

Full Length Research Paper

Genetic divergence study in improved bread wheat varieties (*Triticum aestivum*)

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The genetic divergence study was conducted to estimate the nature and magnitude of diversity in improved varieties of bread wheat during four Winter season, 2008 to 2012. The divergence analysis including Tocher's, canonical (vector) and Euclidian methods indicated the presence of appreciable amount of genetic diversity in the experimental materials. The thirteen wheat genotypes were grouped into four clusters by both Tocher's and Euclidian methods of divergence study. But the clusters of both methods were different on the basis of the genotypes and their numbers present in the cluster. The result obtained from different methods of divergence study was slightly different from each others. The suitable genotypes for the different characters have been drawn from the all three methods of divergence study. The result of principal component analysis revealed that only three principal component accounted more than 80% of the total variation. 3D diagram based on PCA scores and Euclidian distance matrix reflected highest diversity between PBW343 and HS375 while minimum between RSP564 and RSP561. The information obtained from this study can be used to plan crosses and maximized the use of genetic diversity and expression of heterosis.

Key word: Wheat, genetic divergence, cluster analysis.

INTRODUCTION

The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Maniee et al., 2009; Kahrizi et al., 2010a, b). The more the genetic diverse parents, the greater the chances of obtaining higher heterotic expression in F₁s and broad spectrum of variability in segregating population (Shekhawat et al., 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin, 1985). The

study of genetic divergence can assist in the choice of genotypes to be used in breeding programs for the development of new populations as it estimate the extent of diversity existed among selected genotypes (Mondal, 2003). Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat et al., 2001; Arega et al., 2007; Haydar et al., 2007; Ahmadizadeh et al., 2011; Daniel et al., 2011). The present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat

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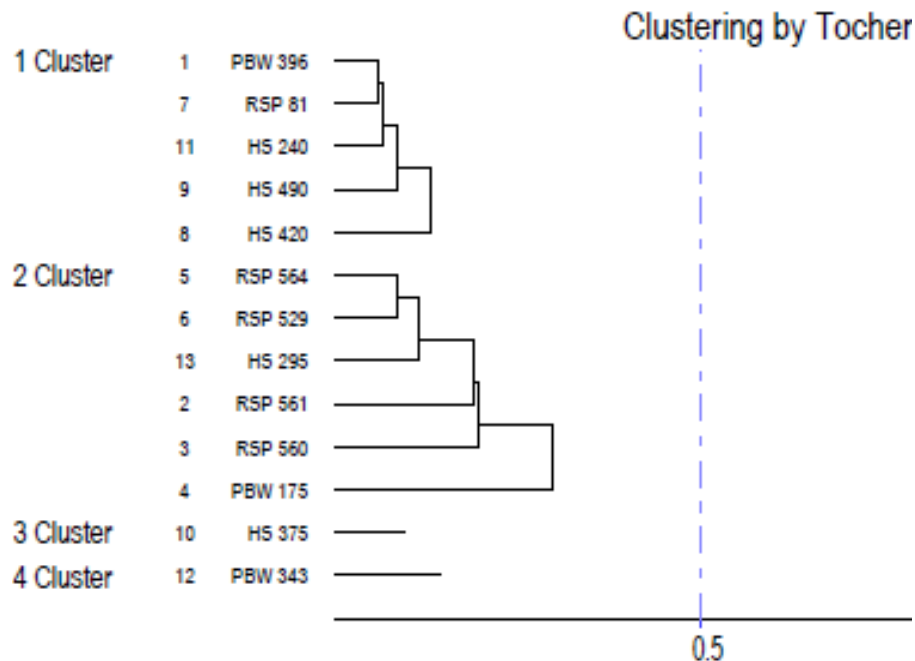


Figure 1. Clustering pattern of wheat varieties by Tocher method.

genotypes for utilization in wheat breeding programme.

using computer package (Windostat version 8.5).

