

Assessment of Genetic Diversity for Heat Tolerance in Advanced Breeding Lines of Bread Wheat (*Triticum aestivum* L. em.Thell.)

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ABSTRACT

Food security and public health are becoming major concerns for the global leaders due to climate change. The uneven distribution of rainfall and temperature has increased the global food demand with quality food. The current study was carried out for analysis of genetic diversity among 64 bread wheat genotypes for heat tolerance based on 21 morpho-physiological traits. The sixty four genotypes were grouped into five different clusters. Maximum number of genotypes was in Cluster V (17) with lowest intra cluster distance (3.866) followed by Cluster II (15), I (14), III and IV (each having 9 genotypes). Genotypes of Cluster IV and I were more genetically diverse due

to maximum inter cluster distance between them (8.873). The Cluster II was designated as “highly tolerant” while Cluster I and V as “moderately tolerant” and “highly sensitive” respectively, to heat stress on the basis of comparison of Cluster mean values for yield and its major contributing traits like, peduncle length, flag leaf length, grain filling duration and so on. By collating their mean performance, the genotypes P-13348, P-13676, P-13820 and P-14114 were found to be more heat tolerant in Cluster II. Similarly, genotypes P-13808, P-13638 and P-14050 were found more moderately tolerant among cluster I genotypes and genotypes P-14106, P-14112 and P-14121 were most sensitive among the Cluster V genotypes to terminal heat stress.

Keywords Climate change, Food security, Genetic diversity, Heat stress, Cluster.

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INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a 2nd most important food crop of world which feeds the growing global population to cater their daily protein and calories need (Mishra *et al.* 2021). Due to modernization and globalization, world is facing consequences of the climate change and heat stress is one of them. Global population is growing day by day that has put pressure

on food demand which is threatening the food security (Secretary-General 2020).

Though, incidence of growing temperature particularly at grain filling stage (terminal heat stress) has triggered the demand. The impact of heat stress on the plants is not of single way but it has multi way effect. The damage to molecular mechanisms and plant physiological processes are interrelated that has profound negative effect on the activities of enzymes which participate in photosynthesis process, membrane stability, metabolic process, source to sink system (Mathur *et al.* 2014) and induce the activities of enzymes that play role in production of reactive oxygen species (ROS), ethylene and chlorophyllase (Hays *et al.* 2007). Heat stress causes male sterility (Kaur and Behl 2010), increase photorespiration (Fu *et al.* 2012, Jagadish *et al.* 2016) and senescence process which retards greenness due to breakdown of photosynthetic system that ultimately short the grain filling duration leading to loss in grain quantity and quality (Hedhly *et al.* 2009).

According to estimates from Asseng *et al.* (2015), the yield of wheat grains decreases by 6% globally for every one degree Celsius rise in the temperature. The creation of resistant cultivars is a long-term strategy for reducing the effects of heat stress. The most crucial strategy continues to be conventional breeding, which entails selecting tolerant germplasm lines, then transferring the tolerance characteristics into commercial lines. Therefore, it is necessary to create genotypes that are adapted to these challenging conditions. To create genotypes for the intended environment, the availability of genetic variation for these qualities is a must. Breeders can identify suitable parents for intentional hybridization by studying variance among germplasm lines with recognized potentialities. Given this context, the current study's goal was to categorize 64 wheat genotypes for heat tolerance based on different morpho-physiological traits.

MATERIALS AND METHODS

To classify the 64 bread wheat genotypes into different clusters based on 21 morpho-physiological traits, an experiment was conducted at Research Area of Wheat and Barley Section, Department of Genet-

ics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Hisar (latitude 29°10' North and longitude 75° 46' East, respectively with an altitude of 215.2 meters above the mean sea level) comes under category of semi-arid region that leads to a type of climate under which crops experience stresses during different periods of growth which not only affects produce yield but quality of produce. The planting material was consisted of 60 advanced breeding lines and four standard heat tolerant check varieties namely WH 1124, WH 1021, HD 3059 and DBW 90 (pedigree has been referred, Bhatti *et al.* 2022). To induce the effect of high temperature at reproductive stage or more specifically during grain filling stage, the material was sown under late sown conditions (16-12-2019) by adopting Randomized Block Design (RBD) with three replications and recommended package of practice was followed to raise a good crop. The mean maximum and minimum temperature at reproductive stage was 30.70° C and 15.12° C, respectively.

