GENETIC DIVERGENCE IN SPRING WHEAT GENOTYPES (*Triticum aestivum* L.)

MS Rahman[1*] MS Hossain[2] MK Akbar[3] MS Islam[1] and L Ali [4]

Address
[1]Plant Breeder, Research and Development Wing, Lal Teer Seed Ltd. Dhaka [2]Professor Dept. of Genetic Engineering and Biotechnology, University of Rajshahi, Rajshahi [3]Stock Seed Manager, Lal Teer Seed Ltd. Dhaka [4]Lecturer, Dept. of Genetics and Plant Breeding BSMRAU

Correspondence*
sajedurgpb@gmail.com

Abstract

Genetic divergences of 24 spring wheat genotypes were estimated using Mahalonobis D^2-statistics and principal component analysis. The genotypes under study were grouped into three clusters. Cluster III had the maximum (12) and cluster II had the minimum (3) number of genotypes. The intra cluster value was maximum in cluster III and minimum in cluster II. The inter cluster distance were larger than the intra cluster distance suggesting wider genetic diversity among the genotypes of different groups. The genotypes of cluster II and III exhibited maximum divergence, as their inter cluster distance was the highest followed between I and II. So, genotypes from these groups could be used as parents in hybridization program to generate the highest possible variability. The characters like days to anthesis, days to maturity and grain yield per plant were major contributors towards the total genetic divergence.

Key Words: Genetic diversity, wheat, *Triticum aestivum* L, cluster and hybridization

Introduction

Study on genetic divergence is very important in evaluating the variation in a breeding population. In addition genetic diversity is essential to meet the diverse goals of plant breeding such as producing cultivars with increased yield (Joshi and Dhawn, 1966), wider adaptation, desirable quality, pest and disease resistance (Nevo *et al.,* 1982). In addition, genetic divergence is studied to identify specific parents for wider genetic variation and heterosis when they are crossed (Aditya, 1995). Mahalanobis D^2-statistics has extensively been used by several workers to study the genetic diversity in different agronomic crops and to identify the characters or characters responsible for such type of divergence. Using Mahalanobis D^2-statistics, the population can be classified in to different groups. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity in a collection of spring wheat genotypes by multivariate analysis.

Materials and Methods

The experiment was laid out in a randomized complete block design (RCBD) with three replications at the field laboratory of department of Genetic Engineering and Biotechnology, Faculty of Agriculture, University of Rajshahi.

This study was performed with 24 genotypes of spring wheat (Table-1) collected from regional Wheat Research Center of Bangladesh Agricultural Research Institute, Shyampur, Rajshahi to assess the genetic diversity among the genotypes. Each replication was consisted of 25 plots and each of the plots was 2.0 m long with five rows. The spacing was 40 cm between rows and 5 cm between plants in a row. The space maintained between the plots was 80 cm and between the replication was one meter. Seeds were sown continuously by hand in rows and after complete emergence; 5 cm distance was maintained between plant after thinning and gap filling in a row of the plot. Urea, Triple Super Phosphate (TSP), Muriate of Potash (MP), Zypsum and Cowdung were applied at the rate of 220 Kg, 180 Kg, 50 Kg, 120 Kg and 6000 Kg/ha respectively.

Data were recorded on individual plant basis from 10 randomly selected plants of each genotype from the five rows per plot in each replication. Among the characters studied as reproductive traits, days to booting, days to heading, days to anthesis, days to maturity were recorded on plot basis and grain yield were recorded in the laboratory after harvesting. Data were subjected to D2 analysis following canonical root method of Rao (1952), which was originally developed by Mahalonobis (1936). All the statistical analysis were carried out using the GENSTAT 5.13 software in IBM computer.

Results and Discussion

Analysis of variance revealed that all the genotypes showed significant variation for most of the character studied as reproductive traits.

Cluster analysis
By the application of non-hierarchical clustering using covariance matrix 24 wheat genotypes for physiological traits were grouped into three distinct clusters. Similar clustering patterns were reported by Majumder *et al.* (2004) and Hossain *et al.* (2006) in wheat. In the present study, cluster III was the largest

group, containing twelve genotypes followed by cluster I and the cluster II contained three genotypes respectively.

Table1. List of 20 spring wheat genotypes with their breeder institute and sources

Sl. No.	Varieties / lines	Breeder Institute	Source
1.	Shatabdi	BARI	Regional
2.	Kanchan	BARI	Wheat
3.	Kalyan Sona	IARI	Research
4.	BAW-1082	BARI	Center,
5.	Ananda	BARI	Shyampur,
6.	Akbar	BARI	Rajshahi.
7.	Seri-82	CIMMYT	
8.	Inia-66	CIMMYT	
9.	Gourab	BARI	
10.	BAW-1083	BARI	
11.	Prodip	BARI	
12.	Kheri	Local	
13.	Sufi	BARI	
14.	Sonalika	IARI	
15.	BAW-1056	BARI	
16.	Balaka	BARI	
17.	Barkat	BARI	
18.	Sourav	BARI	
19.	BAW-1004	BARI	
20.	Pavon-76	CIMMYT	
21.	Bijoy	BARI	
22.	Aghrani	BARI	
23.	Sonara-64	CIMMYT	
24.	Protiva	BARI	

