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Selection of parents for hybridization in wheat (*Triticum aestivum* L.)

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Abstract

This experiment was carried out during Rabi 2013-14 at the research field and laboratory of the department of Genetics and Plant Breeding, HSTU, Dinajpur with 24 wheat genotypes to study the heritability, genetic advance, divergence and to select parents for hybridization program. Twenty four genotypes were evaluated in Randomized Completely Blocked Design (RCBD). The study revealed a wide range of genetic advance and high broad sense heritability for most of the traits. Genetic advance in percent of mean suggested that there is yet scope for further improvement of genotypes for the characters studied. The grain weight of 10 spike, grains/spike and thousand grain weight had high genotypic and phenotypic co- efficient of variation. So selection for these three characters will be highly effective and efficient for improvement. Twenty four genotypes were grouped into five different clusters. The inter cluster distances was the highest between cluster I and cluster II (10.24) and the lowest between cluster V and cluster III (7.29). The result revealed that genotypes located in cluster I and II were far diverse than the genotypes located in cluster V and cluster III. So hybridization with the genotypes of cluster I will be more effective with the genotypes located in cluster II and V. Considering diversity pattern, cluster distance ,cluster mean and other agronomic traits the genotypes E-11,E-21, E-24 of cluster I, E-2 , E-6, E-20 of cluster II, E-19 of cluster IV and E-10, E-15, E-16, E-17 of cluster V may be used as parents for fruitful improvement of yield and yield contributing characters in wheat.

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Introduction

Wheat (*Triticum spp.*) is an ancient most widely cultivated cereal crop in the world which ranks first globally and second in Bangladesh. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. The total area under wheat crop has been estimated 1061602 acre (429602 hectares) as compared to 1029268 acres (416522 hectares) of the year 2013 which is 3.14% higher than previous year. Average yield of wheat has been estimated 3.03 metric tons per hectare which is 0.66% of the higher than the last year. (BBS, 2014). The highest production of wheat in 2013 is estimated in EU 143.3 million metric ton followed by China (121.7 mmt), India (93.5 mmt), United States (60.00 mmt), Russia (52.1), Canada (37.5) Pakistan 24.2 (FAO, 2013) where as the production of wheat in Bangladesh is 1.302 million metric ton (BBS, 2014). So selection of parents is important to produce high yielding variety. One of the important approaches to wheat breeding is hybridization and subsequent selection. Parent's choice is the first step in plant breeding program through hybridization. In order to benefit transgressive segregation, genetic distance between parents is necessary (Joshi *et al.*, 2004).The higher genetic distance between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966; Anand and Murrty, 1968). Local varieties are low yielding and exotic parents had higher yield but with longer maturity, small, red grain color and less adaptive to our environment. So, both are not suitable for selection of parents. The released varieties are high yielding highly adaptive to the local climate and have greater farmers demand. So selection of parents from released varieties and advance lines according to genetic divergence is very suitable. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004). Some appropriate methods, cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity,

and study interaction between the environment are currently available (Bhatt, 1970; Carves *et al.*, 1987; Mohammadi and Prasanna, 2003; Eivazi*et al.*, 2007) Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety (Benadeki, 1992). Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. The choice of parents is of paramount in breeding program. So the knowledge of genetic diversity and relatedness in the germplasm is a pre requisite for crop improvement program. (Barma *et al.*, 1990).The parents will be selected for hybridization to produce a new high yielding variety. Many works were conducted on the genetic divergence of wheat with physiological characters. So the present study was undertaken for parent selection by analyzing the genetic divergence of 24 wheat genotypes collected from WRC, Dinajpur to ensure effective improvement.

Materials and methods

The experiment was set up at the central research farm and laboratory of Genetics and Plant Breeding Department, Hajee Mohammad Danesh Science and Technology University (HSTU), Dinajpur during October 2013 to June 2014. The experimental site is situated under the Dinajpur Sadar Upazila and located at 25⁰39′ N latitude and 88⁰41′ E longitude with an elevation of 37.58 meter above the sea level. For conducting the present study, the base materials were collected from the Wheat Research Center (WRC), Dinajpur. The experimental material materials of the study were consisted of twenty four wheat (*Triticum aestivum* L.) genotypes. The experiment was conducted in a Randomized Complete Block Design. The unit plot size was 2.0 m x 5.0 m where showing was done in ten rows with 20 cm interval between rows. The distance between plots

