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GENETIC DIVERSITY ANALYSIS IN SPRING WHEAT (*Triricum aestivum L.*)

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Abstract

Genetic divergences of 50 wheat lines were studied through Mohalanobis's D^2 and principal component analysis for fourteen characters. Genotypes were grouped into four different clusters. Cluster II comprised maximum number of genotypes (twenty one) followed by cluster IV. The inter-cluster distance was maximum between clusters I and III (12.29) indicating wide genetic diversity between these two clusters followed by the distance between cluster I and cluster II (8.28), and cluster III and cluster IV (7.97). The minimum inter-cluster distance was observed between cluster II and cluster IV (4.193) followed by cluster I and cluster IV (4.339) and cluster II and cluster III(4.390) indicating that the genotypes of these clusters were genetically close. The intra cluster distance of all the four clusters was more or less low which indicated that the genotypes within the same cluster were closely related. The highest inter genotypic distance (0.9166) was observed between the genotypes G 40 and G 41and lowest (0.0993) between the genotypes G 22 and G 43. Among the characters, heading days, maturity days, plant height (cm), canopy temperature at vegetative stage, canopy temperature at grain filling stage, grain filling rate (g $d^{-1}m^{-2}$), 1000- grain weight (g), and grains spike^{-1} contributed most for divergence in the studied genotypes. Cluster I had the highest mean for grain yield (4711.2 kg/ha), grain filling rate (17.5 g $d^{-1}m^{-2}$), chlorophyll content at anthesis, and plant height (93 cm). Crosses between I & III, I & II, and III & IV have greater chances to generate more heterotic F_1s. Considering magnitude of genetic distance, contribution of different traits toward the total divergence, magnitude of cluster means for different traits and performance the genotypes G10, G 11, G12, G35, G40, G48 of cluster I, G7 of cluster II, G41, G5,and G3 of cluster III and G46, G21 of cluster IV may be considered as good parents for future hybridization program to produce high yielding genotypes.

Keywords: Wheat, parents, genetic divergence.

Introduction

Wheat (*Triticum aestivum* L.) is the world's leading cereal grain, especially for temperate zone. The present cultivated species of *Triticum* is mostly hexaploid

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(2n=6x=42). Over last three decades wheat has become one of the leading economic crop in Bangladesh. The climate and soil condition of Bangladesh is suitable for wheat cultivation but yield potentiality of the genotypes in Bangladesh is less than those of temperate country (Sufi *et al.,* 2001). Wheat Research Centre (WRC) of Bangladesh Agricultural Research Institute (BARI) now has a wide range of spring wheat germplasm collected from different sources. Most of these have been collected from International Maize and Wheat Improvement Centre (CIMMYT), Mexico and few from Nepal, India, Pakistan, Australia, etc. In the present study, attempts have been made to characterize a set of wheat germplasm for various morphological characters and estimate the variabilities available in the collections, which can be utilized as donors in hybridization programme. There is a need for improved varieties in respect to heat, drought, and disease tolerant and germplasm is the important natural resource that could be used by the breeders to develop new cultivars. Selection of diverse parent may lead to have a wide gene combination for quantitative improvements of crop varieties (Jain, 1981). So, genetic diversity analysis is a useful tool for choosing efficient parents for hybridization programme to generate high variability for the desired traits. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomoka, 1991).

The multivariate analysis has been established by several investigators for measuring the degree of divergence and for ascertaining the relative contribution of different characters to the total divergence (Natarajan *et al.,* 1988; Sindhu *et al*., 1989; Golakia and Makne, 1992). D^2 cluster and factor analysis have been proved to be useful in selecting genotypes for hybridization. Mahalanobis's (1928) D^2 analysis has been successfully used in measuring the diversity in several crops. An understanding of nature and magnitude of variability among the existing wheat germplasm is a prerequisite for its improvement. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population of geographical level and to access in assessing relative contribution of different components to the total divergence both at intra and inter cluster levels (Jatasra and Paroda, 1978). Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for purposeful hybridization (Arunachalam, 1981; Samsuddin, 1985).

