



Assessment and role of genetic diversity of component traits for improving grain yield and heat tolerance in bread wheat (*Triticum aestivum*)

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ABSTRACT

The present investigation was carried out in a randomized block design (RBD) with 20 diverse wheat (*Triticum aestivum* L.) genotypes grown under three environments *i.e.* 25th November, 2012 (Environment-I, timely sown), 24th December, 2012 (Environment-II, late sown) and 15th January 2013 (Environment-III, very late sown). The environment wise analysis of variance for grain yield and its contributing traits indicated highly significant differences among the genotypes for all the traits under study. High heritability along with high genetic advance and high coefficient of variation (PCV and GCV) for grain yield across three environments indicated substantial contribution of additive gene action in the expression of desirable traits and thus selection would be effective for genetic improvement of grain yield in wheat. On the basis of multivariate analysis, 20 genotypes were grouped into five clusters based on D² value. The cluster V contained the maximum number of genotypes (6) in Environment-I, whereas cluster II included six genotypes in Environment-II, cluster IV included 07 genotypes in Environment-III and on pooled analysis basis cluster V had 07 genotypes. The highest inter cluster values were observed between cluster II and III (2690.75), followed by cluster I and II (2494.51), cluster II and V (1334.53), cluster III and V (730.74) in the first, second, third environments as well as pooled analysis basis, respectively, and thus genotypes included in these clusters showed wide genetic diversity and thus may be utilized in hybridization programme targeting wheat breeding for obtaining transgressive segregants to improve grain yield under varying environments. Based on the cluster mean analysis, genotype K 512 in E-I (timely sown) and E-II (late sown) while AAI 13 in E-II (late sown), E-III (very late sown) and also in pooled analysis were rated better performing for multiple yield traits and these genotypes can be considered in breeding programme as well as for further study for developing superior wheat genotypes.

Key words: Bread wheat, Genetic diversity, Genetic parameters, Grain yield, Multivariate analysis

Wheat (*Triticum aestivum* L.) is one of the most important staple food crops of the world providing about 20 percent of protein to mankind. India holds second position after China in terms of both area (29.72 million ha) and production (98.61 million tonnes) (Anonymous 2018). Among the abiotic stresses, heat stress caused due to late planting is affecting around 13.5 million ha grown under wheat in India and therefore researchers have focus on improving productivity of wheat under harsh environments, viz. drought and high temperature at the time of maturity. Increase in temperature during crop growth period restricts production and productivity, particularly at germination and grain filling stage. The optimum temperature required for growth and development of wheat is in the range of 18-24°C and high temperatures (28-38°C) may result in significant

decrease in yield. Wheat breeders are trying to incorporate late heat tolerance ability in the wheat to develop genotypes that are early in maturity in order to escape the terminal heat stress. The creation and utilization of genetic diversity is essential to overcome the problems of narrow genetic base and also to solve problems associated with complex genetic structure of heat tolerance. Therefore, research efforts are in progress to breed for heat tolerance in wheat. Generating precise information on genetic diversity required in selecting the parents for targeted hybridization is a part of such efforts. The cluster analysis is an appropriate method for determining family relationship to determine the extent of genetic distance of genotypes from each other. A wide range of genetic variability present in the material under study provides chances for selection of desired plant types. The effects of climate change including temperature fluctuations has forced the breeders to develop genetic material that can yield better even under situations of high temperature stress productivity. Therefore the present investigation was carried out to study the genetic diversity among wheat genotypes planted across sowing conditions (timely, late and very late) and also to identify the promising genotypes for use

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in breeding programmes targeting high productivity under harsh environments.

MATERIALS AND METHODS

The experimental material comprised 20 diverse genotypes of wheat evaluated in a randomized block design (RBD) with three replications under three different dates of sowing, viz 25th November, 2012 (E-I, first environment representing irrigated timely sown), 24th December, 2012 (E-II, second environment representing irrigated late sown) and 15th January, 2013 (E-III, third environment representing irrigated very late sown) at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U P). Plot size was kept as four rows of 2.0 m length with row to row distance of 23 cm and plant to plant distance of 10 cm. All the recommended agronomical practices and plant protection measures were adopted to raise the normal crop.

