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EXPLORING THE GENETIC POTENTIAL OF MAIZE (*ZEA MAYS* L.) FOR HIGH-TEMPERATURE STRESS TOLERANCE

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SUMMARY

Maize (*Zea mays* L.), a vital cereal crop, faces challenges from rising global temperatures. As a C4 plant, maize is highly heat sensitive, which disrupts photosynthesis and reduces growth and productivity. High temperatures during the reproductive phase delay silk emergence and dry pollen, decreasing seed production and yield. Developing heat-tolerant maize varieties is essential. Tolerance can be viable by utilizing genetic diversity in breeding programs. This study evaluated 156 inbred lines for high-temperature stress tolerance, selecting 56 promising lines. Their screening continued under field and screen house conditions. High-temperature stress significantly affected maize growth and reproductive stages, increasing the anthesis-silking interval and reducing flowering synchronization. Principal component analysis identified inbred lines PBG1(X), PBG2(X), PBG3(X), PBG4(X), PBG5(X), PBG7(X), 6200(X), 6201(X), 6205(X), and 6202(X) as the best performers under stress, while 6159(X), 6179(X), 6180(X), 6193(X), and 6199(X) performed poorly. Traits, such as cob diameter, days to silking, grains per cob, 100-grain weight, and leaf area, showed positive correlations with the anthesis-silking interval. Inversely, pollen production potential had a negative correlation, while the days to tasseling positively correlated with grain yield. These findings are crucial for developing heat-resilient maize varieties.

Keywords: Maize (*Z. mays* L.), inbred lines, screening, high temperature, PCA, correlation

Key findings: The rising global temperature poses significant physiological stresses on maize (*Z. mays* L.). Addressing this challenge requires identifying and utilizing heat-tolerant maize germplasm essential for breeding climate-resilient varieties. These findings provide valuable insights for improving high-temperature stress tolerance and developing resilient maize germplasm.

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INTRODUCTION

Agriculture is constantly under pressure to adapt to changing climate and ensure food security for the world's growing population. Among the climate challenges, increasing temperatures significantly affect crop productivity. Predictions indicate a temperature rise of 1.4 °C to 5.8 °C in the 21st century (Levinsky *et al.*, 2007). Rising temperatures particularly upset maize (*Zea mays* L.), a vital cereal crop. As a C4 plant, disruption in its photosynthesis efficiency results from heat, affecting growth and productivity. Understanding the genetic basis of heat tolerance is vital for developing resilient maize varieties. Studies focus on identifying genetic traits and mechanisms for heat tolerance during critical growth stages (Alam *et al.*, 2017; Cairns and Prasanna, 2018).

High temperatures cause physiological disruptions in maize during the vegetative phase, such as impaired photosynthesis, reduced chlorophyll content, and interrupted water relations, leading to stunted growth and lower biomass (Cairns and Prasanna, 2018). Heat stress accelerates leaf senescence, reducing the plant's sunlight capture efficiency (Alam *et al.*, 2017). Identifying heat-tolerant genes and integrating them into commercial maize varieties is crucial for sustaining production under climate change.

During the reproductive phase, heat stress affects maize yield. High temperatures during flowering reduce pollen viability and germination, lowering seed set and grain quality. The optimal temperature for maize flowering is 29 °C to 37.3 °C (Lizaso *et al.*, 2018). Elevated temperatures prolong the anthesis-silking interval (ASI) critical for fertilization, disrupting the synchronization between pollen shedding and silk emergence (Mhike *et al.*, 2012). Heat stress desiccates silks and pollen, impairing fertilization (Ahmad *et al.*, 2022). Extremely high temperatures cause pollen sterility, reducing grain number (Rezaei *et al.*, 2015). Research focuses on genetic traits enhancing pollen viability and ASI synchronization.

Genetic variation underpins a plant's adaptability to changing environments. Combining field-based phenotyping with controlled experiments identifies robust heat-tolerant genotypes (Rahman *et al.*, 2019; Moser *et al.*, 2020). Teosinte, maize's wild ancestor, provides valuable genetic resources for improving heat tolerance. Teosinte maintains chlorophyll content and survives extreme temperatures, making it an excellent candidate for breeding (Niazi *et al.*, 2015). Crosses between maize and teosinte introduce beneficial alleles enhancing heat tolerance (Roitsch *et al.*, 2019). Breeding strategies incorporating teosinte's genetic diversity are progressing to develop heat-adapted maize varieties (Niazi *et al.*, 2015). Utilizing maize germplasm with temperature stress tolerance is important (Alam *et al.*, 2017).

