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Research Article

Estimating genetic diversity of bread wheat (*Triticum aestivum* L.) in different environments

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Abstract
An experiment was conducted to evaluate the genetic diversity in 48 genotypes of wheat for 25 traits under two environments i.e., timely and late sown conditions, at Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during *rabi,* 2019-20. The genetic diversity analysis revealed the formation of seven clusters in both environments. Based on the genetic distance, it was concluded that crossing of genotypes from cluster V with clusters I and IV to get a broad spectrum of variation for both environments. Cluster VII for timely sown and cluster V for late sowing conditions contained genotypes with high mean performance for grain yield and other traits and therefore these genotypes can be utilized for yield improvement. Based on the analysis of percent contribution of different traits to total genetic divergence, it was found that under timely sown condition CTD 1, total gluten content and for late sown condition zinc content, CTD 2 contributed the most.

Keywords: Cluster mean, D^2 statistic, environment, genetic divergence, wheat.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most popular staple foods worldwide after rice and is generally grown in tropical and temperate regions of the world due to its high acclimatization and importance to human nutrition and the agricultural economy. Approximately 20% of daily dietary requirement comes from wheat (Anonymous, 2016). Climate, drought, heat stress and salinity are abiotic stress factors that severely limit the growth, development of plants, as well as the adaptability of the plants, which lowers yields in crops such as cereals (Wang *et al*., 2004). Wheat yield is negatively affected by heat stress because of early senescence and accelerated grain filling activities leading to low grain yields (Paulsen, 1994). The selection of a genotype with the desired combination of naturally occurring characteristics can improve the yield and quality of crops. It is important to understand the extent of genetic divergence and its pattern for breeding and selecting desirable traits (Maniee *et al*., 2009). A successful crop improvement program depends on the genetic diversity in the existing germplasm (Moose and Mumm, 2008). Genetic divergence analysis can be used to estimate genetic diversity among selected genotypes that can be used to determine genetic bonding between families and genetic distance between genotypes using cluster analysis (Mellingers, 1972). Diversity could provide farmers with high yielding crops with important useful traits under unfavorable environmental conditions, thereby improving their livelihoods. By understanding variations among genotypes linked to known potentialities, breeders can select appropriate parents for purposeful hybridization. Apart from these, the Mahalanobis D^2 technique assists in identifying selection parameters to be used as criteria for improving wheat yield by analyzing the degree of divergence and the relative contribution of different components. So, the present study was conducted to study 25 traits, namely morphological, physiological, and quality in wheat under two sowing dates i.e., timely and late sown and to group the genotypes into clusters based on inter and intra cluster distances, along with selecting suitable genotypes that can be recommended for wheat breeding programmes for the development of high yielding cultivars under both normal and heat stress conditions.

MATERIALS AND METHODS

The present study was conducted at Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during *rabi,* 2019-20. The experimental material used in the investigation comprised of 48 advance wheat breeding genotypes from the 9th harvest plus yield trial (**Table 1**). The genotypes were grown in Randomized Block Design (RBD) in three replications both under timely sown (TS) (14 November) and late sown (LS) (18 December) conditions. Each plot consisted of 3 rows of 2 meters in length and row to row distance was kept 20 cm in each replication. The observations were recorded on five randomly selected plants from each genotype in both conditions to assess genetic diversity for 25 traits i.e., days to 50 % heading, days to anthesis, days to maturity, plant height (cm), the number of effective tillers/meter, spike length (cm), the number of spikelets/spike, the number of grains/spike, biological yield/plant (g), harvest index (%), 1000-grain weight (g), grain yield/plant (g), grain appearance score, hectoliter weight (kg/hl) by using the hectoliter weight instrument (Test weight instrument developed at DWR, Karnal), sedimentation value (ml) by Axford *et al*. (1979) , crude protein (%) was recorded by estimating total nitrogen in the sample by conventional Microkjeldahl's method, the total gluten content (%) was calculated by adding wet gluten + dry gluten (%), wet gluten content (%) was estimated by dough method, the total soluble sugar (%) was estimated by the method described by Dubois *et al*. (1956), iron content (ppm) and zinc content (ppm) were calculated by AAS Spectrophotometer, NDVI 1: Normalized difference vegetation index at anthesis was measured by Green Seeker^R, NDVI 2: Normalized difference vegetation index at 21 days after anthesis was measured by Green Seeker^R, CTD 1: Canopy temperature depression at anthesis was measured by infrared thermometer, CTD 2 and Canopy temperature depression at 21 days after anthesis was measured by infrared thermometer. Genetic divergence was estimated by Mahalanobis (1936) and Ward method (1963). Percent contribution towards total divergence was calculated by Mahalanobis D^2 statistic (1936).

