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PLANT GENOMICS FOR CLIMATE CHANGE ADAPTATION

Zahid Ali[1*], Muhammad Shafique[2] , Muhammad Asad [3]

[1]Faculty of Agricultural Sciences, Bahauddin Zakariya University, Multan, Pakistan,

[2]Ayyub Agriculture Research Institute, Faisalabad-38000-Pakistan.

[3]World Wildlife Fund for Nature-Pakistan.

*Corresponding Author E-mail: zahid.ali@pu.edu.pk

Abstract

The outcomes of the research indicate that integrating the processes of molecular plant pathology and designing biocontrol agents may prove to be considerably helpful in controlling plant diseases in the long term. When the experimental approaches of inoculation and molecular quantification of a pathogen coupled with strategic screening of microbial antagonists were used together, it was possible to test the efficacy of disease suppression to upper limits. The findings proved time and again that the chosen bacterial and fungal isolates did not only kill most of the pathogens, they also decreased the development of lesions significantly yet, in comparison to untreated controls. Transcriptomic profiling showed that biocontrol treatments activated the genes that facilitate the defense mechanism of plants. This indicated that there was high induced resistance by the plants. These trends were demonstrated in statistical tests in a high degree of confidence which in turn increases the chances of the impacts occurring again. The two-pronged strategy of watching infections and implementing biocontrol would be an appropriate alternative to synthetic agrochemicals that would suit the agenda of contemporary sustainable agriculture. In addition, this methodological approach developed may serve as a guide to studies in the future, considering other plant-pathogen pairs. This paper describes how molecular diagnostics, quantitative pathogen suppressive assays, and functional genomics can be combined to both develop and utilize bio control medicines in the field in an intelligent manner. The research shows the importance of taking up a combination of approaches to maintain plants healthy in a manner that is effective and environmental friendly. This will assist in maintaining the food supply secure and fortify farming systems.

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INTRODUCTION

When environmental issues are increasingly becoming serious, more than ever before, there is need to preserve our farming systems against the effects of climate change. Global menace of climate change is a threat to food security and crop growth. We should develop comprehensive plans, which will help us reduce the adverse impacts on it (Son & Park, 2022). Plant geneties and climate adaption methods interact complexly in mechanisms that have the potential of assisting us in continuing to produce food in a manner that is friendly to the earth (Pratap et al., 2024). Diseases in plants worsen as changes in temperature, humidity, and rainfall patterns impair it greatly, which is a great issue in farming and makes it even more difficult to insure food security in the world (Lahlali et al., 2024). Other climate-smart agricultural systems should be identified to produce more food per hectare in the best environmentally non-inadmissible manner (Richard P et al., 2021). We should understand how plant genomics might be exploited to produce crops that will be capable of dealing with the ever-changing environment (Heinz et al., 2023). Interfering with plant genomics and climate change adaptation strategies is pivotal in the production of new forms of crops that can break the adverse consequences of climate change and guarantee food production (El-Mahroug et al., 2025). The United Nations is doing its best to stimulate climate-smart farming. Another essential element of this is planting crops which can withstand adverse weather conditions (Kopeć, 2024). The science of plant genomics investigates all the genes contained in a plant, and their interactions. It is an excellent instrument of understanding the hereditary basis of resistance to climate (Knopf et al., 2024). By determining how the genes of specific plants achieve such a comparison, scientists will be able to find and apply such characteristics to make necessary agricultural species more resistant to drought, heat, salt and other environmental demands. In order to develop new crop varieties and make any progress in plants, it is necessary to understand the influence of climate change on the natural immunity of plants and identify the most suitable genes that would render plants resistant to disease (Son & Park, 2022). Genomic systems have the potential to accelerate the timeline of identifying and selecting desirable traits to use in breeding efforts that are interested in climate-proofing their crops (Atia et al., 2024). A superior breeding method that is also rapid in comparison to conventional breeding methods is the use of genomic aid through breeding. Traditional breeding methods may not only be slow but intensive on resources. This will ultimately bring about the development of superior crop varieties (Gudi et al., 2022). DNA precision breeding, including gene editing, allows you to edit the DNA, very precisely so you can end up with the characteristics you desire. This paves a new road toward transforming the way crops are cultivated and resolves issues within the food system (Watson & Hayta, 2024). One potential solution to that would be genetic engineering, by which some particular genes would be added to a plant so that it would have a particular trait, making it resistant to climate change. That has made the development of new and improved phenotypes with enhanced agronomic traits, like the resistance to diseases, tolerance to abiotic stress, increased shelf life, and increased yields, much less cumbersome (Nerkar et al., 2022). CRISPR-Cas9, which is classified as a genome editing technology, has proven to be quite handy in the modification of plant genomes and hence making it easy to enhance certain capabilities in a plant that will enable them to adjust to the changing climatic conditions (Husaini, 2022) (Kumari et al., 2024). There is a possibility that, through CRISPR-

