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## Genetic Diversity for yield and yield traits in wheat

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### Abstract

An investigation about the genetic diversity among 60 wheat genotypes using 15 yield and yield traits was studied at the Department of Agriculture, Mata Gijri College, Sri Fatehgarh Sahib, Punjab. Univariate and multivariate analysis of variance revealed the presence of significant among the genotypes. Based on D<sup>2</sup> statistic, genotypes were grouped in 8 clusters following Tocher's method. Cluster VI consisting of 15 genotypes and was the largest one followed by cluster III and maximum intra-cluster distance was found in cluster VIII followed by cluster VI and cluster VII. The most divergent clusters indicated highest inter-cluster distance which was found between clusters V and VIII followed by clusters II and VIII whereas lowest distance was between cluster III and IV. Grain yield per plant, number of grains per spike and 1000 grains weight contributed maximum towards total divergence. The contribution of various characters towards the expression of genetic divergence should be taken into account as a criterion for choosing parents for wheat crossing programme for the improvement in such characters.

**Keywords:** Genetic diversity, Cluser analysis, Grain yield, Significant

### Introduction

The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Genetic divergence refers to the genetic distance between species or between populations within a species. Smaller genetic distances indicate a close genetic relationship where as large genetic distances indicate a more distant genetic relationship. Genetic distance can be used to compare the genetic dissimilarity between different species. Within a species, genetic distance can be used to measure the divergence between different sub-species or different varieties of a species. 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 environments are currently available. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Maniee *et al.*, 2009) [9]. The more the genetic diverse parents, the greater the chances of obtaining higher heterotic expression in F<sub>1</sub>s and broad spectrum of variability in segregating population (Shekhawat *et al.*, 2001) [13]. Selection and hybridizations techniques are frequently used for improving genetic constitution of a genotype. Genetic divergence analysis is important tool to estimate genetic diversity among selected genotypes which determine family relationships and genetic affinity or distance of genotypes from each other studying cluster analysis (Mellingers, 1972) [10]. The statistical analysis revealed that the diverse clusters showed high inter cluster distances which might generate a wide range of transgressive segregants for development of high yielding wheat varieties (Kumar *et al.*, 2015) [6].

The present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme.

### Methods and Materials

The present investigation was conducted during *Rabi* season 2015-16 at Research Farm, Mata Gujri College, Sri Fatehgarh Sahib, India. This place is situated between 30° - 27' and 30° - 46' latitudes and 76° - 04' and 76° - 38 E latitudes and at mean height of 247 meters above mean sea level. The climate of Sri Fatehgarh Sahib is characterized by subtropical semi arid type of climate with three distinct seasons namely hot and dry summer, monsoon and cold winter. The minimum temperature may go down to 4 °C in December-January while the maximum temperature may go as high as 42 °C in May-June.

The experimental material under the study, comprised of 60 diverse genotype of wheat

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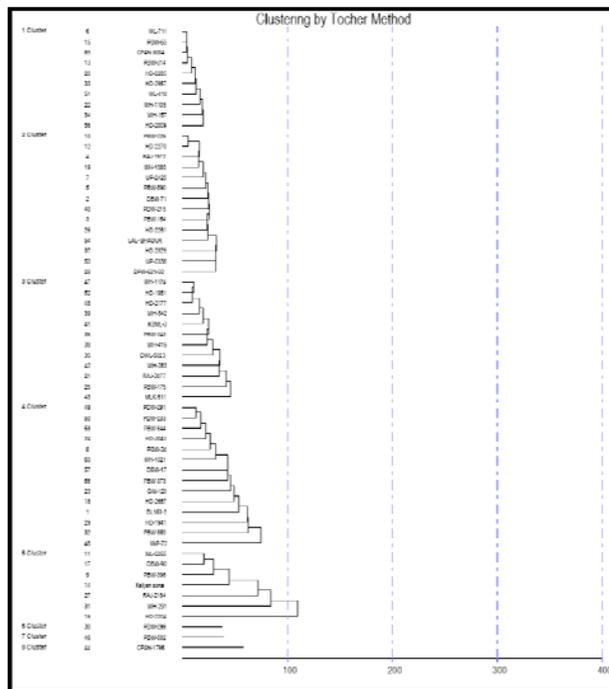
received from Indian Institute of Wheat and Barley Research and were raised in randomized block design with three replications. Data were recorded for 15 traits namely Days to booting, Days to heading, Days to anthesis, Days to maturity, Number of productive tillers per plant, Plant height (cm), Spike length (cm), Peduncle length (cm), Number of spikelet per spike, Number of grains per spike, Number of grains per plant, 1000 grains weight (g), Biological yield per plant (g), Grain yield per plant (g) and Harvest index (%). All the recommended package of practices were applied to raise a good and healthy crop.