The genotypes were evaluated for different four phenological traits like, days to heading, days to anthesis, days to maturity, grain filling duration and different eleven morphological traits at the time of maturity by randomly selecting five plants per line for each replication and their average was taken for evaluation of genetic diversity. The physiological observations were taken at two different stages, first at 7 days after anthesis and second at 14 days after anthesis. Cluster analysis was done according to (Ward 1963) method to compute inter and intra cluster distances on the basis of euclidean distance along with the cluster mean values based on mean values of different traits. The clusters were designated as "highly tolerant group", "moderately tolerant" and sensitive group based on their mean values of yield and its major contributing traits that hold significant potential in determination of tolerance level of genotypes. R-studio software version 2023.03.1+446 was used to analyze the data for genetic diversity analysis.

RESULTS AND DISCUSSION

The mean sum of squares indicates only presence of genetic variability among the accession for a particular condition but extent of genetic diversity

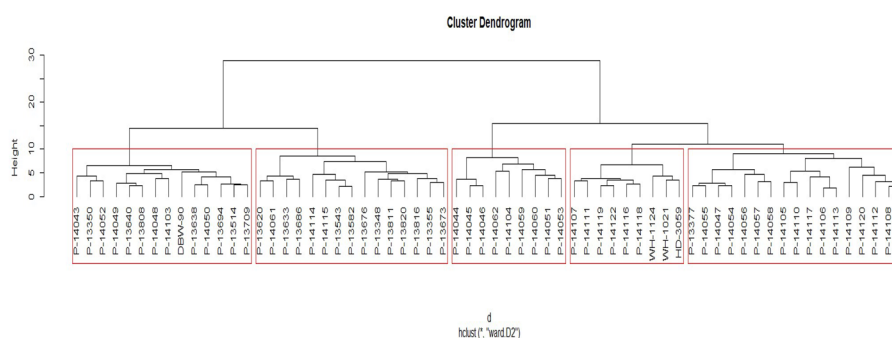


Fig. 1. Dendrogram showing clustering of genotypes.

is given by the D^2 statistics. The presence of genetic divergence and insights of it is very invaluable for crop improvement (Darkwa *et al.* 2020, Sharma *et al.* 2023). So, the presence of genetic variability and effective selection scheme is imperative for any crop improvement programme. In the present investigation, all the 64 genotypes were grouped into the five clusters. Maximum number of genotypes (17) was present in the cluster V (Fig. 1). Cluster II was having next highest number of genotypes (15) followed by I (14), III (9) and Cluster IV (9). The results were in accordance with the findings of Ghodke *et al.* (2019). The number of clusters defines the significance of the extent of diversity among the genotypes. The greater the number of clusters, the more will be genetic dissimilarity among the breeding lines (Darkwa *et al.* 2020). The lowest number of genotypes was placed in Clusters III and IV give an indication that these genotypes were belonging or sharing less ancestry with the genotypes of remaining clusters for the traits under study. Singh *et al.* (2019) also found similar results in his study.

Inter and intra-cluster distances are useful in analysis of the extent of divergence among the breed-

ing lines. The maximum inter cluster distance was exhibited by Cluster I and IV (8.873). The study of Khan *et al.* (2020) was exhibiting the similar kind of interpretation. The Cluster I and III was signifying next highest inter cluster distance (8.373) followed by Cluster I and V (7.693), Cluster IV and V (7.075), Cluster II and IV (6.480), Cluster III and IV (6.004) and so on. Minimum inter cluster distance was found between cluster III and V (5.199) indicating more relatedness among the genotypes of these groups and possess narrow genetic base. The values are depicted in Table 1. Banerjee *et al.* (2020) also found the similar trend in his study. There is direct positive association between the inter cluster distance and genetic divergence (Paw *et al.* 2020). The direct relation between these two helps breeder community to generate hybrids through the hybridization program. More the inter cluster distance more will be genetic divergence among the accessions. The greater genetic differences among the genotypes exploit more heterosis which is governed by the non-additive gene action that further confers wide scope for improvement of yield and its contributing traits. The positive implications of this concept have been achieved in many field crops that helped the worldwide countries

Table 1. Intra (bold, diagonal) and inter (off diagonal) cluster distances.

