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Assessment of genetic diversity for terminal heat tolerance in bread wheat (*Triticum aestivum* L. em. Thell.)

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Abstract
Heat stress in wheat bears very high significance in realsing yield potential of a genotype. Terminal heat stress in particular affects the wheat yields considerably. Keeping this in view the present investigation was carried out with 32 diverse genotypes of bread wheat in completely randomized block design with 3 replications at G.B. Pant University of agriculture & Technology, Pantnagar for studying the genetic diversity for terminal heat stress tolerance under late sown condition. The observations were recorded on 16 agronomic traits and 3 physiological traits. The statistical analysis for genetic divergence was done using Mahalanobis-D^2 statistics and clustering of genotypes was done using Tocher method. On the basis of genetic diversity analysis, it was found that the maximum percent contribution towards genetic divergence was from grain yield/plot i.e. 47.98% and minimum by the harvest index (0.81%). Clustering of genotypes revealed that cluster- I and III have maximum number of genotypes (14) and clusters-II, IV, V & VI each has single genotype only. The highest intra-cluster distance was exhibited by cluster-III (703.41) revealing maximum genetic divergence among its constituents. The highest inter-cluster distance was found between clusters-V and VI (7190.38). The nineteen genotypes were found tolerant. The genotypes bearing desired values from different clusters can be exploited in future breeding programme for improving the yield and physiological traits under late sown condition for mitigating the threat of terminal heat stress in bread wheat.

Keywords: Bread wheat, genetic divergence, clustering, SPAD and heat

Introduction

Wheat is one of the most important and widely grown crops in the world having the area of 224.82 million hectare with the production of about 732.98 million tonnes and productivity of 3.26 tonnes per hectare globally (Anonymous, 2015a) [2]. India is second largest producer of wheat in the world. The area, production, and productivity of wheat in India in 2017-18 was 29.58 million ha, 99.7 million ton and 3.37 ton/ha, respectively (ICAR-IIWBR, 2018) [14]. It is grown in all the regions of the country and the states, and Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, West Bengal, Uttarakhand and Himanchal Pradesh together contribute about 98% to the total wheat production of the country and play an important role of supplying carbohydrate and protein (Tewari *et al.,* 2015) [31].
Wheat crop faces several biotic and abiotic stresses during its life cycle at different growth stages. Among these stresses, temperature stress or heat shocks are most important especially in the regions where temperature fluctuation is abrupt. Howard (1924) [12] stated that 'Wheat production in India is a gamble in temperature', which remains valid even today. Exposure to higher temperature is a major determinant of wheat development and growth, decreasing yields by 3 to 4% per 1 °C increase above average 15 °C in plants (Wardlaw *et al.*, 1989) [33]. The report of Intergovernmental Panel on Climatic Change (IPCC, 2007) [13] indicates that global mean temperature will rise 0.3 per decade reaching to approximately 1 and 3 °C above the present value by 2025 and 2100 respectively (Hays *et al.*, 2007, Singh and Dwivedi, 2015) [11, 29]. Temperatures above the optimum for growth can be deleterious, causing injury or irreversible damage, which is generally called heat stress (Wahid *et al.*, 2007) [32]. High temperature (>30 °C) at the time of grain filling is one of the major constraints in increasing

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productivity of wheat in tropical and sub-tropical countries (Rane and Nagarajan, 2004) [24]. With increase in stress intensity, a progressive and significant decrease was observed in yield and yield attributing traits in all wheat varieties (Singh *et al.*, 2007) [30].

Terminal heat stress during anthesis and grain filling period accelerates maturity and significantly reduces grain size and weight that leads to yield loss upto 40% under severe stress conditions (Hays *et al.*, 2007) [11]. Heat stress during post-anthesis (grain-filling stage) affects availability and translocation of photosynthates to the developing kernels and starch synthesis and deposition within the kernel, thus resulting in lower grain weight and altered grain quality (Mohammadi *et al.*, 2004) [22]. To overcome the problem of heat stress in wheat, genetic diversity analysis is one of the best ways to screen out the best donors for heat tolerance in crop improvement breeding programme.

