Assessment of Diversity for Terminal Heat Tolerance under Different Sowing Conditions in Bread Wheat (*Triticum aestivum* L. em.Thell.)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Wheat crop is facing various abiotic stresses due to changing environmental conditions as a result of global warming and heat stress is one of them which affects wheat crop during different growth stages and ultimately reduces grain yield very significantly. The present investigation was carried out with thirty two diverse genotypes of bread wheat in completely randomized block design with

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three replications at Norman E. Borlaug Crop Research Centre, G.B. Pant University of agriculture & Technology Pantnagar for the screening of wheat genotypes for terminal heat tolerance under three environments viz., timely sown (E1), late sown (E2) and very late sown (E3) conditions and to estimate the effect of high temperature on grain yield. Based on prevailing temperature, timely sown condition was considered as heat stress free environment while late sown and very late sown conditions were considered as heat stress environments. Genotypic performance varied substantially over the non-stress and heat stress environments. The observations were recorded on sixteen agronomic traits and three physiological traits. The statistical analysis forgenetic divergence study was done using Mahalanobis D2 statistics and clustering of genotypes was done using Tocher method. Terminal heat tolerance was measured by calculating heat susceptibility index (HSI) for the stress environments. On the basis of genetic diversity analysis, the maximum percent contribution towards genetic divergence was contributed by plant height while the lowest contribution was from harvest index. The 32 genotypes were grouped into six clusters. Cluster-II had maximum number of genotypes (11) while cluster-VI had only single genotype. Cluster-V exhibited the highest intra-cluster while the lowest intra-cluster distance was exhibited by cluster-VI. The highest inter-cluster distance was observed between cluster-III and cluster-VI whereas the lowest inter-cluster distance was observed between cluster-IV and cluster-I. Cluster-VI exhibited highest cluster means for yield contributing traits like grain weigh per spike, grain yield per plant, harvest index while cluster-V exhibited the highest cluster means for physiological traits like relative water content and canopy temperature depression. On the basis of heat susceptibility index, most of the genotypes were found tolerant and moderately tolerant for heat stress conditions. The genotypes bearing the desired values from different clusters can be exploited in future breeding programme for the improving wheat genotypes for heat stress conditions. These genotypes can be used as donor parents in heat tolerance breeding programme.

1. INTRODUCTION

"Wheat is one of the most important and widely grown crops in the world having the area about 223.04 million hectares holding the position of highest estate among all crops with annual production hovering around 784.91 million tons. In India, it's grown in an area of 31.40 million hectares with a production of 110.55 million metric tons and output of 3.52 metric tons/hectares correspondingly. In India uppermost area under wheat cultivation is 9.54 million hectares" [1]. "India is second largest producer of wheat in the world. 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" [2].

"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" [2]. Howard [3] 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" [4]. The report of Intergovernmental Panel on Climatic Change [5] 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" [6,7]. "Temperatures above the optimum for growth can be deleterious, causing injury or irreversible damage, which is generally called heat stress" [8,9,10,11,12,13,14,15]. "High temperature (>30°C) at the time of grain filling is one of the major constraints in increasing productivity of wheat in tropical and sub-tropical countries" [16,17,14,18,19,15]. "With increase in stress intensity, a progressive and significant decrease was observed in yield and yield attributing traits in all wheat varieties" [20,12,13,14,21,15]. "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" [6]. "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" [22,23,14,24,13,25,15,26]. "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" [27].

"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 F_1 and greater amount of genetic variability in segregating populations" [28].

"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" [29,30,31]. "Precise information on nature and degree of genetic divergence helps the plant breeder in selecting the genetically diverse parents for the purposeful hybridization" [32]. "Genetic improvement of yield especially in self-pollinated

crops depends on nature and amount of genetic diversity" [33].

"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" [34]. "The higher genetic distance between parents, the higher heterosis in progeny can be observed" [33]. "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" [27]. 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 .

2. 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 (Table 1) of bread wheat including three checks, namely, HD-2967, PBW-343 and C-306. The experiment was laid out in randomized complete block design (RBD) with three replications under three sowing conditions viz., timely sown(E1), late sown(E2) and very late sown condition (E3) on 15 November, 2014, 15 December, 2014, 15 January,2015 respectively. 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.

