Analysis of genetic diversity by D^2 -statistics using morpho-physiological traits of late sown wheat (*Triticum aestivum* L.)

ABSTRACT

The sixty-bread wheat (*Triticum aestivum* L.) genotypes were distributed among the seven clusters obtained using D^2 statistics Euclidean distance method on the basis of observation taken on various morphological and physiological 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. Results obtained revealed that the cluster IV had maximum number of genotypes *i.e.,*17 genotypes followed by cluster I (13 genotypes), Cluster IV (10 genotypes), cluster VII, II, III and VI (9, 5, 3 and 3 respectively). The highest inter cluster genetic distance existed between cluster I and VI (6.559) and the average intra cluster distance between the genotypes of cluster VII (3.817) 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 VI. Cluster III had highest mean value for 1000-grain weight and lowest values for plant height indicating genotypes were short. Traits such as days to anthesis followed by canopy temperature, days to maturity, grain filling duration, chlorophyll fluorescence and grain yield per meter contributing a total of 68.1per cent to the total divergence.

Keywords: Wheat, Genetic diversity, cluster analysis, D^2 statistics

INTRODUCTION

Wheat is an important staple crop of tropical countries, and its productivity largely regulates the economy of the country. It is the most widely grown cereal crop in the world. In the period leading up to 2020, demand for wheat for human consumption in developing countries is expected to grow at 1.6% per annum, and for feed at 2.6% per annum. Wheat yield needs to be increased from 2.6 to 3.5 t ha^{-1} within the next 25 year (Ortiz *et al.* 2008) to meet the projected increase in demand. In 2020-21, 765 million metric tonne of global wheat production was reported (Shahbandeh, 2022). In India, wheat production during the period 2020-21 was 109.52 million tonnes recovered from an acreage of 34.6 million hectare (Anonymous, 2020). However, importance of wheat as staple food is even more under changing climate scenario, which at least partially is due to rising temperature. Stress due to high-temperature has emerged as a major constraint for the successful wheat production worldwide (Hays *et al.* 2007; Kumar *et al*. 2012a, b). Nearly 40 % of total irrigated area, where wheat is grown, is severely affected by heat stress (Reynolds *et al.*2001). Yield loss of 29 % is expected by 2080 due to global warming, in wheat. The 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. Especially, under the late sown conditions, wheat crop faces the forced maturity leading to the yield reduction due to heat stress conditions. Days to anthesis and booting decreased due to late sown heat stress condition regardless of the cultivars (Nahar et al., 2010). Thus, to adapt to the changing climatic conditions and to withstand the abiotic stress new varieties need to be developed to fulfil the demand of the ever-increasing population. The present investigation mainly focusses on the diversity analysis present in the experimental material of bread wheat genotypes under late sown conditions.

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, as mentioned below;

No of accessions/ genotypes = 60
Design of experiment = Randomized Block Design
Replications = 3
Plot size = (3m x 0.2m x 2 row) paired row of 3 m length spaced at 0.20 m

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 17 (HD2967, IBWSN1142, IBWSN1162, KRL210, WL711, PBW343, WH1123, WH1105, ATLAS66, WH416, IBWSN1213, PBW725, IBWSN1138, WH1232, WH1179, IBWSN1152, WH542) number of genotypes followed by cluster I with 13 genotypes (WH1184, WH1202, PBW723, IBWSN1205, KRL19, IBWS1170, IBWSN1118, IBWSN1155, WH283, IBWSN1109I, HD3086, WH157, IBWSN1207),cluster V with 10 genotypes (P13647, IBWSN1171, IBWSN1155, P13644, WH1164, P13643, P13649, WH1227, IBWSN1159, WH147), cluster VII with 9 genotypes (DPW621-50, DBW88, IBWSN1145, IBWSN1150, P13648, WH1228, IBWSN1182, C306, IBWSN1151), cluster II with 5 genotypes (WH1021, WH730, HD3059, WH1142, DBW90), cluster III with 3 genotypes (WH1080, Raj 3765, WH1025)and cluster VI with 3 genotypes (WH1124, WH711, WH1226). 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) 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 segregants, selection of parents for hybridization should be properly based on genetic diversity rather than geographic diversity.