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was 0.75 m and block to block distance was 1.5 m. Fertilizer was applied at the rate of 300 kg, 170 Kg, 100 Kg,110 Kg and 6 Kg Urea, TSP, MP, Gypsum and Boron respectively. After land preparation, full dose of P, K, S, Zn, B and one third of N were incorporated thoroughly into the soil as basal dose. The remaining amount of N was applied at 21 and 53 days after seedlings emergence split into two equal amounts. Data on thirteen characters were collected from some randomly and tagged 10 plants from the middle rows excluding borders and some from plant basis. These 10 plants were harvesting by uprooting. Data were recorded for Heading days, Anthesis, Days to maturity, Plant height (cm), Number of plants/ square meter, Number of spikelets per spike, Number of grains per spike, Grain weight of 10 spikes, Thousand grain weight (Kg), Grain yield (Kg/plot), Canopy temperature depression (CTD), Chlorophyll content of flag leaf at 14 days after anthesis (CHL_{21}) (SPAD unit) at either flowering time or physiological maturity. The CTD was recorded at 90 days after anthesis during noon period under bright sunlight and less wind with the help of hand held infra-red thermometer (Model: Crop TRAC item no. 2955L-Spectrum Technologies, Inc.). This trait Chlorophyll content was measured in 5 fully expanded sunlight flag leaves in *vivo* by a Minotola SPAD meter at 14 days after anthesis and expressed in SPAD unit.

Statistical analysis

The data recorded from the present study were analyzed statistically in a computer based statistical package MSTAT – C program and Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2007 software through four techniques *vrz*, principal component analysis, principal coordinate analysis, cluster analysis and canonical vector analysis.

Results and discussions

1. Analysis of variance for different quantitative characters

The analysis of variance for thirteen morpho-physiological characters was carried out to partition the total variance due to genotypes and other sources. The mean squares of 13 characters presented in Table 1. The results indicated that there was significant variation among the genotypes for almost all the characters. Percent of co-efficient of variation (% CV) for all the thirteen characters was good. So there is a scope for improvement through selection. It was varied from the lowest 2.54 in canopy temperature to the highest 9.28 in spikes /m².

Table 1. Mean squares for yield and others characters of wheat genotypes.

Characters	Replication (2)	Genotype (23)	Error (46)	CV (%)
Heading (days)	33.681**	28.246**	4.999	3.19
Anthesis (days)	79.514**	29.536**	13.007	4.56
Plant height (cm)	264.087**	94.415**	8.646	2.88
Maturity (days)	127.042**	21.009**	7.969	2.66
Plants/m²	538.014NS	2184.98**	818.159	8.04
Spikes/m²	230.181NS	1981.27**	887.644	9.28
Grain weight of 10 spike	35.447**	21.064**	3.084	7.32
Grains spike	196.047**	33.767**	7.704	5.82
Tgw	5.173NS	65.615**	13.769	7.54
Spikletes spike⁻¹	1.413NS	4.616**	0.794	4.59
Yield/plot (kg)	0.766**	0.363**	0.094	6.04
Chlorophyll content	3.991NS	14.659**	1.584	3.04
Canopy temp	0.078NS	0.567**	0.245	2.54

**indicates significant at 1% level of provability

*indicates significant at 5% level of provability and

NS indicates non-significant.

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2. Genotypic and phenotypic co-efficient of variation, and heritability and genetic advance

Study of phenotypic and genotypic co–efficient of variation, heritability and genetic advance for yield and its different contributing characters are shown in Table 2 and 3. It was observed earlier that there was significant variation among the varieties / lines for all the characters. The variation among the varieties / lines was judged at phenotypic and genotypic levels. Among the different characters heading days, anthesis, plant height, maturity days, plants/m², spikes/m², grains/spike and 1000-grain weight displayed more than 10% variation at phenotypic level, which could be considered as high enough. At genotypic level, plant height, plants/m², spikes/m², and 1000-grain weight had more than 10% variation

and others had less 8% variation. Navin *et al.* 2014 observed highest estimates of GCV and PCV in grain yield per plant followed by biological yield and harvest index (GCV 22.87 and PCV 23.03). The plants/m², spikes/m² exhibited comparatively higher genetic advance. These characters have low heritability but higher genotypic and phenotypic variance. Heading, plant height, grain weight of 10 pike, grains/spike and 1000 grain weight displayed medium genetic advance. Plant height, grain eight of 10 spikes and 1000 grain weight had higher genetic advance in percentage mean (%). Among them grain weight of 10 spike, grains/spike and thousand grain weight had high genotypic and phenotypic co-efficient of variation. Therefore, selection for these characters would be effective.

