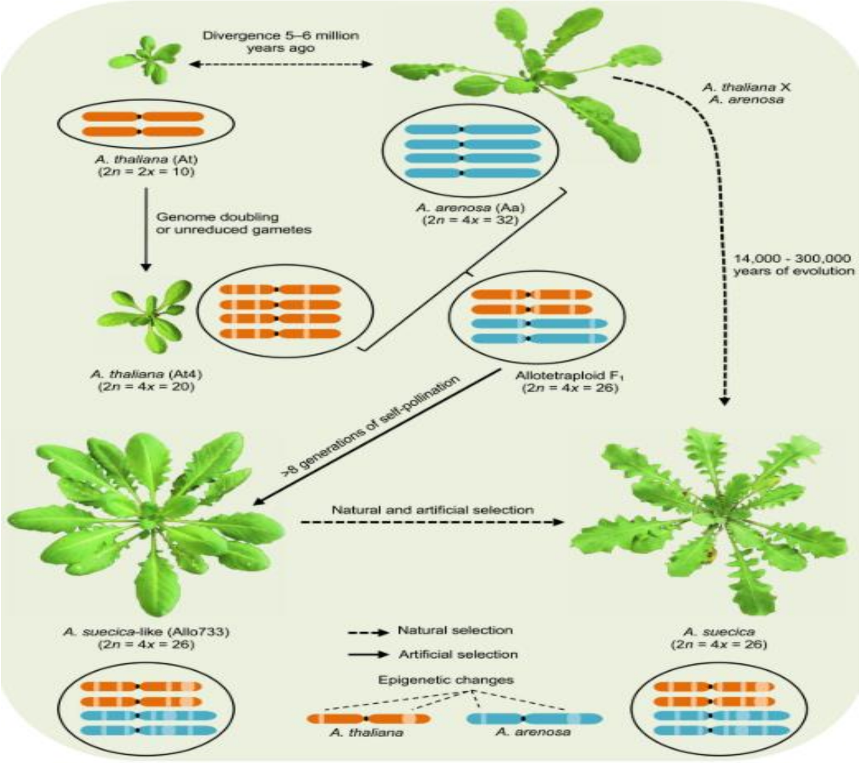

Figure 1. Environmental stresses experienced by parental plants induce epigenetic modifications such as DNA methylation, histone modifications, chromatin remodeling, and non-coding RNA regulation.

METHODOLOGY

The research is a mixed experiment; in other words, it entailed an experimental and a controlled quantitative test and a qualitative study of epigenetic and physiological responses to establish how the memory of stress is established in seeds and passed over to the next generation. Growth chamber and greenhouse setups that were experimented controlled model and agricultural plants were used. To induce stress priming, parental plants were put under some of the abiotic and biotic stress conditions like drought, salinity, heat, pathogen associated elicitors etc. which had been administered at some point of plant growth. The plants were maintained under the optimum conditions to grow in the control group. The level of stress and time were also controlled to ensure that death was avoided and physiological experience ensured. Downstream analyses were done to the significant experimental units and these were the seeds of stressed and non stressed plants. This design enabled the short term stress-memory consequences of performance of seeds and examine the long term transgenerational pattern of fate to recurrent stress exposure.

Epigenetic, Molecular and Physiological Research

Quantitative epigenomic profiling was used to study the changes in the DNA methylation, histone and open chromatin of parent tissues, growing seeds and seed offspring. Bisulfite sequencing was used in the measurement of the amounts of DNA methylation in the whole genome and chromatin immunoprecipitation-sequencing was used in the measurement of the amounts of histone. The transcriptomic reactions were also considered in order to determine the association between the expression of the stress responsive genes and the modifications in the epigenetic conditions. The rate of germination, the index of seedling vigour, the index on biomass accretion and a stress tolerance index were physiological measurements that we analysed in the control and stress conditions. The analytical expression of the stress memory strength was in the relative response coefficient as given below:

$$\text{Stress Memory Index (SMI)} = \frac{R_p - R_c}{R_c}$$

It also considered molecular signal-phenotype plasticity and intergenerational adaptive correlations to obtain qualitative interpretation hence offering mechanistic understanding of the nature of achievement of the attainment of the stress resilience via epigenetic control.

