Character Association and Genetic Divergence in Spring Wheat (*Triticum aestivum l.*)

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Abstract

The present research work was aimed at to study the genetic divergence and relationship between yield and yield contributing characters in 40 genotypes of spring wheat. The characters viz. plant height, spikes/plant, spike length, grains/spike, 1000 grain weight, harvest index, vegetative period, grain filling period, days to maturity, and grain yield/ plant were investigated and significant variations were observed among the genotypes. Divergence analysis clustered the studied genotypes into 7 diverse groups. The maximum number of genotypes were clubbed in cluster I followed by Cluster II, IV, V and VI. The cluster III and VII contained minimum numbers of genotypes. Comparison of cluster means for all the characters indicated considerable genetic divergence between the groups. The highest intra-cluster distance was obtained for cluster VII followed by Cluster VI and cluster III. The maximum inter-cluster distance was observed between genotypes of cluster V and VI followed by cluster VI and VII, and cluster II and V. The scattered diagram revealed that the genotypes G2, G16, G19, G22, G28, G36 and G37 took positions at the periphery of the diagram suggesting that these varieties/lines were more diverged from rest of the genotypes. Considering yield and contributing characters it appears that the genotypes G19 (6.54) and G37 (6.65) were promising for high yield potentiality. Therefore, these two genotypes could be selected for yield improvement program in spring wheat. Study of correlations showed that grain yield/plant was significantly and positively correlated with grains per spike at both phenotypic and genotypic levels and with spikes/plant at phenotypic level. Among the studied characters, spikes/plant showed the highest phenotypic coefficient of variation followed by grain yield per plant, harvest index and 1000-grain weight. Study of heritability indicated that the characters spikes/plant, 1000-grain weight, harvest index and grain yield/plant were highly heritable. Path coefficient analysis also confirmed that spikes/plant, grains/spike, spike length, 1000-grain weight, and harvest index influenced grain yield directly in positive direction. So, these characters should be taken into consideration in selection for yield improvement.

Keywords: Genetic divergence; Character association; Spring wheat; Yield and yield contributing characters; *Triticum aestivum L*

Introduction

Yield in wheat is a complex character and various morphological and physiological characters contribute to grain yield. These yield contributing characters are related between themselves showing a complex chain of relationship of them on yield. The effectiveness of increasing yield depends on the extent to which the variability of yield is dependent on genetic factors [1]. Since, many of the quantitative plant characters which are of economic value are highly influenced by environmental condition; the progress of breeding in such a population is primarily conditioned by the magnitude and nature of variation and interrelationship of plant characters [2]. The magnitude of heritable variability for crop improvement is clearly the most important aspect. The importance of genetic diversity in the improvement of crop has been stressed in both self and cross pollinated crop [3-5]. The quantification of genetic diversity through biometrical procedures [6,7] has made it possible to choose genetically diverse parents for successful hybridization program. Moreover, evaluation of genetic diversity is important to know the source of genes for particular trait within the available germplasm [8]. The Utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution of different characters to the total divergence in self-pollinated crops has been established by several workers [9-12]. Practices of unilateral selection for them frequently end up in retrograde

or less than optimum results in plants breeding [13]. Information on correlation coefficient between yield and its contributing characters has always been helpful as a basis for selection for yield in a breeding program. Therefore, correlation between different characters is an important aspect which should be kept in mind for better planning of selection program. Thus, the study of correlation coefficient and also path coefficient between the characters is important in fact for selection practice, since it permits the prediction of correlation response. Therefore, the present investigation was carried out in wheat to determine the following objectives: 1) To evaluate the performance of some wheat genotypes for yield and yield contributing characters, 2) To study the variability for yield and yield contributing characters, 3) To study the heritability and genetic advance for different characters, 4) To study the genetic divergence among the genotypes, and 5) To study

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the interrelationship between yield and yield contributing characters.

Materials and Methods

The study was conducted at the experimental farm of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207.

Experimental site

Location: The experimental field was located at 90°33.5´ E longitude and 23°77.4´ N latitude at an altitude of 9 meter above the sea level.

Soil and climate: The soil of the experiment site was a medium high land, clay loam in texture and having pH 5.47-5.63. The land was located in Agro-ecological Zone of 'Madhupur Tract' (AEZ no. 28 or, Agro Ecological Zone No. 28). The climate of the experimental site is sub-tropical characterized by heavy rainfall during April to July and sporadic during the rest of the year.

Experimental details

Plant materials: The experimental materials of the study comprised of 40 wheat genotypes (1. G1- Kheri, 2. G2- Kalyansona, 3. G3- Sonora-64, 4. G4- Pavon-76, 5. G5- Ananda, 6. G6- Sonalika, 7. G7- Akbar, 8. G8- Balaka, 9. G9- Aghrani, 10. G10- Barkat, 11. G11- Protiva, 12. G12- Sourav, 13. G13- Gourav, 14. G14- Kanchan, 15. G15- BARI Gom 21, 16. G16- BARI Gom 22, 17. G17- BARI Gom 23, 18. G18- BARI Gom 24, 19. G19- BARI Gom 25, 20. G20- BARI Gom 26, 21. G21- BARI Gom 27, 22. G22- BARI Gom 28, 23. G23- BAW-118, 24. G24- BAW-1130, 25. G25- BAW-1138, 26. G26- BAW-1140, 27. G27- BAW-1051, 28. G28- BD-7550, 29. G29- BD-7606, 30. G30- BD-7620, 31. G31- BD-7615, 32. G32- BD-7575, 33. G33- BD-7607, 34. G34- BD-7559, 35. G35- BD-7554, 36. G36- BD-7553, 37. G37- BD-7651, 38. G38- BD-7546, 39. G39- BD-7625, 40. G40-BD-7652) (where, BAW: Bangladeshi Wheat, BD: Bangladesh). The seeds were collected from Bangladesh Agricultural Research Institute (BARI).

Design and layout: The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. The genotypes were randomly distributed within the replication.