Cluster	I	II	III	IV	V
I	4.610	5.803	8.373	8.873	7.693
II		4.038	5.694	6.480	5.404
III			4.614	6.004	5.199
IV				5.216	7.075
V					3.866

Table 2. Mean cluster values for different morpho-physiological traits.

Traits	I	II	III	IV	V
DH	89.38	89.02	87.51	84.87	93.39
DA	92.85	92.21	91.46	88.63	97.17
PH	95.61	95.52	89.67	95.60	95.58
NPTM	106.61	110.08	100.97	101.43	100.31
PL	30.59	32.26	26.96	28.71	27.50
FL	19.19	21.09	18.38	19.16	17.43
MSL	9.46	9.57	9.03	9.79	9.13
NSPS	19.48	21.15	17.82	18.57	17.92
NGPS	49.72	51.42	47.03	44.80	46.36
DM	129.21	127.81	126.23	125.10	128.11
GFD	35.61	36.36	34.77	36.47	30.95
TGW	37.56	40.24	33.61	36.32	33.55
BY	9.04	9.51	8.19	7.27	7.99
GY	2.93	3.34	2.54	2.57	2.53
HI	32.49	35.14	31.07	35.47	31.59
NDVI 1	0.613	0.733	0.565	0.567	0.559
NDVI 2	0.508	0.643	0.454	0.460	0.452
CTD 1	3.095	4.314	2.349	2.302	2.161
CTD 2	3.307	4.233	2.424	2.594	1.679
CHF 1	38.869	40.570	38.193	37.342	36.458
CHF 2	37.212	39.280	36.590	35.883	35.433

GY: Grain yield per plot, NDVI-1: Normalized difference vegetation index at 7 days of anthesis, NDVI-2: Normalized difference vegetation index at 14 days of anthesis, TGW: Thousand grain weight, NSPS: Number of spikelets per spike, CTD-1: Canopy temperature depression at 7 days of anthesis, PL: Peduncle length, CTD-2: Canopy temperature depression at 14 days of anthesis, FLL: Flag leaf length, BY: Biological yield per plot, CHF-1: Chlorophyll content at 7 days of anthesis, CHF-2: Chlorophyll content at 14 days of anthesis, NPTM: Number of productive tillers per meter, NGPS: Number of grains per spike, DH: Days to heading, DM: Days to maturity, HI: Harvest Index, PH: Plant height, GFD: Grain filling duration, MSL: Main spike length, DA: Days to anthesis.

to target the global food security and human health (Govindaraj *et al.* 2015).

The significance of intra cluster distances lies in the fact that, they indicate the presence of additive gene action which is heritable fixable component of the genetic variation (Bijma 2011). The effective selection scheme depends upon this gene action and skills of the breeders. The gene action is basic foundation for those crop improvement program which exploit the principal of selection for the development of high yielding varieties (Dias 2014). Cluster IV was manifesting greater intra cluster distance (5.216) than rest of the clusters (Table 1). The work of Khan *et al.* (2020) was exploring the same observation for the traits under study. The result reveals that the genotypes of this cluster have more genetic differences among themselves than rest of the clusters. The next cluster which revealed higher distance was Cluster III (4.614) followed by Cluster I (4.610), Cluster II

(4.038) and cluster V (3.866). The study of (Rajshree 2018) also uncovered the similar findings. The development of high yielding and input responsive varieties based on effective selection pressure during green revolution has revolutionized the field of agriculture and decrease the global food security.

The mean values of the clusters for the different traits help the breeders in the selection of the cluster which is having potential for fulfillment of desired objectives. The groups mean values shows genetic potential of genotypes of a particular cluster for the traits under study. If a cluster is performing better in mean values for yield and its contributing traits then genotypes of this group have potential to perform better under the target condition or have tolerance against the stress. The Cluster II was having greater mean values for yield (3.54) and its major associated traits like, number of productive tillers per meter (110.08), peduncle length (32.26), flag leaf length (21.09), grain filling duration (36.36), 1000 seed

Table 3. list of genotypes placed in different groups based on tolerance level to heat stress.

