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Studies on genetic divergence analysis for important agronomical traits in bread wheat (*Triticum aestivum* L. em Thell.)

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Abstract
Thirty six genotypes were tested in a randomized block design with 3 replications. The characters under study were days to flowering, plant height, productive tillers per plant, duration of reproductive phase, days to maturity, spike length, number of spikelets per spike, number of grains per spike, biological yield, harvest index, test weight and grain yield per plant. The computed D^2 and D values varied from 337.95 (18.38) to 5084.74 (71.31) which showed considerable genetic divergence among the different genotypes. The 36 genotypes were grouped into 5 clusters. The intra-cluster distance ranged from 18.38 to 71.31. The maximum inter-cluster distance was between cluster III and V. It suggested the hybridization possibilities between the genotypes included in these clusters by virtue of their being of wide genetic diversity.

Keywords: bread wheat, genetic divergence, tocher method, cluster diagram

Introduction

Wheat occupies a premier position among cultivated food cereals at National and International levels in both area and production. It contributes towards food front to the tune of more than 36 per cent of the world population and provides not less than 20 per cent of the total global calorie supply. It is the leading food grain crop of the temperate climates of the world and its cultivation is mostly concentrated in the northern hemisphere. The most extensive production of wheat is in the areas where winters are cool and summers are comparatively hot.

India has made the spectacular progress in accelerating wheat production and in providing considerable help to the food security system during the last decades. Now India is producing more than 90 million tons of wheat every year from acreage of around 30 million hectares with an estimated productivity of around 32 quintal per hectare (Annual Report 2017-18, Ministry of Agriculture, Govt. of India). There are several reasons for such a remarkable increment in wheat production in the country out of which high yielding varieties with reduced plant height, high biomass and larger spike, photo insensitivity, disease resistance and fertilizer responsiveness to irrigated conditions have played major role.

The knowledge of the factors responsible for high yield is not easy as yield is an interactive effect or multiplication of different traits. Therefore, for attainment of high yield level, the breeder is required to simplify this complex situation through handling of yield components, which have negative correlation with each other. For this rational approach, it is essential to get information on the nature and magnitude of association between different yield components and to resolve and quality /quantity their mode of contribution to yield, [Paroda

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[Paroda and Joshi, 1970 and Bhatt 1973] [6, 2]. Genetic divergence study still today is a powerful tool in the estimating genetic distances in crop plants. Being a numerical estimate this method has an added advantage over other as it permits precise comparisons among all possible traits of population in a group and its commutation offers the automatic removal of the effects of correlations among the genetic variables involved to its efficiencies among the genetic variables involved to its efficiencies and usages.

Material and Methods
Genotypes
The material used in the present study was comprised of 36 diverse strains of wheat (*Triticum aestivum* L. em Thell.). Seed of all the genotypes was collected from Rabi cereals section of C.S.A. University Agriculture & Technology, Kanpur. The detail of the genotypes has been given in Table-1.

Table 1: Detail of Genotypes used in the study

S. No.	Genotype	Origin / Source	S. No.	Genotype	Origin / Source
1.	KYZ 202		11.	KYZ 218	
2.	KYZ 204		12.	KYZ 220	
3.	KYZ 205		13.	KYZ 225	
4.	KYZ 207		14.	KYZ 227	
5.	KYZ 210		15.	KYZ 229	
6.	KYZ 211		16.	KYZ 231	
7.	KYZ 212		17.	KYZ 235	
.8	KYZ 213		18.	KYZ 236	
9.	KYZ 216	C.S.A.U.A & T, Kanpur	19.	KYZ 237	C.S.A.U.A & T, Kanpur
10.	KYZ 217		20.	KYZ 238	
21.	KYZ 240		29.	KYZ 264	
22.	KYZ 241		30.	KYZ 267	
23.	KYZ 243		31.	KYZ 268	
24.	KYZ 244		32.	KYZ 270	
25.	KYZ 246		33.	KYZ 272	
26.	KYZ 248		34.	KYZ 274	
27.	KYZ 254		35.	K 9006	
28.	KYZ 262		36.	HD 2733	I.A.R.I., New Delhi

Statistical Design
The trial was conducted in a Complete Randomized Block Design (CRBD) with 3 replications. Each plot was consisted of 8 rows of 6 m length. The distance between and within rows was kept at 20 cm and 15 cm, respectively. Standard agronomical practices were adopted to raise the good crop.