Observations were recorded on days to maturity, days to 50 % flowering, chlorophyll content (%), plant height (cm), peduncle length (cm), spike length (cm), number of spikelets/spike, number of grains/spikelet, tillers/plant, 1000-grain weight (g), biological yield/plant (g), harvest index (%) and grain yield/plant (g). The mean values from each replication were subjected to statistical analysis using SAS and CROPSTAT computer software. The analysis of variance (ANOVA) was done based on the method suggested by Panse and Sukhatme (1969). Heritability in broad sense was calculated using the method suggested by Burton and De Vane (1953). Genetic advance as percent of mean for each character was calculated following formula as suggested by Johnson *et al.* (1955). Also, data were subjected to non-hierarchical Euclidean cluster statistic (Spark 1973). The analysis of genetic diversity was done through cluster analysis using D² statistics suggested by Mahalanobis (1936) and genotypes were grouped into different clusters using Tochers method suggested by Rao (1952).

RESULTS AND DISCUSSION

The environment wise analysis of variance (Table 1) for grain yield and its contributing traits indicated significant differences among the genotypes for all the traits under study across environments (E-I, E-II & E-III). Similarly, pooled analysis of variance over three environments also showed highly significant differences among genotypes, environments and overall sum (Table 2), indicating thereby presence of genetic and environmental variability among the studied genotypes, for all the thirteen characters, viz. days to 50% flowering, days to maturity, plant height, peduncle length, chlorophyll content, spikelets/spike, grains/spikelet, spike length, tillers/plant, 1000-grain weight, biological yield/plant, harvest index and grain yield/plant. Environment wise analysis of variance also indicated sufficient variability among the genotypes for all the traits under study and therefore, gives a good scope for selection of elite types suitable for varying environments and sowing conditions. Similarly, pooled analysis of variance over environments

Table 1 Analysis of variance for grain yield and its contributing traits in bread wheat under E-I, E-II, E-III environments

Source of variation	D F	Environment	Mean Sum of Squares												
			Days to maturity	Days to 50% flowering	Chlorophyll content (%)	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	Spikelets/spike	Grains/spikelet	Tillers/plant	1000-grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Grain yield/plant (g)
Replication	2	E-I	1.05	3.62	24.22	0.43	0.87	0.00	0.24	0.02	0.09	0.08	0.52	2.54	0.93
		E-II	0.12	3.47	7.16	1.87	0.75	0.11	0.22	0.03	1.35	0.00	27.32	18.87	13.02
		E-III	0.65	9.32	1.46	0.62	0.89	0.04	0.42	0.02	0.05	0.12	0.39	1.88	0.05
Genotypes	19	E-I	4.55**	38.59**	28.04**	267.83**	73.53**	3.92**	9.38**	0.15**	1.72*	16.57**	91.09**	60.58**	28.13**
		E-II	12.71**	13.90**	24.13**	167.81**	39.36**	0.82**	4.56**	0.09**	3.19**	18.16**	62.12**	76.98**	13.52**
		E-III	5.95**	6.43*	13.71**	62.44**	28.66**	1.04**	2.23**	0.33**	0.23**	18.27**	4.66**	117.53**	2.80**
Error	38	E-I	1.21	7.93	7.82	0.62	1.06	0.04	0.24	0.01	0.78	0.12	12.75	4.18	3.03
		E-II	0.96	5.50	5.51	0.48	0.93	0.08	0.21	0.02	0.86	0.15	15.80	6.09	3.46
		E-III	0.69	3.00	5.18	0.93	0.92	0.11	0.15	0.02	0.08	0.17	0.85	3.56	0.51

*, ** Significant at 5% and 1% level of significance respectively.

Table 2 Pooled analysis of variance (ANOVA) for grain yield and its contributing traits in bread wheat

Source of variation	D F	Mean Sum of Squares												
		Days to maturity	Days to 50% flowering	Chlorophyll content (%)	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	Spikelets/spike	Grains/spikelet	Tillers/plant	1000-grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Grain yield/plant (g)
Replication	2	1.07	3.07	14.71	0.30	0.31	0.06	0.43	0.01	0.45	0.07	6.79	13.24	6.51
Genotypes	19	6.78**	27.88**	32.51**	344.57**	114.14**	3.04**	10.27**	0.41**	1.80**	52.65**	49.11**	162.30**	22.76**
Environments	2	17778.67**	8655.67**	59.99**	13474.43**	1607.06**	24.29**	99.55**	2.36**	327.99**	265.89**	8168.34**	2048.33**	1994.23**
Interactions	4	0.37	6.66	9.07	1.31	1.11	0.05	0.23	0.03	0.53	0.07	10.72	5.03	3.74
Overall sum	8	4445.12**	2168.02**	23.21**	3369.34**	402.39**	6.12**	25.12**	0.61**	82.38**	66.53**	2049.14**	517.91**	502.06**
Error	152	2.77	7.99	8.80	19.69	4.16	0.40	0.89	0.04	0.85	0.16	20.95	15.06	4.47

*, ** Significant at 5% and 1% level of significance respectively.

indicated differential response of genotypes selected for the study and differential effects of different environmental conditions.