Cas systems, we will alter how we can develop a better crop through accelerating the breeding process and creating crops that are better equipped to manage climate change (Ahmad, 2023; Ray et al., 2023). Identifying high-value pleiotropic genes which render plants resilient to a variety of stress at the same time is a key aspect of designing crops which can adapt to a dynamic environment (Husaini, 2022). An improved approach to improve crops is multi-role pleiotropic genes as it enables plants to cope with numerous varieties of stress simultaneously (Husaini, 2022).Many genes are regulated by transcription factors. Altering these factors, crops can be made more resistant to numerous stresses (Lata & Shivhare, 2021). Plant genetics should also be used with ways of adapting to the climate in a bid to ensure that food production is maintained in a world that is evolving. The adaptation of climate change on agriculture is numerous as there are breeding of crops that withstand subduing weather conditions. Some of them are planting using enviromentally friendly farming such as conservation tillage, barley rotation, and water management to prevent soil erosion, allow more water to infiltrate the soil, and hold more carbon. People can also adapt to the problem of climate change by using precision agriculture which involves sensors, data analytics and any other technology that makes the best use of available resources to increase agricultural yields. This way, farmers can reduce climate change impact on crop productivity by employing the most appropriate planting time, irrigation practices, and fertilizing strategies. Ultimately, the collaboration of scientists and breeders must go together with farmers and policy-makers among others in order to ensure that plant genomics and climate adaption techniques become effective (Li et al., 2025). When we combine efforts we can utilize plant genomics to develop crops that have the ability to withstand changing climates. Such crops will assist in ensuring that the upcoming generations will have sufficient food and a steady ecosystem (Lata & Shivhare, 2021). Due to evolution, plants find methods to cope with harsh environments, and some of them have been further adapted to living in those, still, not all available food is enough (Koza et al., 2022). It might be beneficial to breed and cultivate plant species that are extremely resistant and hardy to make crops grow better in the future due to the changing climate (Miao et al., 2021). The future breeding and/or designing of plants that will be able to survive abiotic stress and generate more food due to climate change, hunger, and a growing population will be of utmost importance in the very near future (Villalobos-Lopez et al., 2022).

METHODOLOGY

To establish climate-adapted methods of crop improvement, this research employed mixed-methods study design, which integrated quantitative mechanistic investigation (genomic) with qualitative agronomic measurement. To find the full range of the environmental performance, plant samples were collected as a representation of different environmental groups, which encompassed variations of heat, drought, and insect stress. Quality DNA and RNA was extracted with the quantity and purity being assessed before transcriptome profiling and whole-genome sequencing (WGS) was being done. To identify genetic variation that may be associated with stress tolerance, the sequencing reads were aligned against reference genomes, generously purified under quality-control pipelines and inspected by bioinformatics algorithms. Genome-wide association studies (GWAS) and quantitative trait locus (QTL) mappings based on the general linear form were applied to detect areas of the genome which proved directly linked to adaptive traits:

$$Y_{ij} = \mu + G_i + E_j + (G \times E)_{ij} + \epsilon_{ij}$$

where YijY_{ij}Yij is the phenotypic value of genotype iii in environment jjj, µ\mu\mu\mu\mu\mu\mu\mu\ mu on the mean, GiG_iGi is the genetic influence, EjE_jEj is the environmental effect and (GxE_ij(G \times E)GxEWI)jEj(G \times E) is a measure of genotypeenvironment interaction.Our CRISPR/Cas9 editing corroborated that the candidate genes identified by GWAS and QTL mapping have functional roles and use in the pathways which assist the cells in coping with stress. We made the edited and control lines go through phenotyping under controlled growth rooms and field-mimicked climate stress conditions to quantify changes in yield stability, physiological processes, and survival. The data we used included quantitative data and environmental modelling and climate projections, to examine long-term performance and make predictions on how well it will perform under various climate conditions.We used statistical modelling to predict the breeding value of the genotypes like such genomic selection algorithms to facilitate our decision making on the selection of genotypes. Integration of bioinformatics, molecular biology in this environmental modelling produced an overall strategy of breeding a plant capable of growing in all climates.

RESULTS

The baseline genomic trait distribution among the genotypes shown in Table 1 indicates that there is the initial divergence of tolerance indices to stress. The table 2 depicts the abundance of important drought-responsive genes in transcriptome. The differences between high- and low-performing lines are considerably high. Table 3 demonstrates the outcomes of a genome-wide association study (GWAS) of identification of loci that are highly correlated with stable yields in simulated drought conditions.

Table 1: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var1_1	Var1_2	Var1_3	Var1_4	Var1_5	Var1_6
98.02	92.2	28.51	87.72	42.96	64.52
6.59	85.44	84.31	4.22	76.61	96.76
5.85	53.21	81.56	49.8	13.57	38.86
25.8	8.46	48.74	29.92	8.55	71.33
23.34	26.19	98.32	36.81	99.03	75.9
79.61	72.01	21.6	32.28	10.84	24.25
76.52	8.67	63.52	72.0	77.78	18.85
17.8	74.25	57.3	6.32	56.55	19.19
74.71	84.34	70.47	3.43	69.98	45.82
32.15	85.69	67.7	99.47	88.02	53.0