Cluster number	Group	Genotypes
I	Highly tolerant	P-13348, P-13355, P-13543, P-13582, P-13620, P-13633, P-13673, P-13676, P-13686, P-13811, P-13816, P-13820, P-14061, P-14114, P-14115
II	Moderately tolerant	P-13350, P-13514, P-13638, P-13640, P-13694, P-13709, P-13808, P-14043, P-14048, P-14049, P-14050, P-14052, P-14103, DBW-90
V	Sensitive	P-13377, P-14047, P-14054, P-14055, P-14056, P-14057, P-14058, P-14105, P-14106, P-14108, P-14109, P-14110, P-14112, P-14113, P-14117, P-14120, P-14121

weight (40.24), biological yield (9.51) and all the physiological traits than rest of clusters (Table. 2), thus this cluster may be designated as “highly tolerant group”. At the maturity, stem reserve mobilization is a key physiological process that alters the source sink relationship of the plants (Bhatti *et al.* 2022). The more peduncle length is desirable as it leads to more mobilization of sugar towards the sink i.e. grain. The genotypes that manifest less damage to photosynthetic systems and exhibit more physiological stability at the grain filling stage are found to be more efficient in their performance both in yield and quality (Ray and Ahmed 2015). Abrupt increase in temperature at grain filling stage leads to shorten the grain filling period which induces forced maturity of grains and consequently results in formation of light weighted shriveled grains instead of bold types. So, genotypes that take more time for grain filling are found to be more bold and tolerant to heat stress comparatively. The findings of (Jaiswal *et al.* 2019) was also depicted the same result. The selection among the genotypes of this cluster based on comparative performance may yield some more tolerant lines for the future

breeding programs. The cluster I performed moderate in relation to the mean values and may be designated as “moderately tolerant” to heat stress. The Cluster V having minimum mean values for yield and its related traits may be designated as “sensitive group”. The genotypes placed in these three groups are presented in Table 3. The grouping of genotypes into highly tolerant, moderately tolerant and sensitive group is based on cluster mean values for yield and its major contributing traits like, number of productive tillers per meter, peduncle length, flag leaf length, grain filling duration, 1000 seed weight, biological yield and all the physiological traits and further comparison of members of these groups with standard checks and among themselves based on their mean values for yield and its contributing traits provide insight for selection of heat tolerant line P-13348, P-13676, P-13820 and P- 14114 (Table 4) and sensitive lines. Handling of large planting material is a major hindrance in any crop improvement program which slows the progress of the program. So, clustering is like a boon for the researcher community to handle large accession effectively and efficiently (Khan *et*

Table 4. Mean values of yield and its major contributing morpho-physiological traits under late sown condition.

Sl. No.	Genotypes	NPTM	PL	FL	NSPS	NGPS	GFD	TGW
1	P-13348	110.33	34.27	20.27	19.00	52.00	37.33	39.67
2	P-13350	103.00	29.23	18.27	20.00	48.67	36.33	35.07
3	P-13355	106.67	29.10	19.97	21.67	49.33	38.33	38.37
4	P-13377	102.00	28.93	19.43	18.67	44.67	36.00	33.67
5	P-13514	108.33	30.77	21.07	20.67	49.33	37.33	37.80
6	P-13543	115.33	33.53	22.17	22.33	53.67	37.67	41.67
7	P-13582	109.67	34.40	22.17	22.33	54.00	37.67	42.60
8	P-13620	105.00	32.57	20.00	20.33	50.33	32.00	40.53
9	P-13633	98.33	33.13	21.87	21.67	53.67	30.67	41.27
10	P-13638	97.33	30.80	19.27	19.33	49.67	35.33	38.40

Table 4. Continued.