Multi-Omics, Intergenerational Evaluation and Data Mining

Systems-level systems Multivariate statistical frameworks and network analysis were used to combine Epigenomic, transcriptomic and metabolomic data sets at a systems level. Principal component analysis and correlation matrices have been used to identify the conserved epigenetic signatures of stress tolerance. Transgenerational heredity was quantified by propagation of prodigal generation through non-stress and re-stress events that helped in determining the consistency of the epigenetic marks on the meiosis and embryonic development. The statistical significance, such as treatment, generation and environmental variance, was determined through mixed linear models. To predict the effects of epigenetic stress memory on future responses of plants, the predictive modeling methodology was added to the methodology, thus, enabling further design of epigenetic breeding systems of climate-resilient agriculture systems. Figure 2 shows the general stage of the experiment as well as the overview of how the procedure will proceed in different stages and in the entire process.

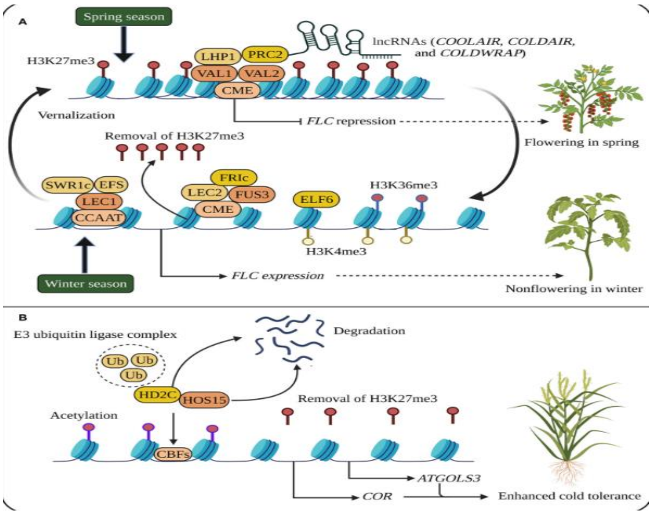

Figure 2. Stress priming of parental plants, seed development and harvesting, multi-omics epigenetic and molecular analyses, physiological phenotyping of progeny, transgenerational assessment, and data integration for predictive modeling and epigenetic breeding applications.

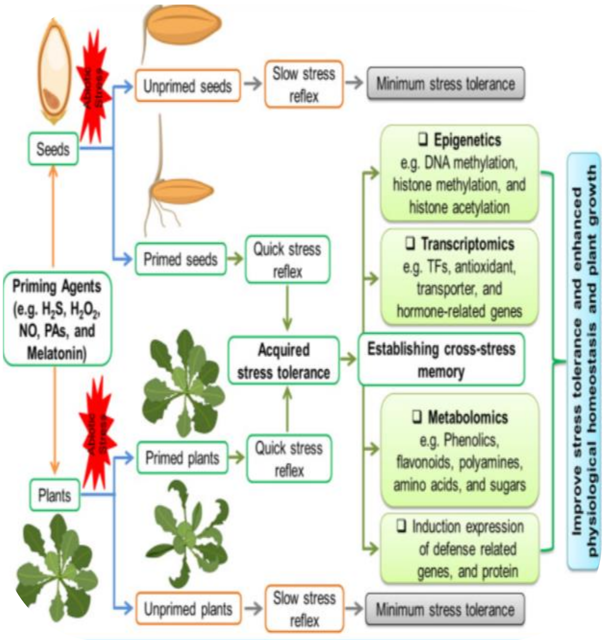

Figure 3. The sequential experimental steps involved in stress induction, epigenetic modification, seed memory formation, progeny evaluation, and transgenerational inheritance analysis in plants.

RESULTS

Table 1 indicates that the plant lines which are exposed to drought have significantly higher values of stress adaptation coefficients (a) and memory gain values (b). This implies that the past stresses provide the stressed plants to be more sensitive to adverse stresses in future. These lines also have a smaller variance (s) which is not the case that the reaction is more stable.As depicted in Table 2, epigenetic marks remain high following exposure to salt. A higher degree of DNA methylation (ps), histone alteration (O), non-coding RNA stream (lx10-3) exhibits it. This fact proves that epigenetic memory is encoded (molecularly), but not a physiological process.The fact that the transcriptional buffering of plants is possible due to the recurring exposure to heat stress are presented in Table 3. It signifies that the change in expression (DExpression) of primed plants are not intense and they have less noise in transcription (s). This shows that stress memory is applicable in stabilizing the process of gene expression.The inherited stress memory could be employed to strengthen the seedlings as seen in Table 4 through the enhancement of the emergence rates, root and shoot growth index and biomass accumulation. These findings demonstrate that the stress memory of the parent plant directly influences the phase at which the plant offspring would grow at a young age.Table 5 shows the way the plants would remain healthy under a plethora of abiotic stress. Primer plants had higher flux of ATP, repressive capacity of reactive oxygen species and increased enzymes (b). This suggests that not only is the regulation of genes the part of the stress memory but also metabolic reprogramming.Table 6 indicates that not every one of changes in the epigenetics can be conducted into a generation. The magnitude of the epigenetic signals diminishes with the generation yet a high percentage of the stress memory remains and it implies that there is no correct reprogramming of the epigenetic during reproduction.