"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 data from selected plants in respect of different character were used for statistical analysis. The

Table 1. List of genotypes/varieties

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

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" [27]. Canopy temperature was recorded four times at the interval of 10 days at different growth stages of the crop from the start of flowering (GS61) to early dough stage (GS 83 as per Zodokset al., [35]) 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 measure the canopy temperature. SPAD value was observed at flowering stage by SPAD meter. The data obtained from all the three sowing conditions were pooled. The statistical analysis for genetic divergence was done using Mahalanobis-D^2 statistics" [36] and clustering of genotypes was done using Tocher method ([37]. 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 [38] to determine the heat tolerance capacity under stress condition. Fisher and Maurer [38] partitioned stress effect on yield (Y) into parameters measuring susceptibility to stress (S) and the extent of the stress (D) and yield potential (Yp).

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

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

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

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, 0.5 < S < 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.

3. RESULTS AND DISCUSSION

Success of any breeding programme depends upon the extent of variability present in the breeding population. The estimation of variability is of utmost importance in a crop for the identification of lines which can generate further variability so that artificial selection of desirable diverse genotypes may be made. Some of the very useful variations would go unutilized if not be identified by the breeder during selection process. In the present investigation material under study observed having high magnitude of variation for plot yield, grain yield/plant, and harvest index and plant height. These results are in agreement with those of Hirachand et al. [39] and Balyaeva [40].

3.1 Percent Contribution of Different Characters towards Genetic Divergence

Percent contribution of different characters towards genetic divergence was estimated (Fig. 2 and Table 3).On the basis of genetic diversity analysis, the maximum percent contribution towards genetic divergence was from plant height (27.22%) followed by plot yield (10.89%), thousand grains weight (9.88%), days to 75% heading (9.27%), canopy temperature depression-I (8.06%), spike length (6.25%), number of grains per spike (5.44), peduncle length (3.83%), grain weight per spike (3.63%), SPAD (3.02%), days to 75% maturity (2.82%), number of spikelets per spike (2.42%), canopy temperature depression-IV (2.22%), relative water content percent (2.22%), biological yield per plant (1.41%), number of tillers per plant (0.81%), canopy temperature depression-II (0.40) while lowest contribution was from harvest index (0.20%).The contribution of plan height in divergence had also been also observed by Khare et al. [41], Kumar et al., [42], Arya et al. [43], biological yield per plant by Arya et al. [43],1000 grain weight by Arya et al. [43] and Dobariya et al., [44], Kumar et al. [42], Kolakar et al. [45]. 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.

3.2 Cluster Information

Under present study, all the 32 genotypes were grouped into six clusters (Fig. 1 and Table 2) suggesting considerable amount of genetic diversity presentin the material. The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity [46,47,19]. The cluster-II consisted of highest number of genotypes (11) followed by cluster-I (8), cluster-V (5), cluster-IV (4), cluster-III (3) while cluster-VI had only single genotype.

Cluster-I: The cluster-I consisted of genotypes viz., RAJ-4083, DBW-14, BWL-1793, HD-2864, HI-1563, RAJ-3765, BWL-9022, and IEPACA RABE. This cluster had high cluster means for yield contributing characters viz., grain filling duration (36.67), grain yield per plant (7.13), 1000 grains weight (37.30), number of grains per spike (50.27), grain weight per spike (1.90), plot yield (1437.14) and physiological traits such as CTD-IV (2.13), CTD-III (2.80), and SPAD (43.89) but low cluster mean for days to 75% heading (72.79), days to 75% anthesis (78.10) and days to 75% maturity (114.75). This cluster represented genotypes with early maturity and good grain yielding capacity.

Cluster-II: The genotypes BWL-1771, SALEMBO, BWL-0814, BWL-0924, HD-2967, PBW-343, OTHERY EGYPT, PBN-51, BACANORA-88, TEPOKO and CHIRYA-3 were grouped into cluster-II. The high cluster mean was observed for yield contributing characters such as plot yield (1748.83), number of grains per spike (52.51), grain weight per spike (1.93), grain yield per plant (6.82), harvest index (36.92) and physiological traits viz., CTD-I (4.93) and relative water content (69.88) and low cluster mean for grain filling duration (35.83), CTD-II (3.28) and CTD-III (2.26) in this cluster. Genotypes in this cluster represented genotypes with mid late maturity with high yield potential.