Sl. No.	Genotypes	NPTM	PL	FL	NSPS	NGPS	GFD	TGW
11	P-13640	108.00	30.57	19.70	20.33	49.33	37.00	39.23
12	P-13673	109.33	32.83	21.20	21.00	49.67	36.00	39.50
13	P-13676	126.67	35.13	20.33	22.00	53.33	35.67	43.20
14	P-13686	107.00	27.13	19.63	21.67	55.33	30.33	35.07
15	P-13694	110.00	30.10	18.07	19.33	48.00	38.00	37.30
16	P-13709	120.67	32.13	19.37	20.33	51.00	37.67	37.27
17	P-13808	110.00	30.73	19.20	19.33	49.00	36.67	37.03
18	P-13811	107.67	31.53	20.67	21.00	51.33	35.67	38.70
19	P-13816	109.00	31.23	18.07	21.33	48.67	36.67	39.60
20	P-13820	108.33	31.20	22.23	21.33	52.00	37.00	40.53
21	P-14043	96.67	30.43	18.97	20.00	49.33	36.00	36.20
22	P-14044	99.67	26.83	14.33	17.00	42.67	29.67	31.67
23	P-14045	100.00	27.27	16.40	17.67	44.00	31.00	32.37
24	P-14046	100.00	28.03	18.13	18.33	47.33	32.67	34.07
25	P-14047	103.33	27.97	16.83	18.00	45.67	34.33	33.73
26	P-14048	121.00	31.07	22.10	18.00	52.33	36.67	37.90
27	P-14049	103.33	29.73	18.37	19.00	48.00	36.67	37.67
28	P-14050	103.00	32.30	17.13	19.67	50.00	36.00	36.87
29	P-14051	112.33	28.03	18.80	17.67	45.00	32.00	35.40
30	P-14052	97.00	26.97	19.30	17.67	45.67	35.00	34.20
31	P-14053	109.33	28.07	17.73	19.00	48.00	32.33	38.90
32	P-14054	110.33	26.60	17.97	18.00	48.67	34.67	35.67
33	P-14055	103.00	27.53	19.20	18.00	42.67	35.33	33.30
34	P-14056	109.00	25.63	17.03	17.33	54.33	36.33	32.00
35	P-14057	100.67	26.77	17.67	18.00	45.33	36.00	33.93
36	P-14058	103.67	26.40	19.33	17.67	50.00	35.67	33.03
37	P-14059	104.00	26.33	19.00	20.00	54.33	31.67	32.17
38	P-14060	99.33	28.57	18.63	19.00	46.67	30.67	34.50
39	P-14061	101.33	30.83	20.97	19.67	50.33	33.34	39.30
40	P-14062	98.33	25.67	14.73	17.00	51.33	31.33	31.87
41	P-14103	114.00	30.10	19.57	18.00	53.00	35.33	37.90
42	P-14104	112.67	28.33	18.17	19.00	47.33	28.67	35.23
43	P-14105	95.67	26.13	16.93	17.67	44.67	33.67	32.87
44	P-14106	95.67	26.47	19.33	17.00	43.33	35.00	32.87
45	P-14107	99.00	26.53	18.00	21.00	44.33	35.00	34.47
46	P-14108	99.00	27.83	18.47	18.33	45.33	31.33	33.90
47	P-14109	92.33	28.60	20.17	16.00	45.33	31.67	34.43
48	P-14110	97.33	26.70	17.77	18.00	49.67	34.00	33.03
49	P-14111	103.67	27.13	20.20	18.33	47.33	36.33	34.87
50	P-14112	90.67	27.70	15.77	17.00	42.00	29.67	33.13
51	P-14113	96.33	26.07	19.57	17.33	45.00	35.33	33.50
52	P-14114	117.00	34.43	23.53	22.67	43.67	38.00	43.73
53	P-14115	108.67	33.73	22.20	22.33	53.00	36.67	42.27
54	P-14116	105.33	26.97	18.87	18.33	41.00	36.00	34.43
55	P-14117	97.33	26.73	16.83	17.33	41.33	36.00	34.10
56	P-14118	101.33	30.80	19.47	18.00	40.33	34.67	34.83
57	P-14119	104.00	28.07	20.30	18.67	45.67	36.67	36.23
58	P-14120	98.67	28.27	18.57	18.33	51.67	30.67	35.17
59	P-14121	95.33	26.80	16.50	18.00	45.00	31.00	33.87
60	P-14122	98.67	28.33	20.00	18.33	42.67	33.33	35.27
61	WH-1124	110.00	32.97	20.17	19.00	46.00	42.33	40.47
62	WH-1021	101.00	31.24	20.97	17.67	49.00	36.67	38.90
63	HD-3059	94.00	28.35	16.77	19.00	50.33	37.67	39.60
64	DBW-90	102.33	32.73	22.77	18.33	53.00	38.00	38.70

Table 4. Continued.

