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ASSESSING HEAT TOLERANCE IN WHEAT GENOTYPES: UTILIZING AGRO-PHYSIOLOGICAL AND QUALITY INDICES WITH MULTIVARIATE ANALYSES

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ABSTRACT

Rising air temperatures pose a significant threat to global wheat harvests, making the development of heat-tolerant genotypes crucial. Using multivariate techniques, plant breeders can enhance the genetic stability of key agro-physiological indicators to boost wheat yield. This study analyzed 48 bread wheat genotypes using 20 characteristics to identify those best suited for heat tolerance, providing valuable insights for breeding programs. Variations in phenotypic and genetic features were identified using multivariate analyses of agro-physiological and quality indices. These were combined to create accurate and consistent selection criteria. The analysis of 20 indicators revealed considerable genotypic and environmental diversity. Our selection process identified eight indices with high heritability and genetic gain, making them useful markers for heat tolerance. The lines GS/2019-20/6046, HTWYT/2019-20/40, and GS/2019-20/7004 were top performers across six principal components with the highest positive scores. The genotypes were classified as follows based on five essential indices [effective tillers/plant (ET), biological yield/plant (BY), chlorophyll content index (CCI), grain filling rate (GFR) and grain yield (GY)] that were obtained *via* correlation, path, and PCA analysis: ten heat-sensitive, fifteen moderately sensitive, seven highly heat-sensitive, seven moderately heat-tolerant, seven heat-tolerant and two highly heat-tolerant. The wheat genotypes GS/2019-20/6046, HTWYT/2019-20/40, SAWYT-2018-19/309, and GS/2019-20/7004 are promising sources for heat-tolerant breeding programs.

Keywords: Heat tolerance, Multivariate, Correlation, Path analysis and PCA analysis.

Introduction

The primary economic sector in the Indian subcontinent, agriculture gives those living in rural areas a source of income, employment, and food security. The last few decades have seen a significant transition in natural ecosystems, agricultural output, and cultivation practices due to the cascading effects of climate change. The wheat crop is typically suited to a wide variety of worldwide climate conditions. For the majority of their developmental stages, particularly during blooming and grain filling, wheat crops require

temperatures between 12 and 22 °C (Rehman *et al.*, 2021). One of the biggest problems facing wheat growers worldwide is a notable increase in air temperature since it has a detrimental impact on grain quality and output (Dubey *et al.*, 2021 and Riaz *et al.*, 2021). Grain quality affects wheat's capacity to generate distinctive baked goods like bread. Compositional characteristics like starch content (SC), protein content (PC), gluten content, and sedimentation value are used to evaluate this feature (Hernández-Espinosa *et al.*, 2018). High canopy temperatures (>31 °C) experienced by late-cultivated wheat crops from

anthesis to maturity have a detrimental effect on the formation of grain yields (Joshi *et al.*, 2007). A 3–4% C increase in seasonal minimum or maximum temperatures in wheat could result in a 15–35% loss in output in Africa and Asia and a 25–35% fall in yield in the Middle East throughout the blooming, pollination, and grain-filling phases (Bitá *et al.*, 2021 and Zhao *et al.*, 2021). Yields are likely to be much lower when such stress happens at key growth stages, such as flowering, grain filling and grain quality might be particularly affected by brief bursts of extremely high temperatures (Dubey *et al.*, 2021 and Fernie *et al.*, 2022) In order to improve wheat performance in hot settings, researchers frequently take advantage of several physiological systems.

The ultimate grain yield is probably influenced by physiological characteristics like early maturity, low canopy temperature, staying green, and high biomass accumulation (Lopes *et al.*, 2012 and Barakat *et al.*, 2020) Because they are more genetically stable and less influenced by the environment than grain yield variables, physiological traits may be employed as an indirect selection method to improve wheat genotypes (Pinto *et al.*, 2010). To detect wheat genotypes that yield well and can withstand high temperatures, more investigation into physiological features is required. These traits can then be used as selection criteria. The only way to do this would be to create early maturing, high-yielding genotypes with extended grain-filling length, climatic intelligence, and abiotic stress tolerance (Mondal *et al.*, 2010). Elite wheat genotypes have been assessed and tested for heat tolerance and traits-linked adaptation before being blended into common varieties for high yielding and heat tolerance (Joshi *et al.*, 2007 and Mondal *et al.*, 2010). Assessing the genetic characteristics related to agro-physiological and quality response is crucial in order to identify the optimal genotypes for use in breeding programs that can withstand abiotic stress while retaining their bread-making capacity (Al-Ashkar *et al.*, 2020). Breeding programs are enhanced by the use of multivariate analysis techniques, which improve accuracy in verification and selection by incorporating multiple traits and features simultaneously. As a result, multivariate analytic methods such as path analysis, cluster analysis, and principle component analysis (PCA) can be used as a model instrument for testing and identifying the causes of variance (Grzesiak *et al.*, 2010 and Al-Ashkar *et al.*, 2019 and El-Hendawy *et al.*, 2020). PCA, for example, reduces the dimensionality of a data set by decreasing the number of variables while preserving as much information as possible. It applies an orthogonal transformation to convert a set of observations of potentially correlated

variables into a set of uncorrelated variables, known as principal components. A simple extension of correlation coefficient is path analysis. Its goal is to categorize the effects of hypothesized causal relationships between sets of variables into direct and indirect effects, as well as assessments of their magnitude and significance. By grouping related genotypes into many clusters according to the values of various variables, cluster analysis is a technique. This study primary objectives were to: (i) create a screening technique to determine the significance of wheat primary heat tolerance indices using multivariate evaluation; and (ii) assess and group the heat tolerance of 48 wheat genotypes.

