Genetic diversity analysis among genotypes of bread wheat (*Triticum aestivum* L.) for yield and its component traits under timely sown condition

ABSTRACT

Genetic diversity analysis for yield and its component traits among 60 genotypes of bread wheat (*Triticum aestivum* L.) under timely sown condition distributed into seven clusters via D^2 statistics using Euclidean distance method which revealed that the cluster IV had maximum number of genotypes followed by cluster II, Cluster VI, cluster I, cluster V and, cluster III and VII. The highest inter-cluster genetic distance existed between cluster IV and VII and the average intra cluster distance between the genotypes of cluster V was maximum. Therefore, genotypes in these clusters may be used to produce the superior hybrids and transgressive segregants. For grain yield and effective tillers had highest mean value in cluster V and cluster VI. Cluster V and VII had highest mean value for 1000-grain weight and plant height respectively. Traits such as by plant height followed by canopy temperature, days to maturity, days to anthesis and grain filling duration contributing total of 50 per cent to the total divergence.

Keywords: Wheat, Genetic diversity, Cluster analysis and morphological traits

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is an annual *Kharif* season cereal crop belongs to the family Poaeceae (grasses). It is a self-pollinating, hexaploid (AABBDD) plant with chromosome number of 42 (2n = 6x = 42) and estimated genome size of 16 GB (Wicker *et al.*, 2018). The global production of wheat during 2020-2021 has been recorded 765 million metric tonne (Shahbandeh, 2022). As per 4th Advance estimates production for major crops during 2020-2021, wheat cultivation acreage were 34.6 million hectares and giving total production of 109.52 million tonne (Anonymous, 2020). During the course of evolution, wheat gained sufficient genetic diversity along the road from einkorn to bread wheat. Today, however, its diversity is weakening due to repeated cultivation of landraces for specific characters, narrow adaptation, farmers' varietal selection and the requirement of uniform varieties in industrial seed grain processing (Bellon 1996; Smale 1997). This depletion has now encouraged the use of genetic resources in wheat breeding programmes. At the same time, high temperature is one of the major abiotic stresses in tropical countries like India that has adverse impact on development, growth and overall yield of wheat. At some particular stage of life cycle of wheat, even a little increase or rise in temperature can lead to a complete loss of crop yield. Genetic diversity is crucial for adaptability and survival of wheat species against the threat of disease attack (Fu and Somers 2009). Hence, it is beneficial to assess the genetic diversity at a particular level that may facilitate the efficient exploitation of the germplasm. Such assessment programmes are imperative for man advanced breeding lines by identifying genotypes for hybridization programme. Thus, the present investigation focuses on the analysis of genetic diversity using cluster distance method.

MATERIALS AND METHODS

The experimental material for the present investigation comprised 60 accessions drawn from wheat gene pool maintained at National Bureau of Plant Genetic Resources (NBPGR), New Delhi and procured by the Indian Institute of Wheat and Barley Research (IIWBR) Karnal. The accessions were raised and followed recommended packages and practices at IIWBR research farm Karnal during *Rabi* season. The sixty accessions/ genotypes were raised under timely sown conditions in Randomized Block Design (RBD) with three replications. Each plot comprises two rows of 3 mts length spaced at 0.20 mts.

Observations were recorded for traits namely days to heading, days to anthesis, days to physiological maturity, grain filling duration, plant height, number of effective tillers, thousand grain weight, grain yield, chlorophyll fluorescence and canopy temperature. Genetic divergence was computed through multivariate analysis using D^2 Statistic as described by Singh & Pawar (2005).

RESULTS AND DISCUSSION

The cluster IV in Table 1 had maximum 19 (HD2967, DBW88, IBWSN1109 WH1124, IBWSN1156, WH711, IBWSN1155, P13648, KRL210, IBWSN1182, IBWSN1138, WH542, IBWSN1205, WH1202, P13644, IBWSN1151, PBW723, WH1227, WH1226) genotypes followed by cluster II with 17 genotypes (KRL19, WH1123, WH283, WH157, WH1228, WH147, WH1232, WH416, HD3086, WH1164, P13643, P13647, WL711, P13649, IBWSN1118, DPW621-50, IBWSN1142), Cluster VI with 14 genotypes (PBW343, IBWSN1145, IBWSN1162, IBWSN1155, IBWSN1152, WH1179, IBWSN1170, IBWSN1213, WH1184, WH1025, IBWSN1207, PBW725, IBWSN1159, IBWSN1171), cluster I with 5 genotypes (WH1021, HD3059, DBW90, Raj3765, WH730), cluster V with 3 genotypes (WH1080, WH1142, WH1105), and cluster III (ATLAS 66) and VII (C306) each having one genotype. The D^2 values amongst various genotypes within a cluster ranged from 0.000 to 3.228. Under both divergence analysis, genotypes related by their place of origin have shown tendency to group in the same cluster to some extent which may be due to dependence upon the directional selection pressure. Similar results were obtained by Dutamo *et al.* (2015) (clustered 60 genotypes of bread wheat into six clusters), Kumar *et al.* (2015) (grouped the 50 genotypes into 10 diverse clusters under both normal and heat stress environment), Kumar *et al.* (2013) distributed the 30 genotypes into 8 clusters and observed that the distribution pattern of genotype in different clusters was random and Jaiswal *et al.* (2010) (grouped the genotypes into twenty three different clusters, each cluster bearing different number of genotypes). To get more heterotic and large number of desirable transgressive segregates, selection of parents for hybridization should be properly based on genetic diversity rather than geographic diversity.