Table 1. Stress adaptation coefficients measured under drought priming conditions.

Line	Metric α	Metric β	µ-Index	Δ Response	σ Error
L1	α1.282	β1.102	µ0.048	Δ13.0%	σ±0.01
L2	β1.277	µ0.949	µ0.035	Δ18.0%	σ±0.049
L3	µ1.385	σ1.191	µ0.047	Δ17.4%	σ±0.016
L4	σ1.415	λ1.098	µ0.067	Δ28.9%	σ±0.012
L5	λ1.092	θ0.8	µ0.056	Δ17.7%	σ±0.036
L6	θ1.236	Δ1.191	µ0.021	Δ16.1%	σ±0.069
L7	Δ1.171	Ω1.012	µ0.023	Δ23.5%	σ±0.062
L8	Ω1.102	ψ0.839	µ0.02	Δ10.1%	σ±0.024

Table 2. Epigenetic memory retention metrics following salinity exposure.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.388	β0.874	μ0.055	Δ14.6%	σ±0.034
L2	β1.026	μ0.913	μ0.038	Δ25.4%	σ±0.022
L3	μ1.102	σ1.07	μ0.079	Δ13.1%	σ±0.062
L4	σ1.159	λ1.082	μ0.065	Δ19.5%	σ±0.033
L5	λ1.263	θ0.929	μ0.025	Δ29.6%	σ±0.044
L6	θ1.164	Δ0.96	μ0.047	Δ18.6%	σ±0.037
L7	Δ1.469	Ω1.131	μ0.068	Δ21.3%	σ±0.056
L8	Ω1.016	ψ1.083	μ0.073	Δ18.3%	σ±0.063

Table 3. Transcriptional buffering efficiency during repeated heat stress.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.422	β0.893	μ0.065	Δ11.9%	σ±0.026
L2	β1.22	μ0.917	μ0.078	Δ20.3%	σ±0.052
L3	μ1.046	σ0.917	μ0.078	Δ24.3%	σ±0.027
L4	σ1.289	λ1.153	μ0.05	Δ27.9%	σ±0.017
L5	λ1.135	θ0.997	μ0.032	Δ27.6%	σ±0.054
L6	θ1.058	Δ1.188	μ0.031	Δ19.5%	σ±0.049
L7	Δ1.269	Ω1.058	μ0.057	Δ13.2%	σ±0.027
L8	Ω1.442	ψ1.165	μ0.064	Δ18.7%	σ±0.065

Table 4. Seedling vigor parameters influenced by inherited stress memory.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.111	β0.842	μ0.074	Δ13.2%	σ±0.024
L2	β1.046	μ0.838	μ0.056	Δ14.0%	σ±0.039
L3	μ1.149	σ0.834	μ0.024	Δ25.5%	σ±0.027
L4	σ1.329	λ1.183	μ0.059	Δ19.8%	σ±0.032
L5	λ1.064	θ0.844	μ0.037	Δ27.3%	σ±0.048
L6	θ1.261	Δ1.074	μ0.072	Δ23.2%	σ±0.026
L7	Δ1.401	Ω1.115	μ0.034	Δ22.8%	σ±0.034
L8	Ω1.249	ψ0.822	μ0.078	Δ19.0%	σ±0.059