Table 1. List of 48 genotypes of wheat used in the study

S. No.	Genotypes	Pedigree
1	HPYT- 403	MAYIL
2	HPYT- 404	ZINCSHAKTHI
3	HPYT- 405	DANPHE #1*2/SOLALA//BORL14
4	HPYT- 406	DANPHE #1*2/SOLALA//BORL14
5	HPYT- 407	VALI//KACHU/KIRITATI
6	HPYT- 408	MANKU//MUTUS*2/TECUE #1
7	HPYT- 409	VILLAJUAREZF2009/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//3*PASTOR/4/WBLL1*2/BRAMBLING/5/WBLL1*2/BRAMBLING//QUAIU
8	HPYT- 410	FRANCOLIN#1/3/IWA8600211//2*PBW343*2/KUKUNA/7/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCONPI94624/AE.SQUARROSA(409)//BCN/4/BL 1496/MILAN/3/CROC_1/AE.SQUARROSA (205)//KAUZ
9	HPYT- 411	C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA8600211//2*PBW343*2/KUKUNA/7/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCONPI94624/AE.SQUARROSA(409)//BCN/4/BL 1496/MILAN/3/CROC_1/AE.SQUARRO
10	HPYT- 412	C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA8600211//2*PBW343*2/KUKUNA/6/MUCUY
11	HPYT- 413	C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA8600211//2*PBW343*2/KUKUNA/6/MUCUY
12	HPYT- 414	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCONPI94624/AE.SQUARROSA(409)//BCN/4/BL1496/MILAN/3/CROC_1/AE.SQUARROSA(205)//KAUZ/7/FRNCLN/3/ND643//2*PRL/2*PASTOR/4/FRANCOLIN #1
13	HPYT- 415	ROLF07*2/KIRITATI/3/IWA 8600211//2*PBW343*2/KUKUNA/4/MANKU
14	HPYT- 416	SHAKTI/2*BORL14
15	HPYT- 417	SHAKTI/2*BORL14

16	HPYT- 418	SHAKTI/2*BORL14
17	HPYT- 419	SHAKTI/2*MUCUY
18	HPYT- 420	SHAKTI/6/KAUZ//ALTAR84/AOS/3/PASTOR/4/873.97/5/MUNAL#1/7/FRET2*2/SHAMA//KIRITATI/2*TRCH/3/BAJ #1
19	HPYT- 421	SHAKTI/7/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/KRONSTADF2004/5/MUNAL/6/MUNAL #1/8/MP4010/MUNAL #1
20	HPYT- 422	SHAKTI/5/WHEAR/KIRITATI/3/C80.1/3*BATAVIA//2*WBLL1*2/4/KIRITATI/2*TRCH/6/BECARD//KIRITATI/2*TRCH/3/BECARD
21	HPYT- 423	KATERE/MUCUY/7/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCONPI94624/AE.SQUARROSA(409)//BCN/4/BL1496/MILAN/3/CROC_1/AE.SQUARROSA (205)//KAUZ
22	HPYT- 424	KATERE/MUCUY/7/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCONPI94624/AE.SQUARROSA(409)//BCN/4/BL1496/MILAN/3/CROC_1/AE.SQUARROSA (205)//KAUZ
23	HPYT- 425	KATERE//ONIX/KBIRD/6/C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA 8600211//2*PBW343*2/KUKUNA
24	HPYT- 426	ZINCOL//BECARD/QUAIU#1/7/INQALAB91*2/TUKURU//WHEAR/6/BAV92//IRENA/KAUZ/3/HUITES/4/T.SPELTA PI348764/5/BAV92//IRENA/KAUZ/3/HUITES
25	HPYT- 427	DANPHE#1*2/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//SHA4/CHIL/4/PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNA/5/MAYIL
26	HPYT- 428	HGO94.7.1.12//WBLL1*2/KUKUNA/3/WBLL1*2/KURUKU/4/PBW343*2/KUKUNA*2//FRTL/PIFED/6/C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA 8600211//2*PBW343*2/KUKUNA
27	HPYT- 429	VALI/3/MUTUS*2//ND643/2*WBLL1/6/C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA 8600211//2*PBW343*2/KUKUNA
28	HPYT- 430	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/T.DICOCCONPI94625/AE.SQUARROSA(372)//SHA4/CHIL/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/6/VILLAJUAREZF2009/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//3*PASTOR/4/WBLL1*2/BRAMBLING/7/TRAP#1/BOW/3/VEE/PJN//2*
29	HPYT- 431	QUAIU#1/SOLALA//QUAIU#2/3/MANKU/4/KACHU#1/KIRITATI//KACHU
30	HPYT- 432	KOKILA/3/MUTUS*2//ND643/2*WBLL1/8/PSN/BOW//SERI/3/MILAN/4/ATTILA/5/KAUZ*2/CHEN//BCN/3/MILAN/6/WBLL1*2/SHAMA/7/IWA 8600211//2*PBW343*2/KUKUNA
31	HPYT- 433	KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/CMH81.530/6/WHEAR/KIRITATI/3/C80.1/3*BATAVIA//2*WBLL1/4/CMH75A.66/SERI/7/VILLAJUAREZF2009/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//3*PASTOR/4/WBLL1*2/BRAMBLING
32	HPYT- 434	WHEAR/KIRITATI/3/C80.1/3*BATAVIA//2*WBLL1/4/CMH75A.66/SERI/5/HUW234+LR34/PRINIA//PFAU/WEAVER/3/CMH83.30/6/KACHU/DANPHE
33	HPYT- 435	DANPHE #1*2/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//SHA4/CHIL/4/MANKU
34	HPYT- 436	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/T.DICOCCONPI94625/AE.SQUARROSA(372)//SHA4/CHIL/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/6/MUU/FRNCLN//FRANCOLIN #1
35	HPYT- 437	MANKU/6/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI
36	3818 BLACK	TA3715/PBW550
37	3831BLACK	TA3972/ PBW621
38	3857 PURPLE	TA3851/ HD2967
39	HPBW 01	T.DICOCCON,CI9309/ AE.SQUARROSA H (409)//MUTUS/3/2*MUTUS
40	PMBB 1	WH711/LASSIK
41	WB 2	T.DICOCCON,CI9309/ AE.SQUARROSA(409)//MUTUS/3/2*MUTUS
42	DBW 187	NAC/TH/AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/..
43	WH 283	HD1981/RAJ821
44	WL 711	DEBARIA/WL-711
45	WH 1127	RL6043/4/NAC//PASTOR/3/BABAX
46	WH 1136	NI5663/RAJ3765
47	WH 1252	P13352/PBW343//WH711/3/PBW550
48	HD 3226	GRACKLE/HD2894