Cluster-III: This cluster had three genotypes namely, SERI-82, SONORA-64, and, IC-118737. This cluster had high cluster mean for yield contributing characters such as number of grains per spike (53.59), number of spikelets per spike (18.06) and physiological traits such as CTD-II (4.05), CTD-III (2.89) and CTD-IV (1.88) but low

cluster mean for days to 75% heading (71.81), days to 75% anthesis (77.37), days to 75% maturity (112.56), grain weight per spike (1.39), grain yield per plant (5.06), 1000 grain weight (29.23), plot yield (1103.85) and relative water content (66.41).This cluster had genotypes with early maturity coupled with poor yield potential.

Cluster-IV: This cluster consisted of four genotypes viz., WH-730, K-9465, BABAX, and RAJ-4037. The high cluster mean was observed for yield contributing traits such as days to 75% heading (78.44), days to 75% anthesis (81.69), days to 75% maturity (117.36), harvest index (40.43), 1000 grains weight (36.74) and physiological traits suchas SPAD (45.01) and CTD-II (3.37) but low cluster mean for grain yield per plant (6.79), grain weight per spike (1.83), number of spikelets per spike (17.82), grain weight per spike (1.83), number of grains spike (46.59), CTD-I (4.08), relative water content (69.23), CTD-III (2.24) and CTD-IV (1.66). This cluster represented genotypes with late maturity and poor yield potential.

Cluster-V: The genotypes GIZA-155, C-306, IC-532653, and DHARWAR DRY were grouped into cluster-V. The high cluster mean was observed for yield contributing traits viz., days 75% heading (81.89), days to 75% anthesis (84.04), days to 75% maturity (122.36), grain filling duration (37.84), number of spikelets per spike (19.22) and physiological traits such relative water content (74.66), CTD-II (3.60), CTD-IV (2.12), CTD-I (4.28), and CTD-III (2.72) but low cluster means for number of grains per spike (46.71), grain weight per spike (1.59), grain yield per plant (5.17), plot yield (1064.18), 1000 grains weight (34.79), harvest index (31.36) and SPAD (40.80). This cluster represented genotypes having late maturity coupled with low yield potential.

Cluster-VI: The cluster-VI had only single genotype CUS/79/PRULLA. This cluster had high cluster mean for yield contributing traits such as grain weight per spike (2.22), grain yield per plant (7.87), 1000 grains weight (42.35), harvest index (40.45), plot yield (1642.67), grain filling duration (36.11) and physiological traits such as relative water content (71.50), CTD-I (4.43), CTD-II (3.37) and SPAD (43.26) but low cluster mean days to 75% heading (78), days to 75% anthesis (80.44), days to 75% maturity (116.56), number of grains per spike (48.41),number of spikelets per spike (16.65) CTD-III (2.43), and CTD-IV (1.72). This cluster represented

genotypes having mid late maturity coupled with high yield potential.

"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" [42,48,43].

3.3 Intra and Inter-cluster Distances

The intra and inter-cluster distances (Table 4) were calculated to determine the genetic relationship among the individuals within a cluster and between members of different clusters. The highest average intra-cluster was exhibited by cluster-V (6.62) followed by cluster-IV (4.19), cluster-III (4.03), cluster-II (3.26), cluster-I (2.22), and lowest by cluster-VI (0.00) suggesting that no genetic diversity in this cluster because of presence of single genotype. The clusters with high intra-cluster distances suggested that genotypes in these clusters were more genetic diverse than the genotypes in other clusters with low intra-cluster distances.

Inter-cluster distance is the main criterion for selection of genotypes using D^2 analysis [41]. The genotypes belonging to those clusters having maximum inter-cluster distance are genetically more divergent and hybridization between these genotypes of different clusters is likely to produce wide variability with desirable individuals. The highest inter-cluster distance was found between clusters-III and VI (15.49) followed by clusters-III and V (14.00), clusters-I and V (12.69), clusters-V and VI (12.20), clusters-II and V (11.78), clusters-IV and V (10.82), clusters-II and VI (9.15), clusters-III and IV (7.89), clusters-I and VI (7.55), clusters-II and III (7.23), clusters-IV and VI (7.05), clusters-I and III (6.07), clusters-II and IV (5.98), clusters-I and II (5.03) while the lowest inter-cluster distance was observed between clusters-I and IV (4.29) suggested a closer relationship between these two clusters and low degree of genetic diversity among the genotypes. The parental material tested for this study showed significant genetic diversity, suggesting that it could be a useful source for choosing varied parents for a hybridization program. Crosses between the various genotypes belonging to clusters separated by large inter-cluster distances should be attempted in order to maximize the likelihood of isolating good trangressive segregants in the segregating generations.