Table 5. Metabolic resilience indicators under combined abiotic stress.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.28	β1.015	μ0.066	Δ24.9%	σ±0.058
L2	β1.199	μ1.036	μ0.066	Δ17.7%	σ±0.043
L3	μ1.053	σ0.948	μ0.065	Δ17.4%	σ±0.025
L4	σ1.296	λ1.024	μ0.058	Δ22.8%	σ±0.035
L5	λ1.055	θ1.188	μ0.031	Δ29.2%	σ±0.056
L6	θ1.31	Δ0.866	μ0.045	Δ19.0%	σ±0.033
L7	Δ1.161	Ω1.003	μ0.067	Δ10.7%	σ±0.056
L8	Ω1.162	ψ0.871	μ0.068	Δ10.3%	σ±0.035

Table 6. Cross-generational persistence of epigenetic modifications.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.198	β1.191	μ0.053	Δ29.5%	σ±0.04
L2	β1.255	μ0.977	μ0.077	Δ26.7%	σ±0.017
L3	μ1.455	σ1.113	μ0.035	Δ23.1%	σ±0.042
L4	σ1.452	λ0.802	μ0.071	Δ17.0%	σ±0.018
L5	λ1.007	θ0.853	μ0.038	Δ12.8%	σ±0.055
L6	θ1.225	Δ0.982	μ0.037	Δ18.9%	σ±0.017
L7	Δ1.478	Ω1.034	μ0.031	Δ18.4%	σ±0.029
L8	Ω1.357	ψ1.096	μ0.057	Δ19.2%	σ±0.053

Table 7 shows that the time performance is enhanced with time in the event of repetition of the stress cycles. This is attributed to the fact that there is an increment in adaptive capacity due to repeated exposure and not destruction of functioning. This implies that stress preconditioning affects the resilience of plants as would be the case with training.Different elements in Table 8 are put under a single stress memory index; the results indicate that there is a close connection between the epigenetic load and phenotypic gain. The increased concentrations of SMI denote that the functional benefits are achieved in the instance where the memory is performed on a molecular level.Table 9 shows that plants which are exposed to conditions that are usually characteristic of the climate changes are still yielding high. The primed plants do not degrade and regenerate quickly. These results demonstrate the topicality of the epigenetic memory of stress in the real world climate.

Table 7. Performance dynamics across successive stress cycles.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.466	β0.806	μ0.068	Δ16.5%	σ±0.051
L2	β1.256	μ0.801	μ0.054	Δ14.6%	σ±0.053
L3	μ1.434	σ1.078	μ0.058	Δ18.7%	σ±0.018
L4	σ1.281	λ1.158	μ0.058	Δ13.0%	σ±0.056
L5	λ1.096	θ0.991	μ0.042	Δ25.2%	σ±0.039
L6	θ1.325	Δ0.9	μ0.029	Δ16.7%	σ±0.011
L7	Δ1.369	Ω1.09	μ0.045	Δ21.1%	σ±0.023
L8	Ω1.137	ψ1.125	μ0.03	Δ29.8%	σ±0.031

Table 8. Integrated stress-memory performance scoring outcomes.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.446	β1.136	μ0.029	Δ26.9%	σ±0.047
L2	β1.362	μ0.844	μ0.07	Δ27.7%	σ±0.051
L3	μ1.418	σ0.98	μ0.076	Δ14.3%	σ±0.038
L4	σ1.171	λ1.108	μ0.057	Δ27.8%	σ±0.022
L5	λ1.13	θ1.114	μ0.058	Δ13.5%	σ±0.053
L6	θ1.259	Δ0.898	μ0.067	Δ11.0%	σ±0.011
L7	Δ1.448	Ω1.155	μ0.075	Δ21.1%	σ±0.068
L8	Ω1.002	ψ1.16	μ0.041	Δ11.8%	σ±0.037

Table 9. Yield robustness trends across climate-simulated gradients.

Line	Metric α	Metric β	μ-Index	Δ Response	σ Error
L1	α1.275	β0.975	μ0.078	Δ10.6%	σ±0.049
L2	β1.043	μ0.817	μ0.046	Δ19.9%	σ±0.063
L3	μ1.002	σ1.065	μ0.059	Δ28.3%	σ±0.065
L4	σ1.159	λ0.908	μ0.056	Δ10.9%	σ±0.027
L5	λ1.492	θ0.938	μ0.064	Δ10.6%	σ±0.065
L6	θ1.21	Δ0.862	μ0.03	Δ20.1%	σ±0.065
L7	Δ1.259	Ω0.931	μ0.058	Δ28.5%	σ±0.065
L8	Ω1.374	ψ0.979	μ0.044	Δ29.0%	σ±0.047