The mean performance of 20 diverse wheat genotypes under three micro-environments (indicated as E-I, E-II, E-III) as well as pooled analysis have been presented (Table 3), that indicated highest mean performance for 12 traits under Environment-I, followed by Environment-II and Environment-III, respectively. The overall performance of wheat genotypes as expected was much higher under timely sown condition as compared to late and very late sown conditions. The range of mean performance was high for days to 50% flowering, chlorophyll content, plant height, peduncle length, spike length, spikelets/spike and grain yield/plant in Environment-I (timely sown); for days to maturity, tillers/plant, 1000-grain weight and biological yield/plant in Environment-II (late sown); grain yield/plant and harvest index in Environment-III (very late sown). The results of the present study revealed that in general, the material under study had wide range of variability for most of the traits. The present study results are in accordance with the earlier findings of Singh *et al.* (2012), Dhakar *et al.* (2012), Singh *et al.* (2013), Singh *et al.* (2014) and Kumar *et al.* (2016) in wheat crop grown at different locations in India.

The data on coefficient of variation (Table 3) indicated that the phenotypic coefficient of variation (PCV) was higher than their corresponding genotypic coefficient of variation (GCV) for all the traits among the genotypes in all three environments (E-I, E-II & E-III) and also in pooled analysis. The highest GCV was recorded for grain yield/plant (18.81%) followed by biological yield/plant (14.46%), peduncle length (12.88%) and spike length (10.02%) in Environment-I (timely sown); for grain yield/plant (15.05%), biological yield/plant (13.72%), tillers/plant (13.68%), harvest index (11.39%) and peduncle length (10.14%) in Environment-II (late sown); for grain yield/plant (20.91%), harvest index (18.72%), peduncle length (10.82%) and grains/spikelet (10.81%) in Environment-III (very late sown) and for grain yield/plant (13.48%) and harvest index (10.20%) in pooled analysis. Singh *et al.* (2013), Das *et al.* (2014), and Singh *et al.* (2014) also reported high PCV and GCV for grain yield, tillers/plant; Singh *et al.* (2012) for peduncle length; Kumar *et al.* (2016) for spikelets/spike; Singh *et al.* (2018) for grain yield and harvest index under normal condition in wheat crop at different locations in India. A close examination of PCV and GCV values suggested that environmental variations had effects in the expression of grain yield in all three environments indicated as (E-I, E-II & E-III); biological yield in E-I & E-II and tillers/plant in E-II. The highest PCV&GCV were recorded for grain yield in all three Environment (Indicated as E-I, E-II & E-III) indicating better opportunity for improvement of grain yield through selection.

The estimates of heritability (broad-sense) in general were low to high under all three environments (E-I, E-II & E-III) as well as pooled analysis (Table 3). In the present study, high heritability estimates (>60%) coupled with high

Table 3 Estimates of genetic parameters for grain yield and its contributing traits in bread wheat under E-I, E-II, E-III and pooled analysis