RESULTS AND DISCUSSION

There was a considerable amount of diversity for all the traits among the advance lines of bread wheat. Seven clusters were formed in both timely (**Table 2**) and late sown (**Table 3**) conditions, by grouping all the genotypes in such a way that genotypes within each cluster had smaller D^2 values than between clusters. Dendrogram showed that seven clusters were formed in Ward's minimum variance dendrogram as shown in **Fig. 1** (TS), **Fig. 2** (LS).

Under the timely sown condition, cluster II and cluster III had a maximum of 12 genotypes followed by cluster VI with 10 genotypes. Cluster V and cluster VII, each had five genotypes. Cluster I and cluster IV each had two genotypes. Under the late sown condition, cluster II had maximum of 18 genotypes followed by cluster VI with VII genotypes. Cluster V and cluster VII each had six genotypes. Cluster III had five genotypes. Cluster IV had four genotypes. Cluster I had two genotypes.

Intra and inter cluster distances are given in both timely (**Table 4**) and late sown (**Table 5**) wheat. The higher inter cluster distance indicated the presence of more diversity among the 48 genotypes included in clusters. With the help of D^2 values, a cluster diagram is drawn showing the relationship between different genotypes for TS (**Fig. 3**) and LS (**Fig. 4**).

For timely sown condition, the genotypes of clusters I and V exhibited maximum divergence (9.98) followed in descending order by the genotypes of I and VI (8.571), IV and V (8.453), VII and V (8.262), VI and IV (8.117), VII and I (8.066), V and II (7.981), V and III (7.981), I and III (7.947), IV and VII (7.867), I and IV (7.821), VI and III (7.373), I and II (7.339), II and IV (7.198), IV and III (7.124), VI and V (6.991), VI and II (6.939), VII and VI (6.700), II and III (6.674), VII and II (6.577), VII and III (6.555). The average intra cluster distance between the genotypes of cluster VI (6.275) was maximum followed by clusters III, II, I, IV, V and VII. For late sown wheat, the genotypes of clusters I and V exhibited maximum divergence (9.269) followed in descending order by the genotypes of I and VII (9.091), III and I (8.765), I and VI (8.597), I and II (8.501), I and IV (8.419), IV and V (7.888), V and VII (7.693), III and IV (7.581), II and V (7.458), II and VI (7.329), III and V (7.307), IV and VI (7.159), III and VII (7.17), II and VII (7.041), IV and VII (6.963), III and VI (6.948), V and VI (6.927), VI and VII (6.837), II and III (6.774), II and IV (6.537). The average intra cluster distance between the genotypes of cluster I (6.476) was maximum followed by clusters VII, V, III , II , VI and IV.

Table 2. Clustering of 48 genotypes of wheat under timely sown condition

Cluster	Number of genotypes	Genotypes
I	2	HPYT - 404, HPYT – 405
II	12	HPYT – 419,HPYT – 424, HPYT – 425, HPYT – 428, HPYT-421, HPYT – 427, HPYT -422, HPYT – 426, HPYT – 430, HPYT – 433, HPYT – 431, HPYT – 434
III	12	HPYT – 409, 3857 PURPLE, HPYT – 436, HPYT – 429, HPBW 01, 3831 BLACK, WL 711, 3818 BLACK, DBW 187, WH 1252, HPYT – 437, WH 1127
IV	2	WH 283, WH 1136
V	5	HPYT – 406, HPYT – 407, HPYT – 408, HPYT - 403, HPYT - 410
VI	10	HPYT - 411, HPYT – 420, HPYT – 416, HPYT – 417, HPYT - 414, HPYT – 415, HPYT – 412, HPYT – 413,HPYT – 418, HPYT – 432
VII	5	HPYT – 423, WB 2, HPYT – 436, PMBB 1, HD 3226