This study will help to determine the extent of genetic diversity for different traits that are present in the currently available breeding materials to classify them into groups and to identify the appropriate germplasm. Results of this study will also help in designing future improvement program for the development of new varieties.

Materials and Method

Fifty wheat genotypes were grown in a randomized complete block design with three replications at the experimental field of Bangladesh agricultural Research Institute, Gazipur during first week of December 2010 to first week of April 2011. The experimental site was at 23.46 ^{0} N latitude and 90.23^0 E longitude with an elevation of 8 meter from sea level. The experimental field was prepared thoroughly by ploughing with tractor followed by harrowing and removing the stubbles. The crop was fertilized with NPKS and B @ 100, 28, 40, 20, and 2.5 kg/ha, respectively, to ensure proper growth and development. The elements N, P, K, S and B were applied in the form of Urea, Triple Super Phosphate, Muriat of Potash, Gypsum and Boric acid, respectively. Two-thirds of urea and the entire quantity of other fertilizers were applied at final land preparation along with Furadon 3G @ 8 kg/ha (Anon., 2011). The rest one-third urea was top-dressed at crown root initiation stage (17-21 days after sowing) following first irrigation. Data were collected on days to heading (DH), days to anthesis (DA), days to maturity (DM), grain filling period (days), grain filling rate (g/m^2/d), plant height (PHT) in cm, chlorophyll content at anthesis in SPAD unit, canopy temperature (^{0}C) at vegetative, anthesis and grain filling stage, spikelets/spike (no.), grains/spike (no.), 1000-grain weight (g), and grain yield/m^2 (g). Grain yield/m^2 of each genotype was converted into grain yield (kg/ha). Mean data of each character was subjected to multivariate analysis viz, principal Coordinate Analysis (PCO), Principal Component Analysis (PCA), Cluster Analysis, and Canonacil Variate Analysis using GENSTAT 513 (Mahalanobis, 1936; Digby *et al*., 1989).

Results and Discussion

The computations from distance matrix gave non-hierarchical clustering among 50 genotypes and grouped them into four clusters (Table 1). The distribution pattern indicated that the maximum number of genotypes (21) were incluted in cluster II followed by cluster IV (17) , and cluster III (6) and cluster I (6). Samsuddin (1985) grouped 16 genotypes of spring wheat into three clusters.

According to Naidu and Satayanarana (1991), the number of genotypes in each cluster varied with the environments. Chaturvedi and Gupta (1995) studied 44 genotypes of wheat and grouped into 13 clusters where the maximum number of genotypes were included in cluster IV (19 genotypes) followed by cluster II (14 genotypes) and cluster I (7 genotypes). Genetic diversity is generally associated with geographical diversity. The genotypes within the same cluster although formed specific clusters but were collected from different places, which indicated that the geographical distribution and genetic divergence did not follow the same trend. Murty and Arunachalam (1966) stated that genetic drift and selection in different environment could cause greater diversity than geographical distance. Further more, there was a free exchange of seed material among the different regions. As a consequence, the trait constellation might be associated with particular region and in nature loose their individuallity under human interference. However, in some cases, effect of geographical origin influenced clustering. So geographic distribution was not the sole criterion of genetic diversity. This suggests that it is not necessary to choose diverse parents from diverse geographic regions for hybridization (Rashid, 2000).

Table 1. Distribution of 50 spring wheat genotypes in four different clusters.

Cluster	Number of genotypes	Percent of total entries	Genotypes
I	6	12	G10, G 11, G12, G35, G40, G48
II	21	42	G 6, G 7, G 8, G13,G14,G15,G16, G20,G22,G24, G26, G27,G28,G29 G30,G31,G33,G37,G43, G47,G50
III	6	12	G 3, G 5, G18, G 25, G41,G45
IV	17	34	G 1, G2, G4, G9, G17,G19,G21, G 23, G 32, G34 , G36, G 38, G39, G42, G44, G 46, G49

Intra (bold) and inter cluster distances are presented in Table 2. The inter-cluster distances were larger than the intra cluster distances. Intra cluster distances were estimated using the inter genotypic distance followed by Singh and Chaudhuary (1985). The maximum inter-cluster distance was observed between the clusters I and III (12.294) followed by the distance between cluster I and II (8.275) and between clusters III and IV (7.970). The maximum value of inter-cluster distance indicated that the genotypes belonging to cluster I was far diverged from those of cluster III. Similarly the higher inter-cluster values between cluster I and III, clusters I and II indicated that the genotypes belonging to each pair of clusters were far diverse.