Character	Environment	Mean	Range	PCV	GCV	Heritability (broad sense)	GA as percent of mean
Days to maturity	E-I	138.40	136.00 - 141.00	1.10	0.76	47.95	1.08
	E-II	116.71	113.00 - 120.33	1.89	1.69	80.33	3.13
	E-III	104.40	101.33 - 107.00	1.49	1.26	71.92	2.21
	Pooled	119.83	117.88 - 121.44	1.49	0.55	13.87	0.42
Days to 50% flowering	E-I	92.36	85.00 - 97.66	4.61	3.46	56.30	5.35
	E-II	78.61	74.33 - 81.66	3.66	2.12	33.73	2.54
	E-III	68.43	66.33 - 71.66	2.97	1.56	27.55	1.68
	Pooled	79.80	76.22 - 82.77	4.00	1.86	21.67	1.78
Chlorophyll content (%)	E-I	41.25	35.33 - 44.76	9.25	6.29	46.28	8.82
	E-II	41.43	36.26 - 45.00	8.26	6.01	52.96	9.01
	E-III	43.06	39.30 - 71.66	6.57	3.91	35.47	4.80
	Pooled	41.91	37.68 - 45.07	8.06	3.87	23.03	3.82
Plant height (cm)	E-I	94.83	75.93 - 109.00	9.98	9.95	99.31	20.43
	E-II	86.41	73.86 - 101.80	8.67	8.64	99.15	17.72
	E-III	65.71	56.60 - 72.73	7.04	6.89	95.65	13.88
	Pooled	82.32	68.80 - 89.97	9.07	7.29	64.69	12.09
Peduncle length (cm)	E-I	38.14	29.93 - 46.80	13.16	12.88	95.77	25.97
	E-II	35.27	28.93 - 41.93	10.51	10.14	93.21	20.18
	E-III	28.09	22.73 - 32.86	11.35	10.82	90.94	21.26
	Pooled	33.83	27.55 - 39.84	9.07	7.29	64.69	12.09
Spike length (cm)	E-I	11.34	9.13 - 13.33	10.18	10.01	96.75	20.29
	E-II	11.21	10.46 - 12.20	5.09	4.44	76.22	7.99
	E-III	10.18	9.40 - 11.13	6.39	5.47	73.29	9.65
	Pooled	10.91	10.04 - 12.15	7.63	4.95	42.15	6.63
Spikelets/spike	E-I	18.54	14.53 - 21.00	9.77	9.41	92.76	18.68
	E-II	17.41	15.73 - 19.73	7.40	6.92	87.38	13.32
	E-III	15.97	14.53 - 18.33	5.74	5.21	82.33	9.74
	Pooled	17.30	15.40 - 19.20	8.02	5.89	54.00	8.93
Grains/spikelet	E-I	3.32	2.93 - 3.86	7.46	6.57	77.54	11.92
	E-II	3.27	3.00 - 3.60	6.49	4.64	51.12	6.84
	E-III	2.95	2.46 - 3.86	11.96	10.81	81.25	20.07
	Pooled	3.18	2.80 - 2.80	8.74	6.35	52.85	9.51
Tillers/plant	E-I	7.24	6.22 - 8.66	14.47	7.69	28.22	8.41
	E-II	6.43	4.58 - 9.03	19.90	13.68	47.28	19.36
	E-III	2.85	2.33 - 3.44	12.80	7.88	37.93	10.00
	Pooled	5.51	4.71 - 6.38	17.76	5.89	11.01	4.03
1000-grain weight (g)	E-I	40.89	35.98 - 45.82	5.78	5.72	97.84	11.66
	E-II	39.86	34.45 - 45.02	6.22	6.14	97.60	12.51
	E-III	36.84	32.02 - 42.22	6.76	6.66	97.22	13.54
	Pooled	39.20	34.15 - 44.35	6.24	6.16	97.41	12.52
Biological yield/plant (g)	E-I	35.32	27.56 - 46.66	17.65	14.46	67.17	24.42
	E-II	28.62	20.30 - 39.99	19.52	13.72	49.42	19.88
	E-III	12.61	10.34 - 15.25	11.54	8.94	60.01	14.27
	Pooled	25.52	21.52 - 30.70	19.22	6.93	12.99	5.14
Harvest index (%)	E-I	43.39	30.78 - 48.05	11.04	9.99	81.78	18.61
	E-II	42.64	36.11 - 56.66	12.78	11.39	79.48	20.93
	E-III	32.91	24.53 - 53.41	19.58	18.72	91.42	36.87
	Pooled	39.65	31.95 - 50.19	14.13	10.20	52.06	15.16
Grain yield/plant (g)	E-I	15.37	9.89 - 20.66	21.96	18.81	73.37	33.19
	E-II	12.16	9.49 - 18.45	21.47	15.05	49.16	21.74
	E-III	4.17	2.65 - 7.10	27.06	20.91	59.69	33.28
	Pooled	10.57	8.04 - 13.79	24.11	13.48	31.27	15.53