Advanced breeding techniques, including genomic and marker-assisted selection, accelerate the development of heat-tolerant maize varieties. These methods identify and select desirable traits at the molecular level, improving breeding efficiency and precision (Naveed *et al.*, 2016). Biotechnological approaches, such as CRISPR/Cas9 gene editing, offer promise for directly modifying genes associated with heat tolerance, providing a faster route to resilient cultivars (Naveed *et al.*, 2020; Zafar *et al.*, 2020). Climate-resilient cultivars can enhance maize output by 5%–25% (Cairns and Prasanna, 2018).

High temperatures trigger molecular and physiological responses in plants, including heat shock protein (HSP) activation, changes in membrane fluidity, and oxidative stress pathways. These responses help plants adapt and mitigate heat stress's damaging effects. Alterations in lipid composition and antioxidant enzyme activation are crucial for maintaining membrane integrity and reducing oxidative damage (Hussain *et al.*, 2018).

Despite progress, challenges remain in breeding for heat tolerance in maize. The complexity of heat tolerance, involving multiple genes and pathways, requires a comprehensive approach combining genomics, phenomics, and environmental studies (Roitsch *et al.*, 2019).

Future research should integrate these approaches to develop effective breeding strategies. Collaborations between international research institutions and advanced breeding technologies are vital for addressing the global challenge of rising temperatures (Alam *et al.*, 2017; Cairns and Prasanna, 2018). Understanding the genetic basis of heat tolerance in maize is essential for mitigating climate change's adverse effects. By leveraging genetic diversity, advanced breeding techniques, and biotechnological innovations, researchers aim to enhance maize's heat resilience, ensuring food security and sustainable agriculture amidst global warming.

MATERIALS AND METHODS

From 2020 to –2023, the research area, laboratories, greenhouse, and screen house at the University of Agriculture, Faisalabad, Pakistan, served as the experimental site for this work. This district of about 184.5 meters above sea level had a semi-arid classification (Bhalli *et al.*, 2012).

Screening of Inbred Lines

During the spring and autumn of the first year (January 07, 2020 to June 30, 2021), maize germplasm collection transpired. The following amounts were 18 lines from the Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera; 18 lines from the Maize and Millet Research Institute (MMRI), Yosafwala; 15 lines from the Plant Genetic Resource Institute (PGRI), NARC, Islamabad; 90 lines from the University of Agriculture (UAF), Pakistan, and nine lines from the International Maize and Wheat Improvement Center (CIMMYT). The first selection phase had 56 best-inbred lines as choices based on morphological standards linked to high-temperature stress. In the second selection phase, the chosen inbred lines sustained screening against different morphological, physiological, and biochemical standards linked to high-temperature tolerance. There were two phases of screening, i.e., field and screen house screenings.

Field screening

Under field conditions, sowing all the inbred lines followed the alpha lattice field design of 5 m-long rows, keeping plant-to-plant spacing of 25 cm and row-to-row spacing of 75 cm. Planting two germplasm sets in the field helped provide normal and high-temperature stress conditions. The first sowing began in the first week of February 2020 (standard), with the second sowing done in the last week of March 2020 to expose the reproductive phase to regular high-temperature stress of late May and early June.

Screen house screening

Under screen house conditions, inbred lines sown in earthen pots had two sets of seeds with a time gap of about a month, as the sowing in field condition, to observe the seedling traits by exposing the plants to standard temperature and temperature stress. All the inbred lines reached evaluation for traits, such as germination percentage, anthesis to silking interval, kernel rows, grains per row, grains per cob, cob length, cob weight, plant height, ear height, and pollen production potential under regular and high-temperature stress.

Statistical analysis

Experimental data underwent analysis of variance (Steel *et al*., 1997). The heat map helped to find the mean performance of genotypes. Biplot and correlation analysis using the Pearson method (Pearson, 1901) employed the following formula:

$$\text{Correlation coefficient} = n(\Sigma xy) - (\Sigma x)(\Sigma y) / \sqrt{[n\,\Sigma x^2 - (\Sigma x)^2][n\,\Sigma y^2 - (\Sigma y)^2]}$$

Where n is the number of data points, $\sum xy$ is the sum of the products of corresponding values of x and y, $\sum x$ is the sum of all x values, $\sum y$ is the sum of all y values, $\sum x^2$ is the sum of the squares of all x values, and $\sum y^2$ is the sum of the squares of all y values.