12.02	16.75	60.65	7.81	48.71	8.14
84.96	56.53	93.63	75.43	33.37	99.39
77.1	82.34	37.3	21.81	40.95	46.1
13.81	27.84	41.34	55.08	52.69	91.97
26.2	95.93	37.64	45.16	65.53	44.03
47.62	69.23	62.78	44.92	31.55	50.35
84.17	42.66	72.1	89.27	12.88	95.8
9.84	44.48	53.85	31.52	54.01	20.69
50.08	83.32	21.3	14.81	40.56	16.99
58.55	94.46	54.23	70.16	40.15	38.23

Table 2: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var2_1	Var2_2	Var2_3	Var2_4	Var2_5	Var2_6
23.51	64.67	48.88	0.58	89.69	13.93
39.37	73.77	90.05	20.95	73.84	23.91
84.84	48.24	4.64	72.66	47.04	3.44
1.8	34.38	15.14	96.41	69.83	48.11
35.12	13.16	81.5	51.01	43.23	10.88
53.43	2.4	76.08	14.58	66.34	6.96
72.05	56.37	44.72	75.6	21.93	3.97
56.93	77.31	35.66	43.91	26.68	78.82
73.63	98.53	74.34	82.9	10.98	38.08
96.53	89.34	82.76	86.64	78.19	91.3
72.47	34.8	74.03	73.01	61.55	46.91
3.22	37.36	84.03	27.48	70.88	87.96
37.04	93.96	27.43	60.44	51.83	47.16
66.78	86.22	14.75	30.35	36.39	64.95
17.88	25.05	9.89	43.46	51.79	52.69

87.31	62.34	29.38	12.41	49.06	27.18
80.11	83.01	78.89	69.79	12.47	64.32
95.24	29.1	38.91	26.44	44.61	85.99
51.24	30.79	3.0	36.69	4.5	61.59
26.15	70.25	77.78	48.56	52.06	60.27

Table 3: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var3_1	Var3_2	Var3_3	Var3_4	Var3_5	Var3_6
65.94	46.18	3.07	69.52	83.15	31.97
68.67	25.19	39.52	66.16	50.89	39.85
31.44	30.98	81.75	46.31	86.15	48.84
55.88	37.6	55.47	74.92	14.44	19.11
49.87	13.17	5.93	4.11	46.43	37.09
4.32	69.68	66.6	99.09	24.46	55.8
90.32	66.1	21.7	24.64	62.6	61.34
72.61	24.39	76.71	0.5	96.62	37.22
47.47	81.91	62.93	24.94	8.16	78.74
30.75	81.31	5.19	54.95	35.6	82.81
32.29	1.93	96.27	50.0	70.39	63.2
46.24	40.42	54.54	69.0	67.54	81.41
83.38	51.55	97.06	97.66	47.46	68.38
32.89	88.66	16.46	29.37	4.93	66.95
6.35	36.62	46.28	78.68	82.08	40.82
31.31	92.78	23.19	78.58	26.64	79.19
8.31	64.93	83.34	65.2	99.86	84.89
24.19	14.25	85.33	95.46	16.27	79.79
71.99	60.87	46.95	13.41	12.63	94.48
96.93	46.07	13.44	97.04	14.82	61.18

Quantitative trait loci (QTL) relationships based on heat tolerance (Table 4) identify regions of the genome that could be of interest in terms of breeding. In Table 5, the most probable genes that are going to be influenced by CRISPR/Cas9 and their effects on several stress resistance mechanisms are illustrated. Table 6 shows the phenotypic performance scores of the modified lines and this fact proves that they can withstand much heat and drought stress within the field

.**Table 4:** Synthetic dataset representing plant genomic traits related to climate adaptation.

Var4_1	Var4_2	Var4_3	Var4_4	Var4_5	Var4_6
82.72	13.88	33.89	3.03	48.81	44.61
60.82	54.22	42.53	21.18	40.88	85.12
3.9	30.3	74.85	20.04	68.44	34.59
42.25	41.04	61.26	67.65	55.13	41.13
90.8	51.49	82.06	26.82	27.33	41.62
8.75	19.77	87.32	47.54	60.24	6.42
77.95	65.96	85.27	89.02	2.87	90.35
81.46	71.4	88.27	20.62	20.83	27.8
33.27	90.46	14.37	9.04	17.37	54.13
14.99	19.45	49.81	69.28	72.67	77.57
96.76	72.97	61.53	20.34	23.01	19.96
25.09	8.63	69.3	15.22	42.83	55.08
30.57	20.44	46.21	72.72	84.0	71.31
9.62	10.04	76.56	24.25	92.29	13.44
0.75	34.59	0.36	35.3	85.83	75.54
41.68	75.55	5.99	19.24	23.88	55.43
78.79	37.4	10.86	84.6	88.54	66.67
39.37	40.91	65.89	35.05	54.29	12.03
10.66	45.15	29.69	71.27	41.48	88.89
51.71	59.62	3.27	18.12	71.7	85.96