**Results and Discussion**

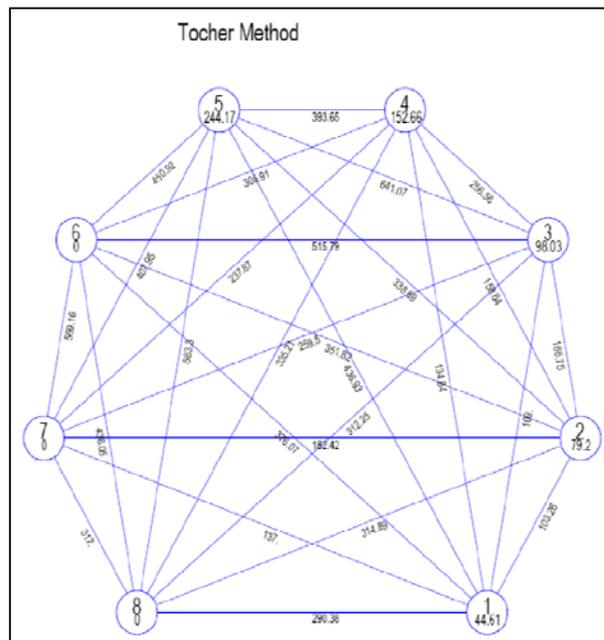
**Genetic Divergence (D<sup>2</sup> – Analysis)-** Variability differs from diversity in the sense that the former has observable phenotypic differences, whereas the latter may or may not have such an expression. One of the powerful techniques for assessing genetic divergence is the D<sup>2</sup>- statistic proposed by Mahalanobis in 1928. This technique measures the forces of differentiation at two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents to be ordered in hybridization programme.

**Cluster Pattern-** The 60 genotypes of wheat were grouped in 8 clusters following Tocher's method Table- 1 and Figure 1. Cluster VI constituted of 15 genotypes and was the largest one followed by cluster III and cluster IV consisting of 12 genotypes and 10 genotypes respectively. Cluster VIII was consisted of 6 genotypes, whereas cluster V and VII consisted of 5 genotypes each. Cluster II and I contains 4 genotypes and 3 genotypes each. The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity (Singh *et al.*, 2009) [14]. The discrimination of genotypes in to discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme.

The average inter and intra cluster distances were calculated and presented in Table-2 and Figure 2. The average inter and intra cluster D- values are presented with the help of a cluster diagram, which represent the average distances among the different clusters. The maximum intra-cluster distance was found in cluster VIII (563.298) followed by cluster VI (400.794) and cluster VII (304.746). The most divergent clusters indicated highest inter-cluster distance which was found between clusters V and VIII (2327.421) followed by clusters II and VIII (2245.737), whereas lowest distance was between cluster III and IV suggested a closer relationship between these two clusters and low degree of diversity among the genotypes. Since, high or optimum genetic divergence is desired between the parents of hybridization plan for obtaining higher frequency of desirable recombinants, the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster are very low. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances.



**Fig 1:** Grouping of genotypes into different Clusters by Tocher Method



**Fig 2:** Average inter and intra cluster distance among different groups of wheat genotypes

**Cluster means-** A comparison of the mean values for fifteen characters of different clusters has been presented in Table-3. Cluster means showed considerable differences among the clusters. Cluster I containing three genotypes were characterized by genotypes/cultivars having highest mean value for days to booting (84.90). Cluster II having four genotypes and having moderate mean days to heading (94.97), days to anthesis (101.40), and lowest mean value for number of spikelet per spike (19.24), number of grains per spike (41.64) and number of grains per plant (249.53). Cluster III comprising twelve genotypes was characterized by highest mean for 1000 grain weight (33.77). Cluster IV having ten