Observations recorded
Five plants from each plot were randomly taken and tagged for recording the following observation. 12 important agronomical traits namely Days to flowering, Plant height, Productive tillers per plant, Duration of reproductive phase, Days to maturity, Spike Length, Number of spikelets per spike, Number of grains per spike, Biological yield, Harvesting index, Test weight, Grain yield per plant,

Statistical Analysis for Genetic Divergence
Genetic divergence was analyzed as per the Mahalanobis method which is involved in measurement of D^2 as given below:
(a) Mahalanobis's generalized distance (D^2): A measure for group distance based on multiple characters was given by Mahalanobis (1928) [4].

After analyzing (v) statistic, pivotal condensation method was used to compute inverse of the error dispersion matrix (Rao, 1952) [8].
The D^2 value between the variables on the basis of characters are:

$$D^2c = Xij\ di\ dj$$
$$i = ij = 1$$

Where,
ij = Reciprocal matrix of (Xij), the pooled common dispersion obtained from error matrix.
d = Difference in the mean value for character for respective treatment as indicated by i and j.

(b) Determination of population constellation: The varieties were grouped into five clusters. Grouping of varieties into various clusters was done by Tocher's method (Rao, 1952) [8]. The criteria used for clustering by this method is that any two varieties belonging to the same cluster should, at least on the average, show smaller D^2 value than those belonging to the other different clusters. When a cluster is formed, the remaining varieties are used for clustering in the same way.

(c) Average inter-cluster distance: The procedure for calculating the inter-cluster distance is first to measure the distance between I and II, between I and III, between I and IV and between I and V. Likewise, the clusters were taken one by one and their distances from other cluster were cluster.

(d) Average intra-cluster distance: With the help of the following formula, intra-cluster distance was measured.
D^2 i/n, Where, D^2i is the sum of distance between all possible combinations (n) of the population included in a cluster.

(e) Cluster Diagram: With the help of D^2 values between and within the cluster, clusters diagram has been drawn which showed the relationship between the different populations.

(f) Cluster Mean: The cluster mean for a particular trait is the summation of mean values of the strains included in a cluster divided by number of strains in the cluster.

Experimental Results
Analysis of Variance
The analysis of variance of data based on mean values of all the twelve characters was done individually and their mean sums of squares are presented in Table-2. The analysis of variance showed highly significant differences among treatments for all the characters.
The D^2 value corresponding to all possible combinations taking two varieties at a time were computed. The 36 diverse genotypes were grouped into five clusters with consideration that the genotypes within cluster had smaller D^2 values among themselves than those from the inter-cluster. Grouping of genotypes into 5 clusters is presented in Table-3. Intra-cluster distances showed divergence among the genotypes within the clusters and inter-cluster distances expressed relative divergence between the clusters. The intra- and inter-cluster distance has been presented in Table-4. Cluster means for twelve characters among the 5 clusters are presented in Table-5.

Cluster Number 1: The clusters consisted of 5 genotypes viz., KYZ 207, KYZ 241, KYZ 246, KYZ 248 and K9006. The genotypes included in this cluster had maximum value for spike length and minimum for both at days to maturity and harvest index. The cluster had the maximum distance from cluster IV and minimum from cluster II. Average intra-cluster distance was 1954.15.

Clusters Number 2: The cluster consisted of 11 genotypes viz., KYZ 205, KYZ 213, KYZ 216, KYZ 227, KYZ 231, KYZ 235, KYZ 237, KYZ 238, KYZ 244, KYZ 254, and KYZ 274. This cluster showed maximum distance from cluster IV and minimum from cluster III and genotype included in this cluster are minimum value for productive tillers per plant, biological yield and grain yield per plant and for the remaining characters values are medium. Average intra-cluster distance was 512.13.