3.4 Cluster Means

Cluster means were calculated for all the physiological and agronomic traits which exhibited considerable differences among the clusters (Table 5). The mean performance of the clusters was used to select genetically diverse and agronomically superior genotypes out of 32 genotypes studied. The highest cluster mean for days to 75% heading was exhibited by cluster-V(81.89) followed by cluster-IV (78.44), cluster-II (78.27), cluster-VI (78.00), cluster-I (72.79) and lowest by cluster-III (71.81).The highest cluster mean for days to 75% anthesis was observed in cluster-V (84.04) followed by cluster-IV (81.69), cluster-II (81.35), cluster-VI (80.44), cluster-I (78.10), and lowest by cluster-III (77.37) (Table 5).

The highest cluster mean for days to 75% maturity was exhibited by cluster-V (122.36) followed by cluster-IV (117.36), cluster-II (117.14), cluster-VI (116.56), cluster-I (114.75), while lowest by cluster -III (112.56). The highest cluster mean for grain filling duration was observed in cluster-V (37.84) followed by cluster -I (36.67), cluster-VI (36.11),cluster -IV (35.92),cluster- II (35.83), and the lowest in cluster-III (35.67).The highest cluster mean for plant height was exhibited by cluster-V (105.87) followed by cluster-VI (101.98),cluster-II (84.15),cluster-IV (83.87),cluster-I (81.24), and lowest by cluster-III (80.61).The highest cluster mean for peduncle length was observed in cluster-V (41.71)followed by cluster-VI (37.18),cluster-I (34.38),cluster-IV (33.34),cluster-II (31.59), and lowest in cluster-III (31.06).

The highest cluster mean for spike length was exhibited by cluster-VI (12.09) followed by cluster-IV (10.72), cluster-I (10.51), cluster-II (9.75), cluster-V (9.73), and lowest by cluster-III (9.62). The maximum cluster mean for number of spikelets per spike was observed in cluster-V (19.22) followed by cluster-I (18.26), cluster-III (18.06), cluster-II (18.03), cluster-IV (17.82), and minimum in cluster-VI (16.65). The highest cluster mean for number of grains per spike was exhibited by cluster-III (53.59)followed by cluster-II (52.51),cluster-I (50.27),cluster-VI (48.41),cluster-V (46.71), and the lowest by cluster-IV (46.59).The maximum cluster mean for grain weight per spike was observed in cluster-VI (2.22)followed by cluster-II (1.93),cluster-I (1.90),cluster-IV (1.83), cluster-V (1.59), and lowest in cluster-III (1.39).The maximum cluster

mean for number of tillers per plant was exhibited by cluster-VI (7.17), cluster-I (6.54), cluster-V (6.35),cluster-II (6.32),cluster-IV (6.01), and minimum by cluster-III (5.88).

The highest cluster mean for biological yield per plant was observed in cluster-VI (19.84)followed by cluster-II (18.56), cluster-I (18.46), cluster-V (16.62), cluster-IV (16.52), and the lowest in cluster-III (14.23).The maximum cluster mean for grain yield per plant was exhibited in cluster-VI (7.87)followed by cluster-I (7.13), cluster-II (6.82),cluster-IV (6.79),cluster-V (5.17), and minimum in cluster-III (5.06).The highest cluster mean for plot yield was observed in cluster-II (1748.83)followed by cluster-VI (1642.67), cluster-I (1437.14), cluster-III (1103.85),cluster-V (1064.18), and lowest in cluster-IV (1046.61). The maximum cluster mean for 1000 grain weight was exhibited by cluster-VI (42.95) followed by cluster-I (37.30), cluster-IV (36.74), cluster-II (36.06), cluster-V (34.79), and minimum by cluster-III (29.23).

The highest cluster mean for canopy temperature depression-I was observed in cluster-II (4.93) followed by cluster-VI (4.43),cluster-V (4.28),cluster-IV (4.08),cluster-III (2.69), and the lowest in cluster-I (2.07).The maximum cluster mean for canopy temperature depression–II was observed in cluster-III (4.05) followed by cluster-V (3.60),cluster-IV (3.37),cluster-VI (3.37),cluster-I (3.30), and minimum in cluster-II (3.28).The highest cluster mean for canopy temperature depression –III was exhibited by cluster-III (2.89) followed by cluster-I (2.80),cluster-V (2.72),cluster-VI (2.43),cluster-II (2.26), and lowest in cluster-IV (2.24).The maximum cluster mean for canopy temperature depression –IV was observed in cluster-I (2.13)followed by cluster-V (2.12),cluster-III (1.88),cluster-II (1.76),cluster-VI (1.72, and minimum in cluster-IV (1.66).