Table 3. Clustering of 48 genotypes of wheat under late sown condition

Cluster	Number of genotypes	Genotypes
I	2	HPYT - 404, HPYT – 409
II	18	HPYT – 405, 3857 PURPLE, HPYT – 431, HPYT – 437, HPYT – 419, HPYT-424, HPYT – 428, HPYT -435, HD 3226, HPYT – 426, HPYT – 422, WH 1252, 3818 BLACK, 3831 BLACK, DBW 187, PMBB 1, WL 711, WH 1127
III	5	HPYT – 412, HPYT - 436, WH 283, HPYT – 415, HPYT - 417
IV	4	HPYT – 429, HPYT – 30, HPYT – 433, HPBW 01
V	6	HPYT – 406, HPYT – 410, HPYT – 407, HPYT - 408, HPYT – 403, HPYT – 414
VI	7	HPYT - 411, HPYT – 423, HPYT – 416, HPYT – 434, HPYT - 418, HPYT – 432, HPYT – 413
VII	6	HPYT – 420, HPYT – 425, HPYT – 421, HPYT – 427, WB 2, WH 1136

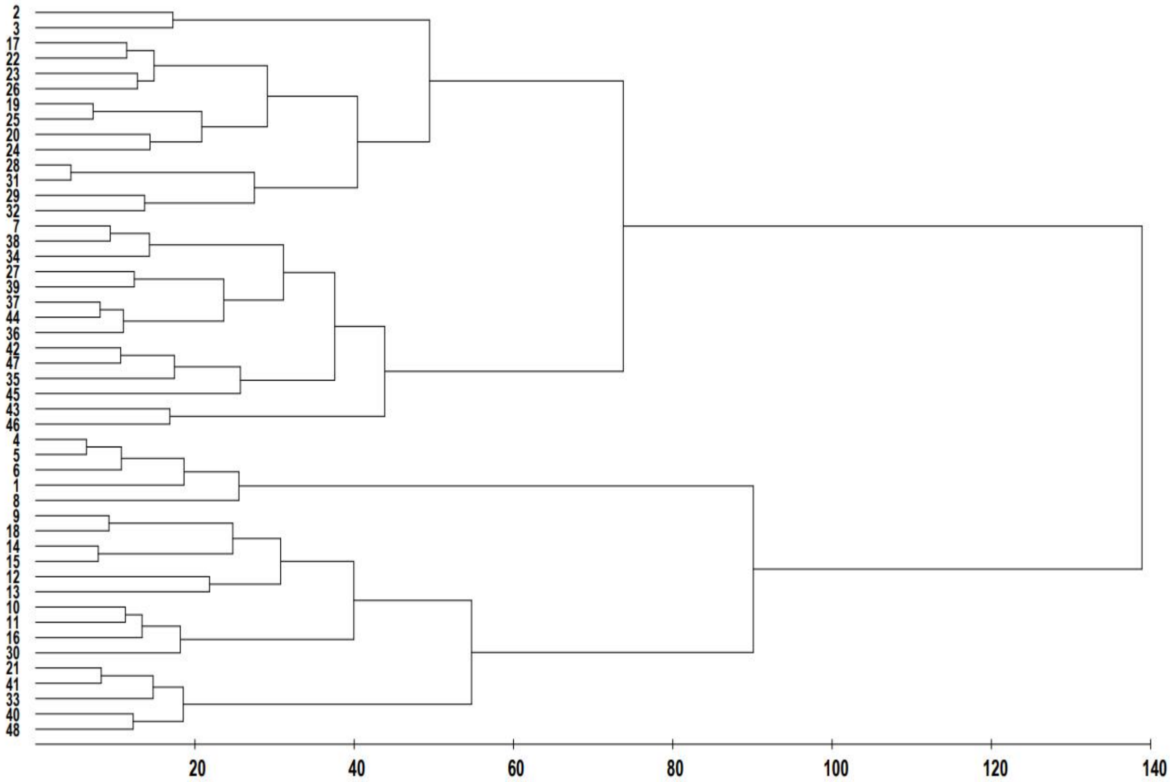

Fig.1. WARD'S Minimum variance dendrogram showing genetic relationship among 48 genotypes of wheat under timely sown condition based on D^2 distance

Y axis: Genotypes (1 - 48) as indicated in Table 1; X axis: Standardized Euclidean^2 distance

Table 4. Average intra (diagonal) and inter (above diagonal) cluster distance values among grouped 48 genotypes of wheat under timely sown condition