Cluster Number 3: The cluster consisted of 10 genotypes viz., KYZ 211, KYZ 212, KYZ 217, KYZ 218, KYZ 220, KYZ 225, KYZ 229, KYZ 240, KYZ 243, and HD 2733. This cluster had the maximum distance from cluster IV and minimum from cluster II. The genotypes included in this cluster had the medium values for all the characters. Average intra-cluster distance was 1728.02.

Cluster Number 4: The cluster consisted of 6 genotypes viz., KYZ 262, KYZ 264, KYZ 267, KYZ 268, KYZ 270 and KYZ 272. This cluster showed maximum distance from cluster V and minimum from cluster II and the genotypes included in this cluster had maximum value for days to flowering and days to maturity and minimum value for plant height, duration of reproductive phase, spike length, number of spikelets spike, number of grains per spike and test weight and for the remaining characters. The values are medium average intra-cluster distance was 337.95.

Cluster Number 5: The cluster consisted of 4 genotypes *viz.*, KYZ 202, KYZ 204, KYZ 210 and KYZ 236. This cluster showed maximum distance from cluster IV and minimum from cluster II and genotypes included in this cluster are with minimum value for days to flowering and medium values for days to maturity and spike length and for remaining characters the values were the highest. Average intra- cluster distance was 1039.37.

Contribution of Individual characters towards total divergence
The results on portioning of the contribution of each character towards total divergence are presented in Table-6. In all the combinations, each character was ranked on the basis of per cent contribution of that character. Character 11 i.e. Test weight, was ranked first. The weight contributed 70.63 per cent followed by days to flowering (14.76), plant height (7.78) biological yield (6.67) and days to maturity (0.16) and remaining characters had no contribution. Test weight, which contributed maximum, was ranked first (445 times) followed by days to flowering which appeared second in the sense of total contribution which ranked first 93 times.

Table 2: Analysis of variance for different characters in 36 genotypes of bread wheat

S. No.	Source of variation	D.F.	Mean Sum of Squares for different Characters											
			1	2	3	4	5	6	7	8	9	10	11	12
1	Replication	2	0.09	3.25	0.97	0.06	0.37	0.18	1.44	9.69	2.53	4.27*	0.01	2.33
2	Genotype	35	9.22**	247.33**	10.59**	3.21**	1.78**	1.87**	3.87**	31.08**	402.42**	2.81**	10.99**	47.18**
3	Error	70	0.03	1.72	0.34	0.14	0.10	0.17	0.47	2.41	3.26	0.77	0.01	1.17

Characters: 1-Days to flowering, 2-Plant height (cm), 3-Productive Tiller/ Plant, 4-Duration of Reproductive Phase, 5-Days to Maturity, 6-Spike length (cm), 7-No. of Spike- lets/ Spike, 8-No. of grains/ Spike, 9-Biological Yield (g), 10-Harvest Index, 11-Test weight (g), 12-Grain yield/ plant (g)
*Significant at 5% level of significance, **Significant at 1% level of significance

Table 3: Composition of cluster based on D^2 statistic in 36 genotypes of bread wheat

No. of cluster	No. of genotypes	Name of genotypes
I.	5	KYZ207, KYZ241, KYZ246, KYZ248, K9006.
II.	11	KYZ205, KYZ213, KYZ216, KYZ227, KYZ231, KYZ235, KYZ237, KYZ238, KYZ244, KYZ254, KYZ274.
III.	10	KYZ211, KYZ212, KYZ217, KYZ218, KYZ220, KYZ225, KYZ229, KYZ240, KYZ243, HD2733.
IV.	6	KYZ262, KYZ264, KYZ267, KYZ268, KYZ270, KYZ272.
V.	4	KYZ202, KYZ204, KYZ210, KYZ236.