RESULTS

Analysis of variance

The analysis of variance tested the difference between groups. Data recording under normal and temperature stress conditions ensued for the ANOVA. Recorded data of 56 inbred lines underwent the analysis of variance at significance levels of 1% to assess the level of diversity among studied traits. Results revealed the presence of significant variability for all the studied traits among blocks (used) and genotypes/treatments (adjusted and unadjusted). Table 1 and table 2 shows the mean square values of studied traits under normal and stressed conditions respectively, which provided information about data trends. Comparing the results of the respective design continued with a randomized complete block design. Relative efficiency estimates were more than 75% for all traits under normal and stressed conditions.

Principal component analysis

PCA is a dimension reduction multivariate analysis that research widely employs. It increases selection efficiency since all traits have simultaneous computation and presentation. Two separate principal component analyses (PCA) proceeded, one for overall traits under standard temperature (Figure 1a), which depicted 55.4% variability as explained by the first two principal components (PC1- 37.8% and PC2- 17.6%). The second was for overall traits under temperature stress conditions (Figure 1b), which depicted variability as explained by the first two principal components (PC1-38.6% and PC2-15.8%). Traits, such as cob length, pollen production potential, reproductive phase parameters, anthesis-silking interval, internodal distance, and kernel rows, were distinct contributors to genotype performance. Best-performing genotypes, including PBG1(X), PBG2(X), PBG3(X), PBG5(X), PBG7(X), 6200(X), 6201(X), and 6202(X), were choices based on their trait vector on the PCA biplot, while poor-performing genotypes, such as 6179(X), 10004(X), 10003(X), and 6193(X) also surfaced.

Correlation using correlogram

Under normal and high-temperature stresses, correlation coefficients between various traits, such as germination percentage, plant height, ear height, days to tasseling, days to silking, pollen production potential, number of rows per cob, number of grains per row, 100-grain weight, and grain yield per plant, reached estimations. High heritability of the trait and a positive correlation with yield are prerequisites for indirect selection (Saba *et al*., 2017). Using a correlogram helped to represent the association graphically, as shown in Figure 2.

Cob diameter, days to silking, days to tasseling, grain per cob, 100-grain weight, kernel rows, and leaf area showed a significant positive correlation with anthesis to silking interval. Cob diameter displayed substantial correlation except for days to silking, germination percentage, grain per cob, and internodal distance. Cob length exhibited a nonsignificant correlation with days to tasseling, days to silking, germination percentage, and kernel rows. Days to silking showed a significant positive correlation with grain per cob. Under conditions of extreme temperature stress, days to tasseling exhibited a positive correlation with days to silking. As noted by Yousaf *et al*. (2018), the relationship between days to tasseling and grain yield was not significant but favorable, indicating that an increase in days to tasseling could boost grain yield in maize, but nonsignificantly. However, Yousaf *et al*. (2017) found a significant positive correlation between days to tasseling and grain yield. Ear height and plant height have no discernible relationship with days to tasseling. Ear height and plant grain yield indicated a positive and sizable association. Except with plant height, kernel rows demonstrated a strong connection with all traits. Leaf area significantly correlated with the number of leaves and plant height. No significant correlation occurred between pollen production potential and moisture contents of leaves. Pollen production potential has a significant

Table 1. Analysis of variance for different agronomic, physiological, and yield-contributing traits in maize under normal temperature.