Genetic diversity and relationship among genotypes is a prerequisite for any successful breeding programme.Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development. Genetic divergence explains the genetic distance between different populations within a species or between species. Less genetic distance indicates close genetic relationship while more genetic distance reveals distant genetic relationship among different genotypes. Genetic similarity or dissimilarity can be compared by genetic distance between different individuals. Genetic distance can be used to measure the genetic divergence between different sub-species or different varieties of a species. The parents having more genetic distant relationship result into higher heterotic expression in F1 and greater amount of genetic variability in segregating populations (Shekhawat *et al.*, 2001) [27].

The genetic diversity of genotypes is not always based on factors such as geographical diversity, place of release and ploidy level etc. Hence characterization of genotypes should be based on statistical procedures. Different statistical methods have been developed to assess the genetic diversity such as D^2-statistics and hierarchial ecludean cluster analysis. These methods determine the genetic divergence using the similarity or dissimilarity based on aggregate effect of different economic important traits. Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Bhatt, 1970; Carves *et al.*, 1987; Mohammadi and Prasanna, 2003) [5, 6, 23]. Precise information on nature and degree of genetic divergence helps the plant breeder in selecting the genetically diverse parents for the purposeful hybridization. (Arunachalam, 1981) [3]. Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic diversity (Joshi and Dhawan, 1966) [16].

One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic distance between parents is necessary (Joshi *et al.*, 2004) [17]. The higher genetic distance between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966) [16]. Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase.

In view of the above, there is need to screen the bread wheat genotypes based on morphological and physiological parameters to find out their suitability across the sowing times and identify stable genotypes for yield and heat tolerance traits.

Materials and Methods
The initial research related to screening was carried out in the experimental area of N.E. Borlaug Crop Research Centre (NEBCRC), G.B. Pant University of Agriculture and Technology. Pantnagar, District U.S. Nagar, Uttarakhand during *rabi*, 2014-15. The experimental material consists of 32 genotypes of bread wheat including 3 checks, namely, HD-2967, PBW-343 and C-306. The experiment was laid out in randomized complete block design (RBD) with three replications under late sown condition on 15 December, 2014. All the thirty two genotypes were evaluated during Rabi 2014-15. Each entry was planted in 5 meter long four rows plot. The rows were spaced 20 cm apart. All the recommended package of practices for wheat was followed to raise a healthy crop.

Table 1: List of genotypes/varieties

Sl. No.	Genotype
1.	PBN-51
2.	BWL-1793
3.	BWL-0814
4.	HD-2967 (check)
5.	BWL-1771
6.	BWL-0924
7.	C-306 (check)
8.	IC-11873
9.	IC-532653
10.	DHARWAR DRY
11.	GIZA-155
12.	ARIANA-66
13.	PBW-343 (check)
14.	BABAX
15.	IEPACA RABE
16.	OTHERY EGYPT
17.	HI-1563
18.	HD-2864
19.	RAJ-3765
20.	RAJ-4083
21.	DBW-14
22.	WH-730
23.	RAJ-4037
24.	SERI-82
25.	SONORA-64
26.	BACANORA-88
27.	SALEMBO
28.	CHIRYA-3
29.	BWL-9022
30.	CUS/79/PRULLA
31.	K-9465
32.	TEPOKO

All the yield attributing and physiological observations on most of the characters were recorded on single plant basis except for days to 75 per cent heading, maturity and canopy temperature depression (CTD). Five representative plants from each plot were randomly selected and tagged for recording the observations on single plant basis. Average datafrom selected plants in respect of different character were used for statistical analysis. The observations were recorded for the sixteen yield attributing traits like days to 75% heading, days to 75% anthesis, days to 75% maturity, plant height, peduncle length, number of tillers per plant, grain filling duration, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000 grain weight, biological yield per plant, grain yield per plot, harvest index and three physiological traits, canopy temperature depression (CTD), relative water content percent (RWC%) and chlorophyll content (SPAD value) of leaf. Canopy temperature was recorded 4 times at the interval of 10 days at different growth stages of the crop from the start of flowering (GS 61) to early dough stage (GS 83 as per Zodoks *et al*., 1974) [34] and it was mentioned as canopy temperature -I (CT –I), canopy temperature-II (CT-II), canopy temperature-III (CT-III) and canopy temperature-IV (CT-IV), and difference between canopy temperature and ambient temperature was calculated and it was designated as canopy temperature depression (CTD I, II, III and IV). The infrared thermometer was used to measue the canopy temperature. SPAD value was observed at flowering stage by SPAD meter. The statistical analysis for genetic divergence was done using Mahalanobis-D^2 statistics and clustering of genotypes was done using Tocher method (Rao 1952) [25]. The statistical analysis was performed by Indostat Hyderabad.

