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Genetic diversity in wheat genotypes under early heat stress in Bangladesh

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Abstract

Twenty-four wheat (*Triticum aestivum* L.) genotypes/lines were assessed in alpha lattice design with three replications during winter season of 2014-15 at the Regional Wheat Research Centre (RWRC), Bangladesh Agricultural Research Institute (BARI), Rajshahi. The main aim of this experiment was to find out the degree of genetic diversity for characters related to early heat tolerance in wheat. Five different clusters were formed among the genotypes. The number of genotypes in cluster I and V were same i.e. three and they formed the smallest cluster. The cluster III was the largest containing eight entries followed by the cluster IV that contained six genotypes and cluster II also had four members. The inter-cluster distances ranged from 3.4496 to 6.8221 and principal component analysis scores also showed that the genotypes had a wide range of genetic diversity. The maximum inter-cluster distance was observed between the clusters IV and V (6.8221) after that cluster I and IV (5.8935) and clusters III and V (5.2913) respectively. The maximum inter-cluster distance value showed that the genotypes under cluster IV were far diverged from the cluster V. Also, the genotypes under the cluster pair I and IV and cluster pair III and IV were far diverged. The genotypes were genetically closed in between cluster III and IV (3.4018), cluster I and V (3.4496), cluster I and II (3.6163) and cluster II and IV (4.1373) due to their minimum inter-cluster diversity. However, the highest spike length, spikelets spike^{-1} and grain yield were found in cluster I may show high heterosis for grain yield. The characters; short growing period, dwarf stature and bold grain were aggregated in cluster IV may show higher heterosis for dwarf stature and earliness. Canonical variate analysis (CVA) revealed that The traits 1000-grain weight and spike length had the highest contribution towards the divergence due to their positive values in both vectors. Based on these results, the genotypes under cluster I, cluster V and cluster IV might be taken for selecting suitable parents or crossing combinations for future early heat tolerance wheat breeding program.

Keywords: Wheat, divergence, cluster, genotype, heat, heterosis

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1 Introduction

Wheat (*Triticum aestivum* L.) is the world leading important winter cereal grain crop and member of the family Graminae (Poaceae). In Bangladesh, it is most important grain crop after rice. The increasing trend of wheat cultivation and production was found up to the year 2000 then decreased due to lack of abiotic stress tolerant varieties specially heat and drought. The competition of wheat for area with potato, maize and Boro rice in winter is another factor of decrease. Now the area and production was 351243 ha and 1099373 metric tons respectively in 2017-18 (BBS, 2019). The world average yield of wheat needs to be boosted up from 2.6 to 3.5 tons ha^{-1} for the coming 25 years to feed the people and to ensure global food security (Ortiz et al., 2008). Scientists of Bangladesh, developed wheat varieties only for irrigated areas where genotypes for stress conditions are considered as less priority. The Wheat Research Centre (WRC) of Bangladesh Agricultural Research Institute (BARI) has released 33 improved varieties for non-stressed irrigated environments. Most of the wheat in Bangladesh (>60%) is cultivated under late sowing condition (December sowing) that faces high temperature at reproductive stage (Badruddin et al., 1994). In the world, heat stress upset wheat around seven million hectares in its life duration and 40% wheat exposed to terminal heat stress (Ruwali and Bhaswar, 1998). Bangladesh and south-east Asia facing terminal heat stress (heat stress at reproductive and grain filling stage) from long time. But early heat stress (heat stress at seedling stage) is a new issue in Bangladesh and neighbor countries. Now a days, a large amount of wheat growing lands become available for sowing in the last week of October to early November for widely cultivation of short duration varieties of T. Aman rice. Generally, farmers don't like to remain their land fallow after harvest of T. Aman to avoid the loss of soil residual moisture. But wheat seeding at this time has not yet been recommended due to prevalence of higher temperature at that time. Wheat germination and crop development hampered in high temperature and finally causing significant yield injury. Bangladesh is a wheat deficit country and to increase wheat production and area, development of early heat tolerant wheat line/variety is essential. The wheat crop exposed at high temperature in early vegetative stage as a result crop become thinned and produced less tillers, decreased chlorophyll, reduced length of shoot and root, reduced shoot and root dry mass despite the favorable condition at heading and grain filling period but the crop did not minimize the previous stress ultimately produced poor yield (Gupta et al., 2013; Hossain et al., 2013; Kumer et al., 1994; Fischer, 1990).Variability for heat tolerance may have exists in wheat varieties/advanced lines for early heat environments. But efforts to screen or transfer early heat tolerance traits into existing varieties/lines have not yet been made scientifically in Bangladesh. Now new high yielding varieties need to be developed that can tolerate early heat situation without reducing grain yield.