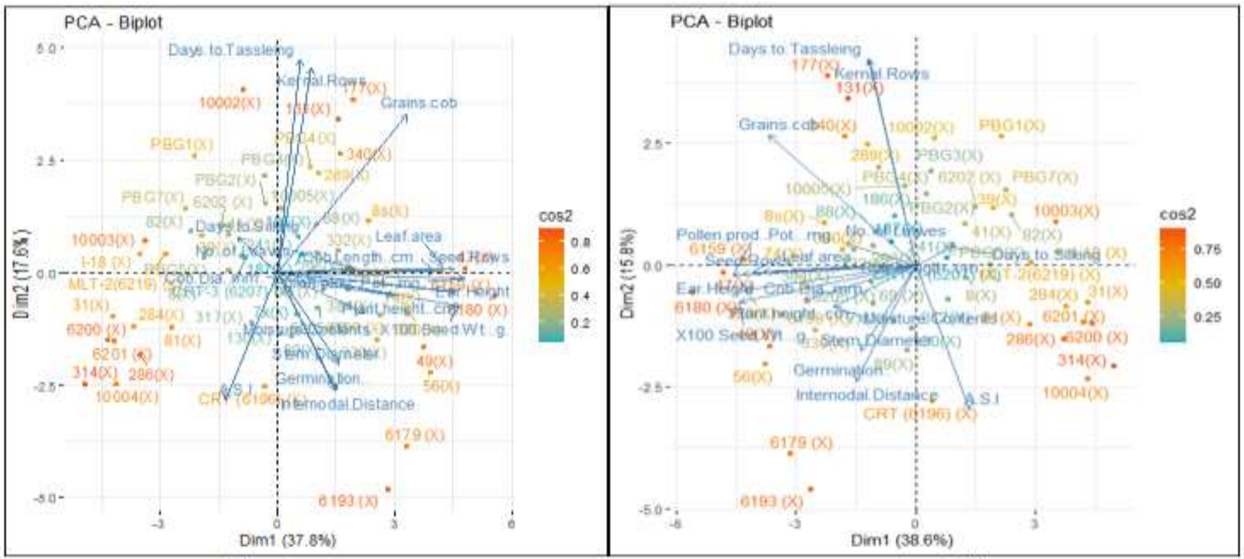
SOV	DF	GP	DT	DS	A.S.I	IND	LA	NOL	EH	PH	SD	CL	KR	SPR	SPC	CD	HSW	PPP	MC
Replication	1	96.6	108.0	3.6	108.0	0.6	58761.4	237.2	37.6	39.5	0.9	0.1	78.9	360.7	6580.6	1185.0	281.0	27625.7	92.0
Blocks within replication	14	136.2	0.4	7.0	7.2	1.6	417.8	0.6	21.1	20.9	0.0	4.7	0.6	1.6	1479.2	2.0	1.6	143.6	0.7
Treatments																			
Unadjusted	55	234.25**	2.00**	2.69**	3.61**	2.39**	2900.08**	3.82**	75.35**	75.72**	0.04**	8.10**	2.31**	11.07**	6868.04**	12.62**	8.70**	904.12**	4.03**
Adjusted	55	233.92**	1.96**	3.44**	4.57**	2.40**	3029.11**	3.76**	74.53**	74.89**	0.03**	7.68**	2.30**	11.22**	6954.78**	12.52**	8.25**	911.97**	3.72**
Error																			
Effective	41	120.51	0.31	3.24	3.63	1.26	312.89	0.51	19.58	19.34	0.00	3.68	0.57	1.28	1372.7	1.34	0.84	92.48	0.41
RCB Design	55	121.22	0.31	3.86	4.18	1.28	322.39	0.51	19.63	19.38	0.01	3.76	0.57	1.31	1375.8	1.41	0.95	98.65	0.45
Intrablock	41	116.11	0.29	2.80	3.16	1.18	289.81	0.49	19.11	18.88	0.00	3.44	0.56	1.19	1340.5	1.22	0.74	83.31	0.36
Relative Efficiency		100.59	101.23	118.92	115.05	101.82	103.04	100.75	100.24	100.24	128.95	102.13	100.07	102.20	100.23	105.19	112.87	106.67	111.17

Table 2. Analysis of variance for different agronomic, physiological, and yield-contributing traits in maize under temperature stress.

SOV	DF	GP	DT	DS	A.S.I	IND	LA	NOL	EH	PH	SD	CL	KR	SPR	SPC	CD	HSW	PPP	MC
Replication	1	7212.068	190.32	2.893	104.14	1.57	58866.81	220.08	36.91	36.68	0.85	0.311	72.32	375.22	460.08	1190.16	273.43	28003.93	90.54
Blocks within replication	14	15.45	0.54	7.021	7.14	1.86	417.95	0.74	21.11	20.75	0.01	4.59	0.69	1.847	738.23	2.05	1.45	137.61	0.72
Treatments																			
Unadjusted	55	120.318**	2.1**	2.67**	3.45**	2.45**	2901.1**	3.71**	75.19**	75.09**	0.039**	8.08**	2.17**	11.29**	3569**	12.7**	8.48**	895.29**	4.03**
Adjusted	55	120.363**	1.98**	3.42**	4.42**	2.50**	3029.71**	3.6**	74.4**	74.37**	0.033**	7.68**	2.16**	11.52**	3642**	12.6**	8.06**	901.63**	3.73**
Error																			
Effective	41	13.24	0.37	3.146	3.48	1.089	313.31	0.74	19.6	19.43	0.004	3.7	0.608	1.35	663.24	1.36	0.8	90.51	0.41
RCB Design	55	13.36	0.39	3.802	4.07	1.195	322.76	0.57	19.65	19.46	0.005	3.77	0.612	1.4	666.27	1.44	0.89	96.02	0.45
Intrablock	41	12.65	0.34	2.703	3.019	0.966	290.26	0.51	19.15	19.02	0.003	3.48	0.58	1.25	641.7	1.23	0.7	81.82	0.36
Relative Efficiency		100.9	105	120.86	116.87	109.77	103.02	103.01	100.22	100.18	125.02	101.75	100.72	103.39	100.46	105.87	111.87	106.09	111.57