Materials and Methods

During the *Rabi* 2021–2022, field trials were held at the Navsari Agricultural University (20°37' N, 72°54' E, and 11.98 m asl). Three independent replicates and a randomized entire block comprised the experimental design. The two dates of sowing were used for this study., i.e., the optimum sowing (29th November in 2021) and late sowing (6th January in 2022). Each genotype 4.0 m-long two rows made up the experimental plot. There may be roughly 80 plants in two rows if the spacing between plants and rows was kept between 10 and 22.5 centimeters. Every 8–10 days, the experiment was irrigated to prevent the confounding effects of high temperature and drought stress. To produce healthy wheat crops, the suggested practice packages for weeding, fertilizing, and crop protection in this area were implemented. The experimental plot's soil was medium-black in color, with a pH range of 7.5 to 7.8, adequate water-holding capacity, and moderate to poor drainage. In this investigation, 48 distinct genotypes of wheat were employed, comprising 6 check varieties and 42 lines (Table 1).

We evaluated twenty physio-agronomic and qualitative parameters across all 48 genotypes of wheat. In order to minimize the influence on the environment, the middle rows were randomly chosen to provide the mean value of five samples or plants per genotype for the purpose of assessing all physio-agronomic properties. At each step, five physiological crop properties were estimated. These include the normalized differential vegetative index (NDVI), canopy temperature (CT), chlorophyll content index (CCI), and grain filling duration (GFD) and rate (GFR). In short, a handheld CCM-200 gadget (OPTI-SCIENCES, USA), a FLIR 180 TG165 imaging infrared thermometer, and a FIELDSCOUT® CM 1000 NDVI Meter made by Spectrum Technologies, Inc. were used to measure CCI, CT, and NDVI,

respectively. GFD was computed using the time interval between DM and DA. Before and/or after harvest, eleven agronomic attributes were estimated: plant height (PH, cm), spike length (SL), effective tillers/plant (ET), biological yield/plant (BY, g), harvest index (HI, %), days to heading (DH, days), days to anthesis (DA, days), days to maturity (DM, days), and grain yield/plant (GY, g). DH, DA, and DM were noted when 50% of the plants headed, flowered, and had yellow peduncles, respectively. The crops were threshed to measure TGW, BY, HI, and GY characteristics after harvest. The FOSS, 198 Sweden Company's Near Infrared Transmittance (Infratec TM) machine was used to measure the following: wet gluten (%), protein content (%), sedimentation value (ml), and starch content (%). With the help of this quick and non-destructive analysis technique, grain quality features may be efficiently assessed, yielding useful information for breeding and selection.

Based on the attributes data, the Heat tolerance index (HTI) for each attribute were calculated, providing a quantitative measure of the heat tolerance of various traits. Heat tolerance index (HTI) was calculated for grain yield and other quantitative traits over high temperature stress (late sown) and non-stress environment (normal sown) by using the formula as suggested by Fernandez (1992). The genotypes with high HTI values are more tolerant to heat stress.

$$HTI = \frac{(X_p \times X_s)}{X_p^2}$$

Where,

X_p = Mean of individual genotype under normal condition for each attribute

X_s = Mean of individual genotype under stress condition for each attribute

X_p^2 = Mean of all genotypes under normal condition for each attribute

Microsoft Excel was utilized for calculating indices. The variance analysis, variability parameters and path analysis for every morpho, physiological and quality attributes were calculated using the package in R software. Correlation, principal component analysis (PCA), biplot diagrams and cluster analysis for the identification of tolerant and susceptible genotypes were generated using PAST Statistics version 4.16c.

Results and Discussion

Analysis of Variance and Genetic Parameters of the Studied Indices

The analysis of variance for twenty characters, as presented in Table 2, shows significant mean square

values for all the traits in genotypes. This indicates the presence of enough variability among the genotypes for each character studied. For the majority of indices, the PCV and GCV converged, with the PCV being greater than the GCV (Table 3). For 15 assessed indices, ranging from 63.58% (PH) to 93.70% (ET), the broad-sense heritability (h^2) displayed high values (>60%) (Table 3). Ten evaluated indices ranging from 20.89% (DH) to 93.76% (ET) had high values (>20%) for the genetic gain; four measured indices ranging from 10.44% (PC) to 19.90% (DA) had moderate values (>10%) (Table 3). The genetic stability of the characteristic (heritability, genetic gain, and GCV) is the main factor that plant breeders rely on. The DH, ET, SL, GS, TGW, BY, GFD and CCI indices demonstrated close relationships between GCV and PCV, high heritability ($h^2 > 60\%$), and genetic gain (>20%). This suggests that the genetic control of indices are additive gene effects the primary source of the genotypic variances. As a result, these indices are trustworthy when employed as direct phenotypic selection criterion for assessing heat tolerance. Similar result was obtained by Falconer *et al.* (1996), Abdolshahi *et al.* (2015), Grzesiak *et al.* (2019) and El-Hendawy *et al.* (2020).

