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

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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 very late sown condition. The observations were recorded on 16 agronomic traits and 3 physiological traits. The statistical analysis for genetic divergence wasdoneusingMahalanobis-D²statisticsandclusteringofgenotypeswasdoneusingTochermethod.On the basis of genetic diversity analysis, it was found that grain yield/plot and minimum by CTD-IV. Clustering of genotypes revealed that cluster-III had maximum number of genotype followed by cluster-I,cluster-II,cluster-IV,cluster-Vandcluster-VI.Thehighestinter-clusterdistancewasobservedbetween cluster-IV and VI while lowest inter-cluster distance was observed between cluster-I and II. The highest intra-cluster distance was observed in cluster-III revealing maximum genetic divergence among its constituents while lowest intra-cluster distance was observed in cluster-VI. The five genotypes were found tolerant to heat stress. The genotypes bearing desired values from different clusters can beexploited in future breeding programme for improving the yield and physiological traits under very 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 tones 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 productivity of wheat

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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 D²-statistics and hierarchical euclidean 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 32genotypes 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 very late sown condition on 15 January, 2015.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.

Table 1: List of genotypes/varieties

S. 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.	DHARWARDRY	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.	IEPACARABE	23.	RAJ-4037	31.	K-9465
8.	IC-11873	16.	OTHERY EGYPT	24.	SERI-82	32.	TEPOKO

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(GS61)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 measure 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 (Mahalanobis, 1936) 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).

$$Y=Yp (1-Sx D)$$

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, 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 (Figure2 and Table 3). On the basis of genetic diversity analysis, the maximum percent contribution towards genetic divergence was from grain yield per plot (60.89) followed by biological yield per plant (7.66), canopy temperature depression-I (6.85), canopy temperature depression-II (5.85), canopy temperature depression-III (5.65), plant height (4.84), relative water content (3.23), 1000 grain weight (2.02), grain yield per plant (1.81) and canopy temperature depression-IV (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.
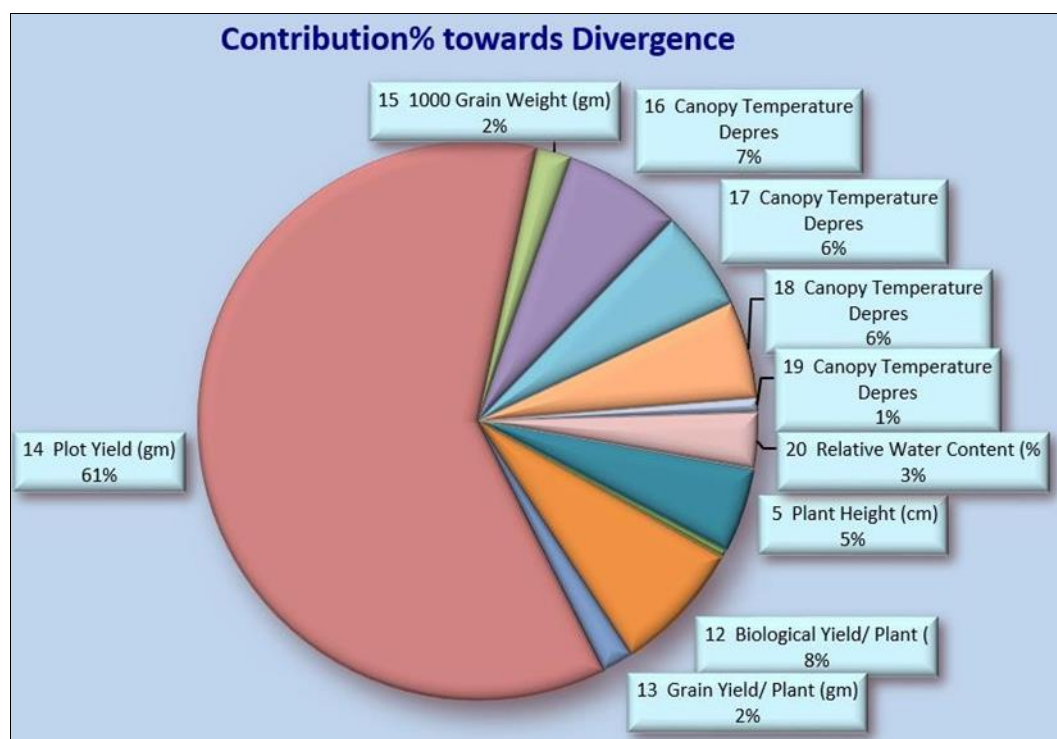

Fig 2: Percent contribution of different characters towards genetic divergence.