a) Intra and inter cluster distances

`The intra and inter cluster distance values between seven clusters under timely sown condition are presented in Table 2.The genotypes of cluster IV and VII exhibited maximum divergence (8.905) followed in descending order by the genotypes of II and VII (8.845), V and VII (8.581), III and VII (8.381), I and VII (8.344), III and V (7.653), III and VI (7.255), VI and VII (7.094), I and III (7.077), III and IV (6.706), II and III (6.384), V and VI (6.303), I and V (6.215), II and V (5.834), I and VI (5.752), IV and V (5.591), I and IV (4.891), II and VI (4.623), I and II (4. 270), IV and VI (3.915), II and IV (3.466). The higher inter cluster distance indicated the presence of more diversity among the genotypes included among these clusters. The average intra cluster distance between the genotypes of cluster V was maximum followed in descending order by clusters VI (3.228), II (3.119), I (3.066), IV (2.570), III (0.000) and VII (0.000). With the help of D2 values a cluster diagram between and within clusters is drawn showing the relationship between different genotypes (Figure 1). Therefore, the genotypes of cluster IV and VII exhibited maximum cluster divergence indicated that these genotypes may be used to produce a greater number of the superior heterotic F_1's and large number of desirable transgressive segregants. The genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selection in addition to geographical diversity. Similar finding was also reported by Sharma and Panwar (2007), Mohanty *et al.* (2017), Arya *et al.* (2017), Naik *et al.* (2016), Gupta *et al.* (2002), Singh *et al.* (2005), Yashpal *et al.* (2005), Verma *et al.* (2006), Ribadia *et al.* (2007) and Marker and Tripathi (2008). Dutamo *et al.* (2015) recorded the lowest intra cluster distance in cluster V (0.00), which shows the absence of genetic variability within this cluster. The inter cluster distance was range from 44.83 to 179.72 and cluster IV and VI showed maximum inter cluster distance of 179.72. This indicates that the crossing between superior germplasm of above diverse cluster pair's might provide desirable recombinants for developing high yielding bread wheat varieties.

b) Cluster means of different clusters for various characters

Mean values of seven clusters of 60 genotypes under timely sown condition are presented in Table 3. Difference in cluster means existed for all characters. Cluster III had lowest mean values for days to heading and days to anthesis indicating earliness whereas, late genotypes were observed in cluster VII. For days to maturity, lowest mean value was observed in cluster I whereas, cluster VII had higher values. For plant height lowest values were in cluster V indicating these genotypes were shortest while cluster VII had the tallest genotypes. Cluster VI had highest mean values for effective tillers per meter while cluster VII had lowest mean. For chlorophyll fluorescence cluster III, VI and VII had highest mean value while cluster II had lowest mean values. Cluster III had highest mean values for canopy temperature and cluster I had lowest mean values. For grain yield per meter cluster V had highest whereas cluster VII had lowest mean values. Cluster V had highest and cluster VI had lowest mean values for 1000-grain weight. Similar findings were also observed by Gartan *et al.* (2003), Dwivedi *et al.* (2005), Dobariya *et al.* (2006), Jaiswal *et al.* (2010), Kumar *et al.* (2013), Arya *et al.* (2017), Verma *et al*. (2013), Ahmad *et al.* (2014) and Naik *et al.* (2016).

Table 1: Distribution pattern of 60 bread wheat genotypes under timely sown condition

Clusters	Number of genotypes	Bread wheat genotypes
I.	**5**	WH1021, HD3059, DBW90, Raj3765, WH730
II.	**17**	KRL19, WH1123, WH283, WH157, WH1228, WH147, WH1232, WH416, HD3086, WH1164, P13643, P13647, WL711, P13649, IBWSN1118, DPW621-50, IBWSN1142
III.	**1**	ATLAS 66
IV.	**19**	HD2967, DBW88, IBWSN1109 WH1124, IBWSN1156, WH711, IBWSN1155, P13648, KRL210, IBWSN1182, IBWSN1138, WH542, IBWSN1205, WH1202, P13644, IBWSN1151, PBW723, WH1227, WH1226
V.	**3**	WH1080, WH1142, WH1105
VI.	**14**	PBW343, IBWSN1145, IBWSN1162, IBWSN1155, IBWSN1152, WH1179, IBWSN1170, IBWSN1213, WH1184, WH1025, IBWSN1207, PBW725, IBWSN1159, IBWSN1171
VII.	**1**	C306