genotypes which can be characterized by highest mean value for plant height (96.71) and lowest mean value for days to booting (79.04), days to heading (88.96), spike length (9.83) and harvest index (40.15). Lowest mean value for biological yield per plant (12.99), 1000 grains weight (22.09), grain yield per plant (8.18) and high cluster mean value for days to heading (100.91), days to anthesis (109.11), days to maturity (128.32) and harvest index (63.21) was the characteristic of the Cluster V which consisted of five genotypes. Cluster VI contains moderate mean value for number of spikelet per spike (24.39), number of grains per spike (59.95) and low mean value for 1000 grains weight (29.55). Cluster VII was characterized by maximum mean value for number of productive tillers per plant (10.50), spike length (12.53), peduncle length (34.09) and number of spikelet per spike (26.07). Cluster VIII exhibited maximum mean value for number of grains per spike (65.88), number of grains per plant (464.19), biological yield per plant (36.27) and grain yield per plant (16.06).

Cluster VIII exhibited highest cluster mean value for grain yield per plant, biological yield per plant, number of grains per spike whereas Cluster VII exhibited high cluster mean for spike length, number of productive tillers. The genotypes present in cluster VIII and VII may be used as parents in hybridization programmes for developing high yielding wheat varieties

For yield improvement cluster III which contains 12 genotypes exhibited highest mean value for 1000 grains weight and cluster VIII which exhibited highest mean value for number of grains per spike also would be promising if taken for hybridization programmes. Cluster VIII contains 6 genotypes also exhibited highest cluster mean for biological yield per plant can be used to improve straw yield contents in wheat hybridization programmes. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement

### Contribution of Traits in Divergence

The contribution of different characters towards the expression of genetic divergence was calculated Table- 4. On the basis of number of first rank earned by every character out of 1 to 15 in each combination of genotypes (total no. of combination in present study were 1770.02) during the calculation of  $D^2$  values. Each character was ranked on the basis of  $d_i = Y_j^i - Y_k^i$  values, where  $d_i$  represents the mean difference between the same character for two different genotypes and  $Y_j^i$  and  $Y_k^i$  represents the mean value of  $i^{\text{th}}$  character for genotype  $j$  and  $k$ . Rank 1<sup>st</sup> was given to the highest mean difference and rank 15<sup>th</sup> to the lowest mean

difference. Percent contribution was calculated by taking total number of combination as 100 per cent, *i.e.* 1770.02 = 100%. By the above stated method it was found that grain yield per plant (25.88), number of grains per spike (25.42) and 1000 grains weight contributed maximum towards total divergence followed by number of spikelet per spike (9.15), plant height (6.44), biological yield per plant (6.05), spike length (5.25), number of grains per plant (3.45), peduncle length (2.99), number of productive tillers per plant (0.90), harvest index (0.56), days to maturity (0.11), days to heading (0.06), days to booting (0.00), days to anthesis (0.00) respectively.

The contribution of grain yield per plant in divergence had also been also observed by Rahman *et al.* (2015) [11], Khare *et al.* (2015) [5], Lal *et al.* (2009) [7], Salavati *et al.* (2008) [12], Jishan and Zhu (2008) [4], number of grains per spike by Lal *et al.* (2009) [7], 1000 grain weight and number of spikelet per spike by Dobariya *et al.* (2006) [3], Arya *et al.* (2017) [1], plant height by Khare *et al.* (2015) [5] and biological yield per plant by Arya *et al.* (2017) [1]. The contribution of days to booting, days to anthesis to the divergence was found to be nil in the selected set of genotypes and days to maturity, days to heading, contributed minimum towards the total divergence. 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.

It is observed from the clustering pattern Table-1, that distribution of various wheat genotypes into clusters occurred randomly irrespective of their geographical origin. Similar type of results was obtained in the studies of Rahman *et al.* (2015) [11], Khare *et al.* (2015) [5], Bhanupriya *et al.* (2014) [2] showed that genetic drift and selection in different environments could cause greater diversity among genotypes than their geographical distances. So, selection of parental material for hybridization simply based on geographical diversity may not be rewarding. It could be inferred from the present study that genotypes showing greater divergence may be considered for utilization in crossing programme, irrespective their origin.

It is worthy to note that in calculating cluster mean, the superiority of a particular genotype with respect to a given character could be get diffused by other genotypes that are grouped in the same cluster but are inferior or intermediate for the character in question. Hence, apart from selecting genotypes from the clusters which have an increased inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest within a cluster.