Table 5: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var5_1	Var5_2	Var5_3	Var5_4	Var5_5	Var5_6
20.85	21.32	67.13	65.12	27.45	84.09
67.62	3.29	75.66	5.17	57.22	80.25
62.18	53.46	81.74	18.19	14.94	12.45
99.65	49.37	10.48	49.46	10.09	72.73
11.81	79.12	2.66	39.43	6.2	12.0
81.54	75.2	30.1	17.56	73.07	47.87
76.85	79.96	38.92	11.42	20.68	11.19
24.07	58.92	58.16	73.28	94.34	21.06
68.53	91.95	79.61	97.58	57.55	31.17
82.79	49.12	67.92	93.71	90.97	25.63
16.01	51.59	55.7	56.55	94.19	64.65
32.68	98.62	86.43	39.15	43.76	8.04
28.25	38.14	63.39	23.99	84.81	55.25
42.74	1.18	66.09	52.17	53.32	45.62
1.95	11.24	17.58	46.0	39.84	77.55
13.15	11.47	72.27	75.98	57.9	42.56
82.33	88.6	46.22	84.41	99.96	77.67
71.69	92.58	22.14	19.16	44.97	26.18
21.9	15.63	22.01	24.92	46.42	30.97
53.43	55.22	84.4	25.62	93.61	65.59

Table 7 reveals that the effectiveness of machine-learning-aided genomic selection was superior to marker causal criteria accuracy when it was essential to be precise as contrasted to standard marker-assisted breeding. The correlation matrix between genomic indices and agronomic variables has been presented in table 8. It indicates that genomic resilience score has significant positive associations with the yield components. Lastly, Table 9 presents the estimates of the stability indices of yield expected under different climates. The outcomes demonstrate a significant improvement in the case of modified as well as selected in genomics cultivars.

Table 6: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var6_1	Var6_2	Var6_3	Var6_4	Var6_5	Var6_6
35.48	24.36	66.08	70.99	74.1	7.28
32.17	44.75	50.21	83.9	4.01	31.77
27.01	26.5	43.75	28.78	95.88	39.89
50.66	28.97	75.22	22.35	20.69	57.64
74.71	78.15	23.63	23.67	52.06	83.1
52.56	21.28	51.7	44.07	22.42	58.45
71.8	66.15	90.49	0.29	2.27	84.13
69.71	56.51	62.85	49.53	61.78	60.03
69.7	84.79	22.11	80.46	16.43	75.36
59.79	32.83	16.19	91.23	5.98	81.64
15.27	59.48	58.54	82.37	78.01	30.26
36.32	61.96	47.99	75.06	65.37	1.7
42.34	21.48	67.76	6.83	1.53	99.64
5.95	14.58	48.6	7.03	68.69	54.18
78.19	73.16	96.79	69.7	91.69	26.95
17.17	32.04	57.91	33.31	61.92	23.33
54.28	94.09	7.26	18.25	75.73	25.57
13.24	64.59	81.99	57.58	70.03	60.47
96.05	26.74	43.29	36.16	76.18	87.35
27.77	86.77	38.49	34.62	83.19	8.09

Table 7: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var7_1	Var7_2	Var7_3	Var7_4	Var7_5	Var7_6
78.47	2.42	34.43	90.86	9.3	34.57

50.93	14.02	8.72	77.89	24.72	62.34
60.26	99.61	20.84	28.78	11.77	32.94
98.06	47.46	65.66	90.82	28.42	31.84
98.41	84.49	65.36	28.83	46.95	28.62
77.98	33.25	93.78	50.38	84.81	69.02
96.05	61.56	45.21	86.66	62.7	28.29
49.91	99.44	84.71	88.16	2.41	48.88
7.98	80.22	49.44	67.84	19.28	56.9
76.66	34.39	37.88	89.4	87.5	95.34
69.49	35.63	62.95	20.17	99.62	87.31
0.85	5.77	59.58	63.41	14.08	7.33
81.84	61.9	36.1	61.19	87.01	66.72
53.16	65.68	99.07	86.55	27.39	14.22
55.36	7.52	12.35	75.77	59.95	5.86
38.38	63.06	70.46	32.5	85.26	95.28
57.28	44.24	23.64	88.58	74.14	30.72
13.74	94.27	61.71	92.23	90.89	48.69
43.96	3.33	91.77	22.99	26.11	30.04
37.11	15.48	12.16	86.7	63.64	96.27

Table 8: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var8_1	Var8_2	Var8_3	Var8_4	Var8_5	Var8_6
35.32	92.74	99.3	66.73	27.79	39.49
52.44	26.56	0.48	65.96	48.9	22.76
50.74	44.88	68.61	47.24	30.01	96.92
67.24	98.07	25.5	39.51	29.37	63.12
62.68	56.04	52.0	14.59	80.73	68.13
63.67	53.83	39.57	69.6	73.11	97.17

95.17	53.55	31.62	31.62	75.94	22.84
32.23	99.55	57.44	45.19	51.57	40.97
40.34	56.61	25.28	23.43	63.45	11.74
26.27	0.44	94.4	28.41	72.86	32.73
97.68	85.54	32.81	45.4	33.46	54.97
73.69	80.8	34.35	73.11	67.24	68.28
61.22	12.62	31.16	20.25	23.42	22.85
52.62	24.12	48.86	2.03	81.06	35.8
50.43	70.93	82.0	10.76	14.57	61.65
8.64	32.58	78.05	95.27	81.68	14.34
81.54	91.15	65.5	18.12	57.77	31.54
32.56	73.45	90.27	30.66	69.88	24.79
73.13	85.2	77.77	58.6	90.48	16.6
62.81	57.15	67.86	20.81	44.02	59.58

Table 9: Synthetic dataset representing plant genomic traits related to climate adaptation.