Table 4: Average intra and inter-cluster D^2 and D value [in parenthesis] among 5 clusters for 36 genotypes of bread wheat

| Cluster No.	I	II	III	IV	V
I	1954.15 (44.21)	1327.09 (36.43)	1927.27 (43.90)	2786.05 (52.78)	2062.81 (45.42)
II		512.13 (22.63)	1208.69 (34.77)	1809.69 (42.54)	1794.28 (42.36)
III			1728.02 (41.57)	3001.47 (54.78)	2066.29 (45.46)
IV				337.95 (18.38)	5084.74 (71.31)
V					1039.37 (32.24)

Table 5: Intra-cluster mean for twelve characters in 36 genotypes of bread wheat

S. No.	Cluster No.	Characters											
		1	2	3	4	5	6	7	8	9	10	11	12
1	I	74.61	75.58	4.77	41.84	116.58*	13.49**	20.89	62.72	31.56	32.14*	37.44	9.85
2	II	77.21	76.64	4.56*	40.21	117.35	12.15	19.69	59.05	26.44*	32.71	37.83	8.71*
3	III	76.80	75.89	7.95	40.50	117.41	12.19	20.03	59.86	47.44	33.10	38.23	15.63
4	IV	79.13**	70.84*	5.27	39.71*	118.73**	11.44*	18.63*	55.97*	30.10	32.29	35.32*	9.81
5	V	74.17*	84.09**	8.12**	42.33**	116.80	13.48	22.27**	65.40**	53.11**	34.34**	39.39**	17.86**

Characters: 1-Days to flowering, 2-Plant height (cm), 3-Productive Tiller/ Plant, 4-Duration of Reproductive Phase, 5-Days to Maturity, 6-Spike length (cm), 7-No. of Spike- lets/ Spike, 8-No. of grains/ Spike, 9-Biological Yield (g), 10-Harvest Index, 11-Test weight (g), 12-Grain yield/ plant (g) *Lowest value of cluster, ** Highest value of cluster

Table 6: Contribution of 12 important characters towards total genetic divergence in 36 genotypes of bread wheat

S. No.	Characters	Percent Contribution towards Genetic Divergence
1	Days to flowering	14.76
2	Plant height (cm)	7.78
3	Productive Tillers/ Plant	0.00
4	Duration of Reproductive Phase	0.00
5	Days to Maturity	0.16
6	Spike length (cm)	0.00
7	No. of Spikelets/ Spike	0.00
8	No. of grains/ Spike	0.00
9	Biological Yield (g)	6.67
10	Harvest Index	0.00
11	Test weight (g)	70.63
12	Grain yield/plant (g)	0.00
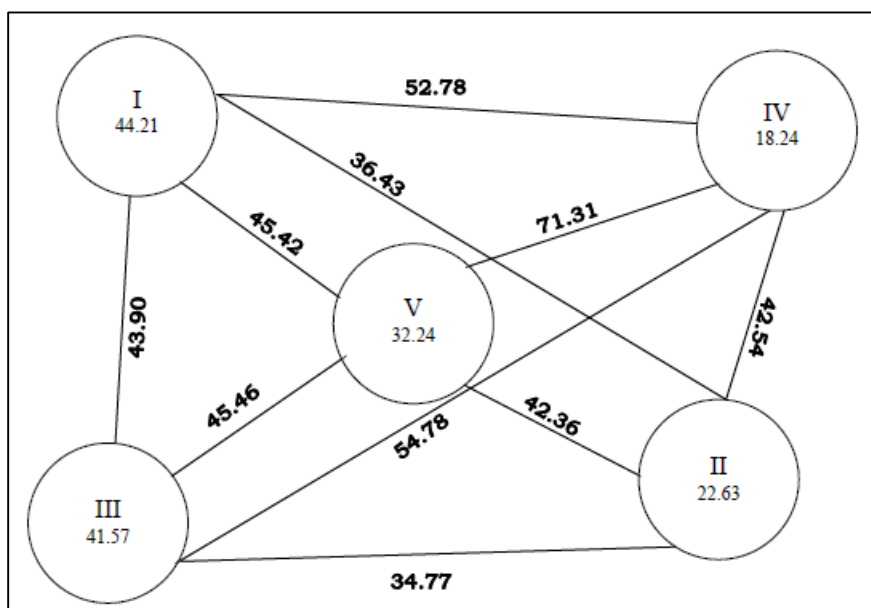
Fig 1: Cluster diagram showing average inter and intra-cluster distances for 12 characters in 36 genotypes of bread wheat