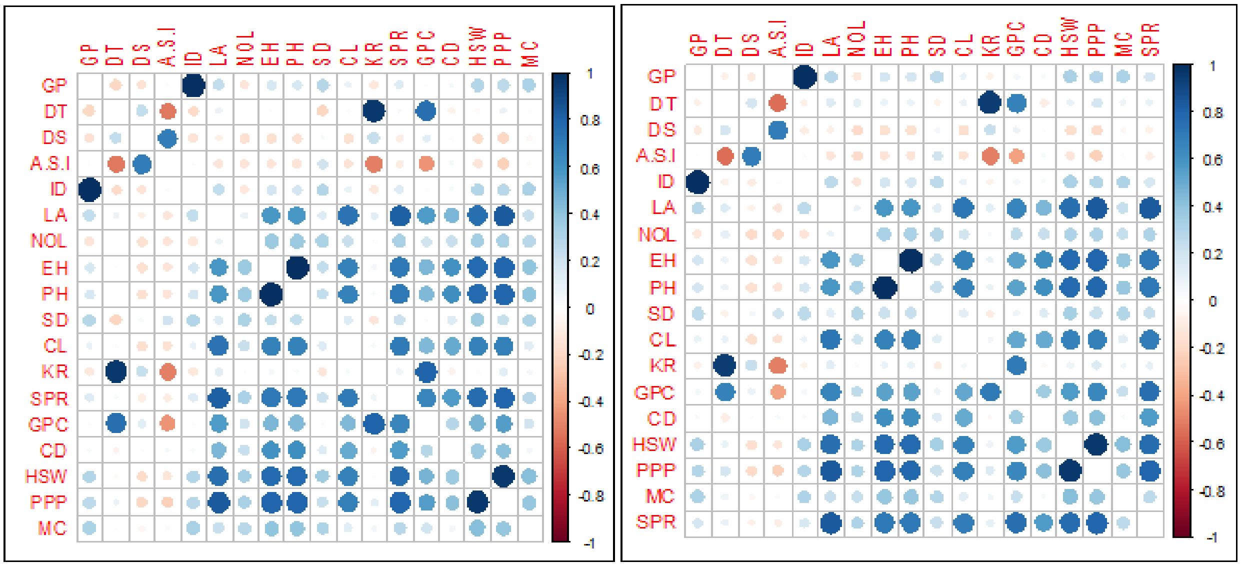
*: significant at 5%, **: significant at 1%

GP: Germination Percentage (%), DT: Days to Tasseling, DS: Days to Silking, A.S.I: Anthesis to Silking Interval, IND: Internodal Distance (cm), LA: Leaf Area (cm), NOL: Number of Leaves, EH: Ear Height (cm), PH: Plant Height (cm), SD: Stem Diameter (cm), CL: Cob Length (cm), KR: Kernel Rows, SPR: Seeds Per Row, SPC: Seeds Per Cob, CD: Cob Diameter (mm), HSW: Hundred Seed Weight (g), PPP: Pollen Production Potential (mg), MC: Moisture Content $^{(\%)}$



(a) (b)

Figure 1. Principal Component biplot for different agronomic, physiological, and yield-contributing traits in maize - the biplot indicates the distribution of the studied genotypes along the studied parameters to determine the most suitable combination of genotypes for their respective parameters. (a) for normal temperature; (b) under temperature stress.



(a) (b)

Figure 2. Correlogram indicates the relationship among the studied parameters for the studied genotypes under two conditions to determine the interrelationship among various parameters. (a) for normal temperature; (b) under temperature stress.
(GP: Germination Percentage, DT: Days to Tasseling, DS: Days to Silking, A.S.I: Anthesis to Silking Interval, IND: Internodal Distance, LA: Leaf Area, NOL: Number of Leaves, EH: Ear Height, PH: Plant Height, SD: Stem Diameter, CL: Cob Length, KR: Kernel Rows, SPR: Seeds Per Row, SPC: Seeds Per Cob, CD: Cob Diameter, HSW: Hundred Seed Weight, PPP: Pollen Production Potential, MC: Moisture Content).