Identification of Indices Related to Yield Tolerance Index

The association between the GY index and each heat tolerance index (HTI) was examined. Figure-1 shows that there was negative association for the CT, PC, WGC, and SV index, whereas eleven HTI (GFR, BY, ET, SL, GS, CCI, TGW, NDVI, HI, DH, and DM) exhibited a positive association with yield, which indicated that it is possible to improve these traits simultaneously with YP through direct phenotypic selection. To determine which indices are best-measured and related to heat tolerance, as well as how they affect the performance of the GY index as a dependent indicator, all of the indices were examined using path analysis in each genotype as independent indices. According to the path analysis, the GY index was directly impacted by the indices BY, GFR, and HI, with high direct effects of 0.99, 0.52, and 0.35 respectively (Table 4). Path coefficient analysis is used to divide the three indices of the GY index variation into various indirect impacts with the other indices and direct effects of each index separately. Path coefficients are useful instruments for comprehending how independent and dependent variables relate to one another (Khan *et al.*, 2003 and Al-Ashkar *et al.*, 2020). Additionally, they discovered that effective breeding programs would not benefit from a straightforward correlation study including interactions between

independent and dependent indices (Del Moral *et al.*, 2010). The primary goal of plant breeding projects for identifying genotypes of heat-tolerant wheat should be the low CT trait. In wheat breeding programs, CT is a reliable physiological marker that is utilized as an affordable, nondestructive method of finding genotypes that are heat-tolerant (Reynolds *et al.*, 2007, Reynolds *et al.*, 2009 and Rebetzke *et al.*, 2013).

Principal Component Analysis

The sample suitability, measured by the Kaiser-Meyer-Olkin (KMO) test, indicates a high value (KMO > 0.5), suggesting that the data is well-suited for factor analysis. The six principal components (eigen value > 1) that the PCA created from the absolute values of each eigenvector contained the estimated variables (20 indices) with contribution rates of 29.47% (PC1), 16.46% (PC2), 12.90% (PC3), 8.59% (PC4), 6.81% (PC5), and 5.86% (PC6) (Table 5). The cumulative contribution rate reached 80.11%. ET, SL, GS, TGW, BY, GFR, CCI, NDVI, and GY were all connected to PC1. PC2 was associated with WGC, SV, and PC. DH, DA, DM, and SC were associated with PC3; PH and CT were associated with PC4; and HI and GFD were associated with PC5, respectively (Table 5). The germplasm lines GS/2019-20/6046, HTWYT/2019-20/40, and GS/2019-20/7004 are those that show the highest positive PC scores and are commonly found in PC1 through PC6. Based on their correlations, the biplot analysis successfully distinguished between the heat-related traits: negatively associated traits ($>90^\circ$), independently associated traits ($=90^\circ$), and favorably associated characteristics ($<90^\circ$). The very low angle between the respective lines in the in character biplot GY and CCI indicates a strong relationship (Figure-2). Even though there was a lesser angle between PC and WGC, PC showed more variances because its associated lines were longer. The genotypic performance in biplots can be measured as the distance between the genotype and the biplot origin. The distant genotypes may have the highest values for one or more characteristics. 3-D representation of different genotypes based on heat tolerance index using different traits for PC1, PC2 and PC3 (Figure-3). The PCA biplot divides the distant genotypes, GS/2019-20/6046 and GS/2019-20/7004 respectively. Many recent literatures have employed the stress tolerance index typically used as a criterion to assess tolerance to screen genotypes (De Leon *et al.*, 2015, Al-Ashkar *et al.*, 2019, Al-Ashkar *et al.*, 2020 and Yu *et al.*, 2021). Even though the number of applied genotypes might seem little, when multivariate analysis techniques were used to discriminate their heat tolerance, the results were correct and the selection criteria were dependable

(Sandhu *et al.*, 2017, Al-Ashkar *et al.*, 2019, El-Hendawy *et al.*, 2019 and Yu *et al.*, 2021).

Clustering and Genetic Relationships between the Genotypes for Heat Tolerance

After conducting correlation, path, and PCA analysis we chose to utilize the tolerance index of the five indices (ET, BY, CCI, GY and GFR) for cluster analysis of 48 wheat genotypes' heat tolerance utilizing genetics dissimilarity matrix. Based on the genotype range of wheat heat tolerance, cluster analysis revealed six main groups (Figure-3). Cluster I, classified as highly tolerant (HT), comprise of two genotypes (SAWYT-2018-19/309 and GS/2019-20/6046); cluster II or tolerant (T) with seven genotypes (HPYT-2019-20/416, GS-2018-19/1007, GS/2019-20/5042, EHT-2018-19/443, RWP-2019-29, HTWYT/2019-20/30 and GW-499), cluster V of moderately tolerant (I) seven genotypes (CWYT 2018-19-644, HTWYT/2019-20/17, EHT-2019-20/732, HTWYT/2018- 19/36, EHT-2019-20/735, HTWYT/2019-20/2 and EHT-2018-19/407), cluster VI or moderately sensitive (MS), of 15 genotypes (GW 11, GS/2018-19/7042, K 1317, GS/2019-20/1003, DBW-166, LOK 1, CWYT 2018-19-630, GS/2019-20/3060, HD 2932, HTWYT/2019-20/8, HTWYT/2019-20/34, RWP 2019-31, WYCYT 2018-20, DT RIL 110 and GS/2019-20/7004). Cluster IV was classified as sensitive (S) ten genotypes (QST 1910, EHT-2018-19/406, HI 1628, DT RIL 1, HTWYT/2019-20/40, HTWYT/2019-20/11, GS/2019-20/3056, HPYT-2019-20/449, EHT-2018-19/403 and WYCYT-2018-13). Cluster III was classified as highly sensitive (HS), consisting of seven genotypes (GS/2018-19/6027, GW 173, HTWYT/2019- 20/39, EHT-2018-19/401, GS/2019-20/4003, GS/2018-19/4049 and HPYT-2019-20/418) (Figure-3). Numerous researchers have ranked the tolerant wheat genotypes according to various agro-physiological properties using cluster analysis (Zeng *et al.*, 2002, Abdolshahi *et al.*, 2015, Al-Ashkar *et al.*, 2019, Al-Ashkar *et al.*, 2021 and Al-Ashkar *et al.*, 2022).