Table 1: Distribution pattern of 60 genotypes into 7 clusters under late sown condition

Cluster no.	No. of genotypes	Name of the genotypes	Intra-cluster Distance
1	**13**	WH1184, WH1202, PBW723, IBWSN1205, KRL19, IBWS1170, IBWSN1118, IBWSN1155, WH283, IBWSN1109I, HD3086, WH157, IBWSN1207	2.975
2	**5**	WH1021, WH730, HD3059, WH1142, DBW90	2.939
3	**3**	WH1080, Raj 3765, WH1025	3.812
4	**17**	HD2967, IBWSN1142, IBWSN1162, KRL210, WL711,	2.656

		PBW343, WH1123, WH1105, ATLAS66, WH416, IBWSN1213, PBW725, IBWSN1138, WH1232, WH1179, IBWSN1152, WH542	
5	**10**	P13647, IBWSN1171, IBWSM1155, P13644, WH1164, P13643, P13649, WH1227, IBWSN1159, WH147	2.868
6	**3**	WH1124, WH711, WH1226	3.686
7	**9**	DPW621-50, DBW88, IBWSN1145, IBWSN1150, P13648, WH1228, IBWSN1182, C306, IBWSN1151	3.817

a) Intra and inter cluster distances

The inter and intra cluster distance values for all the seven clusters under late sown condition are presented in Table 2. The genotypes of cluster I and VI exhibited maximum divergence (6.559) followed in descending order by the genotypes of III and VI (6.513), III and V (6.468), III and VII (6.194), II and VII (5.496), VI and VII (5.328), I and VII (5.038), I and V (5.009), II and V (5.000), II and VI (4.980), I and II (4.913), III and IV (4.820), I and III (4.686), IV and VII (4.647), II and III (4.607), IV and VI (4.605), V and VII (4.332), V and VI (4.319), IV and V (4.144), I and IV (4.093) and II and IV (3.705). 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 VII (3.817) was maximum followed in descending order by clusters III (3.812), VI (3.686), I (2.975), II (2.939), V (2.868) and IV (2.656). With the help of D2 values between and within clusters a cluster diagram is drawn showing the relationship between different genotypes (Figure 1).

Table 2: Inter and intra (diagonal) cluster average of D^2 among different clusters in Wheat under late sown condition

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**
Cluster 1	**2.975**	4.913	4.686	4.093	5.009	6.559	5.038
Cluster 2		**2.939**	4.607	3.705	5.000	4.980	5.496
Cluster 3			**3.812**	4.820	6.468	6.513	6.194
Cluster 4				**2.656**	4.144	4.605	4.647
Cluster 5					**2.868**	4.319	4.332
Cluster 6						**3.686**	5.328
Cluster 7							**3.817**