In plant breeding, genetic diversity has a significant function to produce heterosis and productive wide recombinants for breeding (Rahman et al., 2015) The significance of genetic diversity for identifying parents for hybridization in wheat to develop superior transgressive segregants has also been repeatedly emphasized (Murthy and Anand, 1966; Jatasra and Paroda, 1983; Pandey et al., 2017). In this study, 24 selected wheat genotypes were taken for diversity evaluation and yield was considered as a main selection standard. The measurement of extent of divergence and determination of influence of different traits towards the total divergence were analyzed using multivariate analysis which was established by different investigators. Therefore, this study would help to evaluate promising high yielding genotypes that can tolerate high temperature in early seeding and also selecting superior lines for crossing block as parent.

2 Materials and Methods

2.1 Experimental details

Twenty-four early heat tolerant genotypes (Table 1) (including Shatabdi and BARI Gom 26 as check) of wheat were grown at experimental field of regional wheat research center of BARI, Rajshahi during 2014-15 winter cropping season. The soil of this field was silty clay and slightly alkaline (pH = 7.1-8.5) in nature and belongs to high Ganges River Floodplain Agro-Ecological Zone (AEZ-II) of Bangladesh. The sub-tropical monsoon and uneven rainfall is the characteristics of the climate of the experimental site. The rainfall is mostly concentrated in summer and winter is almost rainless. In crop season, the maximum temperature at seedling stage was above 32°C which was harmful for wheat seedling. About 28 mm rainfall was occurred in the whole wheat growing season. Experiment was conducted in alpha lattice design with three replications. Seeds were continuously sown manually in line sowing method and maintained 20 cm line to line spacing between rows. Fertilizers were applied @ 100-26-50-20-1 kg Nitrogen (N), Phosphorus (P), Potassium (K), Sulphur (S) and Boron (B) per hectare for optimum growth of crops. The elemental form of N P K S and B were converted into commercial form of Urea, Triple Super Phosphate, Muriate of Potash, Gypsum and Boric acid respectively. Two-third of the urea and all the fertilizers were applied as basal during final land preparation. The rest 1/3rd urea was top dressed at 18 days after seeding (DAS) after 1st irrigation. The seed were sown on

05 November 2014 to expose the seedlings at high temperature and harvested on 02 March 2015. The crop was grown in irrigated condition and all intercultural operations were done following WRC, BARI recommended wheat management package. Heading days, maturity days, spike length (cm), spikes m^{-2}, spikelets $spike^{-1}$, grain $spike^{-1}$ and plant height (cm) data were collected at physiological maturity. At maturity, yield of grain (t ha^{-1}) and thousand grain weight were measured after harvesting, threshing and sun drying the crop and adjusted the grain moisture at 12% level.

2.2 Statistical analysis

The data were analyzed to find out genetic diversity using principal component analysis (PCA) and Mahalanobis (1949) generalized distance (D^2) extended by Ruwali and Bhaswar (1952). The cluster (Intra and inter) analysis and cluster distances were computed following the way of Singh and Chowdhury (1985). All the data were analyzed with the help of Genstat software 5.13 edition.