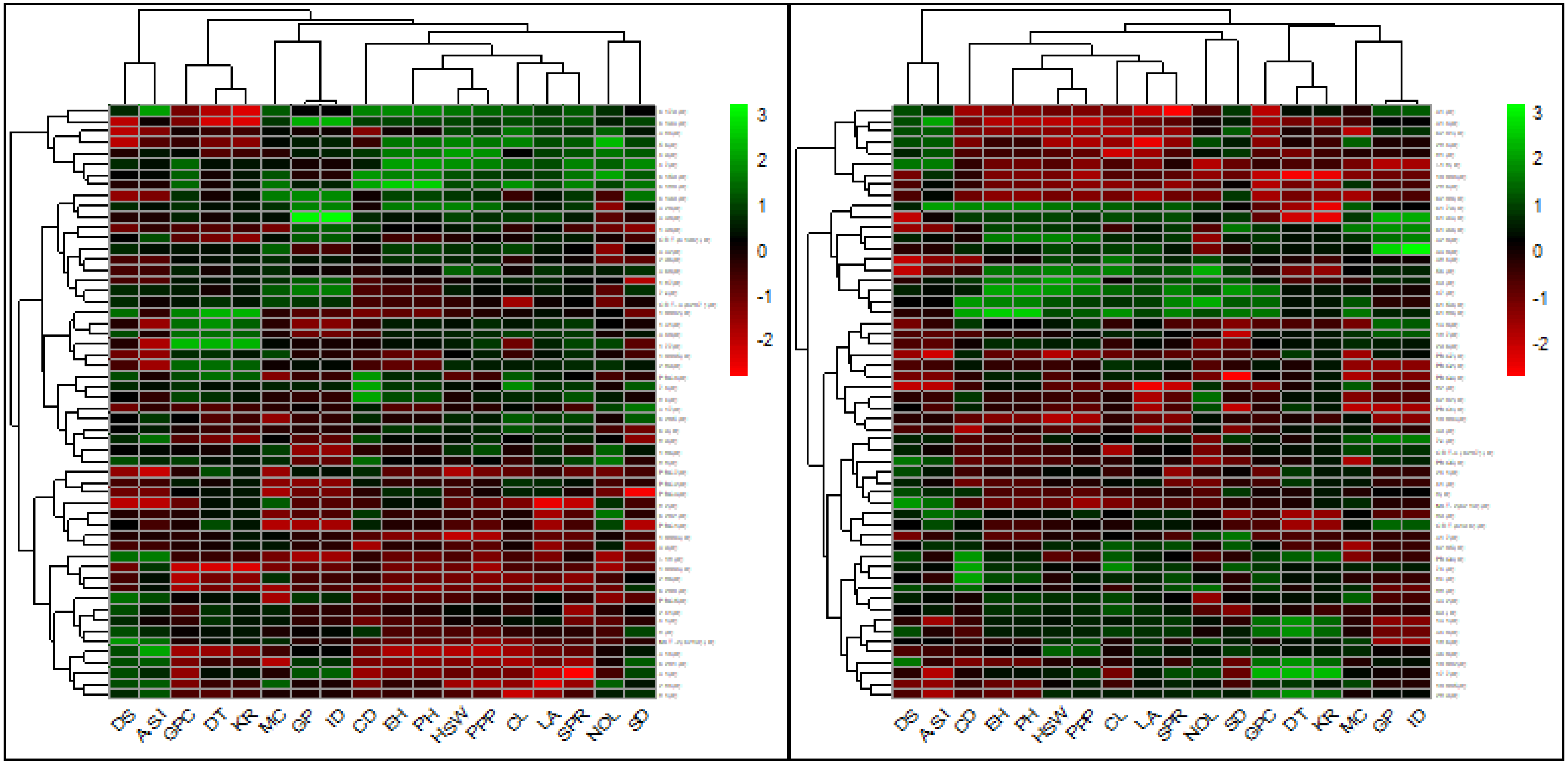
negative correlation with anthesis to silking interval.

Heat map

A heat map is a 2-dimensional representation of mean data in colors. Heat map aided in representing the mean performance of inbred lines under standard and temperature stress conditions for various traits under study.