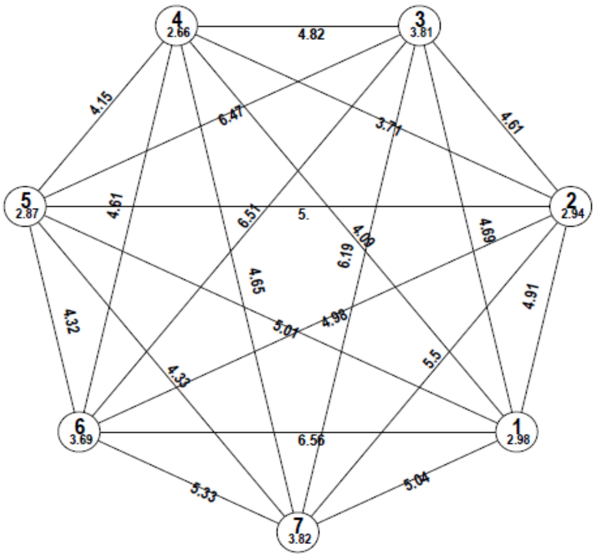

Figure 1: Euclidean Cluster Distances for the 7 clusters

Therefore, the genotypes of cluster I and VI exhibited maximum cluster divergence indicated that genotypes WH1184, WH1202, PBW723, IBWSN1205, KRL19, IBWS1170, IBWSN1118, IBWSN1155, WH283, IBWSN1109I, HD3086, WH157, IBWSN1207 (Cluster I) and genotypes WH1124, WH711, WH1226 (Cluster VI) that showed more divergence may be used to produce the superior hybrids and transgressive segregants. Similar finding was also reported by Sharma and Panwar (2007), Mohanty *et al.* (2017), Naik *et al.* (2016), Gupta *et al.* (2002), Singh *et al.* (2005), Verma *et al.* (2006), Ribadia *et al.* (2007) and Marker and Tripathi (2008). Dutamo *et al.* (2015) observed the lowest intra cluster distance in cluster V (0.00), indicates genetic variability within this cluster is not present. 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, indicates superior germplasm of above diverse cluster pair's when crossed might develop desirable recombinants.

b) Cluster means of different clusters for various characters.

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

Table 3: Cluster mean values of different clusters for various characters under late sown condition

Characters	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**
Days to heading	78.18	80.27	78.22	80.86	83.90	83.89	82.67

Days to anthesis	82.72	84.73	82.56	85.47	88.63	88.89	87.44
Days to maturity	120.03	118.80	118.22	118.80	123.46	124.22	122.63
Plant height (cm)	96.33	100.55	92.85	99.87	102.04	104.78	104.09
Effective tillers per meter	60.19	77.27	69.00	77.16	70.30	87.67	63.52
Chlorophyll fluorescence	0.66	0.66	0.61	0.66	0.66	0.63	0.67
Canopy temperature	29.16	23.90	25.44	28.73	28.92	27.24	28.33
Grain yield per meter (g)	50.45	71.89	59.78	70.57	64.97	83.00	53.46
1000-Grain weight (g)	39.06	41.8	41.87	41.83	36.98	40.70	37.80
Grain filling duration	32.61	33.13	30.22	31.98	34.00	31.67	28.46

c) Percent contribution towards total divergence

Percent contribution towards total divergence was calculated as per Mahalanobis D^2 statistic (1936). The maximum contribution towards the total divergence under late sown condition (Table 4) was exhibited by days to anthesis (14.44%) followed by canopy temperature (12.92%), days to maturity (11.07%), grain filling duration (10.00%), chlorophyll fluorescence (9.88%), grain yield per meter (9.79%), days to heading (9.57%), plant height (9.10%), 1000-grain weight (8.98%) and effective tillers per meter (4.25%). The characters viz., days to anthesis canopy temperature, days to maturity, grain filling duration, chlorophyll fluorescence, grain yield per meter, contributed more than 60% per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in process for improvement of yield and its component traits. In the same way, Dobariya *et al.* (2006) reported maximum contribution toward total divergence by days to flowering, number of tillers per meter, days to maturity and 1000 grain weight, Peshattiwar *et al.* (2009) by days to maturity, days to 50 per cent flowering, plant height and number of spikelet's per ear and Naik *et al.* (2016) by plant height, grain yield and sedimentation value and Singh *et al.* (2005) days to 50 per cent flowering, plant height, spikelet's per ear, biological yield per plant and 1000 grain weight. Hence, these characters should be given importance during hybridization and selection in process for improvement of yield and its component traits.

Table 4: Percent contribution towards variability of each character under late sown condition

Sr. No.	Characters	Contribution (%)
1	Days to heading	9.57
2	Days to anthesis	14.44
3	Days to maturity	11.07
4	Plant height (cm)	9.10
5	Effective tillers per meter	4.25
6	Chlorophyll fluorescence	9.88
7	Canopy temperature	12.92
8	Grain yield per meter (g)	9.79
9	1000-Grain weight (g)	8.98

10	Grain filling duration	10.00

Conclusion

Genotypes of cluster I and VI under late sown condition exhibited maximum cluster divergence indicated that these genotypes may be used to produce the superior hybrids and transgressive segregants. Traits such as days to anthesis followed by canopy temperature, days to maturity, grain filling duration, chlorophyll fluorescence and grain yield per meter contributed maximum to the total divergence present in the study material. Thus, these characters should be given importance during hybridization and selection in the segregating population for improvement of yield and its component traits. In view of the sufficient genetic diversity found in present study, showed considerable scope for genetic improvement through hybridization between the genotypes from divergent clusters.

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