Sl. No.	Genotypes	BY	GY	NDVI 1	NDVI 2	CTD 1	CTD 2	CHF 1	CHF 2
1	P-13348	10.42	3.50	0.770	0.653	5.333	5.697	40.550	39.637
2	P-13350	9.58	2.89	0.637	0.507	2.973	3.603	40.790	39.340
3	P-13355	9.33	3.29	0.667	0.617	3.703	3.870	39.433	38.130
4	P-13377	8.25	2.60	0.577	0.463	2.787	3.313	38.000	35.960
5	P-13514	9.42	3.07	0.650	0.580	3.453	3.843	38.550	34.378
6	P-13543	9.13	3.47	0.750	0.637	4.633	4.580	40.575	39.188
7	P-13582	9.85	3.46	0.737	0.633	3.697	4.520	41.593	40.580
8	P-13620	9.33	3.18	0.683	0.623	3.847	2.727	39.998	38.855
9	P-13633	9.75	3.41	0.800	0.677	3.923	3.063	38.900	37.800
10	P-13638	9.08	2.93	0.640	0.560	3.640	3.720	37.750	36.287
11	P-13640	8.92	3.12	0.613	0.480	3.107	3.223	39.720	38.197
12	P-13673	9.92	3.23	0.697	0.607	4.057	4.417	40.167	39.167
13	P-13676	9.83	3.45	0.767	0.633	4.890	4.983	40.667	40.197
14	P-13686	9.67	3.45	0.753	0.687	4.493	4.017	39.097	37.143
15	P-13694	9.50	2.91	0.670	0.540	3.443	3.667	38.137	36.330
16	P-13709	9.50	3.07	0.610	0.523	3.100	3.910	37.107	35.743
17	P-13808	8.25	2.90	0.587	0.483	2.670	3.300	38.947	37.557
18	P-13811	9.67	3.19	0.750	0.667	5.150	3.423	40.477	39.237
19	P-13816	9.67	3.22	0.683	0.563	4.100	3.550	43.545	42.118
20	P-13820	9.57	3.28	0.783	0.690	5.157	5.830	42.610	41.837
21	P-14043	9.17	3.00	0.517	0.417	3.287	1.243	41.500	40.915
22	P-14044	8.83	2.35	0.500	0.417	0.760	0.663	34.563	33.387
23	P-14045	8.65	2.44	0.533	0.423	1.827	1.337	35.823	34.357
24	P-14046	9.17	2.59	0.550	0.440	1.703	1.127	37.950	36.383
25	P-14047	8.52	2.58	0.580	0.490	2.200	2.830	37.713	37.368
26	P-14048	9.17	3.25	0.680	0.620	4.077	3.973	39.950	38.638
27	P-14049	8.83	2.93	0.617	0.607	3.010	3.783	38.430	36.113
28	P-14050	9.25	2.89	0.600	0.497	2.827	3.140	36.563	35.318
29	P-14051	7.98	2.64	0.540	0.417	1.660	0.440	39.250	38.067
30	P-14052	8.17	2.53	0.590	0.483	2.693	3.347	39.440	39.633
31	P-14053	8.75	2.74	0.643	0.493	2.897	3.283	39.550	37.588
32	P-14054	9.25	2.65	0.583	0.477	2.510	3.070	37.653	36.193
33	P-14055	9.08	2.54	0.583	0.450	2.417	2.037	36.607	35.280
34	P-14056	8.58	2.48	0.563	0.453	2.260	2.873	40.500	37.508
35	P-14057	8.38	2.59	0.503	0.417	1.487	0.750	37.747	37.057
36	P-14058	7.67	2.50	0.513	0.397	0.813	0.583	38.477	33.787
37	P-14059	7.75	2.36	0.513	0.397	1.190	0.470	35.387	34.613
38	P-14060	8.58	2.71	0.617	0.507	2.860	3.613	36.000	35.843
39	P-14061	8.83	3.10	0.670	0.627	3.783	3.927	41.087	37.957
40	P-14062	6.92	2.38	0.523	0.413	3.930	0.477	38.500	38.083
41	P-14103	7.97	2.98	0.580	0.463	3.200	3.480	39.775	38.508
42	P-14104	6.83	2.73	0.603	0.497	2.717	2.403	37.040	35.857
43	P-14105	7.40	2.46	0.593	0.473	4.473	2.843	39.440	37.573
44	P-14106	7.32	2.37	0.547	0.417	1.720	1.507	36.393	35.677
45	P-14107	7.67	2.61	0.573	0.467	2.037	3.000	39.600	37.738
46	P-14108	7.60	2.58	0.587	0.497	2.213	1.750	38.827	37.743
47	P-14109	8.17	2.67	0.630	0.513	3.557	3.613	31.715	31.188
48	P-14110	8.03	2.58	0.597	0.497	2.590	3.390	38.647	37.947
49	P-14111	7.40	2.65	0.593	0.443	2.507	2.960	39.990	36.588
50	P-14112	7.33	2.37	0.553	0.453	1.843	2.057	35.333	33.893
51	P-14113	7.70	2.37	0.527	0.417	1.793	1.883	36.147	35.150
52	P-14114	8.83	3.48	0.767	0.687	3.820	5.100	42.217	41.530
53	P-14115	9.13	3.41	0.770	0.663	4.367	4.057	38.567	36.473
54	P-14116	7.43	2.52	0.553	0.443	2.333	2.880	36.845	35.958
55	P-14117	7.18	2.59	0.517	0.417	1.900	0.660	39.785	38.518
56	P-14118	7.10	2.43	0.593	0.487	1.927	2.673	36.030	34.603

