



Statistical analysis of yield components in the genotypes of wheat (*Triticum aestivum* L.)

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Abstract

Twenty-four genotypes of wheat have shown important variations in yield and other features that contribute to yield. The number of spikelets/spike and weight of 1000 grain showed an elevated genotypic coefficient of variability and heritability with a large proportion of mean genetic progress. The amount of tillers / m² with the amount of spikes / m² and the amount of tillers / plant with the amount of tillers / m² was discovered to be significantly positive. Number of spikes / m², number of spikelets / spike and weight of 1000 grain seemed to be the efficient yield enhancement criteria. The largest amounts of genotypes were found in clusters III and V (6). The maximum inter-cluster distance was observed between clusters III and V (18,689) and the largest intra-cluster distance was recorded in cluster I (2,847) and broad variation range was also noted for the characters studied in cluster mean results.

Keywords: genetic variability, correlation, diversity, cluster

1. Introduction

Wheat (*Triticum aestivum* L.) is the chief cereal of the temperate regions and of the most widely grow and the most important of wheat races. It has been recognized as the source of principal food of man for centuries. About fifty countries of the world, wheat regarded as the staple food. Wheat offers a great wealth of material for genetically studies due to its wide ecological distribution and enormous variation encountered for various morphological and physiological characters^[1].

Wheat is the second important cereal crop after rice in Bangladesh. It covers 645.5 thousand hectares of land in the year 2012-2013, which produced 1960 thousand tons grain in the same year^[2]. During the long association man has improved the yield and other agronomic characters of wheat plant by selection man have improved the yield and other agronomic characters of wheat plant by selection among the exaction genotypes. Modern plant breeding methods have accelerated the rate of improvement of wheat for yield and other agronomic characters. Grain yield in wheat is a complex phenomenon as it is polygenically controlled. For effective selection, information on nature and magnitude of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary. In such situations, correlation and genetic variability analysis could be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components. Singh and Singh^[3] reported positive correlation between number of tillers per plant and peduncle length.

Baisak and Nayak^[4] observed positive correlation of peduncle length with grain yield. According to Gupta *et al.*^[5] there was positive correlation between spike length and grain yield. Khan *et al.*^[6] and Chowdhury *et al.*^[7] also conducted such studies and concluded that yield components like tillers/plant, grains/spike and 1000 grain weight are main contributors to grain yield in wheat. Narwal

et al.^[8] concluded that tillers per plant have positive direct effect and indirect effect via plant height. Correlation and genetic variability analysis leads us to a clear understanding of the genetic association of various plant traits and their contribution to yield. Keeping these facts in view the present studies were conducted to have such valuable information's.

The present research was conducted to evaluate genetic diversity among different genotypes of wheat to compare them for association of morphological traits under water stress conditions, as well as to use in breeding programs and to identify near and far groups of genotypes for using them in suitable cluster.

2. Materials and methods

The experiment was conducted during Rabi season of 2016-2017 at Experimental Research Field of Islamic University, Kushtia, Bangladesh, and Soil pH ranged from 7.0-7.5. Genetically pure and physically healthy seeds of 24 diverse genotypes of wheat were collected from Biometrical Genetics Laboratory, Department of Botany, University of Rajshahi., Wheat Research Centre, Dinajpur., Bangladesh Agricultural Research Institute, Joydebpur, Gazipur and Wheat Research Centre, Shampur, Rajshahi. The experimental material consists of twenty four varieties of spring wheat Such as. Akbar, Ananda, Aghrani, BAW-1059, BAW-1064, Bijoy, Balaka, Barkat, Durum, Gourab, Inia, Kheri, Kanchan, Kalyansona, Pavon-76, Prodip, Protiva, Sufi, Seri-82, Sourav, Sonora-64, Sonalika, Shatabdi and Triticale. These genotypes were planted in the field according to RCBD with three replications. Recommended agronomic package and practices were applied to raise a healthy crop. There were three lines per genotype in each replication. Seeds were sown with the hand and to maintaining row to row distance of 25 cm, plant to plant distance of 15 cm and the replication to replication distance of 125 cm. Recommended doses of major nutrients such as N: P: K; 120:60:60. Normal cultural practices were

followed. All other agronomic practices were kept uniform. Observations were recorded on ten randomly and competitive plants of each genotype from each replication for different quantitative spike characters at maturity stage *viz.*

1. Number of tillers/plant
2. Number of fertile tillers/plant
3. Number of tillers/m²
4. Number of spikes/m²
5. Number of spikelets/spike
6. Number of grains/spike
7. 1000-grain weight (gm)
8. Straw yield (ton/ha)
9. Grain yield/plant
10. Grain yield (ton/ha)

Data from five plants of each genotype were averaged replication wise and mean data was used for statistical analysis. The collected data were analyzed following the biometrical techniques of analysis as developed by Mather [9] based on mathematical model of Fisher [10]. The analysis of variance and covariance for all above mentioned traits were performed following Steel and Torrie [11]. Correlation matrix was prepared using formulae developed by Kwon and Torrie [12].