genetic advance (>20%) was recorded for plant height, spike length, peduncle length, grain yield/plant and biological yield/plant, whereas high heritability with moderate genetic advance was estimated for spikelets/spike, harvest index and grains/spikelet in Environment-I (timely sown). While, high heritability coupled with high genetic advance was recorded for harvest index and peduncle length. Also, high heritability with moderate genetic advance was estimated for spikelets/spike and plant height in Environment-II (late sown). High heritability with high genetic advance was recorded for peduncle length, grains/spikelet and harvest index, whereas high heritability with moderate genetic advance was recorded for plant height, biological yield/plant and 1000-grain weight in Environment-III (very late sown). High heritability coupled with moderate genetic advance was recorded for plant height, peduncle length and 1000-grain weight in pooled analysis. High heritability for days to maturity, plant height and grain yield was reported by Emeka *et al.* (2015) for both timely sown as well as late sown condition in wheat crop in Syria which is similar to the findings of present investigation. In the present study, traits like peduncle length and grain yield/plant that showed high heritability with high genetic advance in all three environments indicated substantial contribution of additive gene action in the expression of these characters. These results are in agreement with the earlier findings of Singh *et al.* (2013), Singh *et al.* (2014), Kumar *et al.* (2016) and Singh *et al.* (2018). High heritability along with high genetic advance and high coefficient of variability (PCV & GCV) for grain yield/plant exhibited good scope for improving grain yield through selection. However, expression of traits, viz. days to maturity and flowering, chlorophyll content, 1000-grain weight, spike length and spikelets/spike that showed high to moderate heritability but moderate to low genetic advance, may be due to non-additive gene action, therefore in such cases simple selection may not be very rewarding and hybridization followed by selecting desirable transgressive segregants would be the better option for improving these traits.

The results of genetic diversity among 20 diverse wheat genotypes in three environments (E-I, E-II & E-III) as well as pooled analysis for 13 yield components presented, revealed that clustering pattern of genotypes was not consistent over environments. Based on the results of genetic diversity analysis, 20 genotypes were grouped into five clusters by non-hierarchical Euclidean cluster statistic in such way that the genotypes within a cluster had a small or low D^2 values than those of in between the clusters. The compositions of cluster revealed that Cluster V (6), Cluster II (6), Cluster IV (7) and Cluster V (6) had the largest number of genotypes in E-I, E-II, E-III and also in pooled analysis respectively, whereas Cluster II in E-III included only one genotype (Table 4). These results showed that number of genotypes in different clusters as expected varied under different environments. The grouping of genotypes based on multivariate analysis has also been reported earlier by Singh *et al.* (2012), Dhakar *et al.* (2012), Singh *et al.* (2014),

Table 4 Distribution 20 genotypes into five clusters based on D^2 value under E-I, E-II & E-III and pooled analysis

Cluster	No. of genotypes	Genotype
<i>Environment- I</i>		
I	2	SVPW 1, K 512
II	4	K 910-4, AAI 13, K 307, NW 1014
III	5	HUW 648, AAI 16, HUW 658, HD 2733, K 9162
IV	3	K 607, K 911, AAI 12
V	6	K 612, K 910-30, AAI 11, NW 4035, NW 4081, NW 6007
<i>Environment- II</i>		
I	2	SVPW 1, HD 2733
II	6	K 910-4, K 512, AAI 11, AAI 13, AAI 16, K 307
III	3	K 612, K 910-30, NW 4035
IV	5	K 607, K 911, HUW 648, AAI 12, HUW 658
V	4	NW 4081, NW 6007, NW 1014, K 9162
<i>Environment- III</i>		
I	4	SVPW 1, K 512, K 607, HUW 648
II	1	NW 6007
III	3	AAI 11, NW 4081, HD 2733
IV	7	K 910-4, K 910-30, K 911, AAI 12, AAI 16, HUW 658, K 307
V	5	K 612, AAI 13, NW 4035, NW 1014, K 9162
<i>Pooled analysis</i>		
I	3	SVPW 1, K 512, HUW 658
II	5	K 910-4, K 910-30, K 911, HUIW 648, K 307
III	4	K 612, AAI 13, AAI 16, NW 1014
IV	2	K 607, AAI 12
V	6	AAI 11, NW 4035, NW 4081, NW 6007, H 2733, K 9162

Tewari *et al.* (2015) and Singh *et al.* (2018).