3 Results

The principle component axis, eigen values and percent contribution of this data are presented in Table 2. The principal component analysis (PCA) describes the rank of the largest contributors to the total variation at each principle component axis. The sum total of the aigen values is usually equal to the number of original variables and aigen values frequently used to determine how many factors to retain. Nine principal component axes extracted from the original data. In this analysis, first principal component axis contributed 56.67% of the total variables. The first four axis contributed 84.44% of the total variation and first two axis contained latent root more than one having 68.69% cumulative influence in the total variation. The genotypes differed significantly among them in different characters and grain yield. Based on the extent of diversity, 24 genotypes were clustered (Table 3) with the help of cluster analysis using Mahalanobis' D^2 statistics and Tocher's method. Five different clusters were formed among the genotypes. The number of genotypes in cluster I and V were same i.e. three and they formed the smallest cluster. The cluster III was the largest containing eight entries followed by the cluster IV that contained six genotypes and cluster II also had four members.

In the present study, intra and inter-cluster distance of the genotypes are presented in Table 4. The range of the intra-cluster distance was 2.1455 to 3.0303 and was smaller than all inter-cluster distance. The cluster V produced the lowest intra-cluster distance where cluster III (3.0303) produced the highest intra-cluster distance among the clusters. The highest inter-cluster distance value was found between cluster IV and V (6.8221) after that the pair of cluster I and IV (5.8935) and between clusters III and V (5.2913). The inter-cluster distance in cluster pair between the clusters II and V (4.6999) after that the cluster I and III (4.3752) and also the cluster pair between clusters II and III (4.1738) produced the intermediate inter-cluster distance. The lowest inter-cluster distance was produced by the clusters III and IV (3.4018), cluster I and V (3.4496), cluster I and II (3.6163) and clusters II and IV (4.1373).

The highest cluster means for head days, plant height, maturity days, grains $spike^{-1}$, spikes m^{-2} and the second highest spike length (cm) and spikelets $spike^{-1}$ with the lowest 1000-grain weight and moderate yield were found from cluster V. The highest spike length (cm), spikelets $spike^{-1}$ and grain yield were found in cluster I. The minimum cluster means for head days, maturity days, spike length (cm), spikes m^{-2}, grains $spike^{-1}$, spikelets $spike^{-1}$, and grain yield were obtained in cluster IV (Table 5). The short plant height, short life cycle (head days and maturity days), bold grain, lower spike length and the lowest yielder genotypes were accumulated into group IV while genotypes with the highest spike length (cm), spikelets $spike^{-1}$ and grain yield having moderate yield traits were observed in the cluster I. The second highest gran yield, head days and plant height (cm) were accumulated in cluster II. The large numbers of genotypes with maximum expected characters were accumulated in cluster V.

The relative contribution of the studied traits towards the total divergence was find out with the help of Canonical Variate Analysis (CVA) and showed in Table 6. There were two vectors (the axis of differentiation) in Canonical Variate Analysis (CVA) and negative values against characters in any vector described lower contribution where positive value means higher contribution towards divergence. In case of vector I, spike length (cm) and 1000-grain weight showed positive values and considered as important responsible characters for genetic divergence. In vector II, positive values were found in maturity days, spike length, spikes m^{-2} , 1000-grain weight, grains $spike^{-1}$ and grain yield which indicated that those were vital traits. It was also observed that spike length and 1000-grain weight contained positive values in both vectors.

4 Discussion

In the study, Principal component analysis (PCA) and the eigen values of the first four components accounted 84.44% of total variation among the nine characters indicated that these components have significant responsibilities in genetic diversity. Princi-