Genotypic and phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation were estimated as suggested by Singh and Chaudhary [13]. Broad sense heritability was calculated as suggested by Johnson *et al.* [14], genetic advance (GA) and genetic advance as percent of mean (GA%) were calculated by Johnson *et al.* [14] and Hanson *et al.* [15]. Genotypic and phenotypic covariances were estimated according to the formulae suggested by Singh and Chaudhary [13]. Genotypic correlation coefficients were calculated using the formulae suggested by Miller *et al.* [16]. Multivariate analysis was done based on Mahalanobis analysis, D²-statistics [17] using GENSTAT-5 computing software.

3. Results and discussion

Mean performances of different characters of the genotypes are shown in Table 1. Significant differences were found among most of the genotypes in respect of different characters. Highest mean performance was recorded for number of tillers/m² which was followed by number of spikes/m² and minimum in grain yield/plant (Table 1). The result revealed that genotypic coefficient of variability was less than its corresponding estimates of phenotypic coefficient of variability for all the characters indicated significant role of environment in the expression of these characters.

Relatively higher estimates of genotypic coefficient of variability for number of spikes/m², 1000 grain yield and number of tillers/m² suggest that the selection can be effective for these characters. Small differences existed between the value of genotypic and phenotypic variance for the characters were less influenced by the environment. Similar findings were also found by Khan *et al.* [18, 19] and [20]. Most of the characters had high heritability in a broad sense estimates indicating preponderance of dominance gene action. Higher genetic advance in percentage of mean for 1000 grain weight, straw yield, number of spikelet's/spike, number of grains/spike and grain yield/plant depicts dominance gene effects. Highest

heritability estimated were observed in case of 1000 grain weight followed by number of grains/spike which also indicated that these characters were also less influenced by the environments. Heritability estimates along with genetic advance in % of mean are more helpful in predicting gain under selection than heritability estimate alone [21].

In the present study, 1000 grain weight number of spike/m² and number of spikelet's/spike indicating broader genetic base and wider adaptability thus greater scope for selection in these traits. Ahmadi and Bajelan [22] and Khan and Naqvi [23] also reported the presence of high heritability and genetic advance in % of mean different yield related attributes in wheat. High heritability in a broad sense estimates for plant height, number of grains/ear [24-27].

In this study, the characters studied had positive correlation with grain yield (Table 2). The highest significant positive correlation with grain yield was shown by number of grains/spike followed by 1000 grain weight at genotypic level. These findings are in good in agreement with earlier results [28-30].

Thus from the estimates of heritability, genotypic coefficient of variation and genetic advance in percentage of mean the 1000 grain yield, number of spikelet/spike and number of spike/m² could be suggested as the effective criteria in breeding wheat for yield improvement.

Twenty four wheat genotypes were grouped into five different clusters by using clustering techniques. The wheat genotypes distribution is presented in Table 3. The maximum genotypes numbers (6) are in clusters II and V which were followed by cluster I (5). The cluster III contained three genotypes and occupied least position.

The D² analysis carried out involving 24 wheat genotypes for 9 characters revealed that altogether 5 clusters have been formed (Table 4). Inter and intra-cluster distance ($D = \sqrt{D^2}$) values were worked out from divergence analysis and are presented in Table 4.

From the table it was revealed that the inter-cluster distance was larger than the intra-cluster distance indicating wide diversity among the genotypes of different groups. The maximum intra-cluster distance (2.847) was observed in cluster I followed by cluster II (1.822) and IV (0.712). The highest inter-cluster distance (18.689) was observed between clusters III and V followed by clusters I and III (16.040) and III and IV (14.452) contained approximately same values, suggesting more variability in genetic makeup of the genotypes included in these clusters. These finding were supported by Azad *et al.* [31] and Zaman and Alam [32]. The cluster mean values were estimated for different characters (Table 5) and it was observed that cluster II had the highest mean values for all the traits in desired direction followed by cluster IV and cluster V. Highest number of tillers/m² and number of spikes/m² were observed in cluster III and selection for these traits will be very effective from cluster III.

The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 6. The values of vector 1 and vector II revealed that both the vectors had positive values for number of fertile tillers/plant, grain yield/plant. Negative values in both the vectors were for most of the characters indicated these two characters had lowest contribution to the total divergence. So, the greater divergence in the present materials due to these three characters will offer a good scope for improvement of yield through selection of genotypes. These results get sufficient

validation from the findings of Azad *et al.* [31] and Zaman and Alam [32].