The highest cluster mean for relative water content was observed in cluster-V (74.66)followed by cluster-VI (71.50), cluster-II (69.88),cluster-IV (69.23), cluster-I (68.10), and lowest incluster-III (66.41).The maximum cluster mean for SPAD value was exhibited by cluster-IV (45.01)followed by cluster-I (43.89),cluster-VI (43.26), cluster-II (42.36), cluster-III (40.83), and minimum bycluster-V (40.80).The highest cluster mean for Harvest Index was observed in cluster-VI (40.45)followed by cluster-IV (40.43),cluster-II (36.92),cluster-I (38.50),cluster-III (35.57), and lowest incluster-V (31.26).

3.5 Terminal Heat Tolerance Ability

Terminal heat tolerance ability (Table 6 and Fig. 3) of different genotype were calculated under heat stress conditions viz., late sown and very late sown conditions. The results revealed that nineteen genotypes were found tolerant and thirteen moderately tolerant under heat stress condition in late sown condition whereas five genotypes were observed tolerant and twenty seven were moderately tolerant under very late sown condition. None of the genotype was found susceptible to terminal heat stress. Five genotypes viz., HD-2967, IC-118737, CHIRYA-3, CUS/79/PRULLA, and BWL-0814 were found tolerant under both the stress conditions indicating high yield potential under all sowing condition.

The findings of present study were found similar with the findings of earlier researchers Ali et al., [49], Dias et al., [50], Kumar et al. [43], Ramya et al. [51], Marcella et al. 2017; Djanaguiraman et al. [52], Fleitas et al., [53], Mukhtar et al. [11], Yodulash et al. [54], Bellete et al. [55], Ding et al. [56], Kamra et al. 2021; Farheen et al. [12], Macro-Barbero et al. [24], Riaz et al. [57], Shahbaz et al. [17], Eman et al. [13], Ullah et al., [25], Bhatti et al. [58], Mazeed et al. [15], Singh [59].

Table 2. Distribution pattern of 32 genotypes under different clusters

| Clusters	Number of genotypes	Name of genotypes
Cluster-I	8	RAJ-4083, DBW-14, BWL-1793, HD-2864, HI-1563, RAJ-3765, BWL-9022 and IEPACA RABE
Cluster-II	11	BWL-1771, SALEMBO, BWL-0814, BWL-0924, HD-2967, PBW-343, CHIRYA-3, OTHERY GYPT, PBN-51, BACANORA-88 and TEPOKO
Cluster-III	3	SERI-82, SONORA-64 and IC-118737
Cluster-IV	4	WH-730, K-9465, BABAX and RAJ-4037
Cluster-V	5	GIZA-155, C-306, IC-532653 and DHARWAR DRY and ARIANA-66
Cluster-VI	1	CUS/79/PRULLA
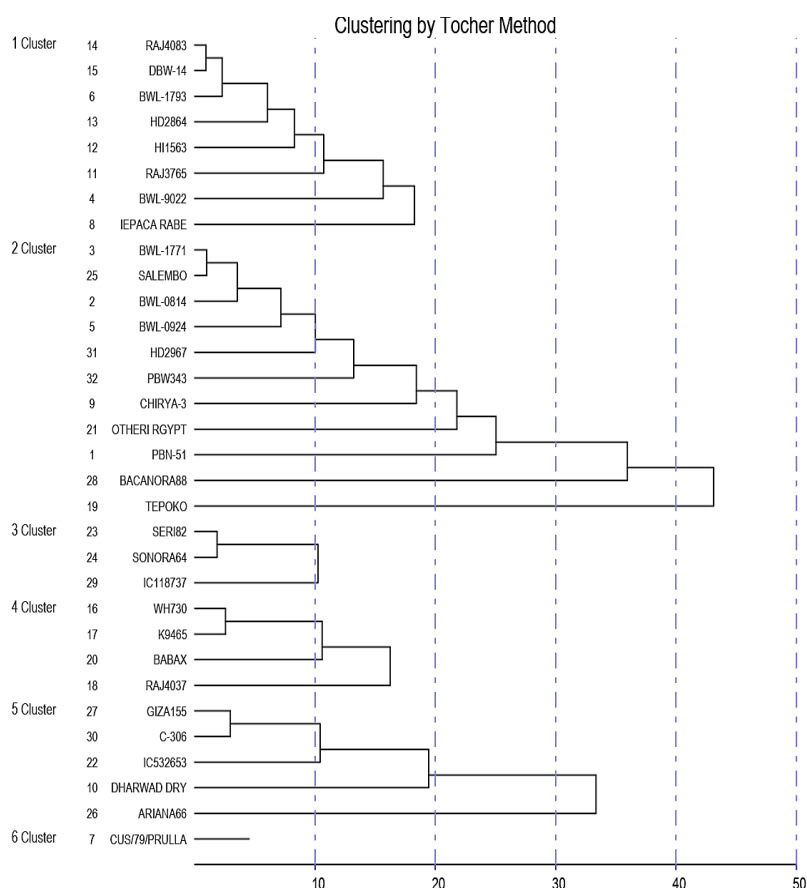
Fig. 1. Clustering of different genotypes by Tocher's method