Methods

Land preparation and fertilization: The land was prepared by plowing with power tiller followed by harrowing and laddering. All the stubbles and weeds were removed from the field. Seeds were sown at 120 kg ha^{-1} in lines 20 cm apart. Recommended fertilizer doses, 100-27-40-20-1 kg ha^{-1} of N-P-K-S-B respectively, were applied

Sowing of seeds and intercultural operations: Before sowing, seeds were treated with Provax-200 WP an effective seed treating fungicide containing of Carboxin and Thiram. Irrigations were applied at crown root initiation, booting and grain filling stages. Intercultural operations were done properly as and when necessary. Hand weeding was done after first irrigation to control weed.

Data collection: Data on ten characters were collected from the ten plants which were randomly selected from the central rows. These ten plants were harvested by uprooting.

Plant height (cm): Height of the main culm from the base to the top of the panicle excluding awn was measured in cm as plant height; **Spikes/plant:** Number of spikes were counted from each of the sample plants and were averaged over per plant; **Spikes length (cm):** Spikes length were counted from each of the sample plants and were averaged over per plant; **1000-grain weight (g):** One thousand clean sun dried grains were randomly counted from each plot and weighed in gram; **Grains/spike:** Grains from ten main spikes of the sample plants were counted and were averaged; **Harvest index:** It was recorded as the ratio of grain yield to the biological yield as per plot basis: Harvest Index = (Grain Yield / Biological Yield) × 100;

Vegetative period: Days required from germination to 50% flowering were counted as vegetative period; **Grain filling period:** Days required from 50% flowering to 50% physiological maturity were counted;

Days to maturity: Days required from germination to 50% physiological maturity;

Grain yield/plant (g): Weight of the total grains of individual plant in gram was taken as grain yield/plant.

Data analysis

The data were recorded for each character was averaged to obtain mean plot data and analysis of variance was performed using the mean values. Duncan's Multiple Range Test (DMRT) was performed using the mean values. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test differences between mean of the genotypes.

Estimation of genotypic and phenotypic coefficients of variation: Genotypic and phenotypic variances were estimated according to the formula given by Johnson et al. [14] - Genotypic variance, $\sigma^2_g =$ (VMS- EMS)/r. Where, VMS: Variety mean square; EMS: Error mean square, and r: Number of replication; Phenotypic variance, $\sigma^2_{ph} = \sigma^2_g +$ EMS. Where, σ^2_g: genotypic variance, and EMS: Error mean square. TThe genotypic and phenotypic coefficient of variation were estimated as follows: Genotypic coefficient of variation, $\sqrt{(\sigma^2_g/\bar{x})}$ X 100, $PCV = (\sqrt{\sigma^2} ph/ \bar{x}) \times 100$. Where, σ^2_g: genotypic variance, and $\bar{x}$: population mean. Similarly, the phenotypic coefficient of variation was also calculated by the formula given below: Phenotypic coefficient of variation, $PCV = (\sqrt{\sigma^2} ph/ \bar{x}) \times 100$. Where, σ^2_{ph} = phenotypic variance, and $\bar{x}$ = population mean..

Estimation of heritability: Heritability in broad sense was estimated by the formula suggested by Johnson et al. [14]. Heritability in broad sense, $h^2_b = (\sigma^2_g / \sigma^2_{ph}) \times 100$. Where, σ^2_g: genotypic variance, and σ^2_{ph}: phenotypic variance.

Estimation of genetic advance: The expected genetic advance and genetic advance in percent of mean were calculated according to Comstock and Robinson [15] - Genetic advance, GA = $h^2_b \times K \times \sigma_{ph}$. Where, h²b: heritability in broad sense, K: selection differential, the value of which is 2.06 at 5% selection intensity, and σ_{pH}: phenotypic standard deviation. Genetic advance in percent of mean, GA (%) = (GA / $\bar{x}$) × 100. Where, GA: genetic advance and $\bar{x}$: population mean

Analysis of genetic divergence: Genetic divergence among the genotypes studied was assessed by using Mahalanobis' D²-statistics and principal components and its auxiliary analyses. Both techniques estimate divergences among a set of genotypes on multivariate scale.

Mahalanobis' D²-statistics: First the variation among the materials were tested by Wilkin's criteria,

$$\frac{|W|}{|S|} = \frac{| \text{Deter min ant of error matrix} |}{| \text{Deter min ant of error variety matrix}}$$

Now, ' $V'(Stat) = -mloge^{\wedge} = -(n - \frac{p+q+1}{2})loge^{\wedge}$

Where, m = n – (p + q + 1) / 2, P = number of variables or characters, q: number of varieties = – 1 (or, d.f. for population), :d.f. for error + varieties, and e = 2.7183

Data were then analyzed for D2-statistics according to Rao [6]. Error variance and covariance matrix obtained from analyses of variance and covariance were inversed by pivotal condensation methed. Using the pivotal elements the original means of the character (X_1, X_2,............X_{11}) were transformed into a set uncorrelated variables (Y_1, Y_2,............Y_{11}). Now, the genetic divergence between two varieties/lines (suppose V_i and V_j) was calculated as $D_{ij}^2 = \sum_{k=1}^{11}(Vik - Vjk)^2$. Where, D_{ij}^2 = genetic divergence between 'ith' and 'j' th genotypes, V_{ik} = transformed mean of the ith genotype for kth character, and V^{jk} = transformed mean of the jth genotype for kth character. The D^2 values between all genotypes were arranged in order of relative distances from each other and were used for clusters formation, as suggested by [6]. Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chaudhary [16]. Average intra-cluster, $D_i^2 = \frac{\sum Di^2}{n}$ Where, $\sum Di^2$ sum of distances between all possible combinations (n) of genotypes included in a cluster, and n = all possible combinations.