Cluster	I	II	III	IV	V	VI	VII
I	**5.873**	7.339	7.947	7.821	9.98	8.571	8.066
II		**5.978**	6.674	7.198	7.981	6.939	6.577
III			**6.049**	7.124	7.981	7.373	6.555
IV				**5.802**	8.453	8.117	7.867
V					**5.537**	6.991	8.262
VI						**6.275**	6.700
VII							**5.185**

Table 5. Average intra (diagonal) and inter (above diagonal) cluster distance values among grouped 48 genotypes of wheat under late sown condition

	I	II	III	IV	V	VI	VII
I	**6.47**	8.501	8.765	8.419	9.269	8.597	9.091
II		**6.025**	6.774	6.537	7.458	7.329	7.041
III			**6.083**	7.581	7.307	6.948	7.17
IV				**4.757**	7.888	7.159	6.963
V					**6.092**	6.927	7.693
VI						**5.6**	6.837
VII							**6.174**

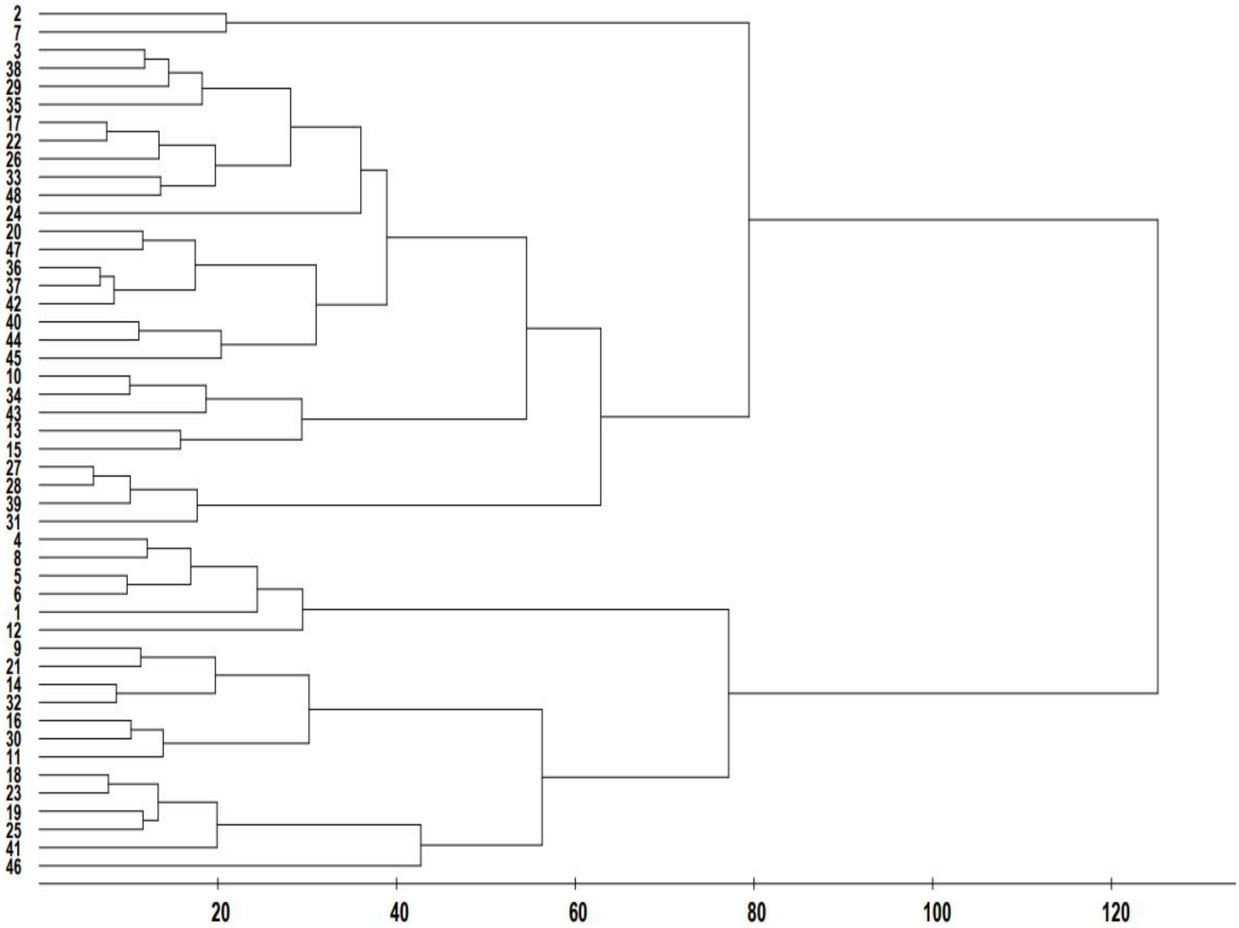

Fig.2. WARD'S Minimum variance dendrogram showing genetic relationship among 48 genotypes of wheat under late sown condition based on D^2 distance.