Table 1. Pedigree of Early Heat Tolerance Wheat genotypes used in the experiment

Genotypes	Cross/Pedigree	Source
G1	Shatabdi	Shatabdi
G2	BARI Gom 26	BARI Gom 26
G3	BAW 1064/ BAW 1059 BD(DI)1766S-0DI-0DI-0DI-030DI-3DI	BAW 1208
G4	PRODIP/SHATABDI//PRODIP BD(DI)1584T-0DI-0DI-0DI-030DI-18DI	BAW 1209
G5	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP# I /3/KAUZ*2/TRAP//KAUZ CGSS05B00153T-099TOPY-099M-099NJ-099NJ-5WGY-0B	BAW 1224
G6	GOURAB/BAW 1027 BD(JE) 1494S-0DI-0DI-0DI-03 0DI-5DI	BAW 1217
G7	BIJOY/PRODIP BD(DI)1698S-0DI-16DI-0DI-5DI	BAW 1219
G8	BIJOY/KRL 1-4//SOURAV BD(JE) 1464T-0DI-5DI-0DI- 1DI	BAW 1220
G9	SHATABDI/GOURAB BD(DI) 1686S-0DI- 1DI-0DI- 1DI	BAW 1222
G10	SHATABDI/GOURAB BD(DI)1686S-0DI-1DI-0DI-2DI	BAW 1223
G11	SOURAV/7/KLAT/SOREN//PSN/3/BOW/4/VEE#5. 10/5/CNO 67/MFD// MON/3/ SERI/6/NL297 BD(DI) 112S-0DI-030DI-030DI-030DI-9DI	BAW 1151
G12	BAW677/Bijoy BD(JA) 1365S-0DI- 15DI-3DI-HRI2R3DI	BAW 1161
G13	BAW923/BAW 1004 BD(DI) 1207S-0DI-4DI-010DI-010DI-0DI-DIRC6	BAW 1157
G14	CHIR7/CBRD//GOURAB BD(DI) 1375S- 10DI-010DI-010DI-010DI- 1DI-DIRC2	BAW 1170
G15	PRODIP/GOURAB BD(JOY)459S-0DI-8DI-010DI-010DI-R5DI	BAW 1177
G16	KAL/BB/YD/3/PASTOR CMSS99M00981S-0P0M-040SY-040M-040SY- 16M-0ZTY-0M...	BAW 1182
G17	SHATABDI/PRODIP BD(DI) 1691S-0DI-6DI-0DI-ODI-2DI	BAW 1194
G18	G.162/BL1316//297/BL 1883 BD(JE) 1446-0DI- 1DI-0DI-0DI-6DI	BAW 1195
G19	MINIVET/PRODIP// SHATABDI BD(DI) 1539T-0DI-7DI-0DI-ODI-3DI	BAW 1200
G20	GOURAB/3/BULBUL//BAW 824/BAW 1087 BD(JO)106T-0DI-0DI-0DI-030DI-2DI	BAW 1202
G21	GOURAB/BAW 1027 BD(JE) 1494S-0DI-0DI-0DI-030DI-5DI	BAW 1203
G22	WBLLI *2/TUKURU//FN/2*PASTOR/3/FRET2/KIRITATI CMSS06B00926T-099TOPY-099ZTM-099Y-OFUS- 18WGY-0B	EHTWSN-23
G23	ATTILA*2/PBW65 *2/4/CROC_1/AE.SQUARROSA (205)//BORL95/3/2 *MILAN CMSS06Y00586T-099TOPM-099Y-099ZTM-099Y-099M-12WGY-0B	EHTWSN-29
G24	ATTILA*2/PBW65 *2/4/BOW/NKT//CBRD/3/CBRD CMSS06Y01026T-099TOPM-099Y-099ZTM-099Y-099M-6WGY-0B	EHTWSN-30

Table 2. Eigen values (Latent root) and percent contribution of traits towards divergence in 24 early heat tolerant wheat genotypes

Principal component axes	Eigen values	Percent contribution	Cumulative percentages
I	5.0999	56.67	56.67
II	1.0818	12.02	68.69
III	0.8083	8.98	77.67
IV	0.6094	6.77	84.44
V	0.55	6.11	90.55
VI	0.397	4.41	94.96
VII	0.2587	2.87	97.84
VIII	0.1224	1.36	99.19
IX	0.0724	0.81	100

Table 3. Distribution of 24 early heat tolerant wheat genotypes in different cluster based on D^2 values

Cluster	Member of genotypes	% of total entries	Genotypes
I	3	12.5	G1, G3, G23
II	4	16.67	G2,G6,G12, G13
III	8	33.33	G4, G8, G9,G11, G15, G16, G18, G19
IV	6	25	G5,G7, G14,G17,G20, G21
V	3	12.5	G10, G22, G24

Table 4. Average intra (bold and diagonal) and inter cluster distances of 24 early heat tolerant wheat genotypes

Cluster number	I	II	III	IV	V
I	2.7112	3.6163	4.3752	5.8935	3.4496
II		2.3363	4.1738	4.1373	4.6999
III			3.0303	3.4018	5.2913
IV				3.0186	6.8221
V					2.1455