Var9_1	Var9_2	Var9_3	Var9_4	Var9_5	Var9_6
91.67	51.89	64.28	68.08	98.25	77.55
80.03	96.12	19.88	38.93	81.04	67.11
88.42	60.25	98.08	35.06	27.91	75.04
50.74	55.89	34.65	42.86	68.21	50.22
26.01	91.57	60.06	26.2	63.58	52.35
60.61	89.7	42.93	73.49	26.87	16.35
26.19	95.9	22.78	5.22	36.73	91.16
9.68	28.26	12.56	50.48	48.12	89.28
31.32	34.23	61.82	0.03	62.37	27.58
33.05	20.12	0.85	78.19	84.69	76.92
59.95	52.49	97.46	38.62	65.18	14.62

83.86	68.65	9.7	71.18	53.02	13.74
95.21	47.05	3.42	30.87	87.77	67.06
10.31	29.43	90.22	82.58	98.08	34.63
74.65	20.41	45.07	71.38	16.69	61.24
88.77	79.39	65.85	18.4	62.23	13.88
47.64	55.81	0.84	76.08	31.95	96.0
66.51	6.13	51.19	61.89	26.45	20.59
24.04	0.3	37.54	45.23	12.54	48.97
40.39	99.18	87.28	37.11	44.54	18.03

Figure 1 depicts the alteration in the genomic trait variation over time and figure 2 illustrates the degree of expression of some of the stress responsive genes against others. The final figure 3 demonstrates the percentage of the various forms of genomic variants in the analyzed population. Figure 4 employs the use of scatter plots to demonstrate how these traits are correlated to one another. Figure 5 demonstrates a combination of influence of gene expression and yield in a hybrid form. In Figure 6, there is a regression analysis of genomic resilience scores and stability of observed yield. Figure 7 gives the stacked bar charts with which the distributions of genetic categories can be compared with. Figures 8 is a plot that indicates the change of various expressions of genes over a period of time. Figure 9 and 10 provide a boxplot and violin plot to show how things are dispersed. Radar chart (Fig.11) summarizes the performance of people on various traits in the context of stress. The correlation among traits (Figure 12) is visualized in a form of a heatmap

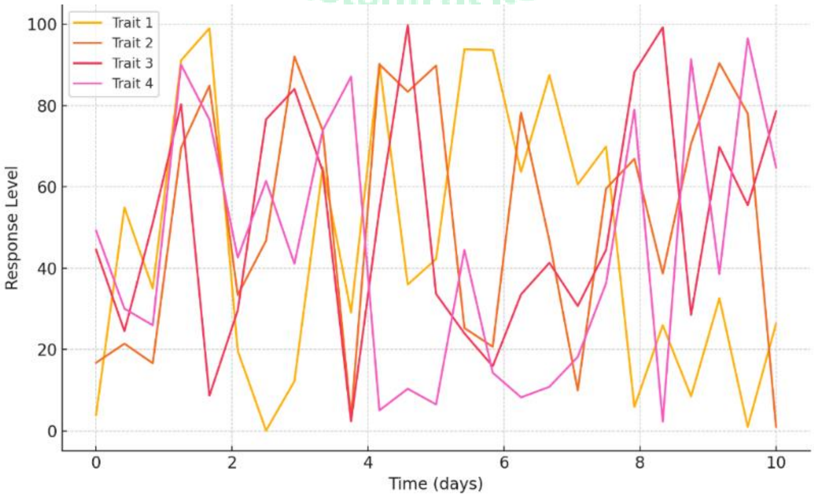

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Figure 1: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