Table 4. Continued.

Sl. No.	Genotypes	BY	GY	NDVI 1	NDVI 2	CTD 1	CTD 2	CHF 1	CHF 2
57	P-14119	7.57	2.78	0.587	0.520	2.673	3.583	37.967	35.933
58	P-14120	8.17	2.71	0.590	0.470	2.793	3.083	39.750	36.533
59	P-14121	8.07	2.58	0.553	0.447	1.677	2.200	37.103	35.787
60	P-14122	7.23	2.73	0.597	0.487	2.743	2.757	36.145	35.883
61	WH-1124	7.00	2.45	0.547	0.447	2.297	2.387	35.053	33.820
62	WH-1021	7.00	2.50	0.533	0.440	2.150	2.287	36.030	34.627
63	HD-3059	7.07	2.43	0.580	0.447	2.450	2.753	35.977	35.157
64	DBW-90	9.33	2.63	0.600	0.460	2.633	2.800	38.480	37.483

al. 2020).

CONCLUSION

Agriculture is also not unique from the adverse effects of climate change and one of the consequences of this is appearance of terminal heat stress which has negative impact on the grain quantity and quality threatening the food security. So, presence of genetic variability and effective selection scheme is need of hour for selection of the heat tolerant lines and their further utilization either through conventional or modern approaches. The highest inter cluster distance was deciphered between Cluster I and IV and highest intra cluster distance was revealed by Cluster IV indicating the extent of divergence among the genotypes. Cluster II was deciphering better performance in relation to cluster mean values for yield and its major associated traits so this cluster may be designated as the “highly tolerant group”. Cluster I and Cluster V may be designated as “moderately tolerant” and “sensitive group” respectively, based on their performance of cluster mean values. The genotypes P-13348, P-13676, P-13820 and P-14114 were found to be more heat tolerant and lines may hold potential that make them ideal candidates for the development of heat tolerant varieties. Similarly, the genotypes P-13808, P-13638 and P-14050 were found more moderately tolerant among cluster I genotypes while genotypes P-14106, P-14112 and P-14121 were most sensitive among the cluster V genotypes to terminal heat stress. Therefore, characterization of genotypes is imperative for any crop improvement program for development of varieties tolerant to biotic or abiotic stress to meet the goals of food security mission.

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