Table 3. Percent contribution of different characters towards genetic divergence

| SI No.	Source	Contribution (%)	Times Ranked 1st
1.	Days to 75% Heading	9.27	46.000
2.	Days to 75% Anthesis	0.01	0.000
3.	Days to 75% Maturity	2.82	14.000
4.	Grain Filling Duration	0.01	0.000
5.	Plant Height (cm)	27.22	135.000
6.	Peduncle Length (cm)	3.83	19.000
7.	Spike Length (cm)	6.25	31.000
8.	Number of Spikelets/ Spike	2.42	12.000
9.	Number of Grains/ Spike	5.44	27.000
10.	Grain Weight/ Spike (gm)	3.63	18.000
11.	Number of Tillers/ Plant	0.81	4.000
12.	Biological Yield/ Plant (gm)	1.41	7.000
13.	Grain Yield/plot (gm)	0.01	0.000
14.	1000 Grain Weight (gm)	9.88	49.000
15.	Canopy Temperature Depression-I	8.06	40.000
16.	Canopy Temperature Depression-II	0.40	2.000
17.	Canopy Temperature Depression-III	0.01	0.000
18.	Canopy Temperature Depression-IV	2.22	11.000
19.	Relative Water Content (%)	2.22	11.000
20.	SPAD Value	3.02	15.000
21.	Harvest Index (%)	0.20	1.000
22.	Plot Yield (gm)	10.89	54.000
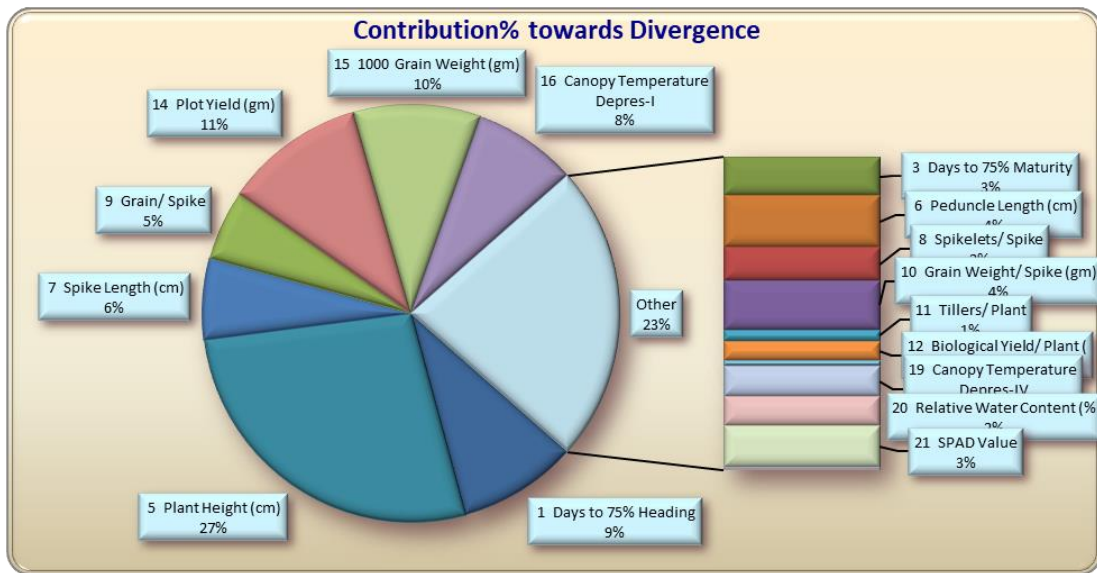
Fig. 2. Percent contribution of different characters towards total genetic divergence