Principal component analysis (PCA): Principal Component Analysis (PCA) is a multivariate technique, is being used to investigate the interrelationships among several characters and can be done from the sum of squares and products matrix for the characters. The principal component analysis finds out the linear combinations of a set of variation that maximize the variation contained within a group of genotypes. So, principal components were computed by the using correlation matrix and genotypes. So principal components were computed by the using correlation matrix and genotypes scores obtained from the first components (Which have the property of accounting for maximum variance) and succeeding components discuss the contribution of the different characters toward divergence.

Estimation of correlation: The genotypic and phenotypic correlation were estimated by the formula suggested by Miller et al. [17] - Genotypic correlation, $r_{g1.2} = \frac{Cov.g1.2}{\sqrt{\acute{o}^2g1 \times \acute{o}^2g2}}$ (Where, Cov. g$_{1.2 =}$ genotypic covariance between the trait x_1 and x_2, σ^2 g1= genotypic variance of the trait x_1, and σ$^2_{g2}$ = genotypic variance of the trait x_2.

Similarly, phenotypic correlation, $r_{ph12} = \frac{Cov.ph1.2}{\sqrt{\acute{o}^2 ph1 \times \acute{o}^2 ph2}}$ Where, Cov. ph1.2= phenotypic covariance between the trait x_1 and x_2, σ^2 ph$_1$= genotypic variance of the trait x_1, and σ^2 ph$_2$ = genotypic variance of the trait x_2.

Estimation of path coefficient analysis: The components of correlation coefficients of different characters with yield/plant were separated into direct and indirect effects through path coefficient analysis. Path coefficient analysis was done according to the procedure quoted by Singh and Chaudhary [16]. Assuming eight independent (x_1, x_2,..............., and) and one dependent variable (x_9), the relationship between them can be represented as follows: $P_{19} + r_{12}P_{29} + r_{13}P_{39} + r_{14}P_{49} + r_{15}P_{59} + r_{16}P_{69} + r_{17}P_{79} + r_{18}P_{89} = r_{19}$; $r_{12}P_{19} + P_{29} + r_{23}P_{39} + r_{24}P_{49} + r_{25}P_{59} + r_{26}P_{69} + r_{27}P_{79} + r_{28}P_{89} = r_{29}$; $r_{13}P_{19} + r_{23}P_{29} + P_{39} + r_{34}P_{49} + r_{35}P_{59} + r_{36}P_{69} + r_{37}P_{79} + r_{38}P_{89} = r_{39}$; $r_{14}P_{19} + r_{24}P_{29} + r_{34}P_{39} + P_{49} + r_{45}P_{59} + r_{46}P_{69} + r_{47}P_{79} + r_{48}P_{89} = r_{49}$; $r_{15}P_{19} + r_{25}P_{29} + r_{35}P_{39} + r_{45}P_{49} + P_{59} + r_{56}P_{69} + r_{57}P_{79} + r_{58}P_{89} = r_{59}$; $r_{16}P_{19} + r_{26}P_{29} + r_{36}P_{39} + r_{46}P_{49} + r_{56}P_{59} + P_{69} + r_{67}P_{79} + r_{68}P_{89} = r_{69}$; $r_{17}P_{19} + r_{27}P_{29} + r_{37}P_{39} + r_{47}P_{49} + r_{57}P_{59} + r_{67}P_{69} + P_{79} + r_{78}P_{89} = r_{79}$; $r_{18}P_{19} + r_{28}P_{29} + r_{38}P_{39} + r_{48}P_{49} + r_{58}P_{59} + r_{68}P_{69} + r_{78}P_{79} + P_{89} = r_{89}$. Where, P_{19}, P_{29},............, P_{89} = path coefficient of the variables x_1, x_2, x_3,..........., x_8 on variable x_9

respectively; r_{19}, r_{29}, r_{39},................, r_{89} = correlation coefficient of x_1, x_2, x_3,..............., x_8 with x_9 respectively. The residual effect was estimated as follows: Residual effect, R $\sqrt{\{1 - (r_{19}P_{19} + r_{29}P_{29} + \ldots \ldots \ldots + r_{89}P_{89})\}}$.

Results and Discussions

The data pertaining to twelve characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

Performance of the genotypes of wheat

Analysis of variance for the characters showed that there were significant variations among the genotypes for plant height, spikes/plant, grains/spike, spike length, 1000-grain weight, harvest index, vegetative period, grain filling period, days to maturity and grain yield/plant (Table 1). Sharma et al. [18] and Joshi et al. [19] also found similar result.

Variation, heritability and genetic advance

The extent of variation among the genotypes in respect to ten characters was studied and mean sum of square, phenotypic variance (σ$_{2p}$), genotypic variance (σ$_{2g}$), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h2b), genetic advance (GA) and genetic advance in percent of mean presented in Table 2. Performance of the genotypes is described below for each character.

Plant height: Significant differences were observed among the genotypes for plant height which ranged from 67.83 cm (G29) to 104.28 cm (G1) with mean value of 84.76. Randhawa et al. [20] and Johnson et al. [14] also found similar significant variation for plant height in wheat. The genotypic and phenotypic variance was observed as 38.42 and 59.21, respectively (Table 2). The phenotypic co-efficient of variation (7.31) and genotypic co-efficient of variation (9.08) were moderate for plant height. The heritability estimates for this trait was moderate with low genetic advance. Also, genetic advance in percent of mean revealed that this trait was governed by additive gene. Singh et al. [21] also reported similar result in wheat.

Spikes/plant: Significant differences were observed among the genotypes for spikes/plant which ranged from 2.33 (G36) to 8.83 (G23) with mean value of 4.19. Maloo [22] and Pawar et al. [23] also found similar significant variation for spikes/plant. The genotypic and phenotypic variance was observed as 3.37 and 3.64, respectively (Table 2). The phenotypic co-efficient of variation (43.82) and genotypic co-

Characters	Sources of variation		Error (d.f.78)
	Replication (d.f.2)	Genotype (d.f.39)	
Plant height (cm)	4.716	136.043**	20.790
Spikes /Plant (no.)	0.625	10.375**	0.274
Grains/spike (no.)	8.764	77.301**	2.827
Spikes length (cm)	3.460	5.204**	1.301
1000 grain weight (g)	2.981	103.269**	1.866
Harvest Index	2.585	276.127**	0.996
Vegetative period (days)	5.081	12.091**	5.069
Grain Filling Period (days)	1.710	25.309**	1.936
Days to Maturity (days)	14.933	54.619**	15.546
Grain yield/plant (g)	0.027	6.002**	0.032

Table 1: Analysis of variance for different morphological plant characters of 40 wheat varieties.