The heat map of mean data of studied traits under a regular temperature appears in Figure 3(a). For days to tasseling, inbred lines 10002(X), 340(X), and 131(X) showed maximum mean values, while 314(X), 286(X), and 10004(X) showed minimum mean values. For days to silking, inbred lines 10002(X), CRT-3 (6207) (X), and 8s(X) gave highest mean values, while 10004(X), 286(X), and 314(X) provided minimum mean values. For anthesis to silking interval, inbred lines CRT (6196) (X), PBG5(X), and PBG3(X) showed maximum mean values, while 332(X), 320(X), and 296(X) had minimum mean values. For internodal distance, inbred lines 330(X), 6193 (X), and 6199 (X) showed maximum mean values, while 186(X), I-18 (X), and PBG1(X) gave the minimum mean values. For leaf area, inbred lines 47(X), 56(X), and 6180 (X) provided the highest mean values, and 31(X), 284(X), and 82(X) had the lowest mean values. For number of leaves, inbred lines 56(X), 6159 (X), and 88(X) showed maximum mean values, while 320(X), I-18 (X), and 10004(X) showed minimum mean values. For plant height, inbred lines 6180 (X), 47(X), and 6179 (X) displayed the maximum mean values, while 10003(X), 6200 (X), and 314(X) showed minimum mean values. For stem diameter, inbred lines 47(X), 6199 (X), and 6180 (X) gave maximum mean values, and PBG1(X), 187(X), and PBG3(X) had minimum mean values. For ears per plant, inbred lines 88(X), 6180 (X), and PBG2(X) provided the maximum mean values, while 10004(X), 10003(X), and 10002(X) showed minimum mean values. For cob length, inbred lines 6180 (X), 74(X), and 56(X) exhibited the maximum mean values, and 314(X), 6201 (X), and 81(X) had the minimum mean values. For kernel rows, inbred lines PBG3(X), 74(X), and 47(X) demonstrated the highest mean values, while 81(X), 6201 (X), and 314(X) showed the lowest mean values. For seeds per row, inbred lines 6180 (X), 47(X), and 6159 (X) showed maximum mean values, and 241(X), 82(X), and 31(X) had the minimum mean values. For cob diameter, inbred lines 6180 (X), 8s(X), and 6179 (X) gave the maximum mean values, while 39(X), 31(X), and 6201 (X) showed minimum mean values. For hundred seed weight, inbred lines 49(X), 47(X), and 56(X) provided maximum mean values, while PBG7(X), 314(X), and 10003(X) expressed the minimum mean values. For the pollen production potential, inbred lines 49(X), 47(X), and 56(X) showed the highest mean values, and 284(X), 10003(X), and 314(X) had the minimum mean values.

The heat map of the studied traits' mean data under temperature stress is in Figure 3(b). For days to tasseling, inbred lines 340(X), 131(X), and PBG7(X) showed maximum mean values, while 314(X), 286(X), and 10004(X) gave minimum mean values. For days to silking, inbred lines PBG1(X), PBG4(X), and CRT-3 (6207) (X) displayed the highest mean values, while 317(X), 286(X), and 314(X) showed the lowest mean values. For anthesis to silking interval, inbred lines PBG1(X), CRT (6196) (X), and PBG5(X) gave maximum mean values, and 332(X), 320(X), and 296(X) had minimum mean values. For internodal distance, inbred lines 330(X), 6193 (X), and 6199 (X) expressed the optimum mean values, while 186(X), I-18 (X), and PBG1(X) showed minimum mean values. For leaf area, inbred lines 47(X), 56(X), and 6180 (X) exhibited maximum mean values, while 31(X), 284(X), and 82(X) delivered the minimum mean values. For the number of leaves, inbred lines 56(X), 6159 (X), and 88(X) showed the highest mean values, and 320(X), I-18 (X), and 10004(X) had minimum mean values. For plant height, inbred lines 6180 (X), 47(X), and 6179 (X) showed maximum mean values, while 6200 (X), 10003(X), and 314(X) gave minimum mean values. For stem diameter, inbred lines 47(X), 6199 (X), and 6180 (X) provided maximum mean values, while PBG1(X), 187(X), and PBG3(X) showed minimum mean values. For ears per plant,



(a)

(b)

Figure 3. Heat Map for different agronomic, physiological, and yield-contributing traits in maize; it shows relationships among inbred lines and studied traits (a) for normal temperature; (b) under temperature stress.

(GP: Germination Percentage, DT: Days to Tasseling, DS: Days to Silking, A.S.I: Anthesis to Silking Interval, IND: Internodal Distance, LA: Leaf Area, NOL: Number of Leaves, EH: Ear Height, PH: Plant Height, SD: Stem Diameter, CL: Cob Length, KR: Kernel Rows, SPR: Seeds Per Row, SPC: Seeds Per Cob, CD: Cob Diameter, HSW: Hundred Seed Weight, PPP: Pollen Production Potential, MC: Moisture Content).