Y axis: Genotypes (1 - 48) as indicated in Table 1; X axis: Standardized Euclidean^2 distance

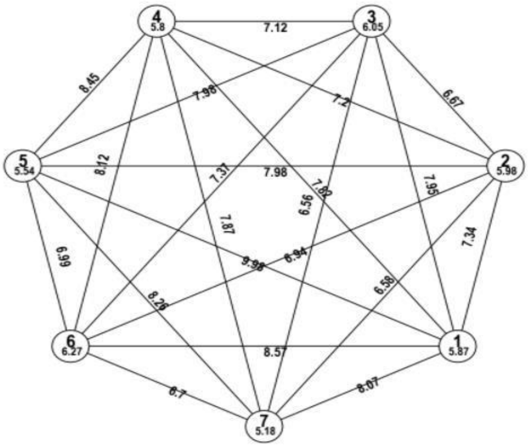

Fig. 3. Intra and inter Euclidean distance between 7 clusters of wheat under timely sown condition

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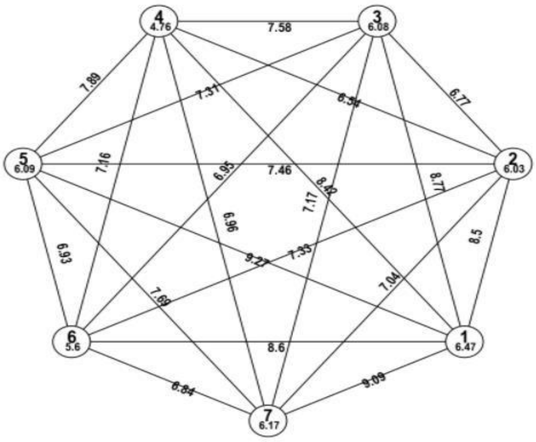

Fig. 4. Intra and inter Euclidean distance between 7 clusters of wheat under late sown condition

By crossing genotypes belonging to different clusters separated by a wide statistical distance in a hybridization program, it would be possible to obtain a wide range of variation in the segregants such as genotypes from cluster V with those from clusters I and IV for both the environments. There was a wide range of variation for several characteristics among single and multi-genotype clusters.

Singh and Pathania (2014) grouped 50 genotypes into six and seven clusters during the first and second years, respectively. The highest inter-cluster distance was observed between cluster III and cluster II (I year) and between cluster V and cluster IV (II year). The genetic diversity analysis revealed the formation of five clusters suggested the presence of wide genetic diversity among the 27 genotypes studied (Gurjar and Marker, 2018). Najaphy *et al*. (2012) assigned the genotypes into four groups, group I included maximum accessions. Naheed *et al*. (2016) evaluated genetic diversity among genotypes with a mean Euclidean distance of 0.522. Cluster analysis based on squared Euclidean distance and ward's method, categorized the cultivars into seven groups (Khodadadi *et al*., 2011). A study by Rahim *et al*. (2010) showed that crosses between genotypes with the greatest genetic distance result in high yields, thus, these crosses can be used in breeding programs to achieve maximum heterosis. The results of this study showed a high degree of genetic divergence between the genotypes of wheat and are consistent with reports by Ali *et al*. (2008) and Singh and Dwivedi (2002) reported the use of cluster analyses in finding high yielding wheat genotypes. D^2 analysis showed the 26 bread wheat genotypes grouped into six clusters (Degewione and Alamerew, 2013). Noorka and Khaliq (2007) did a similar study for the grouping of 100 wheat genotypes. In every cluster, the number of genotypes varies with the environment, according to Naidu and Satyanarana (1991). Chaturvedi and Gupta (1995) examined 44 genotypes of wheat and categorized them into 13 clusters. Intra cluster distances were estimated using the inter genotypic distance by Singh and Chaudhary (1985). The maximum intra cluster distance was reported 26.40 by Vora *et al*. (2017) in wheat.

The difference in cluster means existed for all the studied traits. Cluster means for all the characters studied are presented in **Table 6** TS and **Table 7** LS. Under the timely sown conditions, cluster I showed the highest mean value for plant height, whereas the lowest value for large number of traits i.e. days to 50% heading, days to anthesis, the number of effective tillers/meter, the number of spikelets/spike, harvest index, grain yield, hectoliter weight, iron content, CTD 1 and CTD 2, indicating negative impact towards divergence. Cluster II showed the highest mean value for days to 50% heading and zinc content. Cluster III showed the highest value for the number of spikelets/spike, the number of grains/spike, sedimentation value and total soluble sugar. Days to maturity, the number of effective tillers/meter, spike length, biological yield had the highest mean value for clusters IV, V, VI, VII. Cluster VII showed the highest mean value for most of the traits including grain yield indicating that the genotypes falling in this cluster have the genetic potential to contribute better for yield maximization in breeding programme. Under late sown condition also cluster I showed the lowest mean value for large number of traits, whereas the highest value recorded for plant height alone. However, in heat stress condition cluster V showed the highest mean value for large number of traits i.e. the number of effective tillers/meter, spike length, the number of spikelets/spike, the number of grains/spike, biological yield/plant, grain yield /plant, grain appearance score, hectoliter weight and the total soluble sugar. Similar findings were observed by Deshmukh *et al*. (1999), Dobariya *et al*. (2006), Jaiswal *et al*. (2010), Kumar *et al*. (2013), Kandel *et al*. (2018) and Singh *et al*. (2018) in wheat.