Cluster information
Under present study, all the 32 genotypes were grouped into six clusters (Figure 1 and Table 2) suggesting considerable amount of genetic diversity present in the material. The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity (Singh *et al*., 2009) [28].The cluster-III had highest number of genotypes (11) followed by cluster-I (7), cluster-II (6), cluster-IV (4), cluster-V (3) while cluster-VI had single genotype only. The five genotypes were found tolerant and rest twenty seven genotypes were found moderately tolerant to heat stress belonging to different clusters (Table 6).

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

Clusters	Number of genotypes	Name of genotypes
Cluster-I	7	IC-118737, BWL-1793, K-9465, IEPACARABE, Tepokoand Raj-4083., Bacanora-88
Cluster-II	6	BWL-9022, HD-2864, Salembo, Dharwar Dry, BWL-1771CUS/79/PRULLA,
Cluster-III	11	HI-1563, DBW-14, Raj-3765, BWL-0924, IC-532653, Ariana66, Giza-155, C-306, Raj-4037, WH-730, Seri-82
Cluster-IV	4	Sonora-64, Babax, Othery Egypt, PBN-51
Cluster-V	3	BWL-0814, HD-2967, Chirya-3
Cluster-VI	1	PBW-343

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

Source	Contribution%	Times Ranked 1st
Daysto 75% Heading	0.01	0.000
Daysto 75% Antthesis	0.01	0.000
Daysto 75% Maturity	0.01	0.000
Grain Filling Duration	0.01	0.000
Plant Height (cm)	4.84	24.000
Peduncle Length (cm)	0.01	0.000
Spike Length (cm)	0.01	0.000
Spikelets/ Spike	0.01	0.000
Grain/Spike	0.40	2.000
Grain Weight/Spike (gm)	0.01	0.000
Tillers/Plant	0.01	0.000
Biological Yield/Plant	7.66	38.000
Grain Yield/Plant (gm)	1.81	9.000
Plot Yield (gm)	60.89	302.000
1000 GrainWeight (gm)	2.02	10.000
Canopy Temperature Depression-I	6.85	34.000
Canopy Temperature Depression-II	5.85	29.000
Canopy Temperature Depression-III	5.65	28.000
Canopy Temperature Depression-IV	0.81	4.000
Relative Water Content(%	3.23	16.000
SPAD Value	0.01	0.000
Harvest Index (%)	0.01	0.000
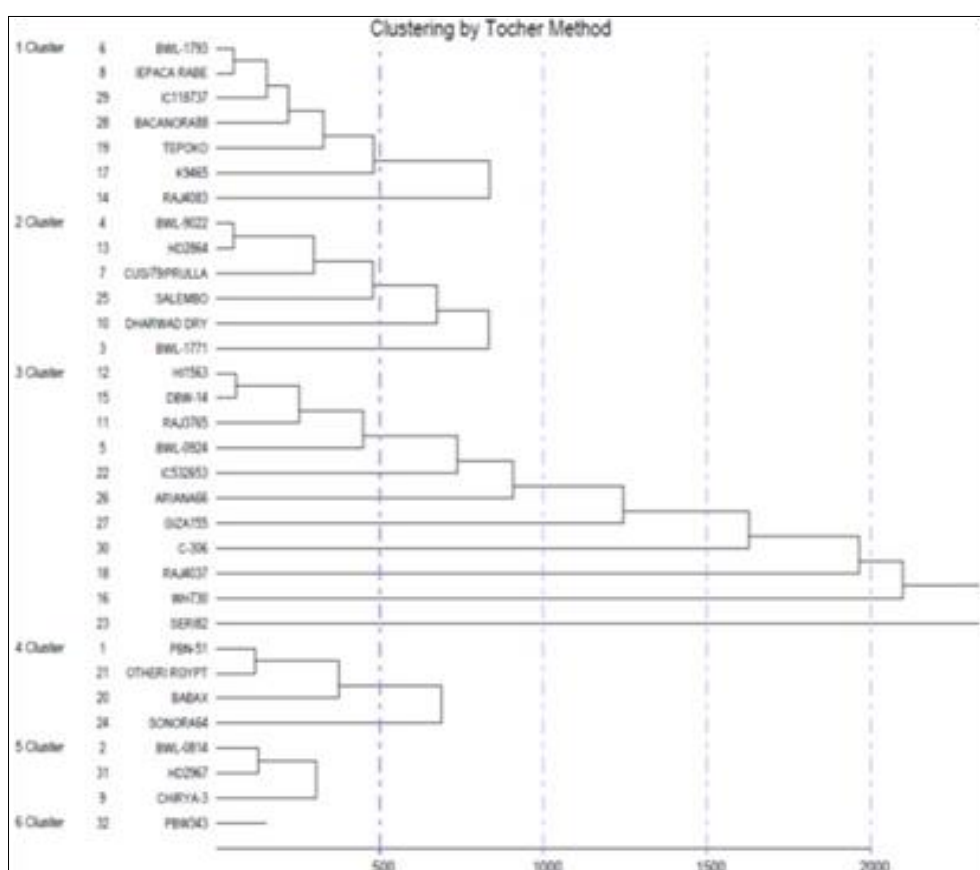
Fig 1: Clustering of Genotypes by Tocher Method.