Conclusion

The study revealed significant variability among the genotypes for all the evaluated traits. Eight indices demonstrated a combination of high heritability and genetic gain, along with a close relationship between GCV and PCV making them useful for identifying heat-tolerant genotypes. Traits such as biological yield per plant, grain filling rate and harvest index revealed high genetic advance as a percentage of the mean, high heritability, positive and significant correlations, and high positive direct effects. Therefore, these traits are advantageous for future breeding programs aimed at

enhancing grain yield in wheat. The grouping of genotypes using multivariate methods in this study is practically valuable for wheat breeders. The tolerated wheat lines GS/2019-20/6046, HTWYT/2019-20/40, SAWYT-2018-19/309, and GS/2019-20/7004 are recommended as prominent genetic sources for heat-tolerant breeding programs.

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Table 1 : A list of wheat genotypes

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	HTWYT/2019-20/2	11	HPYT-2019-20/449	21	HI 1628	31	EHT-2019-20/732	41	GS/2018-19/4049
2	HTWYT/2019-20/8	12	EHT-2018-19/443	22	HTWYT/2019-20/39	32	EHT-2019-20/735	42	WYCYT-2018-13
3	HTWYT/2019-20/11	13	CWYT 2018-19-630	23	GS/2019-20/1003	33	GS/2018-19/6027	43	K 1317 ©
4	HTWYT/2019-20/17	14	CWYT 2018-19-644	24	GS/2019-20/3056	34	GS/2019-20/4003	44	GW 499 ©
5	HTWYT/2019-20/30	15	GS-2018-19/1007	25	GS/2019-20/3060	35	HTWYT/2018-19/36	45	HD 2932 ©
6	HTWYT/2019-20/34	16	SAWYT-2018-19/309	26	EHT-2018-19/401	36	QST 1910	46	LOK 1 ©
7	HTWYT/2019-20/40	17	RWP-2019-29	27	EHT-2018-19/403	37	RWP 2019-31	47	GW 173 ©
8	EHT-2018-19/407	18	GS/2019-20/5042	28	EHT-2018-19/406	38	DT RIL 110	48	GW 11 ©
9	HPYT-2019-20/416	19	DBW-166	29	GS/2018-19/7042	39	WYCYT 2018-20		
10	HPYT-2019-20/418	20	GS/2019-20/6046	30	GS/2019-20/7004	40	DT RIL 1		

Table 2 : Analysis of variance for heat tolerance index of measured traits

Source of Variation	Mean Sum of Square											
	DF	DH	DA	DM	PH	ET	SL	GS	TGW	BY	HI	GFD
Replication	2	0.0009	0.0009	0.0001	0.0016	0.0225	0.0056	0.0012	0.0019	0.0256	0.0049	0.0011
Treatment	47	0.0335**	0.0292**	0.0253**	0.0343**	0.4749**	0.0996**	0.1649**	0.0514**	0.2480**	0.1924**	0.0868**
Error	94	0.0010	0.0009	0.0009	0.0055	0.0105	0.0031	0.0049	0.0038	0.0126	0.0303	0.0056
	DF	GFR	CT	CCI	NDVI	PC	SC	WGC	SV	GY		
Replication	2	0.1845	0.0147	0.0007	0.0003	0.0031	0.0001	0.0004	0.0020	0.0115		
Treatment	47	0.3706**	0.0179**	0.0533**	0.0071**	0.0234**	0.0007**	0.0153**	0.0113**	0.2316**		
Error	94	0.0439	0.0056	0.0016	0.0013	0.0057	0.0001	0.0036	0.0034	0.0162		

DH: Days to heading

DA: Days to anthesis

DM: Days to maturity

PH: Plant height (cm)

ET: Effective tillers/plant

SL: Spike length (cm)

GS: Grains/spike

TGW: Thousand grain weight (g)

BY: Biological yield/plant (g)

HI: Harvest index (%)

GFD: Grain filling duration

GFR: Grain filling rate

CT: Canopy temperature

CCI: Chlorophyll content index

PC: Protein content

SC: Starch content

WG: Wet gluten content

SV: Sedimentation value

GY: Grain yield/plant (g)

NDVI: Normalized difference vegetative index

Table 3 : Genetic variability parameters of heat tolerance index of measured traits studied