SL. No.	Characters	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
1	Plant height (cm)	59.21	38.42	7.31	9.08	64.89	10.29	12.13
2	Spikes /Plant	3.64	3.37	43.82	45.56	92.47	3.63	86.80
3	Grains/spike	27.65	24.82	9.04	9.54	89.78	9.73	17.64
4	Spikes length (cm)	2.60	1.30	7.31	10.33	50.00	1.66	10.64
5	1000 grain weight (g)	35.67	33.80	14.33	14.72	94.77	11.66	28.73
6	Harvest Index	92.71	91.71	35.69	35.50	98.93	19.62	72.73
7	50% Flowering	7.41	2.34	2.31	4.11	31.59	1.77	2.67
8	Grain Filling Period	9.73	7.79	6.38	7.13	80.10	5.15	11.77
9	Days to Maturity	28.57	13.02	3.28	4.85	45.59	5.02	4.56
10	Grain yield/plant (g)	2.02	1.99	32.61	32.35	98.42	2.88	66.12
	PCV: Phenotypic Coefficient of Variation; GCV: Genotypic Coefficient of Variationl; GA: Genetic Advance.							

Table 2: Estimation of genetic parameters for morphological characters related to yield.

efficient of variation (45.56) was high for spikes/plant. Maloo [22] observed high genotypic coefficient of variation for spikes/plant in wheat. Pawar et al. [23] also observed high genotypic and phenotypic coefficient of variations for this character. The heritability estimates for this trait was high with high genetic advance in percent of mean. Mahmood and Shahid [24] reported high heritability with high genetic advance for number of spikes/plant. High heritability estimates with high genetic advance for number of spikes/plant indicated that genetic effect was more pronounced for this character.

Spike length: The mean spike length was noticed as 15.61 cm with a range of 13.22 cm to 19.18a cm. The genotype G32 showed the minimum spike length and the maximum spike length was recorded in the genotype G23. The genotypic and phenotypic variances were observed as 1.30 and 2.60, respectively (Table 2). The phenotypic co-efficient of variation (7.31) and genotypic co-efficient of variation (10.33) was low for spikes/plant. The heritability estimates for this trait was medium with low genetic advance in percent of mean. Biju and Malik [25] observed significant variation for spike length and grains/spike. Bhutta et al. [26] also found highly significant variation for the traits spike length.

Grains/spike: Grains/spike also showed significant difference which ranged from 45.33 (G24) to 64.66 (G36). Joshi et al. [19] and Ehdaie and Waines [27] also found similar significant variation for spikes/plant. The genotypic and phenotypic variances were observed as 27.65 and 24.82, respectively (Table 2). The phenotypic co-efficient of variation (9.04) and genotypic co-efficient of variation (9.54) was low for spikes/plant. The heritability estimates for this trait was high with moderate genetic advance in per cent of mean. Maloo [22] observed high genetic coefficient of variation with high heritability accompanied with high genetic advance indicated additive gene. On the contrary, Singh et al. [21] reported low genotypic and phenotypic coefficients of variation, along with low heritability and low genetic advance which indicated non additive gene.

1000-grain weight: The highest grain weight found in genotype G15 (55.98) and lowest grain weight found in G34 (32.16). The mean value 40.58 was observed. The genotypic and phenotypic variances were observed as 33.80 and 35.67, respectively (Table 2). The phenotypic co-efficient of variation (14.33) and genotypic co-efficient of variation (14.72) was good for spikes/plant with high heritability (94.77) and high genetic advance (28.73). Nessa et al. [28] reported high genotypic and phenotypic coefficients of variation for 1000-grain weight in bread wheat. They estimated high genetic advance accompanied by high heritability suggesting effects of additive gene for this character.

Harvest index: Significant differences were observed among the genotypes for spikes/plant which ranged from 47.34 (G16) to 9.99 (G30) with mean value of 26.98. Austin et al. [29] found similar result. The phenotypic co-efficient of variation (35.69) and genotypic co-efficient of variation (35.50) was good for harvest index with high heritability (98.93) and high percentage of genetic advance (72.73). Austin et al. [29] reported wide range of variation for harvest index. They observed high genotypic and phenotypic coefficients of variation with high heritability accompanied by high genetic advance.

Vegetative period: Vegetative period also showed significant difference which ranged from 63.43 (G10) to 70.90 (G40). The mean value 40.58 was observed. The phenotypic co-efficient of variation (2.31) and genotypic co-efficient of variation (4.11) were low for vegetative period with high heritability (31.59) and low percentage of genetic advance (2.67). Sharma and Kaul [30] reported low genotypic and phenotypic coefficients of variation accompanied by high heritability but low genetic advance. They explained such low genetic advance as they noticed as the cause of presence of dominance and epistasis in the population. Similar results were observed by Pawar et al. [27] and Singh et al. [21].

Grain filling period: Significant differences were observed among the genotypes for spikes/plant which ranged from 50.67 (G38) to 39.67 (G22) with mean value of 43.73. The phenotypic co-efficient of variation (6.38) and genotypic co-efficient of variation (7.13) was low for harvest index with high heritability (80.10) and low percentage of genetic advance (11.77). Miah [30] reported low genotypic and phenotypic coefficient of variation with high heritability but low genetic advance.