Table 4. Intra and inter-cluster distances

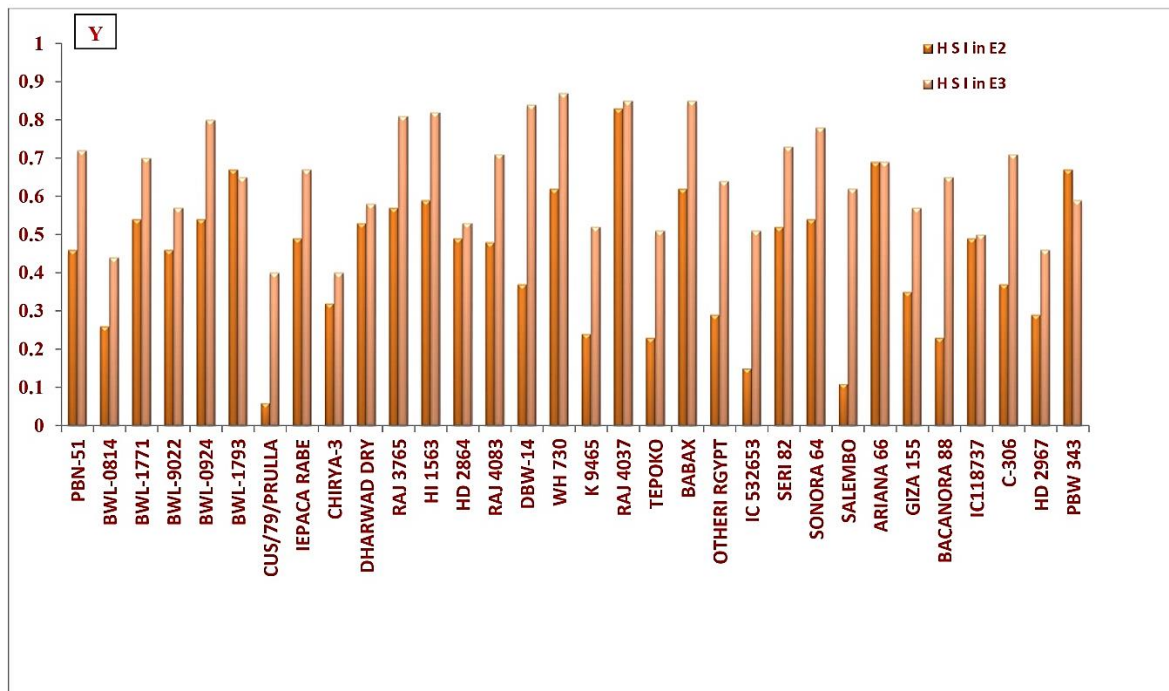|	Cluster-I	Cluster-II	Cluster -III	Cluster-IV	Cluster-V	Cluster -VI
Cluster-I	**2.222**	5.034	6.066	4.293	12.689	7.546
Cluster-II		**3.260**	7.226	5.979	11.777	9.151
Cluster-III			**4.033**	7.887	14.001	15.490
Cluster-IV				**4.104**	10.816	7.048
Cluster-V					**6.618**	12.203
Cluster-VI						**0.000**

Fig. 3. Heat susceptibility index (s) graph in late sown conditions

Table 5. Cluster means for different characters

Clusters	DH	DA	DM	GFD	PH	PL	SL	NSS	NGS	GWS	NTP
Cluster-I	72.792	78.097	114.750	36.667	81.242	34.381	10.508	18.257	50.272	1.901	6.537
Cluster-II	78.273	81.354	117.141	35.828	84.155	31.595	9.747	18.026	52.507	1.931	6.320
Cluster-III	71.815	77.370	112.556	35.667	80.611	31.063	9.616	18.063	53.593	1.391	5.878
Cluster-IV	78.444	81.694	117.361	35.917	83.872	33.341	10.719	17.819	46.594	1.830	6.011
Cluster-V	81.889	84.044	122.356	37.844	105.869	41.713	9.729	19.224	46.713	1.586	6.353
Cluster-VI	78.000	80.444	116.556	36.111	101.978	37.178	12.092	16.648	48.411	2.215	7.167

Continued….