Character	Min	Max	Mean	GCV	PCV	H ² _b (%)	GAM
Days to heading	0.67	1.42	0.98	10.59	11.07	91.60	20.89
Days to anthesis	0.70	1.37	0.96	10.11	10.58	91.26	19.90
Days to maturity	0.63	1.30	0.91	9.89	10.43	90.00	19.34
Plant height (cm)	0.58	1.14	0.95	10.33	12.95	63.58	16.96
Effective tillers/plant	0.35	2.35	0.84	47.01	48.57	93.70	93.76
Spike length (cm)	0.35	1.46	0.94	19.12	20.02	91.22	37.66
Grains/spike	0.38	1.41	0.94	24.52	25.62	91.58	48.33
1000 grain weight (g)	0.60	1.09	0.89	14.17	15.77	80.71	26.24
Biological yield/plant (g)	0.35	1.64	0.88	31.99	34.46	86.17	61.18
Harvest index (%)	0.45	1.97	0.91	25.47	31.83	64.06	41.99
Grain filling duration	0.52	1.22	0.84	19.66	21.60	82.82	36.86
Grain filling rate (g/day)	0.46	1.97	0.92	34.60	40.99	71.27	60.18
Canopy temperature (°C)	1.07	1.36	1.20	5.31	8.17	42.27	7.12
Chlorophyll content index	0.74	1.43	0.96	13.70	14.32	91.49	25.00
NDVI	0.85	1.04	0.91	4.78	6.20	59.38	7.59
Protein content (%)	0.91	1.28	1.08	7.11	9.97	50.86	10.44
Starch content (%)	0.96	1.03	0.99	1.42	1.74	66.67	2.39
Wet gluten content (%)	0.89	1.24	1.06	5.90	8.18	52.00	8.77
Sedimentation value (ml)	0.88	1.15	1.02	4.97	7.55	43.33	6.74
Grain yield/plant (g)	0.41	1.73	0.81	33.14	36.68	81.59	61.66

Table 4 : Genotypic path coefficient analysis of heat tolerance index component characters towards grain yield

Cha.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	'r _g ' with GYP
1	0.24	-0.36	0.16	-0.00	-0.07	-0.11	0.04	0.12	0.04	0.07	0.00	0.13	0.12	-0.00	0.06	0.01	0.05	0.00	-0.00	0.27
2	0.22	-0.38	0.16	-0.00	-0.06	-0.11	0.04	-0.09	0.06	-0.00	0.00	0.07	0.08	-0.00	0.05	0.02	0.07	0.00	-0.00	0.14
3	0.15	-0.26	0.24	-0.01	-0.04	-0.08	0.05	-0.11	0.12	0.03	0.05	-0.07	0.00	-0.00	0.06	0.03	0.04	-0.00	-0.00	0.22
4	0.09	-0.18	0.12	-0.01	-0.01	-0.07	0.05	-0.13	0.23	-0.09	0.02	-0.00	-0.01	-0.00	0.06	0.02	0.03	0.00	-0.00	0.11
5	0.06	-0.08	0.03	-0.00	-0.28	-0.21	0.10	-0.18	0.76	-0.02	0.00	0.37	0.05	0.00	0.13	0.00	0.01	0.00	-0.00	0.76**
6	0.08	-0.13	0.06	-0.00	-0.18	-0.32	0.14	-0.13	0.55	0.03	0.00	0.33	0.08	0.00	0.13	-0.00	0.05	0.00	-0.00	0.69**
7	0.06	-0.09	0.06	-0.00	-0.15	-0.24	0.19	-0.08	0.51	0.04	0.01	0.27	0.01	-0.00	0.11	-0.06	-0.04	0.02	0.00	0.62**
8	0.05	-0.06	0.05	-0.00	-0.10	-0.08	0.03	-0.53	0.55	-0.01	0.00	0.25	0.25	0.00	0.07	0.00	0.07	-0.00	-0.00	0.54**
9	0.01	-0.02	0.03	-0.00	-0.21	-0.18	0.09	-0.29	0.99	-0.14	0.00	0.36	0.02	-0.00	0.13	-0.01	0.00	0.00	0.00	0.78**
10	0.05	0.00	0.02	0.00	0.01	-0.03	0.02	0.01	-0.40	0.35	0.01	0.05	0.12	-0.00	-0.02	-0.02	-0.01	0.00	0.00	0.18
11	0.02	-0.02	0.19	-0.00	-0.00	-0.02	0.03	-0.06	0.08	0.05	0.07	-0.18	-0.06	-0.00	0.03	0.02	0.00	-0.00	-0.00	0.15
12	0.06	-0.05	-0.03	0.00	-0.20	-0.21	0.09	-0.25	0.68	0.03	-0.02	0.52	0.15	-0.00	0.09	-0.03	0.01	0.00	0.00	0.86**
13	-0.07	0.07	-0.00	-0.00	0.04	0.06	-0.00	0.32	-0.05	-0.10	0.01	-0.19	-0.41	0.00	-0.02	0.09	0.02	-0.01	-0.00	-0.26
14	0.08	-0.11	0.08	-0.00	-0.15	-0.18	0.09	-0.21	0.50	0.02	0.01	0.23	0.09	-0.00	0.17	-0.03	0.02	0.01	0.00	0.58**
15	0.06	-0.09	0.06	-0.00	-0.16	-0.18	0.08	-0.15	0.54	-0.03	0.01	0.21	0.04	-0.00	0.23	-0.03	-0.07	0.01	0.00	0.53**
16	0.01	-0.04	0.03	-0.00	-0.00	0.01	-0.05	-0.00	-0.05	-0.04	0.00	-0.07	-0.18	0.00	-0.04	0.21	0.21	-0.04	-0.00	-0.05
17	-0.04	0.09	-0.03	0.00	0.01	0.05	0.02	-0.14	-0.03	0.02	-0.00	-0.02	0.04	-0.00	0.06	-0.16	-0.28	0.04	0.00	-0.07
18	-0.02	0.02	0.01	0.00	0.01	0.03	-0.07	-0.00	-0.08	-0.00	0.01	-0.05	-0.11	0.00	-0.06	0.15	0.19	-0.06	-0.00	-0.03
19	0.00	-0.05	0.03	-0.00	-0.00	-0.00	-0.02	-0.04	-0.11	-0.03	0.00	-0.05	-0.03	0.00	-0.06	0.13	-0.21	-0.04	-0.00	-0.08

Note: Diagonal values are direct effects, Residual factor = 0.0068, Cha. -Characters, *,** Significant at 5% and 1% level of significance, respectively.