Table 1: Estimation of mean performance and genetic parameters for grain yields and yield components in wheat genotypes.

Characters	Mean	MS of Genotypes	PCV%	GCV%	h ² b%	GA(%) of mean
Number of tillers/plant	5.250	0.521	7.512	3.012	40.103	11.565
Number of fertile tillers/plant	4.236	0.376	9.152	2.057	22.480	8.314
Number of tillers/m ²	320.80	2110.15**	570.717	54.210	9.498	2.624
Number of spikes/m ²	273.10	1943.55**	518.543	147.925	28.526	8.654
Number of spikelets/spike	19.830	29.129**	51.173	46.683	91.224	29.937
Number of grains/spike	52.040	256.811**	22.957	14.916	66.903	28.318
1000-grain weight (g)	35.74	119.347**	121.654	119.925	98.578	38.981
Grain yield/plant(g)	1.847	0.418	34.357	5.990	58.315	14.867
Straw yield (ton/ha)	4.740	1.195	15.087	5.486	36.363	22.933
Grain yield (ton/ha)	2.574	0.436	18.458	11.232	60.853	31.516

*** Significant at 5% and 1% level of probability.

Table 2: Genotypic correlation coefficient for different pairs of yield related characters in wheat.

Characters	NFTP	NT/ m ²	NS/m ²	NSt/S	NGS	TGW	GYP	SYP	GY
NTP	0.287	0.991**	0.989**	-0.115	-0.824**	0.150	0.047	0.183	-0.028
NFTP		0.899**	0.919**	-0.181	-0.434	0.022	0.019	0.046	-0.025
NT/m ²			0.999**	0.909**	-0.979**	-0.988**	-0.897**	0.899**	-0.886**
NS/m ²				-0.899**	-0.993**	0.998**	0.796**	0.895**	0.499
NSt/S					0.997**	-0.992**	0.414	0.899**	0.594*
NGS						-0.917**	0.639*	0.889**	0.899**
TGW							0.796**	0.290	0.739**
GYP								0.133	0.121
SYP									0.091

Legend: Number of tillers/plant=NTP, Number of fertile tillers/plant=NFTP, Number of tillers/m² =NTm2, Number of spikes/m² =NS/m2, Number of spikelet's/spike=NSp/S, Number of grains/spike=NGS, 1000-grain weight=TGW, Grain yield/plant=GYP, Straw yield (ton/ha) =SY and Grain yield (ton/ha) =GY, Note: *- Significant at 5% level, ** - Significant at 1% level.

Table 3: Distribution of 24 wheat genotypes for different characters in different clusters.

Cluster No.	No. of Genotypes
I	5
II	3
III	6
IV	4
V	6

=24

Table 4: Average intra (bold) and inter cluster distance (D²) of 24 wheat genotypes obtained on the basis of nine spike related characters.

Clusters	I	II	III	IV	V
I	2.847				
II	7.825	1.822			
III	16.040	8.266	0.481		
IV	3.833	7.032	14.452	0.712	
V	8.295	12.326	18.689	5.655	0.000

Table 5: Cluster mean values for yield related characters of 24 wheat genotypes.

Characters	Clusters				
	I	II	III	IV	V
Number of tillers/plant	3.89	4.50	4.67	3.85	3.52
Number of fertile tillers/plant	2.78	3.33	3.33	2.85	2.57
Number of tillers/m ²	294.78	352.00	371.00	317.42	286.57
Number of spikes/m ²	269.33	274.00	271.33	239.12	210.00
Number of spikelets/spike	19.67	20.33	27.67	19.76	19.86
Number of grains/spike	48.67	52.34	47.67	49.91	47.86
1000-grain weight (g)	37.00	31.50	29.33	32.42	33.19
Straw yield (ton/ha)	2.57	3.44	4.79	2.77	2.99
Grain yield/plant (g)	1.81	1.67	1.51	1.57	1.57
Grain yield (ton/ha)	2.06	2.13	2.16	1.84	2.01

Table 6: Relative contribution of yield related characters to the total divergence in wheat.

Characters	Vector I	Vector II
Number of tillers/ plant	-0.137	0.407
Number of fertile tillers/plant	0.123	0.419
Number of tillers/m ²	-0.149	0.343
Number of spikes/m ²	-0.090	0.355
Number of spiklets/spike	-0.288	-0.210
Number of grains/spike	-0.216	-0.168
1000-grain weight (g)	-0.030	-0.104
Straw yield (ton/ha)	-0.354	-0.046
Grain yield/plant(g)	0.209	0.233
Grain yield (ton/ha)	-0.248	-0.124

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