MATERIALS AND METHODS

The present experiment was carried out at Maize Breeding Research Station, Poonch (India) under rainfed condition situated between 33° 25' to 34° 01' north latitude and 73° 58' to 74° 35' east longitude at height of 3300 MSL and bounded by Kashmir valley and line of control with Pakistan. The experiment materials consist of 13 bread wheat varieties originated and obtained from different genetical back ground and different centres of the country, respectively (Table 4). All the 13 genotypes are pure line wheat varieties well released for commercial cultivation in different states of India. The experiment was conducted in Randomized Block Design for four years, that is, winter 2008-09, 2009-10, 2010-11 and 2011-12 following the agronomical practice for wheat like row to row distance of 25 cm and fertilizer (NPK) doses at rate of 120:100:80 kg/ha under rainfed condition. The data of physiological characteristics like plant height (cm), spike length (cm) and harvest index (%) were recorded from mean of five randomly selected plants from each variety per replication. days to 50% heading, days to maturity and grain yield were recorded on plot basis where the grain yield was converted into kg/ha. The effective no. of tillers was measured in per square meter of the plot. The experiments were sown on different dates in the month of November during four winter seasons 2008 to 2012. The average rainfall during the crop period (November to May) was 730.5 mm. The genetic divergence among the wheat varieties were calculated by canonical (Vector) and non-hierarchical Euclidean methods of divergence estimation. The D2 values were calculated by using the method described by Mahalanobis (1936). Genetic divergence analysis using canonical (vector) method is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively, were derived (Rao, 1952). Non-hierarchical Euclidean cluster analysis (Beale, 1969; Katyal et al., 1985) was conducted

RESULTS AND DISCUSSION

On the basis of results obtained from the present study high degree of genetic divergence was observed. It is evident as more number of cluster (four) formed by the 13 wheat genotypes and high range of values of inter and intra cluster distance. The more diversity of parents, the greater chance of obtaining high heterosis (Zaman et al., 2005). Amongst four clusters formed by Tocher's method (Figure 1), cluster II was largest (with 6 genotypes) and cluster III and IV were smallest with one genotype only (Table 1). The maximum inter cluster distance was observed between cluster III and cluster IV (Table 2), which exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme.

The result obtained from different methods of divergence study was slightly differs from each others. Although D2 statistics using Tocher method for classifying the genotypes is useful in general but non-hierarchical Euclidean cluster analysis (based on Wards minimum variance dendrogram) Figure 2 more critically identifies sub clusters of the major groups at different levels and offers additional opportunity than that of Tocher method to plant breeders in planning of hybridization programme aimed at crop improvement.

All the 13 bread wheat genotypes were divided into four clusters by non-hierarchical Euclidean cluster analysis (Figure 2). Maximum number of genotypes (5) grouped in

Table 1. Distribution of 13 wheat genotypes in to four different clusters based on tocher and Euclidean method of cluster analysis.

Cluster	Method	No. of inbred	Name of inbred
I	Tocher	5	PBW 396, RSP 81, HS 240, HS 490, HS 420
	Euclidean	4	PBW 396, RSP 81, HS 375, HS 240
II	Tocher	6	RSP 564, RSP 529, HS 295, RSP 561, RSP 560, PBW 175
	Euclidean	2	RSP 561, RSP 560
III	Tocher	1	HS 375
	Euclidean	5	RSP 564, RSP 529, PBW 175, HS 420, HS 490
IV	Tocher	1	PBW 343
	Euclidean	2	PBW 343, HS 295

Table 2. Mean inter and intra cluster distance among four clusters in wheat genotypes on the basis of D2 statistics (Tocher's Method (I-IV) and Euclidian method (A-D)).

Cluster	Cluster I Cluster A	Cluster II Cluster B	Cluster III Cluster C	Cluster IV Cluster D
Cluster I	0.329	0.972	0.633	1.917
Cluster A	3.844	17.161	12.918	21.240
Cluster II		0.700	2.175	1.433
Cluster B		2.858	9.089	15.366
Cluster III			0.00	3.094
Cluster C			5.779	15.896
Cluster IV				0.00
Cluster D				4.513

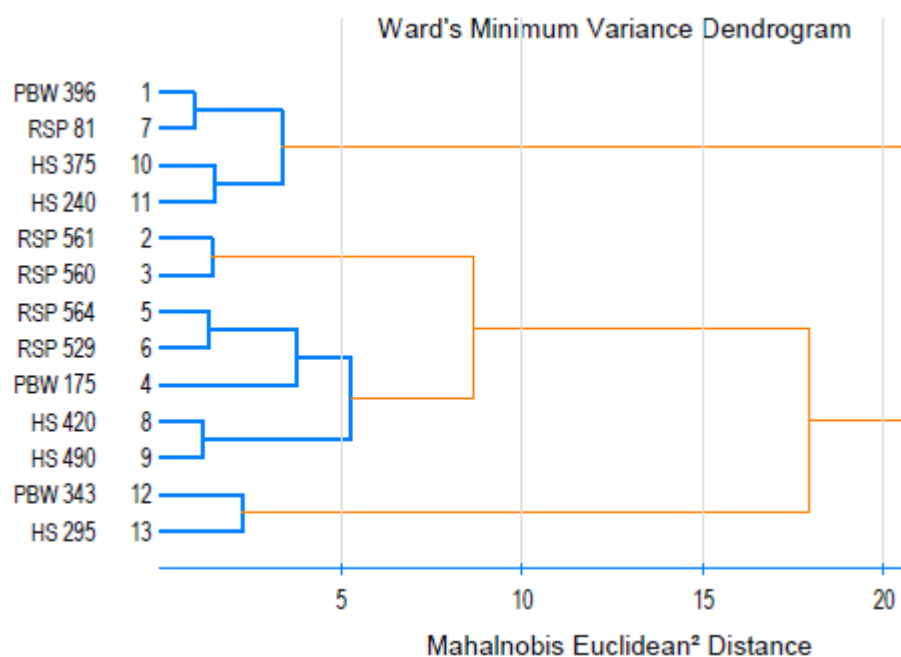
**Figure 2.** Clustering pattern wheat varieties by Euclidean method.