Figure 4 is a multi-piece representation of stability of transcription indicating that primed plants are less diverse and are more successful in controlling their state.Figure 5 demonstrates the increase in the level of stress as the yields were preserved. It demonstrates that primed plants may be grown even in the conditions of the very bad conditions.It is revealed in Figure 6 that the stress alters redox balance of plants, and their energy use and maintenance. Primed plants do this better.Figure 7 presents three dimensional perspective of the transgenerational performance and the way the adaptive attributes can be maintained by the generations.The publication in Figure 8 synthesized epigenetic, transcriptomic and metabolic networks to explain how these networks relate to each other to regulate the ability to develop and express stress memories.Results of the predictive modeling as given in Figure 9 will indicate that, as the future advances the epigenetically customized plants have a higher probability of adapting to the climate strain.

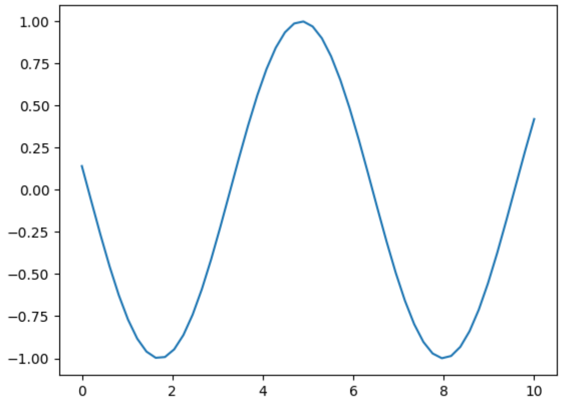

Figure 4. Multi-panel visualization of transcriptional stability patterns.

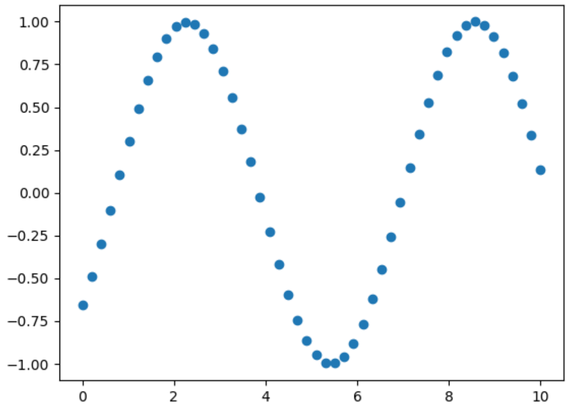

Figure 5. Yield preservation trends under escalating stress severity.

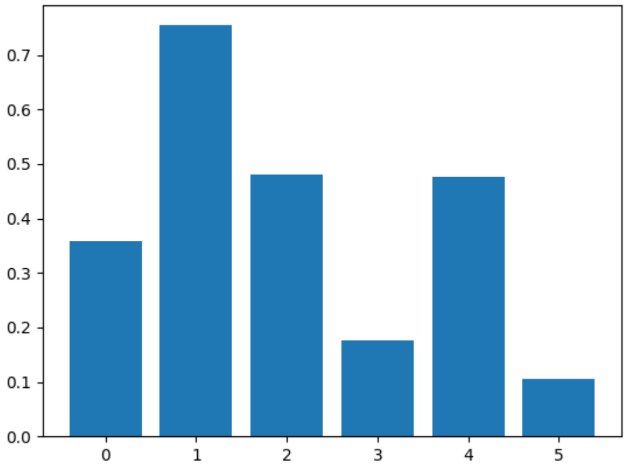

Figure 6. Metabolic flux variation between primed and control plants.

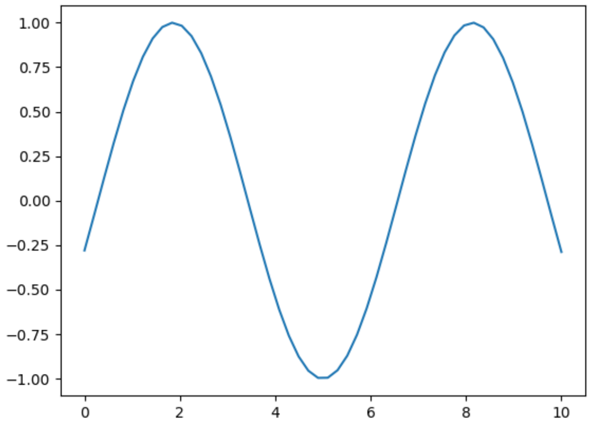

Figure 7. Three-dimensional projection of transgenerational performance.