Heat susceptibility index (S) was calculated for all the 32 genotypes as given by Fisher and Maurer (1978) [10] to determine the heat tolerance capacity under stress condition. Fisher and Maurer (1978) [10] partitioned stress effect on yield (Y) into parameters measuring susceptibility to stress (S) and the extent of the stress (D) and yield potential (Yp).

$$Y = Y_p (1 - S \times D)$$

Where,

D = (1-X/Xp), X and Xp are the mean yields of all genotypes under stress and optimal conditions, respectively. With D being a constant for a particular trait, it can be shown that

$$S = (1 - Y/Y_p) = (Y_p - Y) / Y_p$$

Where, Yp is the potential yield under non- stress condition and Y is the actual yield under stress environment. S is the relative heat stress tolerance of wheat varieties (S< 0.5 stress tolerant, S > 0.5 < 1.0 moderately stress tolerant and S > 1.0 susceptible). Since D is constant for a particular trial, S is a measure of the yield decrease due to the stress relative to the potential yield with a low value of S being desirable. Thus S is the inverse of heat tolerance.

Results and Discussion
Percent contribution of different characters towards genetic divergence:
Percent contribution of different characters towards genetic divergence was estimated (Figure 2 and Table 3). On the basis of genetic diversity analysis, the maximum percent contribution towards genetic divergence was from grain yield per plot (47.98%) followed by relative water content percent (21.57%),

CTD-IV (7.06%), CTD-II (6.85%), SPAD value (3.43%), CTD -I (1.81%), plant height (1.41%), canopy temperature depression-III (1.01%), 1000 grain weight (1.01%) and minimum contribution was from harvest index (0.81%). The contribution of plan height in divergence had also been also observed by Khare *et al*., (2015) [18], Kumar *et al.,* (2009) [21], Arya *et al.,* (2017) [4], biological yield per plant by Arya *et al.,* (2017) [4], Arya *et al.,* (2017) [4], 1000 grain weight by Arya *et al.,* (2017) [4] and Dobariya *et al.,* (2006) [9] Kumar *et al.,* (2009) [21], Kolakar *et al.,* (2014) [20]. The contribution of various characters towards the expression of genetic divergence should be taken into account as a criterion for choosing parents for crossing programme for the improvement in such characters.

Cluster information: Under present study, all the 32 genotypes were grouped into six clusters (Figure1 and Table 2) suggesting considerable amount of genetic diversity prsesent in the material. The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity (Singh *et al*., 2009) [28]. The clusters-I and III have highest number of genotypes (14) while clusters-II, IV, V and VI have single genotype only. The nineteen genotypes were found tolerant and rest thirteen genotypes were found moderately tolerant to heat stress belonging to different clusters (Table 6).

Cluster-I : The cluster-I consists of fourteen genotypes out of which eight genotypes viz., IC-118737, BWL-9022, K-9465, IEPACA RABE, HD-2864, DBW-14, TEPOKO, RAJ-4083 were found tolerant and six genotypes viz. PBW-343, BABAX, HI-1563, RAJ-3765, BWL-1793, and SONORA-64 were found moderately tolerant. This cluster had highest cluster mean value for the characters, spike length (9.98) and harvest index (39.42). This cluster has higher values of yield attributing characters along with early maturity.

Cluster-II: Cluster-II has single tolerant genotype OTHERY EGYPT only. This cluster revealed highest cluster mean value for RWC (76.97%) followed by number of grains per spike (57.87), SPAD value (45.30), grain filling duration (38.67), biological yield per plant (24.80). This cluster represented higher cluster means for yield attributing as well as physiological traits.