Table 2. Average intra (bold) and inter cluster distances (D^2) for 50 wheat genotypes.

Cluster number	I	II	III	IV
I	**0.236**			
II	8.275	**0.235**		
III	12.294	4.390	**0.306**	
IV	4.339	4.193	7.970	**0.332**

However, the distance between cluster II and IV was minimum (4.193) followed by the distance between cluster I and IV (4.339) and between clusters II and III (4.390) indicating genotypes within these pair of clusters were less diverse.

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two-dimensional scatter diagram (Z_2-Z_1) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Fig. 1. The positions of the genotypes in the scatter diagram were apparently distributed into 4 groups, which indicated that there exists considerable diversity among the genotypes. The selection of diverge genotype, from different clusters would produce a broad spectrum of variability for morphological and quality traits which may enable further selection and improvement. The variety developed from the selected genotypes within the limits of compatibility of these clusters may produce high magnitude of heterosis. This would be rewarding in wheat breeding programme.

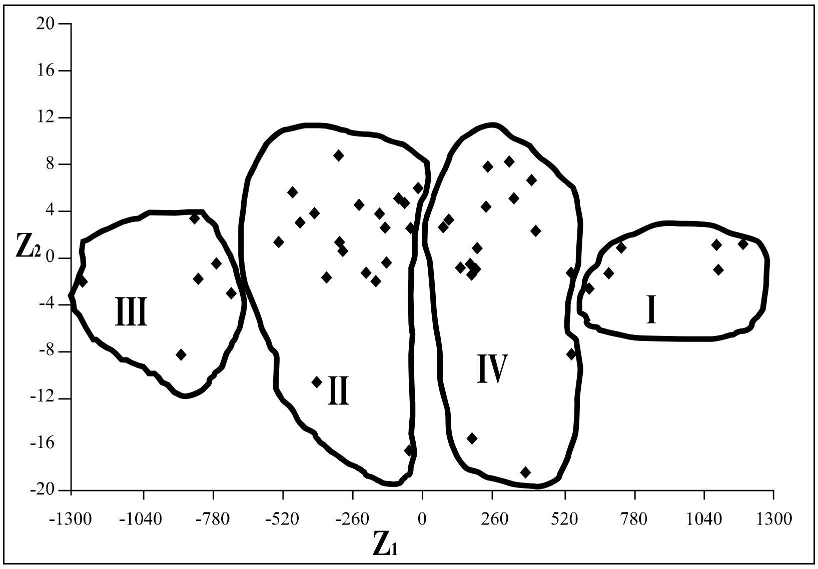

Fig. 1. Scatter distribution of 50 wheat genotypes based on their principal component scores superimposed with clustering.

Jagadev and Samal (1991), Ahmed *et al*. (2002) and Choudhury *et al.* (2006) were in agreement with these findings. Cluster mean value of 14 different characters are shown in Table 3. Difference in cluster means existed for almost all the characters studied. The highest mean value for grain yield (kg/ha) (4711.2), grain filling rate (g $d^{-1}m^{-2}$) (17.5), chlorophyll content at anthesis (51.2), and plant height (cm) (93.00) were observed in cluster I indicating the parental lines fallen in this cluster having the genetic potentiality to contribute better for yield maximization of improved wheat variety. For grain yield (kg/ha) cluster III ranked the lowest (2929.2) which include 6 genotypes. This cluster had the lowest grain filling rate (11.4), plant height (cm) (88.6), chlorophyll content at anthesis (48.8), grain filling duration (25.9), and 1000- grain weight (g) (36). Although this cluster had the highest grains/spike (51.9), anthesis days (78.6), maturity days (104.5), canopy temperature at anthesis stage (22.2), and heading days (74). So, its inability to maintain cooler canopy at the anthesis stage and grain filling stage might have played the key role for all negative attributes.