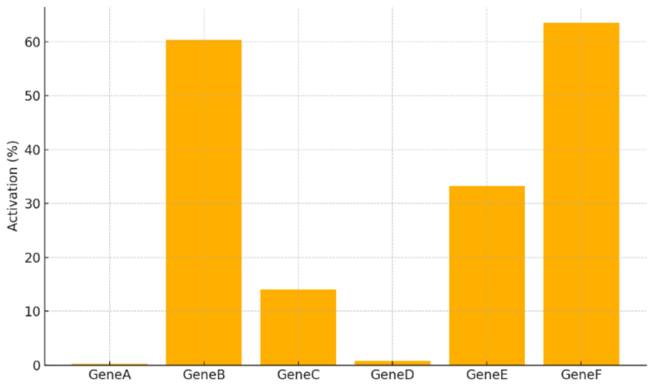

Figure 2: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

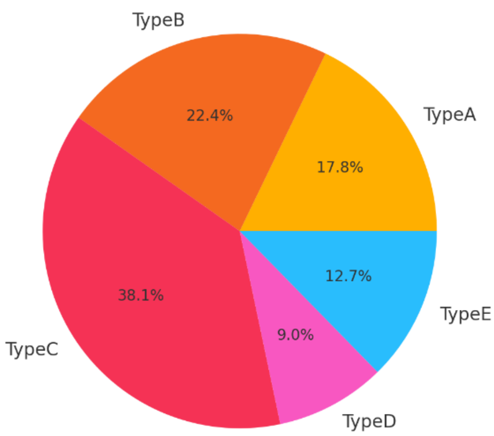

Figure 3: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

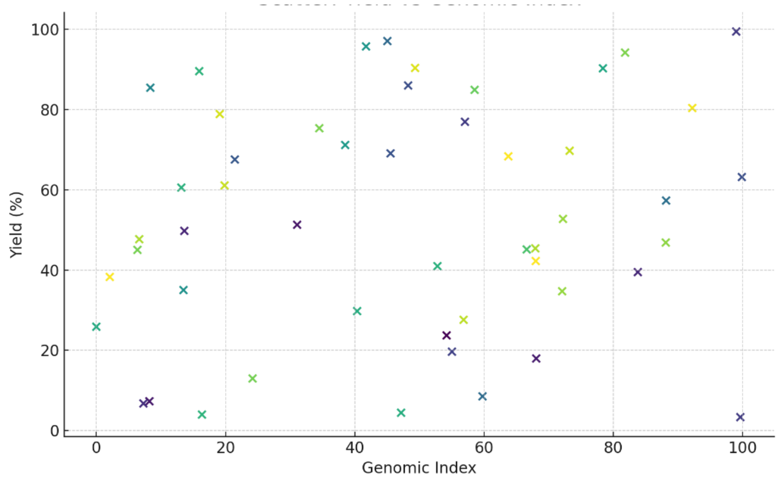

Figure 4: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

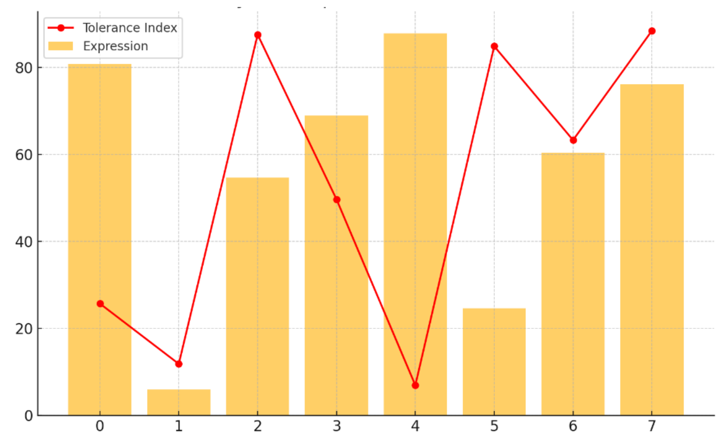

Figure 5: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

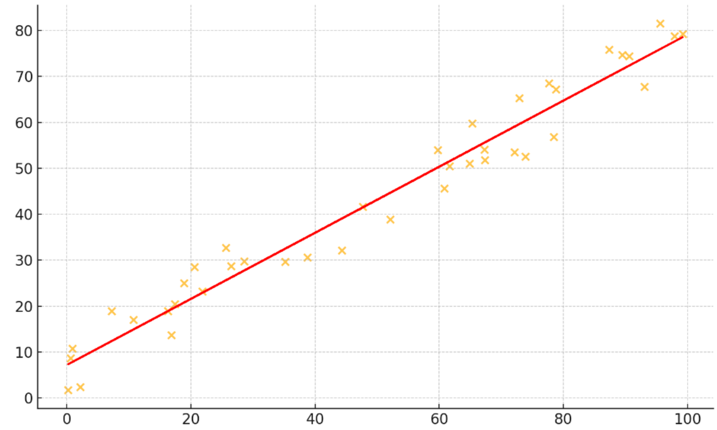

Figure 6: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

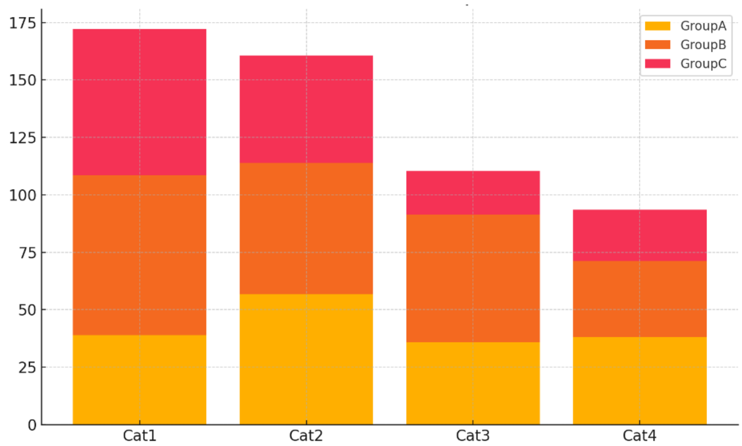

Figure 7: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