Cluster-III: The cluster-III comprised of fourteen genotypes. This cluster has maximum tolerant genotypes (9), namely, PBN-51, CHIRYA-3, BACANORA-88, HD-2967, CUS/79/PRULLA, BWL-0814, IC-532653, GIZA-155, C-306 and five moderately tolerant genotypes viz., BWL-1771, BWL-0924, SERI-82, DHARWAR DRY, WH-730. This cluster revealed II-highest cluster mean value for plant height (89.99) followed by harvest index (35.82) and peduncle length (35.31). This cluster represented maximum genotypes that can cope up with higher temperature and give more yield under stress condition.

Cluster-IV: ARIANA-66 was grouped into cluster-IV and found moderately tolerant. This cluster revealed maximum cluster mean for days to 75% maturity (125.00) followed by plant height (102.80), days to 75% anthesis (96.00),), days to 75% heading (94.33), peduncle length (36.27), number of spikelets per spike (21.15), canopy temperature depression-I (5.73) and II (3.40), II-highest cluster mean for spike length (9.61) and relative water content per cent (72.02), III-highest cluster mean for SPAD value(44.08) along with lower cluster means for the characters number of grains per spike(48.40),

grain weight per spike(1.43), biological yield per plant(16.73) and grain yield per plot (548.0). This cluster was marked with lowest cluster means for grain filling duration, 1000 grain weight, canopy temperature depression- III and IV, harvest index (%) and number of tillers per plant. This cluster has represented less ability to tolerate stress conditions coupled with poor yield.

Cluster-V: Genotype RAJ-4037 was grouped into cluster-V having moderately heat tolerance capacity. This cluster represented highest cluster mean for canopy temperature depression-IV(3.37), II-highest cluster mean for days to 75% maturity(118.33), grain filling duration(38.33), number of tillers per plant(6.80), canopy temperature depression-III(3.27) and lowest cluster means for plant height(67.33), peduncle length(28.23), spike length(9.02), number of spikelets per spike(14.71), number of grains per spike(41.67), grain weight per spike(1.16), biological yield per plant(13.47), plot yield(270), relative water content per cent(65.89) and SPAD value(42.20). This cluster had also represented less ability to tolerate stress conditions coupled with poor yield like cluster-IV.

Cluster-VI: Cluster-VI have single genotype SALEMBO only that was found tolerant. This cluster exhibited maximum cluster mean for grain yield per plot (2722.67) followed by 1000 grain weight (38.88) and canopy temperature depression-III(3.30), II-highest cluster means for days to 75% anthesis (81.67), number of spikelets per spike(19.22), biological yield per plant (21.13), canopy temperature depression-I (4.53) and IV (2.47) and SPAD value (44.77). Lower cluster means for this cluster was observed for peduncle length (30.90), spike length (9.29), number of grains per spike (46.80), number of tillers per plant (6.27) and canopy temperature depression-II (1.77).This cluster had high tolerance ability to heat stress along with higher yield.

The pattern of distribution of genotypes in different cluster exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different clusters and vice-versa (Kumar *et. al.,* 2009) [21]. A number of studies have also reported considerable amount of genetic diversity in wheat materials (Deshmukh *et al.*, 1999; Jaiswal *et al.*, 2010; Khodadadi *et al.*, 2011; Amin *et al.*, 2014, Tewari *et al.*, 2015, Arya *et al.*, 2017, Dhanda and Munjal, 2017 and Sharma *et al*., 2018) [7, 15, 19, 1, 4, 8, 26].

Intra and inter-cluster distances: Intra and inter-cluster distances were estimated (Table 4). The inter-cluster distance was observed higher than intra-cluster distances suggesting wide range of genetic diversity among genotypes. The highest intra-cluster distance was exhibited by cluster-III (703.41) which revealed maximum genetic divergence among its constituents followed by cluster-I (417.08) while lowest intra-cluster distance was observed in clusters-II, IV, V and VI which was zero for these three clusters revealing minimum genetic divergence among their constituents and homogeneous nature of genotypes, hence selection will be ineffective (Arya *et al.*, 2017) [4].