The average intra and inter cluster distances varied in different environments (Table 5), since the genotypes exhibited different clustering patterns in different environments. The maximum inter cluster distance was recorded between clusters II & III (2690.75), clusters I & II (2494.51), clusters II & V (1334.53) and clusters III & V (730.74) in E-I, E-II, E-III and pooled analysis, respectively, which indicated that these genotypes (environments wise) involved in these clusters have wide genetic diversity and thus can be used in wheat hybridization for improving grain yield. The inter cluster values that indicated close relationship were to be considered that hybridization among the genotypes of these clusters would not provide good levels of segregation but will also allow selection of

Table 5 Average inter and intra cluster distances for 5 clusters in wheat under E-I, E-II & E-III and pooled analysis

Cluster	I	II	III	IV	V
<i>Environment-I</i>					
I	261.49	575.50	1568.79	489.81	1172.02
II		304.19	2690.75	1152.71	1834.90
III			286.22	675.93	663.87
IV				283.36	566.49
V					0.00
<i>Environment-II</i>					
I	264.42	2494.51	1318.37	577.36	1241.19
II		243.35	397.35	978.88	593.10
III			85.42	389.94	548.63
IV				202.73	423.79
V					126.27
<i>Environment-III</i>					
I	126.59	210.69	299.85	198.47	1088.60
II		75.11	254.99	259.59	1334.53
III			98.26	208.02	942.44
IV				89.06	801.79
V					0.00
<i>Pooled analysis</i>					
I	23.64	52.96	186.48	73.58	240.08
II		23.81	71.24	163.79	401.42
III			0.00	389.93	730.74
IV				28.06	83.30
V					0.00

superior genotypes for varying conditions of sowing and managing heat stress by least reduction in grain weight under late sowing. It is well recognized that greater the distance between clusters, wider the genetic diversity would be between the genotypes. Therefore, highly divergent genotypes would produce a broad spectrum of segregation in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants. This information would be very useful in planning wheat breeding programme particularly for different temperature regimes. Singh *et al.* (2012), Dhakar *et al.* (2012), Verma *et al.* (2014), Das *et al.* (2014), Tewari *et al.* (2015) and Singh *et al.* (2018) also reported similar findings on genetic diversity under normal condition at different locations of India.

The maximum intra cluster distance was observed in cluster II (304.19) followed by cluster I (264.41), cluster I (126.59), and cluster IV (28.05) in E-I, E-II, E-III and pooled analysis respectively (Table 5). The maximum intra cluster distance was mainly due to wide genetic diversity among the genotypes of these clusters. The low genetic diversity and selection of parents within the cluster having higher

mean values for a particular character may also be useful for further improving wheat genotypes for grain yield. In the earlier studies, Das *et al.* (2014), Tewari *et al.* (2015) and Singh *et al.* (2018) had also reported substantial genetic diversity in wheat crop.

Five clusters showed considerable differences in mean value for different characters under study (Table 6). Two genotypes of cluster-I accounted for highest cluster mean for days to 50% flowering, spikelets/spike, 1000-grain weight, biological yield/plant and grain yield/plant. Four genotypes of cluster-II contributed to highest cluster mean for chlorophyll content, plant height, peduncle length and spike length. Similarly, five genotypes of cluster-III were responsible for highest cluster mean for days to maturity, grains/spike, tillers/plant and harvest index in Environment-I (timely sown). Two genotypes of cluster-I accounted high cluster mean for days to maturity, plant height and peduncle length. Six genotypes in cluster-II were responsible for days to 50 % flowering, grains/spikelets, tillers/plant, biological yield/plant and grain yield/plant. Three genotypes in cluster III for chlorophyll content and five genotypes in cluster V were responsible for highest cluster mean for spikelets/spike, 1000-grain weight, spike length and harvest index in Environment-II. Four genotypes in cluster I were responsible for the highest cluster mean for days to maturity. Only one genotype in cluster II was responsible for highest cluster mean for chlorophyll content and biological yield/plant whereas, four genotypes in cluster III were responsible for days to maturity, plant height and peduncle length. Two genotypes in cluster V were responsible for grains/spikelets, tillers/plant, grain yield/plant, spikelets/spike, 1000-grain weight, spike length and harvest index in Environment-III. These were, thus adjudged to be considered suitable for creating maximum variability by hybridization and selecting the desired genotypes possessing tolerance to late heat stress coupled with higher yield under late or very late sowings of wheat and lowest reduction in grain size and weight. Based on the cluster mean analysis, genotype K 512 in E-I (timely sown) and E-II (late sown) while AAI 13 in E-II (late sown), E-III (vary late sown) and also in pooled analysis were rated better performing for multiple yield traits and these genotypes can be considered in breeding programme as well as for further study for developing superior wheat genotypes.