Table 3. Cluster means for 14 traits of 50 wheat genotypes.

Trait	Cluster mean			
	I	II	III	IV
Days to heading	70.1	73.9	74	71.9
Days to anthesis	73.8	78.1	78.6	75.7
Days tomaturity	100.8	104.1	104.5	102.9
Plant height (cm)	93	92.5	88.6	91.7
Chlorophyll content at anthesis	51.2	49.5	48.8	49.1
Canopy temperature at vegetative stage	21.1	21.1	21.1	20.9
Canopy temperature at anthesis stage	22.1	22.2	22.2	21.9
Canopy temperature at grain filling stage	23.8	23.9	23.7	23.5
Grain filling duration	27	26.1	25.9	27.2
Grain filling rate (g/d/m^2)	17.5	13.8	11.4	15.2
Spiklets/spike	15	16.1	16.2	16.3
Grains/spike	51.3	50.3	51.9	50.7
1000- grain weight (g)	37.3	37.9	36	36.8
Grain yield (kg/ha)	4711.2	3579.6	2929.2	4087.7

Cluster IV showed the highest spiklets/spike (16.3) and grain filling duration (27.2). In contrast, this cluster exibitted lowest canopy temperature at grain filling stage (23.5), canopy temperature at anthesis stage (21.9), and canopy temperature at vegetative stage (20.9). But it had the 2nd highest grain yield (kg/ha) (4087.7). So, its ability to maintain cooler canopy at the late grain growth stage might have played the key role for all the positive attributes.

Cluster II had the highest 1000- grain weight (g) (37.9), canopy temperature at grain filling stage (23.9) (Table 3). But this was not enough to ensure good yield. So, its inability to maintain cooler canopy temperature at the grain filling stage might have played the key role for all negative attributes. In this cluster we observed lowest means for Grains spike^{-1}.

Relative contribution of different characters towards divergence is presented in Table 4. Vector-1 and Vector-2 value were obtained from PCA. In first axis vector-1, all the studied characters had positive impacts towards divergence except for days to anthesis, chlorophyll content at anthesis, grain filling duration and grain yield (kg/ha). In vector-2, days to heading, days to maturity, plant height (cm), chlorophyll content at anthesis, canopy temperature at vegetative stage, canopy temperature at grain filling stage, grain filling duration, grain filling rate (g $d^{-1}m^{-2}$), grains/spike, and 1000- grain weight (g) had positive impact towards divergence.

Table 4. Latent vectors for 14 traits of 50 wheat genotypes.

Trait	Vector I	Vector II
Days to heading	0.1579	0.7224
Days to anthesis	-2.0754	-1.5608
Days to maturity	2.0044	1.2174
Plant height (cm)	0.1063	0.0859
Chlorophyll content at anthesis	-0.0341	0.1627
Canopy temperature at vegetative stage	0.5675	1.485
Canopy temperature at anthesis stage	0.2576	-0.0942
Canopy temperature at grain filling stage	0.1387	1.158
Grain filling duration	-1.7038	0.9073
Grain filling rate (g/d/m^2)	0.2325	3.6718
Spiklets/spike	0.0365	-0.3108
Grains/spike	0.0257	0.0508
1000- grain weight (g)	0.1345	0.2013
Grain yield (kg/ha)	-0.008	-0.0133

The characters heading days, maturity days, plant height, canopy temperature at vegetative stage, canopy temperature at grain filling stage, grain filling rate, grain per spike, and 1000- grain weight (g) showing positive value in both the vectors contributed maximum towards divergence. So, the divergence in the present materials due to these eight traits will offer a good scope for improvement of wheat varieties through selection of parents.

Generally crosses involving parents belonging to most diverse genotypes are expected to exhibit maximum heterosis and create wide variability in genetic architecture. Considering magnitude of genetic distance, contribution of different traits toward the total divergence, magnitude of cluster means for different traits and performance the genotypes G10, G 11, G12, G35, G40, G48 of cluster I, G7 of cluster II, G41, G5,and G3 of cluster III and G46, G21 of cluster IV may be considered as parents for future hybridization program to produce high yielding genotypes.

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