The highest inter-cluster distance was found between clusters V and VI (7190.38) revealing that the genotypes included in these clusters are distantly related and had broad spectrum of genetic diversity and may be used in hybridization programme for crop improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive seggregants. This would be useful in wheat breeding programme for developing varieties having high yield coupled with heat tolerance capacity followed by clusters-IV and VI-(6225.42), clusters-I and VI (2930.44), clusters-III and VI (2582.26), clusters-II and V (2449.69), clusters-III and V (2267.33), clusters –III and IV (1912.70), clusters-II and VI (1868.56), clusters-II and IV (1746.94), clusters-I and IV (1501.35), clusters-I and IV (1381.71), clusters-IV and V (1367.27), clusters-I and III (793.18), clusters-II and III (710.11) while lowest inter-cluster distance was observed between clusters-I and II (539.78) indicating close relationship between these clusters would not provide good results.

Table. 2: Distribution pattern of 32 genotypes under different clusters.

| Clusters	Number of genotypes	Name of genotypes
Cluster-I	14	IC-118737, PBW-343, Babax, HI-1563, Raj-3765, BWL-1793, Sonora-64, BWL-9022, K-9465, IEPACA RABE, HD-2864, DBW-14, Tepoko and Raj-4083.
Cluster-II	1	Othery Egypt
Cluster-III	14	PBN-51, BWL-1771, BWL-0924, CUS/79/PRULLA, Chirya-3, Bacanora-88, HD-2967, BWL-0814, Seri-82, Dharwar Dry, IC-532653, Giza-155, WH-730 and C-306.
Cluster-IV	1	Ariana-66
Cluster-V	1	Raj-4037
Cluster-VI	1	Salembo
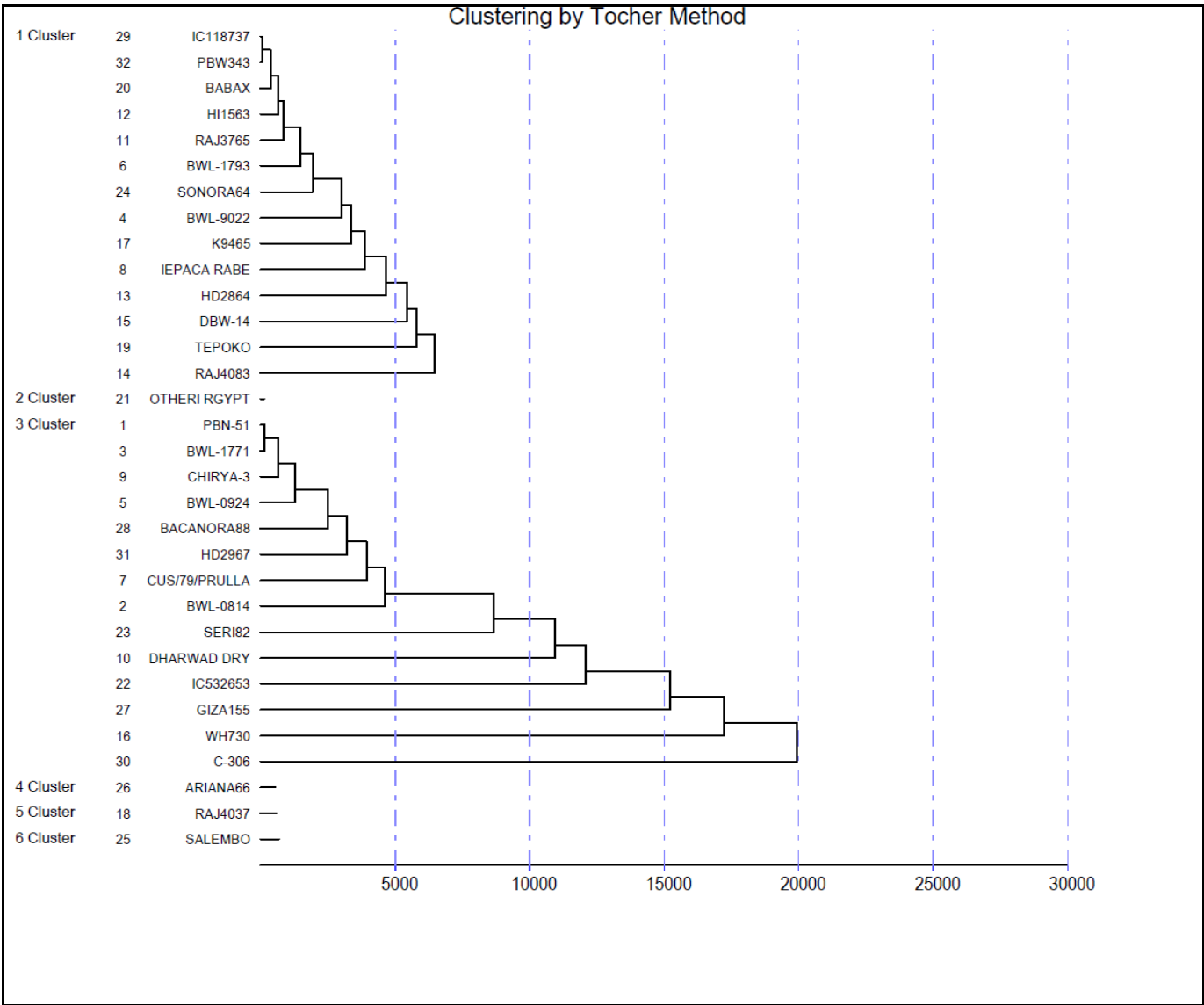
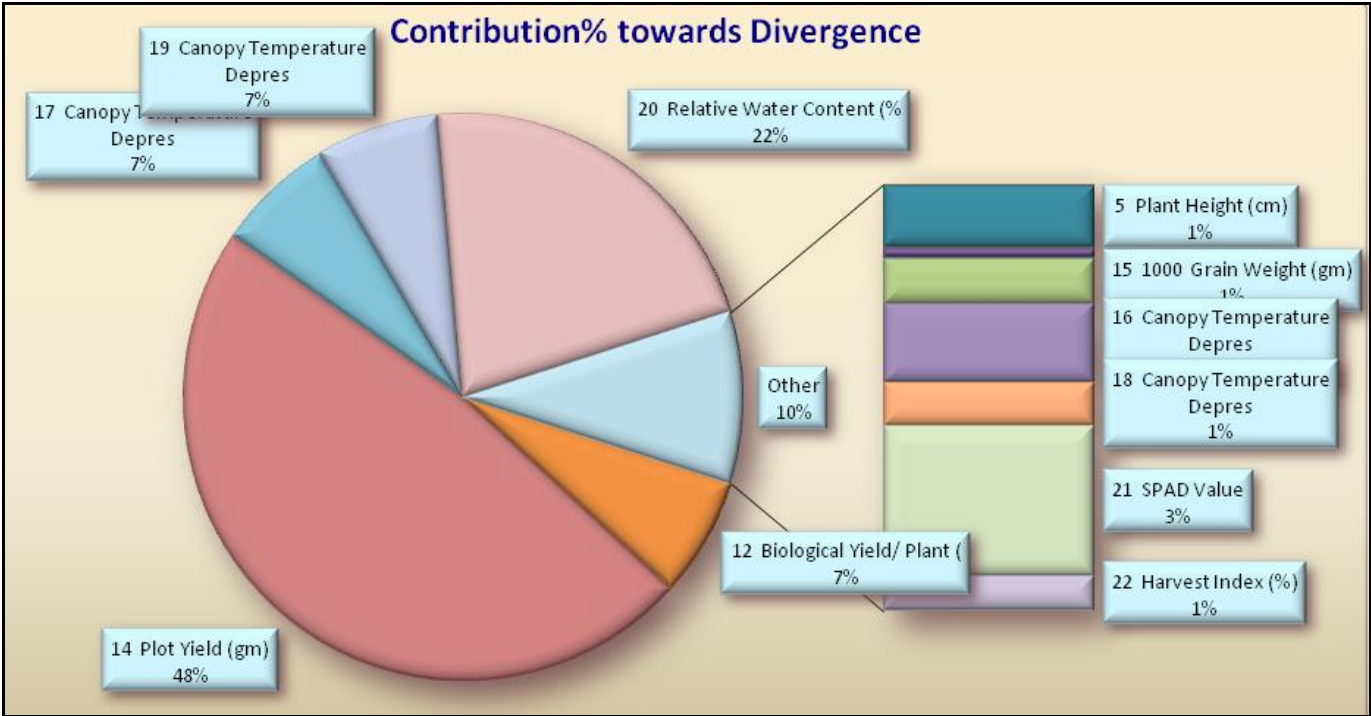**Fig 1:** Clustering of Genotypes by Tocher Method.