Discussion

Genetic divergence present in a crop plays an important role in improvement of the crop for making further improvement. It is necessary to import useful quantitative traits from diverse genetic sources. The D^2 statistic provides the means of grouping genotypes in topological district clusters in order of their relative distance from each other. Such a study is expected to be useful not only in the choice of the parents for hybridization but also to serve as an index effecting selection. The concept of D^2 as a measure of divergence was first introduced by Mahalanobis (1928) [4]. It is based on second degree statistic and is self weighing on the basis of genetic variability. D^2 values between any pair of populations account to a measure of genetic divergence than the one which fall into different clusters. On the basis of magnitude of D^2 values, 36 genetically diverse strains were grouped into 5 clusters.

Five genotypes are grouped in cluster I, 11 in cluster II, 10 in cluster III, six in cluster IV and four in cluster V (Table-3). The maximum value of inter-cluster distance was recorded between cluster IV and V followed by III and IV (Table-4 and Fig-1) suggesting wide diversity between these groups. The corroborative findings were reported by Walia *et al.* (1996) [14], Patil and Bhavsar (1997) [7], Sharma *et al.* (1998) [11] and Singh and Dwivedi (2002) [12]. It is suggested that the genotypes KYZ 202, KYZ 204, KYZ 210, and KYZ 236 of cluster V may be used as a parent for the hybridization programme with any superior genotype of cluster II and/or I to produce desirable recombination.

The lowest value of inter-cluster distance was recorded between cluster II and III (34.77) followed by cluster I and II (36.43) showing close relationship between these groups. Since the genotypes of these clusters had shown close

relationship and hence may not be emphasized to be used in hybridization programme.

The comparison of cluster means for twelve characters under study revealed considerable genetic differences between the clusters regarding one or more characters. Clusters V showed maximum values of cluster mean for plant height, productive tillers per plant, duration of reproductive phase, number of spikelets per spike, number of grains per spike, biological yield, harvest index, test weight and grain yield per plant. Therefore, the genotypes KYZ 2002, KYZ 204, KYZ 210, and KYZ 236 may be used in hybridization programme. Cluster II, I and IV had minimum values of cluster means for 3, 2 and 6 characters, respectively. These are for cluster II (productive tillers per plant, biological yield grain yield), for cluster I (days to maturity and harvest index) and for cluster IV (plant height, duration of reproductive phase, spike length, number of spikelets per spike, number of grains per spike and test weight). The genotypes included in these clusters may not be utilized for the improvement of these traits.

It may be concluded on the study of genetic divergence that the cluster III and V are most divergent. The hybridization programme could be suggested between the genotypes falling under these clusters as it would give maximum heterotic response. Cluster I, II and IV were the closest clusters and had lowest values of inter-cluster distances. Hybridization between the genotypes falling in these clusters would not be advantageous.

For the selection of parents for hybridization purpose on the basis of D^2 values, relative contribution of each character to the total divergence, choice of cluster with maximum genetic divergence and selection of one or two genotypes from such clusters are important.

Contribution of such characters towards total divergence (Table-6) revealed that the test weight contributed maximum towards total divergence followed by days to flowering, plant height, biological yield and days to maturity. The corroborate finding was reported by Singh and Dwivedi (2002) [12]. These clusters were, thus, adjudged to be considered suitable for creating maximum variability by hybridization and selecting the desired genotypes for higher yield. The corroborative findings to total results were reported by Das *et al.* (1984) [3], Raut *et al.* (1985) [9], Murphy *et al.* (1986) [5], Srivastava *et al.* (1987) [13], Redhu *et al.* (1996) [10], Walia and Garg (1996) [14], Patil and Bhavsar (1997) [7], Sharma *et al.* (1998) [11] and Bergale *et al.* (2001) [1].

Conclusion
On the basis of the present study made on genetic divergence, it was suggested that test weight could be used for selection of diverse genotypes and the crosses between the genotypes of cluster III and V might give fruitful results in hybridization programme.

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