1: Days to heading	2: Days to anthesis	3: Days to maturity	4: Plant height (cm)
5: Effective tillers/plant	6: Spike length (cm)	7: Grains/spike	8: Thousand grain weight (g)
9: Biological yield/plant (g)	10: Harvest index (%)	11: Grain filling duration	12: Grain filling rate
13: Canopy temperature	14: Chlorophyll content index	15: Normalized difference vegetative index	16: Protein content
17: Starch content	18: Wet gluten content	19: Sedimentation value	

Table 5 : Eigenvectors and percentage of accumulated contribution of principal components

	PC1	PC2	PC3	PC4	PC5	PC6
Eigenvalue	5.896	3.293	2.581	1.718	1.363	1.173
Variability (%)	29.479	16.463	12.903	8.5909	6.8171	5.8669
Cumulative %	29.479	45.942	58.845	67.435	74.253	80.119
Eigenvectors:						
DH	0.225	0.224	0.305	-0.272	-0.193	0.213
DA	0.196	0.244	0.314	-0.186	-0.307	0.269
DM	0.184	0.295	0.402	0.077	0.144	-0.111
PH	0.141	0.197	0.211	0.212	-0.302	-0.099
ET	0.322	-0.019	-0.210	0.089	0.025	0.123
SL	0.327	0.013	-0.074	0.015	0.120	0.269
GS	0.299	-0.098	0.042	0.124	0.175	0.223
TGW	0.225	0.083	-0.126	-0.182	-0.162	-0.602
BY	0.307	-0.054	-0.244	0.291	-0.124	-0.184
HI	0.021	-0.025	0.100	-0.489	0.573	0.094
GFD	0.073	0.208	0.283	0.264	0.471	-0.382
GFR	0.295	-0.132	-0.302	-0.209	-0.038	0.119
CT	-0.116	0.082	-0.032	0.526	0.160	0.373
CCI	0.310	-0.032	0.066	0.036	0.091	-0.042
NDVI	0.274	-0.081	0.066	0.213	-0.039	0.032
PC	-0.055	0.432	-0.214	0.066	0.029	0.103
SC	-0.005	-0.413	0.288	0.123	0.050	-0.005
WGC	-0.087	0.395	-0.263	-0.017	0.171	0.009
SV	-0.044	0.394	-0.215	-0.015	0.011	0.040
GY	0.349	-0.033	-0.201	-0.055	0.222	-0.063