Table 3. Canonical vectors which supply best linear function of variates, value of canonical roots and percentage of variation absorbed by respective roots.

Parameter	1 Vector	2 Vector	3 Vector	4 Vector
Eigene value (Root)	2.484	1.729	1.504	0.557
% Var. Exp.	35.479	24.694	21.491	7.961
Cum. Var. Exp.	35.479	60.173	81.664	89.625
Days to 50% heading	0.128	0.721	0.087	0.109
Days to maturity	0.395	0.169	0.553	-0.132
Plant height (cm)	0.408	0.255	-0.384	0.607
Effective tillers/ m ²	-0.185	0.003	0.704	0.470
Spike length (cm)	0.546	0.147	0.020	-0.504
Grain yield (kg/ha.)	0.433	-0.397	-0.064	0.357
Harvest index (%)	-0.376	0.455	-0.196	0.006

Table 4. Details of wheat genotypes and their mean values of vectors calculated through canonical (vector) method.

Origin centre	Varieties	Vector 1	Vector 2	Vector 3	Mean yield (Q/ha)
Ludhiana (PAU), India	PBW 396	10.577	15.000	7.342	27.81
Jammu (SKUAST-J), India	RSP 561	10.886	14.301	7.572	38.73**
Jammu (SKUAST-J), India	RSP 560	10.946	14.299	7.599	38.37**
Ludhiana (PAU), India	PBW 175	11.008	14.457	6.624	36.25**
Jammu (SKUAST-J), India	RSP 564	10.906	14.348	7.027	34.73**
Jammu (SKUAST-J), India	RSP 529	10.862	14.219	6.806	32.08**
Jammu (SKUAST-J), India	RSP 81	10.645	15.070	7.277	29.03
New Delhi (IARI), India	HS 420	11.137	14.697	7.057	32.98**
New Delhi (IARI), India	HS 490	10.883	14.868	7.211	34.26**
New Delhi (IARI), India	HS 375	10.773	15.610	7.209	27.54
New Delhi (IARI), India	HS 240	10.921	15.272	7.150	29.89
Ludhiana (PAU), India	PBW 343	9.775	14.256	7.188	27.83
New Delhi (IARI), India	HS 295 (Check)	10.322	14.319	7.016	27.63
CD 1%					4.37

** Significantly different from zero at 0.01 levels of probability.

cluster 3 and minimum (2) genotypes in each of cluster 2 and 4 (Table 1). The relative association among the different genotypes is presented in the form of Wards Minimum Variance Dendrogram which was prepared using the rescaled distance. The resemblance coefficient between two genotypes is the value at which their branches join. The dendrogram elaborate the relative magnitude of resemblance among the genotypes as well as the clusters. It is clear from the perusal of wards minimum variance dendrogram that "fence sitter" single genotype, grouped by Tocher method in cluster III (HS 375) and cluster IV (PBW 343) were precisely accommodated in cluster 1 and II, respectively exhibiting more similarity (less variance) among other members of the respective cluster. Similar type of result was also found by Garg and Gautam (1997) in their experiment.

The result showed that geographical and genetic diversity exhibited no correspondence between them as genotypes from one and different geographic reason are

grouped together, which might be due to free exchange of genetic material from different regions. Sharma et al. (2002) and Sharma et al. (2008) have also revealed that the pattern of distribution of genotypes within various clusters was random and independent of geographical isolation. So there is no association between the geographical distribution and genetic diversity. On the basis of Euclidian method the highest inter cluster distance was recorded between cluster 1 cluster 4 consist of 4 and 2 genotypes, respectively, where as minimum between cluster 2 and 3. Within the cluster, the genotypes with high order of divergence were found in clusters 3 followed by cluster 4 (Table 2).