Canonical variate analysis
The Intra and Inter cluster distance are presented in Table 3. It was revealed from the table that the inter cluster distances were larger than the intra cluster distances, which was suggested that there were wide genetic diversity among the genotypes of different clusters. The intra cluster distances in all the three clusters were more or less low which indicated that the genotypes within the same cluster were closely related. The genotypes of cluster II and III exhibited maximum divergence, as their inter cluster distance was the highest followed between I and II. On the other hand, the minimum genetic divergence was obtained in the members of cluster I and III indicating a close relationships among the genotypes of these clusters. The cluster III which showed the highest intra cluster distance (0.982) was composed of 12 genotypes and cluster II showing the lowest intra cluster distance (0.150) was composed of 3 genotypes. It indicates that within cluster diversity of the genotypes was maximum in cluster III and minimum in cluster II. So, the genotypes of the cluster III would be more stable. Somayajullu *et al.* (1970) reported that the clustering

reflected instability due to relatively lesser divergence, whereas, the widely diverged cluster remained distinct in different environments. So, cluster stability depended on magnitude of divergence. Majumder *et al.* (2004) and Hossain *et al.* (2006) drew similar conclusion. In this present study, it was expected that the crosses between the genotypes of cluster II and III would exhibit high heterosis and likely to produce new recombinants with desired traits.

Cluster means for the characters
From the cluster mean values (Table 4) of grain yield and reproductive components, it was observed that cluster II showed the highest intra cluster mean values for days to booting, days to heading, days to anthesis, days to maturity and grain yield per plant. This indicated that late and high yielding genotypes included in this cluster. Cluster I exhibited intermediate intra cluster mean values for days to booting, days to heading, days to anthesis and days to maturity but lowest value for grain yield per plant. Cluster III, which was composed of the largest number of genotypes and were earliest in booting, earliest in heading, earliest in anthesis and earliest in maturity but medium value for grain yield per plant. This indicated that comparatively early genotypes were included in this cluster.

Table 2. Distribution of 24 wheat genotypes for reproductive traits and grain yield in different clusters

Cluster no.	Total no. of genotypes in cluster	Genotypes included in different clusters
I	9	Shatabdi, Kalyan Sona, Ananda, Prodip, BAW-1056, Barkat, Sourav, BAW-1004, Protiva
II	3	Seri-82, Kheri, Pavon-76
III	12	Kanchan, BAW-1082, Akbar, Inia-66, Gourab, BAW-1083, Sufi, Sonalika, Balaka, Bijoy, Aghrani, Sonora-64

Table 3. Average intra (Bold) and inter cluster distances (D^2) for reproductive traits and grain yield in 24 wheat genotypes.

Clusters	I	II	III
I	**0.284** (0.533)	4.838 (2.199)	3.500 (1.870)
II		**0.150** (0.387)	6.919 (2.630)
III			**0.982** (0.991)

Note: The values on the diagonals (bold) are intra cluster and those on off diagonals are inter cluster distance. Figures in the parentheses are the D- values ($D = \sqrt{D^2}$)]

Table 4. Intra cluster mean values for reproductive traits and grain yield in wheat.

Characters	Clusters		
	I	II	III
Days to booting	55.04	62.33	52.64
Days to heading	64.26	69.55	59.86
Days to anthesis	70.44	76.33	67.42
Days to maturity	110.56	113.78	108.86
Grain yield per plant (g)	5.39	6.31	5.78

Table 5. Relative contributions of reproductive traits and grain yield to the total divergence in wheat

Characters	Vector - I	Vector -II
Days to booting	-0.1307	+0.9186
Days to heading	-0.7047	-1.2203
Days to anthesis	+0.1326	+0.4387
Days to maturity	+0.0163	+0.0256
Grain yield per plant (g)	+0.0228	+0.0519

Contribution of characters towards divergence

Contribution of traits towards the genetic divergence of reproductive traits and grain yield are presented in the Table 5. The Table revealed that in vector I, the important traits responsible for genetic divergence in the major axis of differentiation were days to anthesis, (0.1326), days to maturity (0.0163) and grain yield (0.0228). On the contrary, in vector II which is the second axis of differentiation, days to booting (0.9186), days to anthesis (0.4387), days to maturity (0.0256) and grain yield (0.0519) were important. Considering vector I and vector II, it was observed that days to anthesis contributed maximum towards the divergence, which was followed by days to maturity and grain yield. Again, days to booting contributed to the divergence to some extent as it showed positive value in vector II. On the other side, days to heading to be considered as the lowest contributor among the traits towards the divergence as it had negative vector values in both the vector I and II. Uddin *et al.* (1999)

and Hossain *et al.* (2006) observed that 100 grain weight was the maximum contributor to the total divergence. These information and the results of the present study suggested that the genotypes selected from more diversified clusters between II and III were more diverse and could be utilized in choosing parents for cross combinations for future hybridization program.

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