Clusters	BY	GY	TGW	CTD-I	CTD-II	CTD-III	CTD- IV	RWC	SPAD	HI	PY
Cluster-I	18.458	7.133	37.303	2.071	3.298	2.797	2.131	68.099	43.891	38.502	1437.139
Cluster-II	18.562	6.824	36.064	4.933	3.278	2.257	1.760	69.884	42.358	36.925	1748.828
Cluster-III	14.230	5.059	29.226	2.685	4.048	2.890	1.878	66.408	40.828	35.574	1103.852
Cluster-IV	16.517	6.794	36.742	4.078	3.369	2.244	1.656	69.228	45.009	40.434	1046.611
Cluster-V	16.618	5.173	34.790	4.280	3.598	2.720	2.120	74.656	40.800	31.261	1064.178
Cluster-VI	19.844	7.867	42.950	4.433	3.367	2.433	1.722	71.499	43.256	40.452	1642.667

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 %, PY- Plot Yield

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

		Under Late Sown condition				Under Very Late Sown condition	
Sl. No.	Genotype	Value of Heat Susceptibility Index(S)	Interpretation	Sl. No.	Genotype	Value of Heat Susceptibility Index (S)	Interpretation
1.	PBN-51	0.46	T	1.	PBN-51	0.72	MT
2.	BWL-0814	0.26	T	2.	BWL-0814	0.44	T
3.	BWL-1771	0.54	M T	3.	BWL-1771	0.70	MT
4.	BWL-9022	0.46	T	4.	BWL-9022	0.57	MT
5.	BWL-0924	0.54	M T	5.	BWL-0924	0.80	MT
6.	BWL-1793	0.67	M T	6.	BWL-1793	0.65	MT
7.	CUS/79/PRULLA	0.06	T	7.	CUS/79/PRULLA	0.40	T
8.	IEPACA RABE	0.49	T	8.	IEPACA RABE	0.67	MT
9.	CHIRYA-3	0.32	T	9.	CHIRYA-3	0.40	T
10.	DHARWAD DRY	0.53	M T	10.	DHARWAD DRY	0.58	MT
11.	RAJ 3765	0.57	M T	11.	RAJ 3765	0.81	MT
12.	HI 1563	0.59	M T	12.	HI 1563	0.82	MT
13.	HD 2864	0.49	T	13.	HD 2864	0.53	MT
14.	RAJ 4083	0.48	T	14.	RAJ 4083	0.71	MT
15.	DBW-14	0.37	T	15.	DBW-14	0.84	MT
16.	WH 730	0.62	M T	16.	WH 730	0.87	MT
17.	K 9465	0.24	T	17.	K 9465	0.52	MT
18.	RAJ 4037	0.83	M T	18.	RAJ 4037	0.85	MT
19.	TEPOKO	0.23	T	19.	TEPOKO	0.51	MT
20.	BABAX	0.62	M T	20.	BABAX	0.85	MT
21.	OTHERI RGYPT	0.29	T	21.	OTHERI RGYPT	0.64	MT
22.	IC 532653	-0.15	T	22.	IC 532653	0.51	MT
23.	SERI 82	0.52	M T	23.	SERI 82	0.73	MT
24.	SONORA 64	0.54	M T	24.	SONORA 64	0.78	MT
25.	SALEMBO	0.11	T	25.	SALEMBO	0.62	MT
26.	ARIANA 66	0.69	M T	26.	ARIANA 66	0.69	MT
27.	GIZA 155	0.35	T	27.	GIZA 155	0.57	MT
28.	BACANORA 88	0.23	T	28.	BACANORA 88	0.65	MT
29.	IC118737	0.49	T	29.	IC118737	0.50	T
30.	C-306	0.37	T	30.	C-306	0.71	MT
31.	HD 2967	0.29	T	31.	HD 2967	0.46	T
32.	PBW 343	0.67	M T	32.	PBW 343	0.59	MT

*T- Tolerant, and MT- Moderately Tolerant

4. CONCLUSION

Clustering analysis revealed that all the genotype can be grouped in six clusters. 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 under different stress conditions. Selecting a donor from several clusters based on genetic distances, cluster means, and heat tolerance capacity would be ideal. These results revealed that the experimental material included physiological features responsible for bread wheat's heat tolerance as well as enough genetic variability and diversity to contribute to yield. The process of hybridization can be made more directed and efficient by choosing genotypes of interest from various clusters and designing a program around them. The current study offers important insights into the degree of genetic diversity found in the materials examined, which will aid in the creation of better individuals with higher yields and physiological features resistant to heat stress—that is, late and extremely late sowing conditions.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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