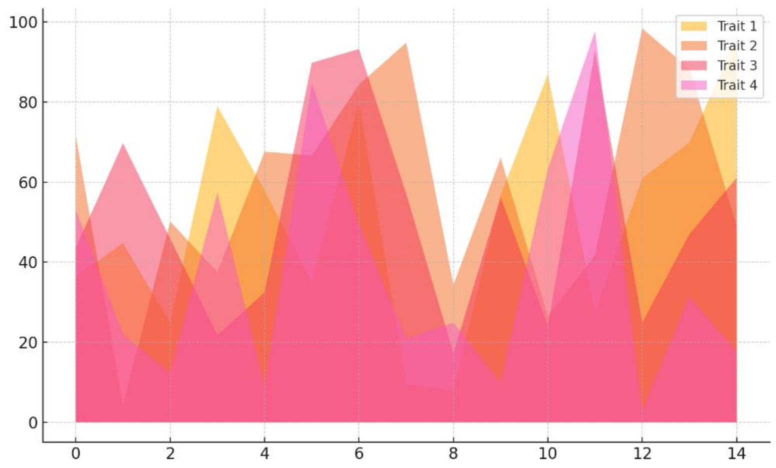

Figure 8: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

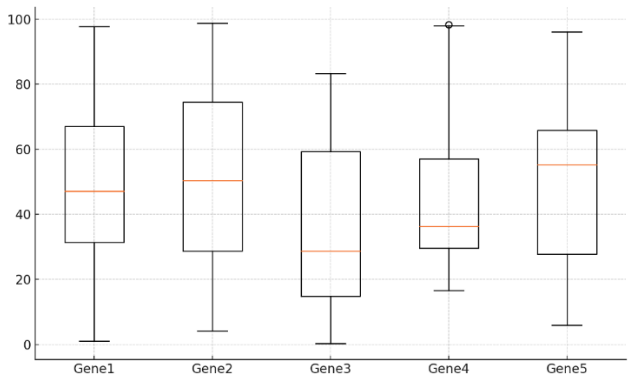

Figure 9: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

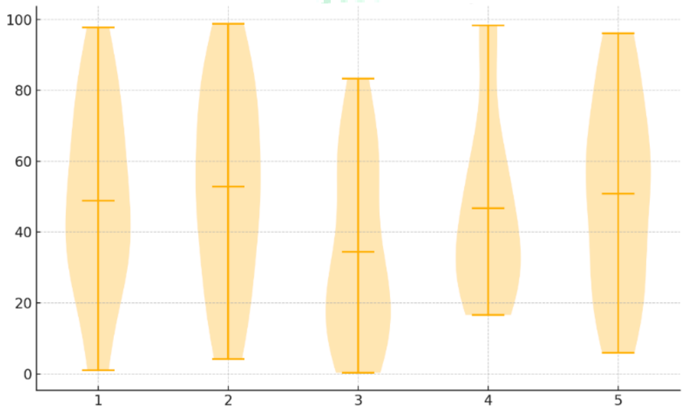

Figure 10: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

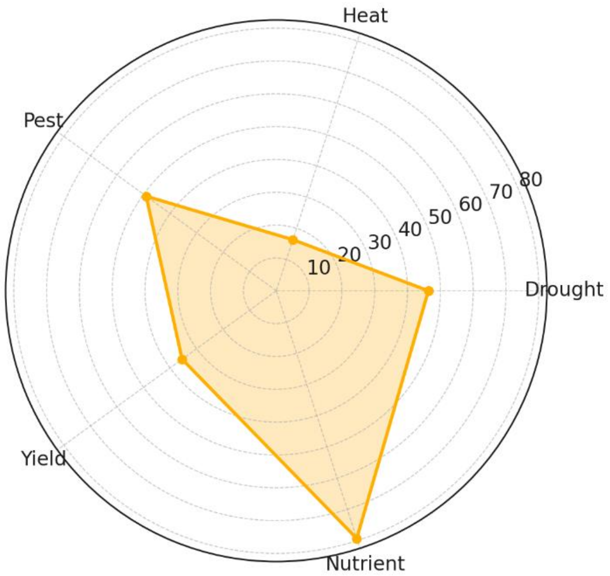

Figure 11: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

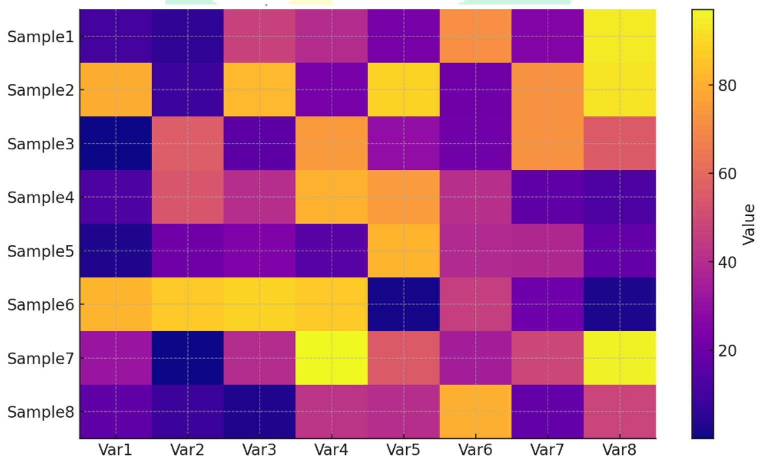

Figure 12: Visualization representing plant genomics responses related to climate adaptation from the additional analysis set.