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Table 6. Mean values of 7 clusters for different traits of wheat under timely sown condition

Cluster	DH	DTA	DTM	PH	NET	SL	NSS	G/S	BY	HI	TGW	GY
I	100.167	104.5	145.333	121.567	92.5	9.767	17.167	40.667	35.5	33.772	40.533	12.017
II	101.889	107.361	145.694	107.764	97.472	9.689	18.056	44.361	34.465	41.389	41.764	14.269
III	105.083	109.833	145.278	109.508	104.028	10.35	18.083	46.111	34.607	39.673	39.614	13.736
IV	101.333	107.167	146.833	111.2	108.833	10.567	17.333	39.333	36.478	34.617	43.467	12.617
V	101.333	107.167	146.833	111.2	108.833	10.567	17.333	39.333	36.478	41.334	45.293	16.9
VI	101.333	107.167	146.833	111.2	108.833	10.567	17.333	39.333	36.478	40.923	43.963	16.62
VII	101.333	167.167	146.833	111.2	108.833	10.567	17.333	39.333	36.478	41.602	38.86	16.927
Mean	103.056	108.319	145.562	110.09	102.278	10.26	18.389	47.486	37.234	40.28	41.769	15.014

Cluster	GA	HW	SV	CP	TG	WG	TSS	Fe	Zn	NDVI 1	NDVI 2	CTD 1	CTD 2
I	5.283	74.455	42.333	15.337	35.015	27.665	1.42	31.683	37.6	0.757	0.615	1.65	1.517
II	5.331	77.43	42.25	15.398	35.288	28.347	1.293	33.572	40.442	0.761	0.581	3.403	2.569
III	5.55	77.724	44.083	14.635	38.058	29.579	1.474	31.814	35.603	0.797	0.566	3.106	2.383
IV	5.7	80.392	34.833	14.91	40.94	32.708	1.208	35.733	40.3	0.815	0.522	3.7	2.417
V	5.92	79.789	38.867	11.677	33.835	24.146	1.164	31.973	35.847	0.717	0.534	4.393	3.427
VI	5.337	77.399	40.733	14.335	33.29	26.808	1.357	32.823	37.947	0.769	0.642	4.32	2.943
VII	5.26	77.921	41.667	15.767	34.829	28.049	1.279	32.287	39.013	0.785	0.655	2.613	1.633
Mean	5.454	77.793	41.674	14.614	35.589	28.019	1.338	32.688	37.96	0.722	0.592	3.48	2.542

Table 7. Mean values of 7 clusters for different traits of wheat under late sown condition

Cluster	DH	DTA	DTM	PH	NET	SL	NSS	G/S	BY	HI	TGW	GY
I	83.5	88.5	123.5	106.45	82.667	8.967	16.167	30.883	39.477	27.19	35.867	10.767
II	88	92.556	127.889	92.7	85.333	9.902	17.463	38.056	33.263	38.455	36.107	12.743
III	88.867	93.667	127.667	98.9	86.8	10.48	17.533	41.267	40.708	32.661	34.8	13.28
IV	84.167	88.917	126.25	95.992	85.833	10.025	18.25	46.25	30.004	41.673	34.567	12.525
V	88.111	92.056	125.944	99.289	89.667	10.794	19.111	48.556	43.954	35.47	36.7	15.583
VI	87	91.81	126.048	95.943	89.571	10.205	18.238	44	41.492	36.401	37.157	15.01
VII	86.111	90.833	127.556	92.672	89.333	9.572	18.222	41.889	35.102	39.956	36.506	14.078
Mean	87.215	91.812	126.993	95.486	87.076	10.048	17.896	41.431	36.792	37.165	36.11	13.551

Cluster	GA	HW	SV	CP	TG	WG	TSS	Fe	Zn	NDVI 1	NDVI 2	CTD 1	CTD 2
I	5.317	73.822	41.333	14.562	36.32	29.402	1.665	28.467	30.85	0.657	0.515	5.6	3.65
II	5.35	76.31	40.333	16.833	45.232	34.281	1.677	29.187	33.322	0.658	0.499	3.976	2.528
III	5.153	74.984	37.733	17.359	51.731	40.368	1.585	30.407	33.787	0.695	0.516	4.84	2.647
IV	5.158	76.939	43.25	17.129	45.959	31.562	1.343	33.55	36.233	0.654	0.491	3.867	2.083
V	5.583	78.625	36.944	15.732	40.759	30.517	1.973	28.706	31.844	0.692	0.496	4.633	2.817
VI	5.176	76.05	39	18.886	37.861	27.901	1.522	32.329	36.124	0.7	0.536	5.971	3.148
VII	5.411	78.531	38.444	17.887	51.781	38.981	1.513	31.117	34.578	0.674	0.537	5.861	3.817
Mean	5.324	76.65	39.493	17.111	44.783	33.672	1.633	30.287	33.891	0.674	0.51	4.733	2.838