Fig 2: Percent contribution of different characters towards genetic divergence.

Table 3: Percent contribution of different characters towards genetic divergence.

SI No.	Source	Contribution (%)	Times Ranked 1st
1	Days to 75% Heading	0.00	0
2	Days to 75% Anthesis	0.00	0
3	Days to 75% Maturity	0.00	0
4	Grain Filling Duration	0.00	0
5	Plant Height (cm)	1.41	7
6	Peduncle Length (cm)	0.00	0
7	Spike Length (cm)	0.00	0
8	Number of Spikelets/ Spike	0.00	0
9	Number of Grains/ Spike	0.00	0
10	Grain Weight/ Spike (gm)	0.20	1
11	Number of Tillers/ Plant	0.00	0
12	Biological Yield/ Plant (gm)	6.85	34
13	Grain Yield/plot (gm)	47.98	238
14	1000 Grain Weight (gm)	1.01	5
15	Canopy Temperature Depression-I	1.81	9
16	Canopy Temperature Depression-II	6.85	34
17	Canopy Temperature Depression-III	1.01	5
18	Canopy Temperature Depression-IV	7.06	35
19	Relative Water Content (%)	21.57	107
20	SPAD Value	3.43	17
21	Harvest Index (%)	0.81	4

Table 4: Intra and Inter-Cluster Distances

	Cluster-I	Cluster-II	Cluster -III	Cluster-IV	Cluster-V	Cluster -VI
Cluster-I	417.08	539.78	793.18	1501.35	1381.71	2930.44
Cluster-II		0.00	710.11	1746.94	2449.69	1868.56
Cluster-III			703.41	1912.70	2267.33	2582.26
Cluster-IV				0.00	1367.27	6225.42
Cluster-V					0.00	7190.38
Cluster-VI						0.00

Table 5: Cluster means for different characters.

Clusters	DH	DA	DM	GFD	PH	PL	SL	NSS	NGS	GWS	NTP
Cluster-I	73.83	77.45	112.95	35.50	81.76	33.42	9.98	17.77	50.33	1.68	6.46
Cluster-II	78.33	79.67	118.33	38.67	88.00	35.00	9.42	17.51	57.87	2.12	7.00
Cluster-III	77.38	79.33	115.69	36.36	89.99	35.31	9.45	17.59	48.96	1.56	6.60
Cluster-IV	94.33	96.00	125.00	29.00	102.80	36.27	9.61	21.15	48.40	1.43	5.90
Cluster-V	77.67	80.00	118.33	38.33	67.33	28.23	9.02	14.71	41.67	1.16	6.80
Cluster-VI	78.00	81.67	117.33	35.67	85.00	30.90	9.29	19.22	46.80	1.62	6.27

Clusters	BY	GY	TGW	CTD-I	CTD-II	CTD-III	CTD- IV	RWC	SPAD	HI
Cluster-I	18.23	1121.79	36.95	2.27	2.48	2.66	1.86	67.94	42.53	39.42
Cluster-II	24.80	1472.00	38.75	2.37	2.63	2.67	1.30	76.97	45.30	33.05
Cluster-III	18.92	1369.41	35.37	3.93	2.82	2.57	1.97	68.80	42.14	35.82
Cluster-IV	16.73	548.00	30.98	5.73	3.40	0.53	0.60	72.02	44.08	30.25
Cluster-V	13.47	270.00	34.18	3.03	1.80	3.27	3.37	65.89	42.20	35.60
Cluster-VI	21.13	2722.67	38.88	4.53	1.77	3.30	2.47	71.28	44.77	35.66