Table 2. Genetic parameters of 13 important characters of wheat genotypes.

Characters	Genotypic variance	Phenotypic variance	Genotypic coefficient of variation	Phenotypic coefficient of variation
Heading (days)	7.75	12.75	3.98	5.10
Anthesis (days)	5.51	18.52	2.97	5.44
Plant height (cm)	28.59	37.24	5.24	5.98
Maturity (days)	4.35	12.32	1.96	3.31
Plants/m²	455.61	1273.76	6.00	10.03
Spikes/m²	364.54	1252.18	5.95	11.03
Grain weight of 10 spike	5.99	9.08	10.21	12.57
Grains spike	8.69	16.39	6.18	8.49
Tgw	17.28	31.05	8.45	11.32
Spikletes / spike	1.27	2.07	5.81	7.40
Yield/plot (kg)	0.090	0.184	5.91	8.46
Chlorophyll	4.36	5.94	5.05	5.89
Canopy temp	0.107	0.352	1.68	3.05

Table 3. Heritability in broad sense, genetic advance in percentage of mean for13 important characters of wheat genotypes.

Characters	Heritability (broad sense)	Genetic advance	Genetic advance in percentage mean (%)
Heading (days)	60.79	4.47	6.39
Anthesis (days)	29.76	2.64	3.34
Plant height (cm)	76.78	9.65	9.46
Maturity (days)	35.29	2.55	2.40
Plants/m²	35.77	26.30	7.39
Spikes/m²	29.11	21.22	6.61
Grain weight of 10 spike	66.03	4.10	17.09
Grains spike	53.00	4.42	9.27
Tgw	55.66	6.39	12.98
Spikletes/spike	61.61	1.82	9.40
Yield/plot (kg)	48.82	0.431	8.51
Chlorophyll	73.34	3.68	8.90
Canopy temp	30.46	0.372	1.91

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3. Principal Component Analysis (PCA)

Principal Component Analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma, 1998). The eigen values are often used to determinate how many factors to retain. The sum of eigen values is usually equal to the no of variables. Eigen values of 13 principal component axes and percentage of total variation accounting for them obtained from principal component analysis are presented Table 4. The result revealed that first axis largely accounted for the variation among the genotypes (27%) followed by second axis (23.90%). The First 5(five) axes accounted 83.42% of the total variation among the 13 traits describing 24 genotypes while the former two accounted 50.90%. Haileaiorgis *et al.* (2011) studied principal components analysis and the result revealed that nine principal components (PC1 to PC9) accounted nearly 80 % of the total variation. Khodadadi *et al.* (2011) found over 97% of genetic variation based on Principal Component Analysis (PCA). Cluster analysis based on PCA using the first five principal components indicated six separate groups of genotypes, with the maximum genetic distance observed between Sardari and Vorona/Kauz (VO) genotypes. Such differences in genetic component of traits studied in this manuscript can be applied as a new source of variation in other breeding programs and crossing nurseries for wheat improvement.

Table 4. Percent of variation in respect of 13 principal components in of wheat genotypes.

Principal component axis	Eigen value	Percent of total variation accounted	Cumulative percent
Heading (days)	3.51	27.00	27.00
Anthesis (days)	3.10	23.90	50.90
Plant height (cm)	1.75	13.53	64.43
Maturity (days)	1.42	10.97	75.41
Plants/m²	1.04	8.01	83.42
Spikes/m²	0.692	5.32	88.75
Grain weight of 10 spike	0.496	3.81	92.56
Grains spike	0.385	2.96	95.53
Tgw	0.228	1.75	97.29
Spikletes spike⁻¹	0.171	1.31	98.61
Yield/plot (kg)	0.094	0.729	99.33
Chlorophyll content	0.071	0.542	99.88
Canopy temp.	0.015	0.119	100.00