Cluster-I: Cluster-I had seven genotypes namely BWL-1793, IEPACARABE, IC-118737, BACANORA-88, TEPOKO, K-9465 and RAJ-4083. This cluster had single heat tolerant genotype i.e. IC-118737 and rest six were moderately tolerant. This cluster had highest cluster means for the characters number of spikelets per spike and grain weight per spike. This cluster has higher values of yield attributing characters along with early maturity.

Cluster-II: Cluster-II had six genotypes which were BWL-9022, HD-2864, CUS/79/PRULLA, SALEMBO, Dharwar DRY and BWL-1771. This cluster has also single tolerant genotype i.e. CUS/79/PRULLA and rest were moderately tolerant. This cluster had highest cluster means spike length, number of grains per spike, 1000 grain weight, canopy temperature depression-III, canopy temperature depression-IV and SPAD value. This cluster represented higher cluster means for yield attributing as well as physiological traits.

Cluster-III: The cluster-III comprised of eleven genotypes which are HI-1563, DBW-14, RAJ-3765, BWL-0924, IC-532653, ARIANA-66, GIZA-155, C-306, RAJ-4037, WH- 730 and SERI-82. This cluster had no tolerant genotype. All genotypes in this cluster were moderately tolerant. This cluster had higher cluster means for different yield and physiological traits such as peduncle length, number of spikelts per spike, grain weight per spike, biological yield per plant, canopy temperature depression-III, canopy temperature depression-IV, and SPAD and harvest index. This cluster had moderate tolerance ability to heat stress.

Cluster-IV: This cluster had four genotypes namely PBN-51, Othery EGYPT, BABAX and SONORA-64. This cluster had only moderately tolerant genotypes. This cluster represented higher cluster mean for days to 75% maturity, grain filling duration, spike length, number of grains per spike, grain weight per spike, canopy temperature depression-I, canopy temperature depression-II, relative water content and harvest index. This cluster had lower cluster mean values for the characters such as days to 75% heading, plant height, panicle length, number of tillers per plant, biological yield per plant, grain yield per plant, plot yield, 1000 grain weight, canopy temperature depression-III, SPAD and harvest index. This cluster had moderate tolerance ability to heat stress.

Cluster-V: This cluster consisted of three genotypes- BWL-0814, HD-2967 and Chirya-3. All the members of this cluster were found tolerant. This cluster represented highest cluster mean for the traits such as plant height, number of tiller per plant, biological yield per plant, grain yield per plant, plot yield, canopy temperature depression-I, canopy temperature

depression-II and relative water content. This cluster was also marked with II-highest cluster mean for the traits such as peduncle length, grain weight per spike, canopy temperature depression-III and SPAD value. This cluster had higher cluster mean for yield attributing traits coupled with physiological traits. This cluster had maximum number of tolerant genotypes. This cluster had high tolerance ability to heat stress along with higher yield.

Cluster-VI: This cluster had single moderately tolerant genotype PBW-343. This cluster exhibited highest cluster mean for the traits such as plant height, number of tillers per plant, biological yield per plant, grain yield per plant, plot yield, canopy temperature depression-I and highest index. This cluster represented II- highest cluster mean for 1000grain weight and lowest cluster mean for the traits such as grain filling duration, plant height, peduncle length, number of spikelets per spike, number of grains per spike, number of tillers per plant, biological yield per plant and SPAD value. This cluster represented lower cluster means for yield attributing traits. This cluster also had moderate tolerance ability.

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 (215.69) which revealed maximum genetic divergence among its constituents followed by cluster-IV (197.01), cluster-II (155.75), cluster-IV (144.25), cluster-I (98.65) and cluster-VI (0.00) 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-IV and V (1279.57) 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- III and V (1165.64), clusters-III and VI (565.36), clusters-V and VI (561.98), clusters- I and V (559.75), clusters-II and IV (549.27), clusters-II and III (483.58), clusters-IV and VI (405.45), clusters-II and V (374.75), clusters-I and IV (347.05), clusters- III and IV (312.34), clusters-I and III (274.52), clusters-II and VI (221.55), clusters-I and VI (210.57), clusters-I and II (180.22) indicating close relationship between these clusters would not provide good results.

Table 4: Intra and Inter-Cluster Distances

	Cluster-I	Cluster-II	Cluster -III	Cluster-IV	Cluster-V	Cluster -VI
Cluster-I	98.654	180.221	274.522	347.049	559.755	210.565
Cluster-II		155.750	483.575	549.274	374.753	221.553
Cluster-III			215.693	312.341	1165.638	565.362
Cluster-IV				197.006	1279.566	405.455
Cluster-V					144.255	561.983
Cluster-VI						0.000

Table 5: Cluster means for different characters.