Days to maturity: Significant differences were observed among the genotypes for days to maturity which ranged from 104.33 (G22) to 119.00 (G35 and G38) with mean value of 110.12. The phenotypic co-efficient of variation (3.28) and genotypic co-efficient of variation (4.85) was low for days to maturity with moderate heritability (45.59) and low percentage of genetic advance (4.56). Sharma and Kaul [30] carried out an experiment with wheat and observed high genotypic and phenotypic coefficients of variation with high heritability and moderate genetic advance for this character. Nessa et al. [28] also found similar result.

Grain yield/plant: Significant differences were observed among the genotypes for grain yield per plant which ranged from 2.16 (G1) to 7.18 (G26) with mean value of 4.36. The phenotypic co-efficient of variations (32.61) and genotypic co-efficient of variation (32.35) was medium for grain yield per plant with high heritability (98.42) and high percentage of genetic advance (66.12). Nessa et al. [28] reported high genotypic and phenotypic coefficients of variation and high heritability with high

genetic advance for grain yield in bread wheat. Considering yield and yield contributing characters, it appears that the genotypes G19 and G37 were promising for high yield potentiality. Both the genotypes had high grain yield. The genotype G19 was also ranked in higher position for harvest index, spike length, grains/spike and 1000-grain weight. It took 105 days to mature. The genotype G37 was the best for plant height, effective tillers/plant and grains/spike. Therefore, in this study, these two genotypes could be selected for yield improvement in spring wheat.

Genetic divergence

Genetic divergence among forty genotypes of wheat was studied through Mahalanobis' D2 –statistics and Principle Component Analysis (PCA) which has been discussed below.

Mahalanobis' D2-statistics analysis: The multivariate analysis using Mahalanobis' D2-statistics was carried out to study the genetic divergence among the forty genotypes of wheat. The genotypes were clustered and it was observed that the D2 values within cluster are low compared to between other clusters, which indicate diversity is low within a cluster. The forty genotypes of wheat were grouped into 7 clusters (Table 3). There were 4 genotypes in the cluster III and 3 varieties in the cluster VII. The number of genotypes in the remaining 5 clusters varied from 6 to 9. The cluster I included 9 genotypes which was the largest one. These were G1, G6, G18, G21, G23, G24, G27, G33 and G34. From the Table 4; it was observed that this cluster produced medium mean values for all the characters. It indicates that the genotypes included in this cluster were semi dwarf and produced medium number of grains/spike. These varieties also gave moderate grain yield with moderate seed size (as 1000 grain weight and lest weight was medium). The cluster II composed of six genotypes namely G2, G3, G4, G5, G13 and G22. It produced minimum mean value

for spike length and intermediate values for all the characters. This suggests that the varieties lines included in this group produced semi dwarf plant, with medium number of spikes plant, grains/spike, these genotypes also produced moderate grain yield with medium seed size. The cluster III contained four genotypes namely G7, G8, G10 and G29. These genotypes produced the lowest mean value for spikes/plant and intermediate values for all the remaining characters indicated that this group had minimum spikes/plant with medium number of spikelet's/spike, grains/spike, semi dwarf plant and medium duration. It also produced moderate grain yield/plant. The cluster IV consisted of six genotypes; they are G9, G11, G12, G14, G17 and G20. The genotypes of this group produced the highest 1000-grain weight, the maximum number of grain/ spike and with long vegetative period and days to maturity. It gave minimum grain yield/plant. The cluster V contained six genotypes namely G15, G16, G19, G25, G26 and G28. This group produced the highest grain yield/plant and the dwarf plant with higher number of spikes/plant and grains/spike. The growth duration of the genotypes of this group was found maximum. It also produced medium size of seeds (as 1000 grain weight) with the highest harvest index. The cluster VI contained six genotypes namely G30, G31, G36, G38, G39 and G40. It produced medium grain yield with the lowest harvest index and lowest 1000-grain weight. It had semi dwarf plant and the medium number of spikes/plant. It took medium days for vegetative period, grain filling period and days to maturity. The cluster VII composed of three genotypes namely G32, G35 and G37. It produced the highest number of spikes/plant and grains/spike. It had highest vegetative period and medium days to maturity but medium grain filling period. It also produced medium 1000-grain weight and harvest index. It contains semi dwarf plant and produced higher grain yield. It was observed from the cluster mean values that all the characters in group I, II and III were more or less similar except harvest index. Group IV contained the tallest plants and the highest 1000-grain weight. Group V had the capability to produce highest grain yield. Group VI produce average grain yield. Group VII contained the highest grains/spike. Shamsuddin [31,32] calculated genetic diversity among ten varieties of spring wheat used, as parents in diallel cross through Mahalanobis' D2-statistics. He grouped the genotypes into three clusters. Chaturvedi and Gupta [33] studied genetic divergence of 40 genotypes by using Mahalanobis' D2-statistics. Genotypes were grouped into 13 diverse clusters. Radhu et al. [34] grouped 121 genotypes of wheat into 27 clusters.

Cluster number	Number of genotypes	Percent (%)	Name of genotypes
I	9	22.50	G1, G6, G18, G21, G23, G24, G27, G33 and G34
II	6	15.00	G2, G3, G4, G5, G13 and G22
III	4	10.00	G7, G8, G10 and G29
IV	6	15.00	G9, G11, G12, G14, G17 and G20
V	6	15.00	G15, G16, G19, G25, G26 and G28
VI	6	15.00	G30, G31, G36, G38, G39 and G40
VII	3	7.50	G32, G35 and G37

Table 3: Number, percent and name of genotypes in different cluster.

Characters	I	II	III	IV	V	VI	VII
Plant height (cm)	87.63	79.99	86.59	92.43	79.40	83.82	83.46
Spikes /Plant	3.40	3.58	2.96	3.44	7.75	4.08	7.99
Grains/spike	53.85	50.12	57.40	58.52	56.83	60.33	61.66
Spikes length (cm)	15.38	14.69	15.65	16.26	15.52	18.81	17.12
1000 grain weight (g)	39.97	38.16	42.08	50.25	36.56	34.56	39.27
Harvest Index	29.44	23.43	33.41	20.51	36.68	17.74	30.23
Vegetative Period	66.61	64.50	64.85	65.88	68.93	68.98	69.79
Grain Filling Period	43.40	42.90	41.04	42.96	48.08	47.53	42.21
Days to Maturity	110.20	107.49	106.00	101.06	117.09	116.56	112.00
Grain yield/ plant (g)	3.76	3.42	5.38	3.05	6.21	4.53	5.34

Table 4: Cluster mean for twelve yield and yield characters of 40 wheat genotypes.