Table 5. Cluster means for nine characters of early heat tolerant wheat genotypes

Characters	I	II	III	IV	V
Head days	63	57	59	56	73
Plant height (cm)	96.7	88.5	83.62	83.67	98.33
Maturity days	110	107	104	99	113
Spikes m^{-2}	375	369	315	301	386
Spike length (cm)	10.67	9.1	9.55	8.9	10.4
Spikelets spike^{-1}	18	16	16	15	18
Grains spike^{-1}	49.7	46.3	44.6	38.5	51
1000-grain weight (g)	43.37	43.17	44.21	46.67	34.67
Grain yield (kg ha^{-1})	5150	5118	4301	3693	4447

Table 6. Relative contributions of the nine characters to the total divergence in early heat tolerant wheat genotypes

Characters	Vector I	Vector II
Head days	-0.1319	-0.1195
Plant height (cm)	-0.0755	-0.0557
Maturity days	-0.082	0.0416
Spikes m^{-2}	-0.0228	0.0045
Spike length (cm)	0.3666	0.2947
Spikelets spike^{-1}	-0.3864	-0.1335
Grains spike^{-1}	-0.1267	0.1039
1000-grain weight (g)	0.2502	0.1273
Grain yield (kg ha^{-1})	-0.0012	0.0013

pal component analysis reflects the significance of the prime contributor to the total variation (Sharma, 1998). According to the cluster analysis, five different clusters were formed that indicating the presence of wider genetic variabilities present among the genotypes of different clusters. It may be due to the adaptability of genotypes to this specific environment. In a study, Ferdous et al. (1970) identified the clusters and variabilities among the bread wheat genotypes. Almost same results were found by Khudadaim et al. (2011) on wheat genotypes in Iran.

The intra-cluster distances were low in all the clusters which indicated that the genotypes within the clusters were genetically closed and homogenous in nature. The findings were supported by Iftekharuddaula et al. (2002) in rice (*Oryza sativa* L.). The higher inter-cluster values were found in between the cluster IV and cluster V, between the cluster I and IV and between the clusters III and IV combined with PCA scores indicating that the higher degree of genetic diversity among the genotypes and each pair of clusters were far diverged. The cluster V produced the balanced inter-cluster distances with other clusters signifying wide divergence and the genotypes of the cluster could be used as parents in hybridization program (Akter et al., 2016). Then it was remarkable that cluster V produced the highest inter-cluster distances with cluster II, III, and IV that the cluster V can be used as one parent in the hybridization and other parents can be taken from the clusters II, III, and IV. Thus information on association of morpho-agronomic traits with grain yield and genetic variability is essential for a fruitful selection (Islam et al., 2017). Joshi and Dhawan (1966) also reported that inclusion of more diverse parents (within a limit) increases the chances for achieving stronger heterosis and wide range of variation in segregating generations.

Canonical variate analysis (CVA) showed that 1000-grain weight and spike length had positive values in both vectors suggesting that the huge divergence in the genotypes because of these two characters would create a good scope for improvement in early heat tolerant wheat genotypes through selection of parents. Grains spike^{-1} and spike length were found to have the highest contribution towards total divergence as observed by Chowdhury et al. (2006). Zaman et al. (1970) also reported that maturity days and 1000-grain weight had higher contribution towards total divergence.

5 Conclusion

In the present study, the highest distance was found between cluster IV and V followed by the distance between cluster I and IV. However, the highest spike length, spikelets spike^{-1} and grain yield were found in cluster I may produce high heterosis for yield. Again, considering short growing period, dwarf stature and bold grain were aggregated in cluster IV may showed higher heterosis for short duration and short plant height. Canonical variate analysis (CVA) showed that 1000-grain weight and spike length had positive values in both vectors suggesting that the huge divergence in the genotypes because of these two characters would create a better option for improvement in early heat tolerant wheat genotypes through selection of parents. Based on these results, the genotypes of cluster I, cluster V and cluster IV could be employed for early heat tolerance wheat breeding program.

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Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

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