**Table 1:** Distribution of 60 genotypes of wheat into different clusters Tocher Method

Cluster	No. of genotypes in cluster	Genotypes
I	3	RAJ-2184, PBW-299, WH-291
II	4	PBW-396, WL-2265, KALYAN SONA, DBW-90
III	12	HD-2687, HD-2285, RAJ-3077, HD-2967, WH-157, DWL-5023, PBW-343, HD-2329, WH-283, PBW-502, PBW-373, HD-2009
IV	10	RAJ-1972, PBW-590, UP-2425, PBW-34, PBW-226, HD-2270, WH-1080, HD-3043, PBW-644, WH-1021
V	5	DL-153-2, PBW-154, HD-2204, PBW-215, DBW-17
VI	15	DBW-71, WL-711, PBW-314, PBW-65, WH-1105, GW-120, PBW-175, HD-2281, DPW-621-50, HD-1981, PBW-550, PDW-233, UP-2338, LAL-BHADUR, CPAN-3004
VII	5	KSML-3, MLKS-511, CPAN-1796, IWP-72, PDW-291
VIII	6	WH-416, WH-542, WH-1124, HD-2177, WL-410, HD-1981

**Table 2:** Intra and inter-cluster distance (D-value) of clusters formed with 60 genotypes of Wheat

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	290.193	442.495	397.03	512.413	954.662	499.109	1388.113	1612.073
Cluster II		275.839	485.358	713.468	932.337	829.894	1671.050	2245.737
Cluster III			230.764	394.54	1000.126	504.642	1059.253	1145.911
Cluster IV				231.842	782.032	462.624	999.840	1178.731
Cluster V					0.000	999.586	1499.453	2327.421
Cluster VI						400.794	767.986	1177.622
Cluster VII							304.746	1352.394
Cluster VIII								563.298

**Table 3:** Cluster means for fifteen yield attributes in 60 genotypes of Wheat

Characters Clusters	Days to booting	Days to heading	Days to anthesis	Days to maturity	No. of productive tillers per plant	Plant height (cm)	Spike length (cm)	Peduncle length (cm)	No. of Spikelet per spike	No. of gains per spike	No. of Grains per plant	1000 grain weight	Biological yield per plant (g)	Grain yield per plant (g)	Harvest index (%)
Cluster 1	86.02	95.49	101.50	122.75	7.03	89.60	11.52	31.07	20.40	52.40	302.71	31.12	22.05	9.38	42.75
Cluster 2	81.36	90.17	97.13	118.95	8.81	87.66	11.81	30.30	19.81	51.87	300.10	33.29	26.30	10.24	39.27
Cluster 3	84.82	95.07	101.45	121.68	7.81	89.96	11.41	30.45	19.11	42.10	247.73	32.33	20.37	8.62	42.54
Cluster 4	83.40	93.17	99.28	122.63	7.97	89.83	10.44	32.67	22.34	59.02	306.07	31.53	22.63	9.44	42.09
Cluster 5	82.05	89.56	95.95	118.70	9.00	95.45	12.27	32.93	22.65	61.19	438.36	32.93	34.96	15.39	45.20
Cluster 6	83.02	91.66	98.67	124.22	10.00	88.76	11.84	34.20	34.20	56.20	294.60	27.90	24.78	10.29	41.60
Cluster 7	88.98	99.78	106.17	119.97	7.80	80.56	11.34	23.40	19.60	50.80	478.20	31.30	20.10	10.44	52.14
Cluster 8	89.84	100.91	109.11	128.32	10.40	96.07	10.05	32.35	20.20	40.80	389.00	22.09	12.99	8.18	63.21

**Table 4:** Percent contribution of each character toward the total divergence in 60 genotypes of wheat

S. No.	Character	Number of times appearing first in the ranking	Per cent contribution
1.	Days to booting	0.01	0.00
2.	Days to heading	1	0.06
3.	Days to anthesis	0.01	0.00
4.	Days to maturity	2	0.11
5.	Number of productive tillers per plant	16	0.90
6.	Plant height (cm)	114	6.44
7.	Spike length (cm)	93	5.25
8.	Peduncle length (cm)	53	2.99
9.	Number of spikelet per spike	162	9.15
10.	Number of grains per spike	450	25.42
11.	Number of grains per plant	61	3.45
12.	1000 grains weight	243	13.73
13.	Biological yield per plant	107	6.05
14.	Grain yield per plant (g)	458	25.88
15.	Harvest index (%)	10	0.56

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