Clusters	DH	DA	DM	GFD	PH	PL	SL	NSS	NGS	GWS	NTP
Cluster-I	66.429	69.333	100.095	30.762	72.771	30.781	9.648	18.133	47.714	1.538	6.348
Cluster-II	67.000	69.500	103.889	34.333	78.089	31.167	10.009	17.867	40.744	1.364	6.939
Cluster-III	67.333	69.758	105.242	34.909	76.733	32.991	9.584	17.691	42.194	1.375	6.012
Cluster-IV	66.667	69.583	106.167	38.167	70.483	29.432	9.610	17.550	47.533	1.374	5.617
Cluster-V	66.778	69.000	100.778	31.778	78.122	31.889	9.007	17.156	46.044	1.498	7.189
Cluster-VI	69.667	73.667	100.333	26.667	66.700	23.967	9.373	15.400	37.333	1.287	5.533

Clusters	BY	GY	TGW	CTD-I	CTD-II	CTD-III	CTD-IV	RWC	SPAD	HI
Cluster-I	14.610	5.419	841.952	32.048	3.667	3.233	2.252	2.219	74.927	44.131
Cluster-II	14.767	4.756	1074.889	35.947	4.506	3.200	2.728	2.683	74.830	46.336
Cluster-III	14.315	4.721	453.303	32.130	3.606	2.933	2.424	2.294	72.604	45.448
Cluster-IV	9.633	2.900	527.500	31.496	4.850	4.000	1.358	1.350	75.161	43.728
Cluster-V	19.422	6.356	1465.556	33.267	5.733	4.067	2.511	2.178	77.822	45.666
Cluster-VI	9.000	3.867	1130.667	34.183	3.867	4.067	2.067	2.000	73.590	42.500

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	SI. No.	Genotype	Value of Heat Susceptibility Index (S)	Interpretation
1.	PBN-51	0.71538681	Moderately tolerant	17.	K 9465	0.52030361	Moderately tolerant
2.	BWL-0814	0.43756504	Tolerant	18.	RAJ4037	0.8511739	Moderately tolerant
3.	BWL-1771	0.70012733	Moderately tolerant	19.	TEPOKO	0.51361102	Moderately tolerant
4.	BWL-9022	0.57229081	Moderately tolerant	20.	BABAX	0.84967513	Moderately tolerant
5.	BWL-0924	0.80444336	Moderately tolerant	21.	OTHERIRGYPT	0.63984551	Moderately tolerant
6.	BWL-1793	0.65180216	Moderately tolerant	22.	IC 532653	0.50619082	Moderately tolerant
7.	CUS/79/PRULLA	0.39951741	Tolerant	23.	SERI 82	0.73248209	Moderately tolerant
8.	IEPACARABE	0.67348485	Moderately tolerant	24.	SONORA64	0.78451716	Moderately tolerant
9.	CHIRYA-3	0.39657895	Tolerant	25.	SALEMBO	0.61648039	Moderately tolerant
10.	DHARWADDRY	0.58136893	Moderately tolerant	26.	ARIANA66	0.68904058	Moderately tolerant
11.	RAJ3765	0.8052169	Moderately tolerant	27.	GIZA 155	0.57408975	Moderately tolerant
12.	HI 1563	0.82009893	Moderately tolerant	28.	BACANORA88	0.65178082	Moderately tolerant
13.	HD2864	0.52902876	Moderately tolerant	29.	IC118737	0.49801114	Tolerant
14.	RAJ4083	0.70873187	Moderately tolerant	30.	C-306	0.37	Tolerant
15.	DBW-14	0.83960211	Moderately tolerant	31.	HD2967	0.29	Tolerant
16.	WH730	0.86803419	Moderately tolerant	32.	PBW343	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, grain yield per plot 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 cluster-V had tolerant genotypes only with higher cluster means for plant height, number of tiller per plant, biological yield per plant, grain yield per plant, plot yield, canopy temperature depression-I, canopy temperature depression-II and relative water content while clusters- III, IV and VI represented only moderately tolerant genotypes with higher cluster means for peduncle length, number of spikelts per spike, grain weight per spike, biological yield per plant, canopy temperature depression-III, canopy temperature depression-IV, SPAD and harvest index etc. clusters-I and II had tolerant as well as moderately tolerant genotypes along with higher cluster means for the traits such as spikelets per spike and grain weight

per spike, spike length, number of grains per spike, 1000 grain weight, canopy temperature depression-III, canopy temperature depression-IV and SPAD value. 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 very late sown conditions.

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