Table 2: Average inter- and intra- (diagonal) cluster D^2 Euclidean distance among different clusters of bread wheat under timely sown condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**3.066**	4.270	7.077	4.891	6.215	5.752	8.344
Cluster II		**3.119**	6.384	3.466	5.834	4.623	8.845
Cluster III			**0.000**	6.706	7.653	7.255	8.381
Cluster IV				**2.570**	5.591	3.915	8.905
Cluster V					**4.726**	6.303	8.581
Cluster VI						**3.228**	7.094
Cluster VII							**0.000**

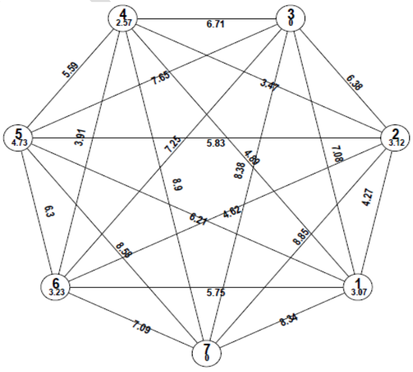

Fig. 1: D^2 Euclidean distance among different clusters of bread wheat under timely sown condition

Table 3: Cluster mean values of different clusters for yield and its component traits under timely sown condition

Yield and its component traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to heading	86.80	87.49	85.66	90.36	88.00	95.19	97.33
Days to anthesis	91.73	92.22	90.00	95.19	93.00	100.07	102.00
Days to maturity	137.27	139.41	150.00	138.97	144.11	141.83	150.33

Plant height (cm)	106.03	105.98	110.11	106.71	105.37	110.32	121.44
Effective tillers per meter	96.53	111.49	94.66	128.98	133.44	115.07	72.66
Chlorophyll fluorescence	0.70	0.69	0.72	0.72	0.70	0.72	0.72
Canopy temperature	21.06	27.11	27.70	26.75	22.67	27.25	21.72
Grain yield per meter (g)	95.51	116.15	100.44	134.35	138.89	119.85	74.25
1000-Grain weight (g)	43.64	43.26	41.76	44.24	44.37	40.98	43.20
Grain filling duration	32.00	31.49	32.33	30.93	51.11	33.59	48.33

c) *Per cent* contribution towards total divergence

Per cent contribution towards total divergence was calculated as per Mahalanobis D^2 statistic (Mahalanobis, 1936). The maximum contribution towards the total divergence under timely sown condition (Table 4) was exhibited by plant height (15.25%) followed by canopy temperature (13.19%), days to maturity (11.48%), days to anthesis (11.28%), grain filling duration (10.30%), 1000-grain weight (8.74%), days to heading (8.14%), chlorophyll fluorescence (8.07%), effective tillers per meter (7.89%) and grain yield per meter (5.68%). The traits viz., plant height followed by canopy temperature, days to maturity, days to anthesis, grain filling duration, contributed more than 60% per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population for improvement of yield and its component traits. Similar results for traits contributing maximum to the total divergence obtained by Singh *et al.* (2002) for days to 50 per cent, flowering, plant height, spikelet's per ear, biological yield per plant, Dobariya *et al.* (2006) for days to flowering, number of tillers per meter, days to maturity and 1000 grain weight, Peshattiwar *et al.* (2009) for days to maturity, days to 50 per cent flowering, plant height and number of spikelet's per ear and Naik *et al.* (2016) for plant height, grain yield and sedimentation value and Singh *et al.* (2005) for days to 50 per cent flowering, plant height, spikelet's per ear, biological yield per plant and 1000 grain weight.

Table 4: *Per cent* contribution of yield & its component traits towards total divergence under timely sown condition

Sr. No.	Yield and its component traits	Contribution (%)
1	Days to heading	8.14
2	Days to anthesis	11.27
3	Days to maturity	11.48
4	Plant height (cm)	15.25
5	Effective tillers per meter	7.89
6	Chlorophyll fluorescence	8.07
7	Canopy temperature	13.19
8	Grain yield per meter (g)	5.68
9	1000-Grain weight (g)	8.74
10	Grain filling duration	10.30

CONCLUSION

The sufficient genetic diversity found in present study, showed considerable scope for genetic improvement through hybridization between the genotypes from divergent clusters. The genotypes of cluster IV and VII followed by cluster II and VII condition exhibited maximum cluster divergence indicated that these genotypes may be used to produce the superior hybrids and transgressive segregants. The traits viz., plant height followed by canopy temperature, days to maturity, days to anthesis, grain filling duration, under timely sown condition contributed maximum to the total variability, thus, these characters should be given importance during hybridization and selection in the segregating population for improvement of yield and its component traits.

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