DF-Days to 75%, DA-Days to 75% anthesis, DM-Days to 75% maturity, GFD-Grain filling duration, PH-Plant height, PL-Peduncle length, SL-Spike length, NSS- Number of spikelets per spike, NGS-Number of grains per spike, GWS-Grain weight per spike, NTP-Number of tillers per plant, BY-Biological yield per plant, GY- Grain yield/plot, TGW-1000 grain weight, CTD-Canopy temperature depression, RWC-Relative water content %, SPAD- Soil-plant analysis development (chlorophyll content), HI-Harvest index %.

Table 6: Heat Susceptibility Index(S) of different genotypes and their heat tolerance capacity.

SI. No.	Genotype	Value of Heat Susceptibility Index (S)	Interpretation
1.	PBN-51	0.46	Tolerant
2.	BWL-0814	0.26	Tolerant
3.	BWL-1771	0.54	Moderately tolerant
4.	BWL-9022	0.46	Tolerant
5.	BWL-0924	0.54	Moderately tolerant
6.	BWL-1793	0.67	Moderately tolerant
7.	CUS/79/PRULLA	0.06	Tolerant
8.	IEPACA RABE	0.49	Tolerant
9.	CHIRYA-3	0.32	Tolerant
10.	DHARWAD DRY	0.53	Moderately tolerant
11.	RAJ 3765	0.57	Moderately tolerant
12.	HI 1563	0.59	Moderately tolerant
13.	HD 2864	0.49	Tolerant
14.	RAJ 4083	0.48	Tolerant
15.	DBW-14	0.37	Tolerant
16.	WH 730	0.62	Moderately tolerant
17.	K 9465	0.24	Tolerant
18.	RAJ 4037	0.83	Moderately tolerant
19.	TEPOKO	0.23	Tolerant
20.	BABAX	0.62	Moderately tolerant
21.	OTHERI RGYPT	0.29	Tolerant
22.	IC 532653	-0.15	Tolerant
23.	SERI 82	0.52	Moderately tolerant
24.	SONORA 64	0.54	Moderately tolerant
25.	SALEMBO	0.11	Tolerant
26.	ARIANA 66	0.69	Moderately tolerant
27.	GIZA 155	0.35	Tolerant
28.	BACANORA 88	0.23	Tolerant
29.	IC118737	0.49	Tolerant
30.	C-306	0.37	Tolerant
31.	HD 2967	0.29	Tolerant
32.	PBW 343	0.67	Moderately tolerant

Summary and Conclusion

The most important trait that causing maximum genetic divergence was grain yield per plot and it was responsible for differentiating the genotypes studied while other traits like RWC, CTD-IV, CTD-II, SPAD value, CTD-I, plant height, CTD-III and 1000 grain weight also had considerable contribution towards genetic divergence. Inter and intra-cluster distances provide index of genetic diversity between and within clusters. Larger the distance between the clusters better the chances of getting transgressive segregants. Different clusters exhibited higher values of cluster means for different yield and physiological traits along with wide range of heat tolerance capacity like clusters-IV and V have only moderately tolerant genotypes with higher cluster means for canopy temperature depression-I, II, III, IV, relative water content percent and lower cluster means for 1000 grain weight, biological yield per plant, plot yield, harvest index(%) etc., clusters-II and VI have only tolerant genotypes with higher cluster means for number of grains per spike, grain weight per spike etc. Clusters-I and III have tolerant as well as moderately tolerant genotypes along with greater values of cluster means for different yield attributing as well as physiological traits responsible for heat tolerance. It would be desirable to choose the donor from different clusters depending upon genetic distances, cluster means and heat tolerance ability. These findings suggested that the experimental material had sufficient diversity for yield contributing as well as physiological traits responsible for heat tolerance in bread wheat. Designing a hybridization programme by identifying genotypes of interest from different clusters will make the process more directional and effective. The present study provides useful information about the level of genetic diversity present in the materials studied and this would help in the development of superior individuals for yield and physiological traits tolerant to heat stress under late sown conditions.

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