Intra-inter cluster distances: The average intra and inter cluster distances (D2 and D values) are presented in Table 5, Figures 1 and 2. The highest distance was noticed between the clusters V and VI and it was followed by the distances between clusters VI and VII, II and VI, I, and VI, V and VII. The distances between clusters I and IV was the minimum preceded by the distance between clusters II and IV; I and II; I and III; and III and IV. From this study, it was also observed that the distances among the genotypes of the cluster VII were higher than genotypes of other clusters. It suggests that cluster VII included more diverse materials. Where the distances among the genotypes of the cluster IV were lowest which suggests that cluster IV included less diverse materials. The Somayajulu at el. [35] reported that the clustering revealed instability due to relatively lesser divergence, whereas the widely divergent clusters remained distinct in different environment. This result supported by Raut et al. [36] and Singh el al. [37]. Therefore, cluster stability dependent on divergence. In present study, it was observed that the cluster V and VI, VI and VII, II and VI. I and VI, V and VII were highly diverged. So they would be more stable.

Principal component analysis: Principal Component Analysis (PCA) also helps in assessment of diversity for multivariate scales. The

Characters	I	II	III	IV	V	VI	VII
I	519.14 (**22.78**)	584.91 (24.18)	744.84 (27.29)	542.70 (23.30)	890.91 (29.85)	1254.03 (35.41)	1032.66 (32.14)
II		645.97 (**25.42**)	969.09 (31.13)	563.39 (23.74)	1339.14 (36.59)	1131.89 (33.64)	1194.98 (34.57)
III			657.59 (**25.64**)	1215.65 (34.87)	840.58 (28.99)	1299.95 (36.05)	1152.41 (33.95)
IV				184.90 (**13.60**)	1160.12 (34.06)	1223.14 (34.97)	1185.99 (34.44)
V					517.21 (**22.74**)	2007.23 (44.80)	1238.66 (35.19)
VI						842.82 (**29.03**)	1508.12 (38.83)
VII							1861.49 (**43.14**)

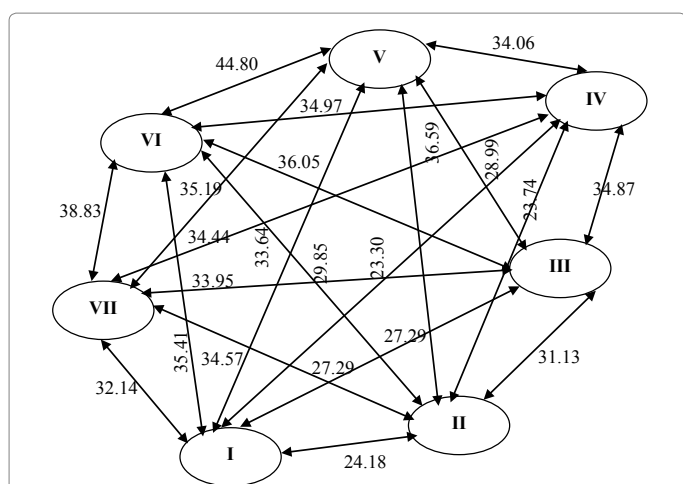**Table 5:** Intra-inter cluster distance.

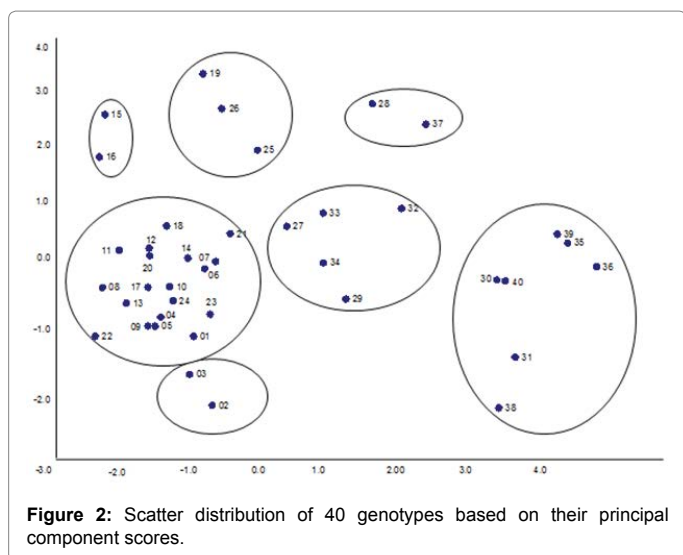**Figure 1:** Diagram showing intra and inter cluster distance of 40 genotypes.

Figure 2: Scatter distribution of 40 genotypes based on their principal component scores.

results of PCA are presented in the Table 6. The latent roots and percent of variation associated with them abstracted ten principal components. All this ten components accounted 100% of variability of which first and second component accounted for 36.92% and 22.54%. Total of these first two components summed to give 59.46% which covered the major part of the total variation. Based on these two principal components using them in axis 1 and 2 a two dimensional scattered diagram of the

Principle components	Eigen value	Percent of variance (%)	Cumulative Percentage (%)
1	3.69	36.923	36.923
2	2.25	22.545	59.467
3	1.14	11.419	70.886
4	0.786	7.870	78.756
5	0.647	6.474	85.230
6	0.527	5.278	90.507
7	0.447	4.476	94.983
8	0.295	2.955	97.938
9	0.204	2.049	99.987
10	0.0013	0.013	100.000

Table 6: Percent of variation in respect of 10 principal components.