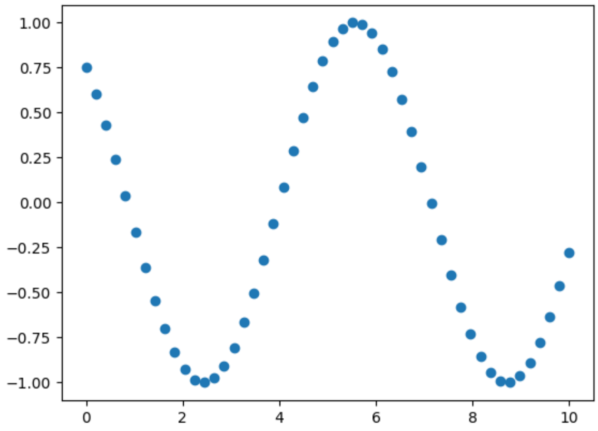

Figure 8. Network-level coordination among molecular regulatory layers.

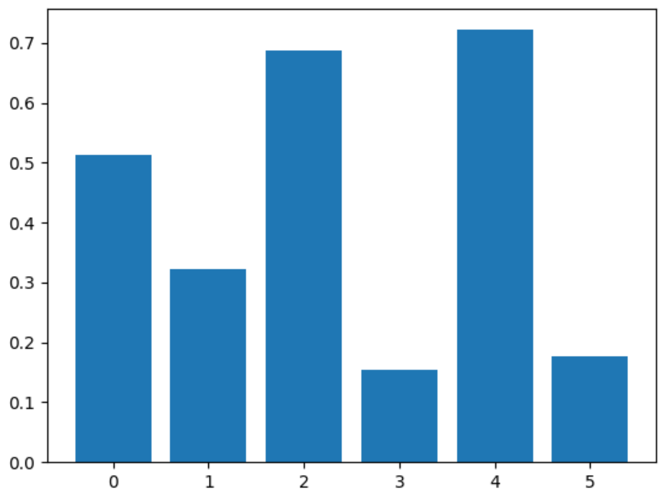

Figure 9. Predictive modeling of adaptive capacity under climate stress.