inbred lines 88(X), 6180 (X), and PBG2(X) demonstrated the highest mean values, while 10004(X), 10003(X), and 10002(X) exhibited the lowest mean values. For cob length, inbred lines 6180 (X), 74(X), and 56(X) showed maximum mean values, and 314(X), 6201 (X), and 81(X) had minimum mean values. For kernel rows, inbred lines PBG3(X), 74(X), and 47(X) gave the optimum mean values, while 81(X), 6201 (X), and 314(X) showed minimum mean values. For seeds per row, inbred lines 6180 (X), 47(X), and 6159 (X) displayed the highest mean values, while 241(X), 82(X), and 31(X) showed the lowest mean values. For cob diameter, inbred lines 6180 (X), 8s(X), and 6179 (X) gave maximum mean values, and 39(X), 31(X), and 6201 (X) had minimum mean values. For hundred seed weight, inbred lines 49(X), 47(X), and 56(X) showed maximum mean values, while 284(X), PBG7(X), and 314(X) expressed minimum mean values. For pollen production potential, inbred lines 49(X), 47(X), and 56(X) showed maximum mean values, and 10004(X), 284(X), and 314(X) had minimum mean values.

DISCUSSION

Crop development programs for heat-stress tolerance rely heavily on genetic variation and parental selection, essential for improving crop resilience against various stresses. Genetic diversity for heat tolerance has been evident in field crops like cotton, mung beans, tomatoes, rice, and wheat (Farooq *et al*., 2011; Golam *et al*., 2012). Maize germplasm shows potential variance in drought and heat-stress resilience. Identifying and classifying genetic differences are crucial for creating tolerant genotypes (Lu *et al*., 2011; Aliyeva *et al*., 2024; Mahdi *et al*., 2024).

In this study, the evaluation of 56 maize inbred lines under normal and elevated temperatures revealed significant differences in various traits, indicating potential utility and heritability. Under both temperature regimes, the analysis of variance (Tables 1 and 2) detailed extremely significant differences among inbred lines for the studied traits. The effect of high-temperature stress was most pronounced on the plant, and the effect of high-temperature stress on internodal elongation may have contributed to the diminution in ear height (Cairns *et al*., 2012). Significant increases in anthesis to silking interval in maize under heat stress may be caused by a delay in silking, meaning that because of the higher temperature (+30 °C), pollen shedding begins much earlier than silks emerge (Mhike *et al*., 2012). High-temperature stress significantly affects maize growth and reproductive stages, leading to increased anthesis-silking interval (ASI) and reduced flowering synchronization (Cicchino *et al*., 2010). Membrane destabilization due to high temperatures affects cell thermo-stability, affecting plant resilience (Savchenko *et al*., 2002; Wahid *et al*., 2007).

Temperature caused decreases in pollen production potential because cereals, particularly, maize are highly vulnerable to high-temperature stress, impacting pollen production and germination, resulting in poor seed set and grain quality (Goose *et al*., 2000). Heat stress during maize reproductive stages affects pollen viability, influencing pollination success and yield improvement (Stone, 2023). Factors, such as pollen sterility and reduced generation, contribute to the decline in viable pollen on stigma, with temperature fluctuations playing a crucial role (Matsui *et al*., 2001). The pollen germination in maize took a toll from prolonged exposure to high temperatures, as described by Kakani *et al*. (2002). The ear of maize emerged susceptible to high temperatures, which leads to poor kernel growth. High temperatures also affect maize ear development, impeding kernel growth and affecting pollen production and silk development (Lizaso *et al*., 2003; Loos *et al*., 2003).

Studies show a 70% reduction in grain output under high-temperature stress due to factors like decreased pollen viability and silk receptivity (Khodarahmpour, 2011). Results showed that under high temperatures, the number of kernels per ear and kernel weight decreased. It can refer to high temperatures causing a decrease in kernel quantity per ear due to several factors, including reduced pollen viability, silk receptivity, and increased kernel abortion frequency (Cicchino *et al*., 2010). Stress post-pollination inhibits kernel formation (Moser *et al*., 2006), while excessive spring temperature stress decreases row and kernel numbers and overall plant yield (Hussain *et al*., 2010). High temperatures above 30 °C affect Rubisco activity, decreasing photosynthesis and kernel development (Steven *et al*., 2002). Additionally, nutrient limitation from reduced photosynthesis results in embryo abortion, contributing to decreased grain yield (Commuri and Jones, 2001).

CONCLUSIONS

In conclusion, genetic diversity is vital for Identifying and categorizing to develop heat-tolerant crop varieties. High temperatures notably influence maize's reproductive phases, affecting pollen viability and kernel development, leading to decreased yield. Evaluation of maize inbred lines under normal and elevated temperatures revealed significant differences in traits like plant and ear height, flowering time, pollen production, and grain yield. Understanding genetic variation and physiological responses to heat stress is important for designing resilient crop varieties and ensuring sustainable agricultural production.

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