Principle components	PCA 1	PCA 2
Plant height (cm)	-0.170	0.336
Spikes/Plant	0.439	-0.037
Grains/spike	0.223	0.418
Spikes length (cm)	0.162	0.319
1000 grain weight (g)	-0.155	0.455
Harvest Index	-0.174	0.377
Vegetative Period	0.436	0.119
Grain Filling Period	0.436	-0.110
Days to Maturity	0.499	-0.013
Grain yield/plant (g)	0.141	0.483

Table 7: Latent vectors yield and yield contributing characters in 1st and 2nd principal components.

genotypes were constructed. The scattered diagram revealed that the variety/line G2, G16, G19, G22, G28, G36, G37 took positions at the periphery of the diagram suggesting that these genotypes were more diverged from rest of the genotypes. Latent vectors or Eigen values in 1st and 2nd principal component were estimated and shown in the Table 7. The Eigen values for all the characters showed less than one in both components (axes). In the first component the character day to maturity, spikes/plant, vegetative period, grain filling period had comparatively high values than others. In the second component the character grain yield/plant, 1000-grain weight and grains/spike had high values. In the first component, the Eigen values for the grain yield/plant were positive and that plant height was negative. This suggests that the first principal component distinguished those genotypes which had higher grain yield/plant but short plant height. In the second principal component the Eigen values of both harvest index and grains/spike were negative suggesting these components distinguished those genotypes which had higher grains/spike with higher harvest index.

Relationship between yield and yield contributing characters

Relationship between grain yield and yield contributing characters of 40 wheat genotypes are studied through genotypic and phenotypic correlation coefficients, the causes of such relations are further analyzed through path analysis.

Correlation coefficients: Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components. As we know yield is a complex product being influence by several inter-dependable quantitative characters. So selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character

highly associated with yield, it simultaneously affects a number of other correlated characters. Hence, knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. Phenotypic and genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of wheat are given in Table 8.

Plant height: Plant height had non-significant positive correlation with grain yield/plant (0.047 and 0.051) at phenotypic and genotypic level (Table 8), which is supported by Shamsuddin and Ali [38]. Plant height had significant positive correlation with spikes per plant (-0.314*and -0.344*) at both levels. However, it had strong positive correlation with grains/spike (0.346* and 0.358*) at phenotypic and genotypic levels respectively.

Spikes/plant: Spikes/pant had positive correlation with grain yield/plant (0.263 and -0.274) at phenotypic and genotypic level (Table 8), which is supported by Shamsuddin and Ali [38]. Spikes/plant had significant positive correlation with grains/spike 0.324* at genotypic level. Sharma and Kaul [30] reported that grain yield was positively and significantly correlated with spikes/plant.

Grains/spike: Grains/spike had significant and positive correlation with grain yield/plant (0.373*and 0.371*) at phenotypic and genotypic level (Table 8). Grains/spike had significant positive correlation with vegetative period (0.407** and 0.320*) at both levels. However, it had negative correlation with harvest index (-0.024 and -0.031) at phenotypic and genotypic levels respectively. Sen et al. (39) observed from their study that grains/spike and 1000-grain weight showed positive and significant correlation with yield both at genotypic and phenotypic levels which support the present findings.

Spike length: Spike length had positive correlation with grain yield/plant (0.311 and 0.320*) at phenotypic and genotypic level (Table 8). Spikes length had significant positive correlation with grains/spike (0.381* and 0.395*) at phenotypic and genotypic levels.

1000-grain weight: 1000-grain weight had significant and positive correlation with grain yield/ plant (0.371* and 0.366*) at phenotypic and genotypic level (Table 8). Sen et al. [39] found the similar result. 1000-grain weight had significant positive correlation with harvest index (0.367* and 0.395*) at both levels. And it had negative correlation with vegetative period (-0.135 and -0.208) at both levels. Payal et al. [40] found positive and significant correlation between harvest index and grain yield/plant which supports the present findings.

Vegetative period: Vegetative period had significant and positive correlation with grain yield/plant (0.286* and 0.296*) at phenotypic and genotypic levels. Vegetative period had significant and positive correlation with grain filling period (0.512** and 0.366**) at both levels.

Grain filling period: Grain filling period had positive correlation with grain yield/plant (0.089 and 0.092) at phenotypic and genotypic levels. Grain filling period had significant and positive correlation with days to maturity (0.912** and 0.816**) at both levels.

Days to maturity: Days to maturity had positive correlation with grain yield/plant (0.199 and 0.207) at phenotypic and genotypic levels. Days to maturity had significant and positive correlation with grain filling period (0.912**and 0.816**) at both levels. Jinbao et al. [41] observed that days to maturity shows negative and significant correction with harvest index which supports these findings.

Path coefficient analysis: The direct and indirect effects of yield contributing characters on yield were worked out by using path analysis. In this study, yield per plant was considered as effect

Characters	correlation	Spikes / Plant	Grains/ spike	Spikes length (cm)	1000 grain weight (g)	Harvest Index (HI)	Vegetative period	Grain Filling Period	Days to Maturity	Grain yield/ plant (g)
Plant height (cm)	r_p	-0.314*	0.346*	0.098	0.294	0.181	-0.202	-0.271	-0.271	0.047
	r_g	-0.344*	0.358*	0.018	0.302	0.188	-0.237	-0.289	-0.299	0.051
Spikes/plant	r_p		0.311	0.085	-0.312*	-0.253	0.685**	0.590**	0.722**	0.263
	r_g		0.324*	0.070	-0.309	-0.251	0.776**	0.614**	0.789**	0.274
Grains/spike	r_p			0.381*	0.238	-0.024	0.407**	0.216	0.340*	0.373*
	r_g			0.395*	0.226	-0.031	0.320*	0.171	0.262	0.371*
Spikes length (cm)	r_p				0.085	0.025	0.278	0.150	0.235	0.311
	r_g				0.080	0.028	0.267	0.144	0.233	0.320*
1000 grain weight (g)	r_p					0.367*	-0.135	-0.259	-0.231	0.371*
	r_g					0.366*	-0.208	-0.287	-0.292	0.372*
Harvest index (HI)	r_p						-0.062	-0.369*	-0.278	0.415**
	r_g						-0.093	-0.385*	-0.313*	0.416**
Vegetative period	r_p							0.512**	0.817**	0.286*
	r_g							0.366*	0.538**	0.296*
Grain filling period	r_p								0.912**	0.089
	r_g								0.816**	0.092
Days to maturity	r_p									0.199
	r_g									0.207

* and ** indicate significant at 5% and 1% level of probability, respectability.