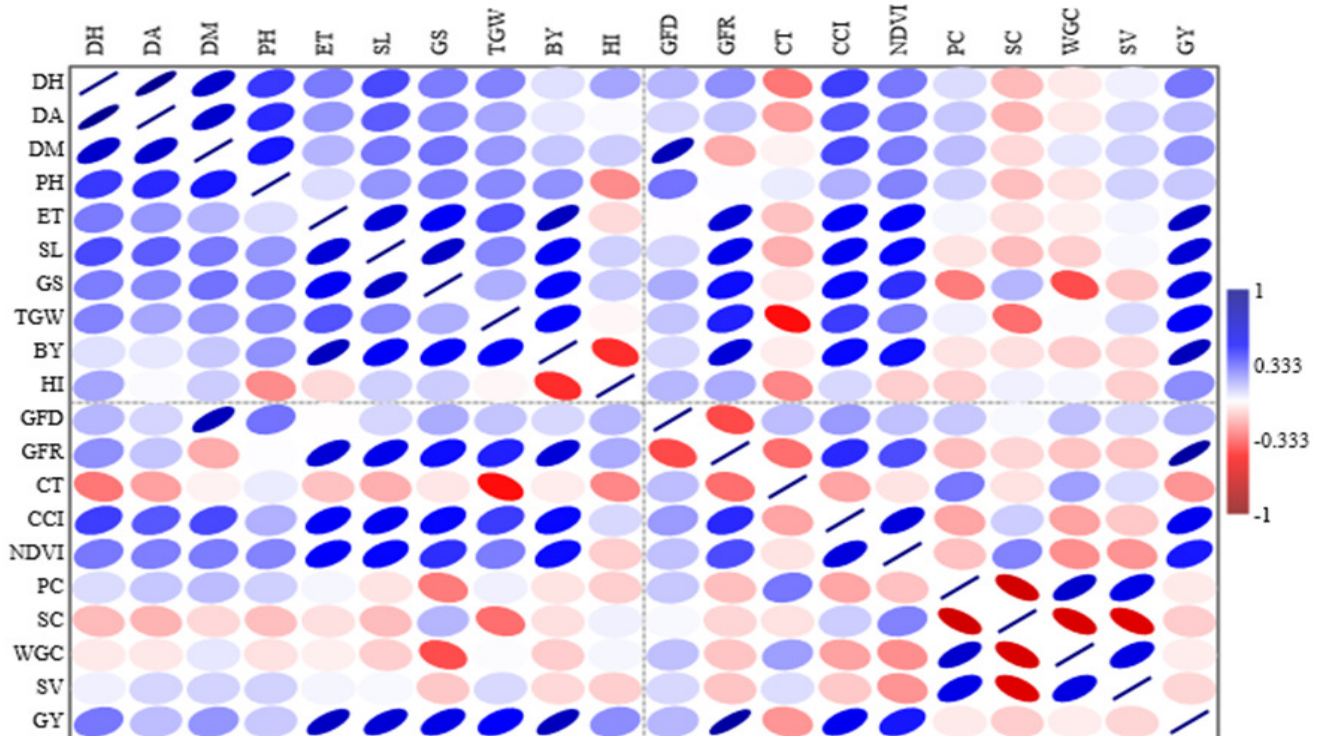


Fig. 1 : Correlation matrix among 20 HTI measured

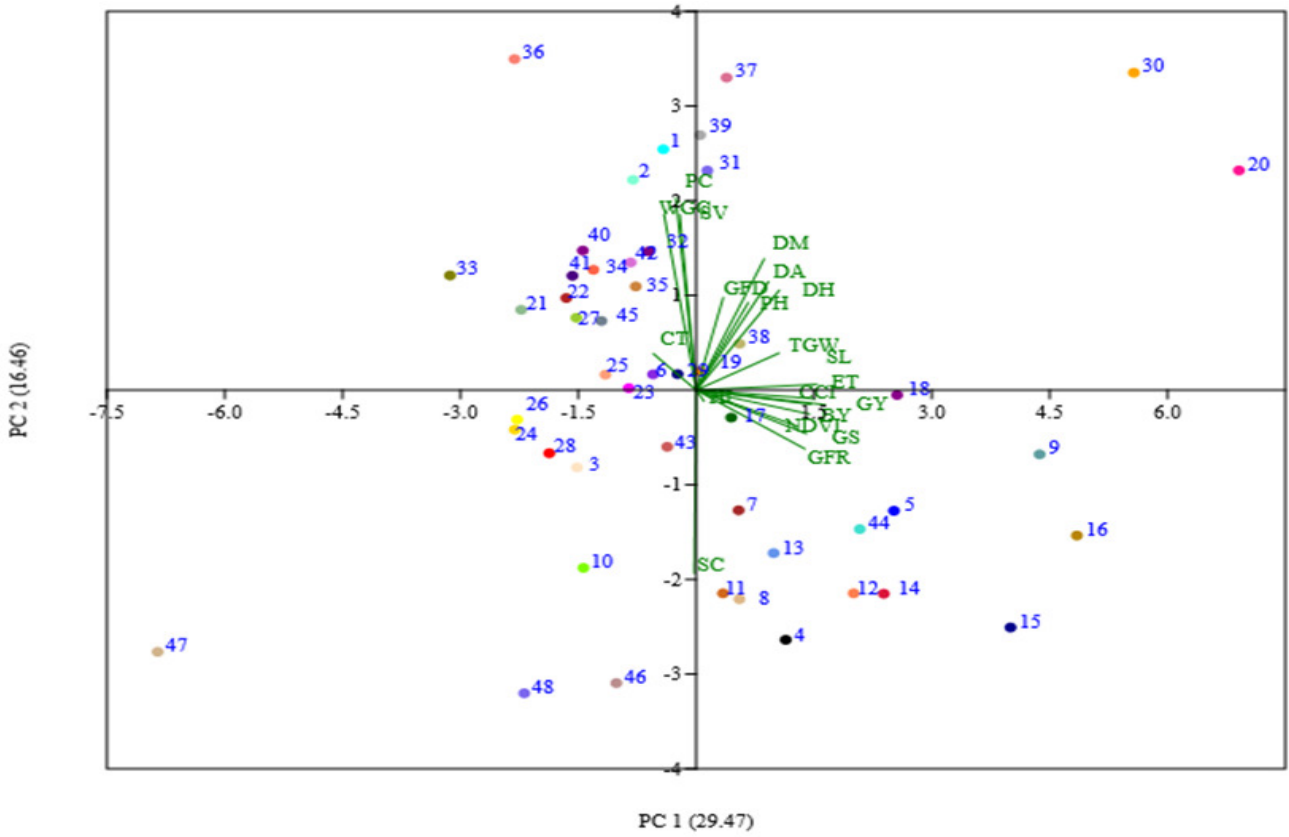


Fig. 2 : Biplot for the first two principal components in the principal component analysis of 48 wheat genotypes for 20 HTI. Scattered numbers over the plot represented the serial number of genotypes mentioned in Table 1.