Based on the above results, it may be concluded that environment wise analysis of variance exhibited significant differences among the genotypes for all 13 traits estimated under present study. The traits which have sufficient variability suggested that hybridization programme involving these diverse genotypes might lead to transgressive segregants and thus an overall genetic improvement in wheat crop under varying environments to mitigate associated problems including late heat stress. Inter and intra cluster distance indicated sufficient genetic diversity between and within clusters. It would be desirable to choose the donor from different clusters. The maximum inter cluster distance was observed in

Table 6 Cluster mean for grain yield and its contributing traits in bread wheat under E-I, E-II & E-III and pooled analysis

Cluster	Days to maturity	Days to 50% flowering	Chlorophyll content (%)	Plant height (cm)	Peduncle length (cm)	Spike length (cm)	Spikelets/spike	Grains/spikelet	Tillers/plant	1000-grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Grain yield/plant (g)
<i>Environment-I (timely sown)</i>													
I	138.39	94.72	41.31	98.73	38.35	11.74	19.41	3.40	7.29	42.83	39.06	44.31	17.21
II	138.08	92.83	42.93	108.21	43.01	11.77	19.40	3.30	7.21	40.38	35.55	43.98	15.88
III	139.66	93.83	37.26	78.50	32.70	10.53	18.73	3.60	7.60	37.44	34.87	45.57	15.86
IV	138.33	90.71	42.21	89.86	37.22	11.30	17.81	3.23	7.20	40.81	32.47	43.45	14.12
V	137.67	85.00	35.33	85.33	34.60	9.13	14.53	2.93	6.55	38.81	32.81	30.78	10.10
<i>Environment-II (late sown)</i>													
I	118.66	78.66	39.87	97.90	40.20	11.36	17.66	3.30	6.44	39.95	28.79	43.49	12.42
II	114.16	79.66	42.38	74.23	29.83	10.73	16.70	3.33	6.86	40.06	30.39	41.79	12.76
III	116.00	78.25	42.66	81.21	35.26	10.80	16.21	3.31	6.36	37.75	28.17	38.19	10.81
IV	116.66	79.14	41.73	88.00	35.19	11.33	17.64	3.21	6.66	39.44	29.65	41.78	12.46
V	116.88	77.11	40.51	82.46	32.53	11.62	18.57	3.28	5.73	43.41	25.39	50.02	12.48
<i>Environment-III (vary late sown)</i>													
I	104.75	69.00	43.85	62.51	28.69	10.02	15.61	2.80	2.81	35.14	12.79	28.91	3.72
II	102.83	67.16	46.41	69.86	27.26	10.13	15.76	3.03	2.88	34.28	12.79	30.86	3.96
III	104.86	68.40	42.01	71.53	30.78	10.45	16.46	2.85	2.86	38.13	12.69	33.66	4.29
IV	104.00	68.25	41.20	63.33	25.03	10.11	15.80	3.13	2.72	38.57	12.06	35.89	4.30
V	104.00	67.33	42.80	63.40	23.73	10.46	17.40	3.86	3.00	42.22	12.62	53.41	7.10
<i>Pooled analysis</i>													
I	120.42	79.77	40.73	86.36	36.41	10.92	17.45	3.14	5.69	39.75	26.09	40.29	11.03
II	119.38	80.36	42.18	80.35	31.38	11.15	17.69	3.20	5.46	41.62	25.79	42.06	11.21
III	120.11	80.44	42.71	80.82	29.11	11.20	18.82	3.66	4.71	44.35	25.86	50.19	12.22
IV	119.39	79.00	43.07	80.47	33.67	10.73	16.59	3.14	5.49	37.24	24.93	36.42	9.62
V	120.33	82.77	40.20	76.33	31.42	10.84	18.20	3.17	5.45	34.15	24.16	37.53	9.74

Environment-I (timely sown), followed by Environment-II (late sown), Environment III (very late sown) and pooled analysis, respectively, which indicates that these genotypes (environment wise) have broad spectrum of genetic diversity and therefore could be useful in wheat hybridization programmes aiming high grain yield under varying environments so as to address the problems of late heat stress by selecting genotypes that show least reduction under delayed sowing of wheat crop across zones and conditions. Two genotypes, viz. K 512 in E-I and AAI 13 were rated better performing for multiple yield traits and these genotypes can be recommended in breeding programme for developing superior wheat genotypes.

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