Scatter diagram analyzes the relationships between two variables. One variable was plotted on the horizontal axis and the other was plotted on the vertical axis. The pattern of their intersecting points can graphically show relationship patterns. Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram using the component score 1 as X –X́axis and component score 2 as Y-Ý axis was constructed and presented in fig. 1. The position of genotypes in the scatter diagram were apparently distributed into five groups, which indicated that there exists considerable diversity among the genotypes.
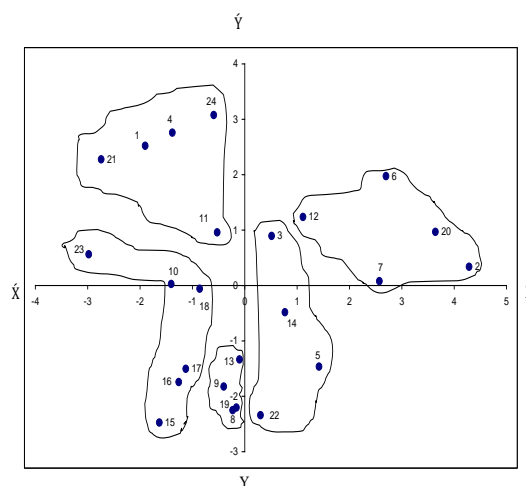

Fig. 1. Scatter diagram of 24 wheat genotypes based on their principal component scores.

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4. Canonical vector analysis

Canonical vector analysis was done to compute the intra cluster Mahalanobis'sD²values.The intra and inter cluster distance (D²) values are presented in table 5. Statistical distances represent the index of genetic diversity among the clusters. The inter cluster distances were larger than intra cluster distances suggesting wider genetic diversity among the genotype of different groups. The genotype within a cluster tends to diverse less from each other possibly due to similarity of percentage. This result supports with the finding of Ahmed *et al.* (2002). Higher inter and intra cluster distances indicate the higher genetic variability among accessions between and within clusters, respectively. The lower inter and intra cluster distance indicates closeness among the accession of two clusters and within the clusters. Choudhery *et al.* (2006) obtained larger Inter-cluster distances than the intra-cluster distances in a multivariate analysis in wheat. The maximum inter cluster distance was observed between the cluster I and II(10.24) followed by the distance between cluster II and III(9.45) and between cluster II and IV(9.07).The maximum value of inter- cluster distance indicated that the genotype belonging to cluster I was far diverged from those of cluster II. Similarly the higher inter cluster values between cluster II and III, cluster II and IV indicated that genotype belonging to each pair of clusters were far diverged. In the present study the inter cluster distances between the cluster with other clusters ranged from 10.24 to 7.29 suggesting crossing E-2 and E-20 genotypes of cluster II with desirable genotypes of other clusters such as 21, E-24 and E-1 of cluster I would express heterotic effect. The intra-cluster distances were computed by the values of inter genotypic distance matrix of PCO. There was no marked variation in intra-cluster divergence which varied from 5.08 to 7.96 (Table 8). The maximum intra-cluster cluster was computed for the cluster II(7.96), consisted of 5 genotypes of diverse origin followed by the cluster V (6.37), composed of 6 genotypes, while the minimum distance (5.08) was observed in the cluster III that composed of 4 genotypes. However, the highest values of intra-

cluster distance in cluster II indicated the genotypes (5) constituted this cluster though included in the same cluster there might have considerable diversity among them. Similarly the minimum distance (5.08) was observed in cluster III which indicated that 4 genotypes indicated in cluster were genetically very close to each other.

Table 5. Average intra (bold) inter-cluster distance (D² and $\sqrt{D^2} = D$) for wheat genotypes.

Cluster	I	II	III	IV	V
I	**43.86**	104.89	70.22	72.58	71.92
	(6.62)	(10.24)	(8.38)	(8.52)	(8.48)
II		**63.42**	89.33	82.24	80.78
		(7.96)	(9.45)	(9.07)	(8.99)
III			**25.77**	55.03	53.21
			(5.08)	(7.42)	(7.29)
IV				**26.84**	58.43
				(5.18)	(7.64)
V					**40.52**
					(6.37)

The pattern of distribution of genotypes into various clusters is given in table 6. The distribution pattern indicated that the maximum number of genotypes (6) were indicated in cluster V followed by cluster I (5), cluster II (5) and cluster III (4) and cluster IV (4). Shamsuddin (1985) grouped into 16 genotypes of spring wheat into three clusters. According to the Nidu and Satayanarana (1991) the number of genotypes in each cluster varies with the environments. Chaturvedi and Gupta (1995) studded 44 genotypes of wheat and grouped into 13 clusters where the maximum number of genotypes were included in cluster V (19 genotypes) followed by cluster II (14) genotypes and cluster I (7) genotypes