Table 8: Coefficients of phenotypic and genotypic correlation among different yield component.

Characters	Plant height (cm)	Spikes / Plant	Grains/ spike	Spikes length (cm)	1000 grain weight (g)	Harvest Index (HI)	Vegetative period	Grain Filling Period	Days to Maturity	Grain yield/plant (g)
Plant height (cm)	**-0.009**	-0.155	0.033	0.004	0.097	0.079	0.011	-0.015	0.005	0.051
Spikes /plant	0.003	**0.449**	0.030	0.016	-0.099	-0.105	-0.037	0.031	-0.014	0.274
Grains/spike	-0.003	0.146	**0.092**	0.089	0.072	-0.013	-0.015	0.009	-0.005	0.371*
Spikes length (cm)	-0.0002	0.031	0.036	**0.225**	0.026	0.012	-0.013	0.007	-0.004	0.320*
1000 grain weight g	-0.003	-0.139	0.021	0.018	**0.320**	0.154	0.010	-0.014	0.005	0.371*
Harvest index	-0.002	-0.113	-0.003	0.006	0.117	**0.420**	0.004	-0.019	0.005	0.416**
Vegetative period	0.002	0.349	0.029	0.060	-0.067	-0.039	**-0.048**	0.018	-0.009	0.296
Grain filling period	0.003	0.276	0.016	0.032	-0.092	-0.162	-0.018	**0.050**	-0.014	0.092
Days to maturity	0.003	0.223	0.024	0.052	-0.093	-0.131.	-0.026	0.041	**-0.017**	0.207
Diagonally bold figures indicate the direct effect					Residual effect = 0.4913					

Table 9: Partitioning of genotypic variance into direct and indirect effects of morphological characters of 40 wheat genotypes by path coefficient analysis.

(dependent variable) and plant height, spikes/plant, grains/spike, spike length, 1000-grain weight, harvest index, vegetative period, grain filling period and days to maturity were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of wheat in Table 9.

Plant height: Plant height had positive direct effect on yield/plant (0.051) (Table 9). It had negative indirect effect through spikes/plant (-0.155) and grain filling period (-0.015). On the other hand, plant height showed positive indirect effect on yield/plant *via* grains/spike (0.033), 1000-grain weight and days to maturity (0.005).

Spikes/plant: Spikes/plant had positive direct effect on yield/plant (0.274) (Table 9). It had positive indirect effect through grains/spike (0.030), spike length (0.016) and grain filling period (0.031). Das [42] studied path analysis and reported that the highest direct effect was obtained for number of spikes/plant on grain yield.

Grains/spike: Grains/spike had positive direct effect on yield/plant (0.371*) (Table 9). It had positive indirect effect through spike/plant (0.146), spike length (0.089), and grain filling period (0.009). On the other hand it showed negative indirect effect on grain yield/plant *via* vegetative period (-0.015) and days to maturity (-0.005). Das and Mondal [43] observed number of grains/spike and a moderate direct effect on grain yield.

Spike length: Spike length had high positive direct effect on yield/plant (0.320*) (Table 9). It had positive indirect effect through spike/plant (0.031), grains/spike (0.036) and grain filling period (0.007). On the other hand, it showed negative indirect effect on grain yield/plant *via* vegetative period (-0.013) and days to maturity (-0.004).

1000-garin weight: 1000-garin weight had high positive direct effect on yield/plant (0.371*) (Table 9). It had positive indirect effect through grains/spike (0.021) and days to maturity (0.005). On the other hand it showed negative indirect effect on grain yield/plant *via* spikes/plant (-0.139) and grain filling period (-0.014). Bhular et al. [44] suggested from path analysis that 1000-grain weight was one of the most important yield component in durum wheat.

Vegetative period: Vegetative period had positive direct effect on yield/plant (0.296) (Table 9). It had positive indirect effect through grains/spike (0.349), grains/spike (0.029) and grain filling period (0.018). On the other hand, it showed negative indirect effect on grain yield/plant *via* 1000-grain weight (-0.067) and days to maturity (-0.009). Rahman et al. [45] observed negative direct effects of vegetative period on yield. This disagreement with present findings might be due to environmental variation.

Grain filling period: Grain filling period had positive direct effect on yield/plant (0.092) (Table 9). It had positive indirect effect through spikes/plant (0.276), grains/spike (0.016), and grain filling period (0.018). On the other hand, it showed negative indirect effect on grain yield/plant *via* 1000-grain weight (-0.092) and days to maturity (-0.014).

Days to maturity: Days to maturity had positive direct effect on yield/plant (0.207) (Table 9). It had positive indirect effect through spikes/plant (0.223), grains/spike (0.024), and grain filling period (0.041). On the other hand it showed negative indirect effect on grain yield/plant *via* 1000-grain weight (-0.093) and harvest index (-0.131). Khan et al. [46] suggested hybridization program should include genotypes with greater number of grains/spike, high grain weight and high grain yield to obtain further improvement grain yield in bread wheat. From this study, it was observed that the characters grains/spike, 1000-grain weight and harvest index has positive and significant direct effect on grain yield. So, these characters should be considered for successful breeding program.

Conclusion

Selection procedure would be applied for desired characters such as lowest days to maturity and increase spikes/plant, number of grains/ spike, grain weight, and grain yield/plant. Wide range of genetic diversity existed among the wheat genotypes. That genetic diversity could be used for future breeding program of wheat in Bangladesh. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters like 1000-garin weight, harvest index and yield /plant were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

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