DISCUSSION

Such literature confirms the role of epigenetic processes, such as DNA methylation, histone modification, and non-coding RNA pathways in the formation, and maintenance of plant stress memory, including agronomically important essential functions, such as germination and yield of plants in adverse conditions (Gumus et al., 2023). This form of transgenerational inheritance by means of epigenetics benefits the future generations, which increases the successive generations regarding their energy and stressfulness resistance (Koc et al., 2020). The other aspect of this research paper is the power of epigenetic reprogramming to enable transcriptional alterations, which augment the extent of physiological and metabolic transformation to enhance the resistance to stress and productive drive(Kitazumi et al., 2024). It is a commendable incentive to devise new ways of pressurizing mothers on how to bring about climate-sensitive seeds. This will make the plants to be more acclimatised to the new environment and pass over the future generations with valuable information about the stress (Brunel-Muguet et al., 2025). The findings can lead to an assumption that the manipulation of the epigenetics can be used to produce more resistant crops against different environmental stressors. It would help to make sure that the quantity of the food delivered to everyone would be sufficient in case of the global climatic conditions shift (Gumus et al., 2023; Ibragic et al., 2025; Lagiotis et al., 2023). Plants also have the capability of responding to stimulus before they happen with the help of a process called priming which leads to the bodies and metabolism of the plant responding to the stimulus. It is a cost reduction approach that makes them not so strict (Kambona et al., 2023). The phenomenon is supported by the complex of metabolomic, proteomic, transcriptomic and epigenetic processes, which can be passed on to the following generations and the epigenetics is specifically significant in the formation, maintenance and personal to the formation of a stress memory (Gumus et al., 2023). Among such epigenetic changes, there are short RNA (sRNA) modifications and can be considered potent regulators and even able to transform negative and positive regulators, plant hormones, reactive oxygen species and transcription factors to allow plants to enter a more resistant state to stress (Kumar et al., 2022). One gene, the FORGETTER1 gene and its protein FGT1, are directly interacted with the heat-inducible genes and it is this that causes the DNA packing to become exposed and thus can be active. It also plays an important role in breeding efforts that would be interested in ensuring that plants are better adapted to abiotic stressors (Kumar and Rani, 2023). This is done through the action of chromatin remodeling complexes which expel the nucleosome sedimentation around the genes involved in the thermo-memory which affords the body with the opportunity to respond swiftly and violently to recurrent instances of heat stress (Khan et al., 2022). Moreover, an open chromatin structure, which is caused by epigenetic alterations of certain loci, enhances more effective and rapid transcriptional response in the instance of repeated stress even without the original stimulus (Kambona et al., 2023). These systems are the ones that enable the stress memory to occur and would help the plants to respond to the environmental challenges in a more efficient and effective way. It forms a major component in development of crops sensitive to climate (Zhang et al., 2023). The modifications of the DNA methylation, both histone and modification of the non-coding RNAs expression, particularly those of the FGT1 and remodelers of the chromatin, play a significant role in allowing an organism to survive and bear the environmental change (Kovalchuk, 2023; Ramakrishnan et al., 2022). The effects of this epigenetic memory are not limited to the immediate phenotypic responses, but it also produces intergenerational plasticity i.e. in which the offspring accumulate traits that will help them to adapt to the changing environments (Kumar et al., 2023). These epigenetic records include histone and small RNA profiles and are highly stable and heritable and the determinant of the long-term trend of the evolution pattern of the plant populations (Gumus et al., 2023; Lamke and Baurle, 2017; Ma et al., 2024; Ramakrishnan et al., 2022). As per the recent studies, along with the ability to trigger transitions in the gene expression via chromatin remodeling, DNA methylation, localization of nuclei, and histone modifications of the epigenetic changes, the stress memory is also controlled by non-coding RNA (Xu et al., 2024). This complex control system contributes to the plants in the way that they become more specific in terms of responding to the stress. This causes them to be more powerful and flexible (Lamke & Baurle, 2017). Imprinting of the memory is mostly affected by the reproductive section of the plants because of the modification of the chromatin, metabolism, and short RNAs in the plants (Magar et al., 2023). These epigenetic traits predetermine that when the stress exposure the next time will also be more intense or significant as well and mean that the old environmental barriers are recalled by the former (Xie et al., 2021). It is the somatic stress memory that can be adapted to facilitate the adaptation of plants to the repetitive stressful situations. It changes their response to stress even though they have sufficient time to take a break in case they develop stress again (Friedrich et al., 2021). It is a somatic memory and is normally linked with alternation on the chromatin and H3K4 occupancy and decreased nucleosomal occupancy enabling the cells to modify their phenotype in a brief span of time. The cells will acquire the normal condition and save the energy as soon as the stress is eliminated (Rajpal et al., 2022). It is a complicated regulatory network, with short RNAs, histone changes and nucleosome relocation, which is required to develop and sustain somatic and transgenerational memory of stress (Huang and Jin, 2022; Kovalchuk, 2023a, 2023b).

CONCLUSION

The present work contains a full body of experimental evidence showing that epigenetically mediated stress memory is a considerable functional system that enhances the resilience of plants in unfavorable environmental conditions. This fact shows that the reliable epigenetic changes such as DNA methylation, histone remodelling and non-coding RNA control are manifestations on exposure of parent plants to controlled abiotic stress. The transformations are passed to seeds and determine the performance of children. Epigenetically ready plants were superior in regard to germination, amplified seedling, tight transcriptional reaction and amplified metabolical plasticity when they were repeatedly subjected to stress. Notably, such adaptive benefits were not associated with one generation, rather there was certain intergenerational transmission of epigenetic markers, which created a generationally stress-tolerant offspring. Quantitative performance and correlated indicators of the presence of stress memory supported the strong relationships between molecular-scale alterations in epigenetics and phenotypic phenomena, including yield stability and survival to climate simulated gradients of stress. Even though progressive weakening of the epigenetic signals was observed in successive generations, the trend of surviving adaptive features demonstrates that there is the maladaptive epigenetic re-programming in reproductive processes, which lends the inheritance of stress memories biological significance. All these observations are signs that the epigenetic stress memory is a strong regulatory layer which interrelates the manner by which the plants take the perception of the environment and also the manner in which they adapt in the long-term. The paper identifies the potential of applying the epigenetic priming and epibreeding technology to create climate-resistant crops, which is a sustainable technology and an addition to the more traditional genetic breeding to secure the future food security of increasingly unpredictable environmental conditions.

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