Intra–cluster means for thirteen traits are presented in table 7. The result revealed that the cluster remarkably distinguished for most of the traits which is indicative of proper clustering. The cluster I had the highest chlorophyll content and canopy temperature. This cluster had the lowest intra-cluster mean for heading, anthesis, plant height, maturity and spikelet per spike. As the genotypes in the cluster I showed

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earlier maturity where as genotypes in cluster III were late maturing and hence the representative genotypes of cluster I can be used for induction of earliness. The cluster II had the height plant height, plants/m² and spikes /m². The genotypes in the cluster II can be used for the improvement of plant height.

Table 6. Distribution of 24 wheat genotypes in different cluster.

Cluster	No. of genotypes	Percent of total Genotypes	Entry/Genotypes number	Entry/Genotypes name
I	**5**	20.83	1, 4, 11, 21, 24	Aghrani, Gourab, BARI-27, PYT-19 and BAW-1135
II	5	20.83	2, 6, 7, 12, 20	Protiva, Sufi, Bijoy, BARI-28 and PYT-18
III	4	16.67	3, 5, 14, 22	Sawrav, Shatabdi, PYT-11 and PYT-20
IV	4	16.67	8, 9, 13, 19	Prodip, BARI-25, PYT-6 and PYT-16
V	6	25.00	10, 15, 16, 17, 18, 23	BARI-26, PYT-12, PYT-13, PYT-14, PYT-15 and PYT-21

This cluster had the lowest grain weight of 10 spike and grains/spike. This cluster III had the highest intra cluster mean for the heading and days to maturity. This cluster had the lowest spikes/m² and thousand grain weight. The cluster IV had the highest anthesis and spikelets per spike and lowest plants/m², yield per plot and lowest canopy temperature. Its ability to maintain cooler canopy at the vegetative growth stage and grain filling stage. The grain filling rate is important in Bangladesh condition. Due to short and mild winter, wheat crop faces terminal heat stress during grain filling period. As a result grain became small and shriveled, consequently yield reduced. So genotypes belonging cluster IV will be effective for develop heat stress variety.

Table 7. Cluster mean for yield and yield contributing 13 characters in wheat genotypes .

Components	Clusters				
	I	II	III	IV	V
Heading (days)	66.26	71.60	74.17	70.08	69.00
Anthesis (days)	75.87	77.87	81.00	82.25	79.33
Plant height (cm)	95.97	108.20	103.24	102.08	100.91
Maturity (days)	103.33	106.53	108.58	107.25	105.72
Plants/m²	345.80	398.86	353.58	338.24	342.00
Spikes/m²	314.47	358.20	308.66	312.75	308.72
Grain weight of 10 spike	23.20	20.40	23.49	25.30	27.03
Grains spike	47.57	44.62	49.21	46.25	50.25
Tgw	48.36	46.31	45.09	52.22	53.08
Spikletes/ spike	18.04	19.68	19.59	21.02	19.16
Yield/plot (kg)	4.89	5.14	5.15	4.64	5.36
Chlorophyll	43.19	40.82	42.20	42.35	39.07
Canopy temp	19.98	19.59	19.41	19.09	19.31

Gartan *et al.* (2003) observed that cluster I had the highest mean value for grain yield and spike length and the second highest mean values for number of tillers and early maturity. Cluster VI also recorded the greatest 100-seed and 1000-seed weights.

The genotypes in cluster V (E-10, E-15,E-16,E-17,E-18 and E-23) showed maximum 1000 grain weight, grain weight of 10 spike, yield (Kg per plot) and grains per spike, and therefore these genotypes could be exploited for their direct release as a variety after testing under wide range of environments. This cluster had the lowest intra-cluster mean for chlorophyll content. In addition to that this cluster had second lowest heading and plant height and maturity days. Moreover, these genotypes can also be used as parents in hybridization programs to develop high yielding wheat varieties.

Conclusion

Finally on the basis of cluster distance and cluster mean and other agronomic traits the genotypes E-11,E-21, E-24 of cluster I, E-2, E-6 and E-20 of cluster II, E-19 from cluster IV and E-10, E-15, E-16, E-17, of

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cluster V may be considered as parents for future hybridization program to produce early, heat stress and high yielding genotypes.

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