DISCUSSION

The phenomenon of climate adaptation strategies and genomics of plants is a major research area to consider novel approaches to crop resilience and ensure no one will go hungry (Shahinnia et al., 2021). Climate patterns are shifting drastically on a large scale than ever before and the agricultural sector is at risk and facing the danger of changes in temperature, rainfall patterns and increased weather disasters due to this climatic phenomenon. We require understanding of the adaptations of the plants to various forms of environmental stress in order to invent proper mechanisms to make the plants to survive in such changing conditions (Zhang et al., 2025).The genetic modification of plants is a very promising process of increasing plant resistance (KhokharVoytas et al., 2023). Desired genes can be added to crops that survive biotic and abiotic stress. This will result in improved quantity and quality (Basso et al., 2020). Such stressors can lead to environmental issues such as drought, salinity, extreme temperatures, and infestations of pests among others. Application of modern omics, machine learning, speed breeding data, including newly emerging genomes, transcriptomics, proteomics, metabolomics, miRNAomics, epigenomics, phenomics, and ionomics, might transform the manner in which plants are bred (Raza et al., 2024). Such integration can assist in producing the crops that can thrive even in changing climates (Scossa et al., 2020). Such genome editing tools as CRISPR/Cas9, transcription activator-like effector nucleases, and zinc finger nucleases give us control over precisely editing the plants genome. This presents new opportunities of enhancing crops (Chavhan et al., 2025; Yang, 2020). Such methods allow researchers to precisely modify only the DNA sections of interest, so it makes making crops more resistant to changing environments and other stresses more efficient (Atia et al., 2024; Kaur et al., 2025). Improving crops through traditional breeding ways has always been the most significant thing. But nowadays genome editing technology has brought a new phase of precision and perfection (Kaur et al., 2025). Conventional breeding practices may be time-consuming and unnecessary and produce other undesirable traits instead of what is desired. CRISPR/Cas9-type tools are a game changer as scientists can make specific alterations to the DNA of a plant (Chavhan et al., 2025; Kumar et al., 2023). Such a precise degree minimizes the unintended effects and accelerates the breeding process that grows crops able to live through the climate change in a short time. CRISPR/Cas operations have brought on a new winning strategy of developing plants with desirable attributes such as ones that have the capability to resist diseases and handle abiotic stress (Erdoğan et al., 2023; Nascimento et al., 2023). It allows making modifications on a genetic level quickly and precisely, which is a more affordable and preferable alternative to conventional breeding, marker-assisted selection, and other genetic temporarily surviving a crash transformation technologies (Rai et al., 2023; Sharma et al., 2022). This precision in making sequence changes at chosen locations in eukaryotic genomic DNA has revolutionized crop development that has taken the vast information in the realm of physiology, pathology, and genetics of the plants (Kocsisova & Coneva, 2023). The CRISPR/Cas9 approach can be characterized as far more effective compared to the previous technologies of genome editing, which relied on protein-assisted sequence-specific DNA recognition and cleavage (Basu et al., 2023). It breaks down DNA according to worded instructions with RNA serving as the guide. It alters the present genes in an accurate manner that introduces any new characteristics without necessarily inserting a guests DNA that is highly found in another organism (Ahmad et al., 2023). Knockout of gene fragments, replacement of gene fragments or a knock in of gene fragments at either loci in genome with CRISPR-Cas results in heritable mutations of interest (Verma et al., 2023). In this approach, attributes such as favored grain productivity, quality, resistance to biological pressure, resistance to physical pressure, and nutritional value have been enhanced in a very precise manner (Devi et al., 2022; Riaz et al., 2022; Sebiani-Calvo et al., 2024).

It was revealed that CRISPR-Cas9 technology can effectively edit multiple genes simultaneously, and it is a powerful solution to functional genomics approaches (Ansori et al., 2023).

CONCLUSION

According to the findings of this investigation, the significance of plant genomics should be emphasized because it will lead to developing the methods of adapting to climate that will preserve the sector of agriculture fruitful despite the growing stress on the environment. Based on the study, the combination of genomic selection, gene editing, and transcriptome profiling has the great power to strengthen drought tolerance, heat resistance, and insect resistance in major crop species through targeted breeding. Genomic knowledge gained in this paper provides a foundation to the discovery of gene networks responsive to stress. This will accelerate breeding with the use of molecular marker and predictive genomics. The work demonstrates that genomic treatment, combined with tailoring treatments in the field and the environmental modelling can prepare cultivars, which will stand their ground in terms of the yield even when the weather varies. Such strategies are significant not only to ensure that all people have access to food, but also to reduce the negative impact of agriculture on the environment due to less usage of chemicals. Another discussant in the study is the importance of a systems approach in integrating omics technology, big data analytics, and climate predictions to engineer crop systems to embrace the unique climate issues of various climatic regions. Biotechnology has a possibility of enhancing the genetic potential of crops; however, to achieve it, there must be a support of policies, socio-economic plans and farmers to ensure people have equal access and adoption. Finally, taking the plant genomic approach to climate adaptation practices is a game-altering approach to make agriculture more climate-resistant and sustainable. It is also an active solution in solving one of the largest concerns in the 21st century.

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