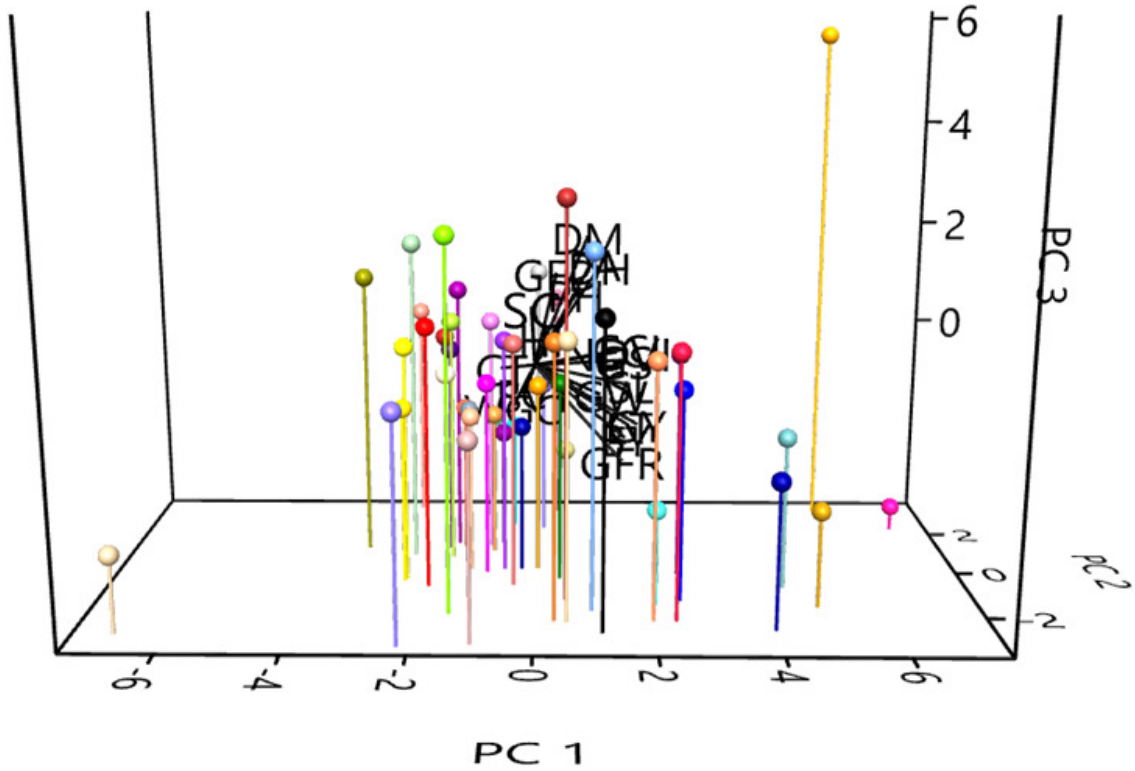


Fig. 3 : 3-D representation of different genotypes based on heat tolerance index of measured traits of 48 wheat genotypes.

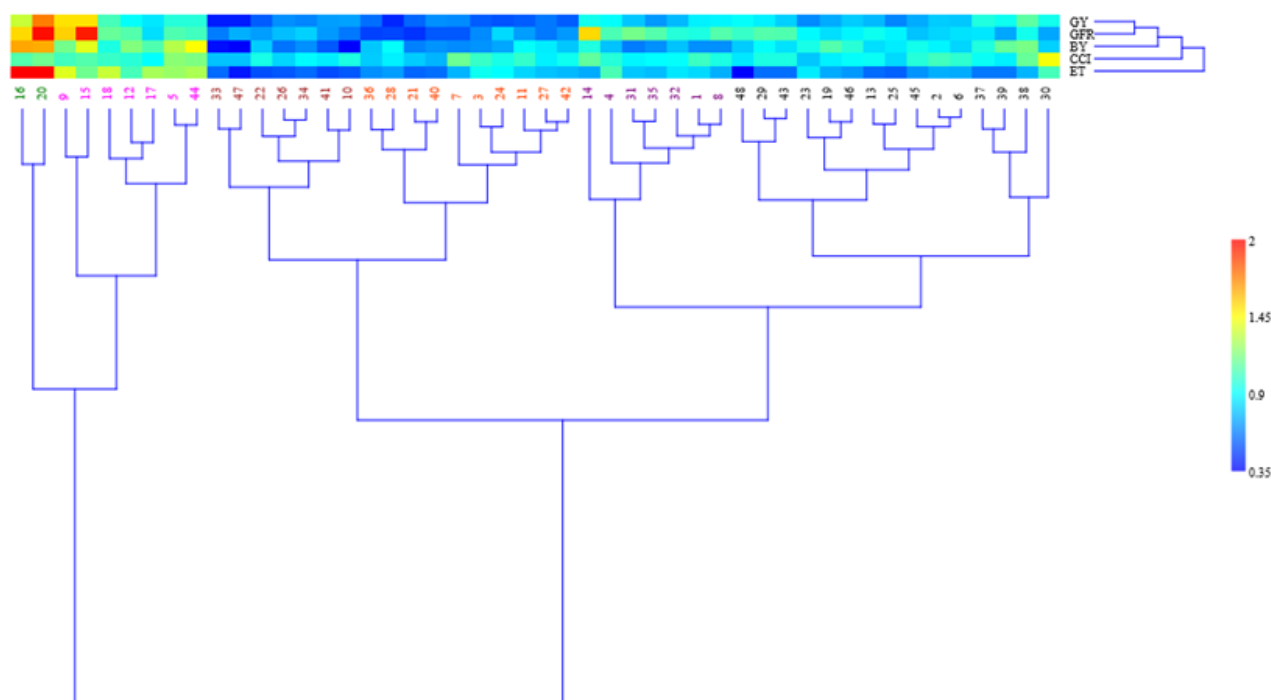


Fig. 4 : Hierarchical clustering of 48 wheat genotypes using five HTI

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