On the basis of cluster mean values, maximum divergence for effective tillers, spike length, grain yield and harvest index was exhibited by cluster 2; days to heading and days to maturity in cluster 1; and maximum divergence for plant height in cluster F (Tables 3 and 4).

Principal factors were carried out using principal

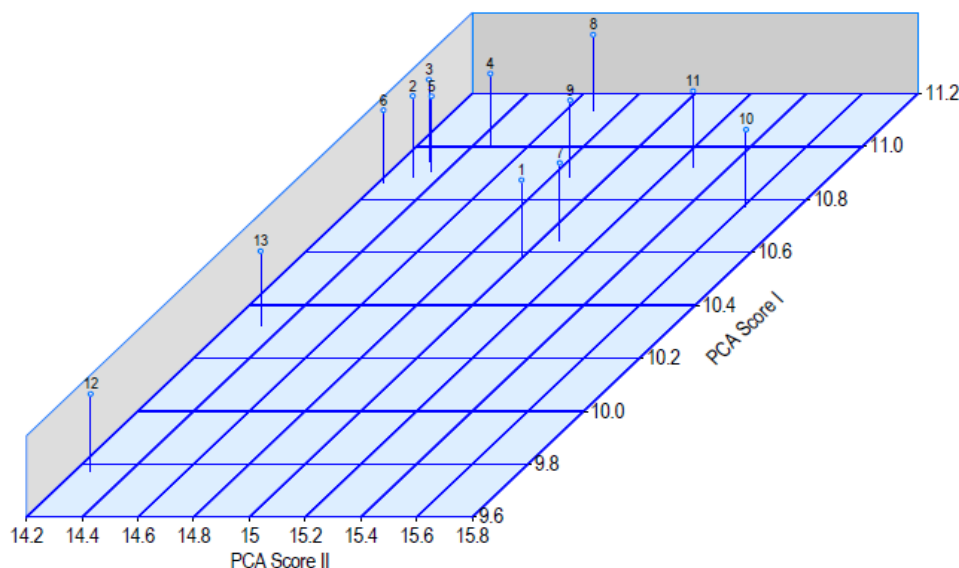


Figure 3. Three dimensional representation of genotypes using 3 principal component based on canonical variates.

component (PC) method for factor extraction. Differentiation among populations occurs in stages, or in other words in different axes of differentiation which accounts for total divergence. Theoretically as many as axes of differentiation can be envisaged as there are characters contributing to total variation, but it is not absolutely. It is possible that most of the variation is accounted for by the first two or more axes of differentiation. In the present investigation only the first three principal components showed eigen values more than one and cumulatively they explained 81.67% variability (Table 3). The first principal component explained 35.48% of the total variation and the second and third principal components explained 24.69 and 21.49% variation, respectively. The first principal component (λ_1) absorbed and accounted for maximum (35.48%) proportion of variability and remaining once accounted for progressively lesser and lesser amount of variation for λ_2 , λ_3 and λ_4 , respectively. The study through canonical analysis revealed that there are three effective axes (vectors) $\lambda_1 + \lambda_2 + \lambda_3 = 81.66\%$. In first axis (vector 1), spike length with element value 0.546; in second axis, days to heading with element value 0.721 and in third axis, effective tillers with element value 0.704, contributed maximum to the total divergence at primary, secondary and tertiary axes of differentiation based on canonical vectors 1, 2 and 3, respectively (Table 4). Similar type of work was also carried out by Tsegaye et al. (2012). Jagadev et al. (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization.

Genetic divergence between genotypes is measured in

terms of spatial distance and resulted in formation of three dimensional (3D) representation based on three PCA scores (λ_1 , λ_2 and λ_3 graphs) as depicted in Figure 3. Three principal factors scores were used to plot all the 13 wheat genotypes using PCA1, PCA2 and PCA3, that is, 3D plot which accounted for most important component traits namely spike length, days to heading and effective tillers.

Amongst 13 wheat genotypes, studied in the present study, exhibited great extent of genetic diversity on the basis of 3D diagram based on PCA scores and Euclidian distance matrix, which reflected highest diversity between PBW 343 and HS 375, while minimum genetic diversity between RSP 564 and RSP 561.

Conclusion

There is significant genetic variability among tested genotypes that indicates the presence of excellent opportunities to bring about improvement through wide hybridization by crossing genotypes with high genetic distance. PCA scores and Euclidian distance matrix reflected highest diversity between PBW343 and HS375 while minimum between RSP564 and RSP561. The information obtained from this study can be used to plan crosses and maximized the use of genetic diversity and expression of heterosis

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