DH : Days to 50 % heading, DTA : Days to anthesis, DTM : Days to maturity, PH : Plant height (cm), NET : Number of effective tillers/ meter, SL : Spike length (cm), NSS : Number of spikelets / spike, G/S : Number of grains/spike, BY : Biological yield/plant (g), HI : Harvest index (%), TGW : 1000-grain weight (g), GY : Grain yield /plant (g), GA :Grain appearance score, HW : Hectoliter weight (kg/ hl), SV : Sedimentation value (ml), CP: Crude protein (%), TG : Total Gluten Content (%), WG : Wet Gluten Content (%), TSS : Total soluble sugar (%), Fe : Iron content (ppm), Zn : Zinc content (ppm), NDVI 1: Normalized difference vegetation index at anthesis, NDVI 2: Normalized difference vegetation index at 21 days after anthesis, CTD 1: Canopy temperature depression at anthesis, CTD 2: Canopy temperature depression at 21 days after anthesis.

Results from the present study indicate that crossing genotypes from different groups with high mean yield may help to achieve higher yield. A broader range of genetic variability is provided in segregating generations by incorporating more divergent parents in hybridization. The results of the divergence and cluster mean suggest that crosses between genotypes in clusters V and VII for timely sown and clusters V, VI and IV on late sown may produce maximum heterosis and good recombination.

Under the timely sown conditions (**Table 8**), the maximum contribution was exhibited by CTD 1 followed by the total gluten content, the total soluble sugar, CTD 2, sedimentation value, the number of effective tillers/meter, the number of grains/spike, 1000-grain weight, NDVI 2, zinc content and wet gluten content. Under late sown condition (**Table 9**), the maximum contribution was exhibited by zinc content, CTD 2, the total soluble sugar, the total gluten content, sedimentation value, grain yield/plant, CTD 1, spike length, NDVI 2, NDVI 1 and crude protein.

These characters should be given importance during hybridization and selection for the improvement of yield and its component traits. Singh *et al.* (2018) evaluated genetic diversity for various morphological and quality traits in bread wheat, among different traits, productive tillers (28.74%), grain yield (19.23%) had a maximum contribution to total genetic divergence. Grain yield per plant followed by the length of the main spike, the number of grains per main spike contributed maximum towards total genetic divergence (Vora and Yusufzai, 2017). In addition, Lal *et al*. (2009) reported that grain yield, plant height and spike length accounted for the greatest amount of genetic diversity. Nagaraju *et al*. (2015) reported that yield, plant height and the number of grains per spike contributed most towards genetic divergence and these traits are major determinants of genetic variability in wheat.

In conclusion, a clustering pattern can be used to select parents and decide cross combinations that produce the highest possible variation for individual traits for both

Table 8. Per cent contribution of different traits towards total divergence of wheat under timely sown condition

S. No.	Characters	Contribution (%)
1	Number of effective tillers/meter	3.1
2	Number of grains/spike	1.86
3	1000-grain weight	1.86
4	Sedimentation value	11.7
5	Total Gluten Content	16.4
6	Wet Gluten Content	1.06
7	Total soluble sugar	15.07
8	Zinc content	1.24
9	Normalized difference vegetation index at 21 days after anthesis	1.6
10	Canopy temperature depression at anthesis	30.14
11	Canopy temperature depression at 21 days after anthesis	12.15

Table 9. Per cent contribution of different traits towards total divergence of wheat under late sown condition

S. No.	Characters	Contribution (%)
1	Spike length	0.89
2	Grain yield /plant	1.33
3	Sedimentation value	2.04
4	Crude protein	0.71
5	Total Gluten Content	24.2
6	Total soluble sugar	29.52
7	Zinc content	44
8	Normalized difference vegetation index at anthesis	0.79
9	Normalized difference vegetation index at 21 days after anthesis	0.8
10	Canopy temperature depression at anthesis	0.98
11	Canopy temperature depression at 21 days after anthesis	35.99

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environments. Seven clusters were formed in both timely sown and late sown environments. For future breeding programs, combining genotypes from cluster V with those from clusters I and IV will result in a very broad range of variation for both environments. Any genotype with a high mean value in a cluster can be used in hybridization programmes for further selection and improvement. Thus, intercrossing of genotypes involved in these clusters might be useful to induce variability in respective traits, and improve them rationally for increased grvain yield. Cluster VII for timely sown and cluster V for late sown had the highest mean values for most of the traits, so genotypes falling into these clusters will contribute more in the breeding program. It is extremely important to give great weight to the traits contributing maximum to the D^2 value when selecting the clusters and parents for hybridization. Under timely sown conditions CTD 1, the total gluten content and the total soluble sugar and for late sown conditions zinc content, CTD 2 and the total soluble sugar should be given importance in breeding programmes.

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