Genetical and Physiological Analysis for Heat Tolerance in Spring Wheat

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Abstract

The experiment was conducted at Agronomy field laboratory, Dept. of Agronomy and Agricultural Extension, University of Rajshahi, Rajshahi during 2019-2020 to identify the diverse genotypes of wheat related to heat tolerance. Twenty wheat genotypes/lines were used as a plant materials in this experiment. The wheat genotypes/lines were evaluated in heat stress environments. Non-hierarchical clustering grouped the wheat genotypes into five clusters. The cluster II indicated the maximum number of genotypes following the cluster V, III and IV. Plant height and spikes m^{-2} were major traits contributed mostly towards genetic divergence. Selection of parents for these two traits has good scope to get broad spectrum of segregates. The cluster V had the highest grains $spike^{-1}$, spikelet's $spike^{-1}$, 1000-grain weight, grain yield and biomass whereas canopy temperature, heading days and maturity days were lowest. Cluster I had the lowest grain yield, spikes m^{-2}, grains $spike^{-1}$, biomass and chlorophyll content, plant height, spikelet's $spike^{-1}$ and 1000-grain weight. Five pairs of clusters viz. the clusters (I and V, I and II, I and IV, III and V and IV and V) may be considered for getting more heterotic F_1. The genotypes G 02 and G 11 of cluster I and genotypes G 6, G 15, G 17, G 18 and G 20 of cluster V may be considered as parents for future hybridization program to obtain diverse genotypes related to heat tolerance.

Keywords: Wheat; Genetic divergence; Heat stress and D^2 analysis

Introduction

Wheat is the most widely grown cereal crop which plays an important role in world food security. It ranks second among major cereals next to rice and ensure a vital role in food security of teeming hungry millions of people of Bangladesh. The climate of our world is changing gradually. Global warming has been a major issue in recent years. Intergovernmental Panel on Climate Change (IPCC) predicted 1.8°C to 4.0°C temperature increase by the end of 21 century. Bangladesh is not an exceptional from it. The length of winter season is so short compared to the summer in northern part of Bangladesh. Here the temperature begins to increase from mid- February when wheat crop starts its physiological stage. As a result, heat is a major factor in wheat production. Late sowing is the main constraint to low yield of wheat in Bangladesh.

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As a result, in grain filling stage, wheat is faced into high temperature reducing the duration of grain filling. This situation greatly hampers its grain filling and also the production of wheat also. Thus, heat stress limiting the yield of wheat. The effect of climate change is the evident on the quality of wheat, as increased heat results in shriveled wheat grains (Tadesse *et al.,* 2013). To adapt new crop varieties to the future climate, we need to understand how crops respond to elevate temperatures and how tolerance to heat can be improved (Halford, 2009). Genetic diversity is crucial for adaptability and survival of wheat species against the threat of high temperature. Success in crop improvement generally depends on the magnitude of genetic variability and the extent to which the desirable characters are important. Germplasm evaluation will be of great significance for selection of heat-tolerant genotypes and for improving grain yield under high temperature. Conceiving the above idea, the present investigation was undertaken, to study the genetic divergence of spring wheat genotypes related to heat tolerance.

Materials and methods

The experiment was conducted out at Agronomy field laboratory, Dept. of Agronomy and Agricultural Extension, University of Rajshahi, Rajshahi during 2019-2020. Twenty wheat

Table 1. Socio-demographic Profile of Study Participants (n=13)

Entry code	Source
G 01 (BARI Gham 21)	BARI
G 02 (BARI Gham 26)	BARI
G 03	CIMMYT
G 04	CIMMYT
G 05	CIMMYT
G 06	CIMMYT
G 07	CIMMYT
G 08	CIMMYT
G 09	CIMMYT
G 10	CIMMYT
G 11	CIMMYT
G 12	CIMMYT
G 13	CIMMYT
G 14	CIMMYT
G 15	CIMMYT
G 16	CIMMYT
G 17	CIMMYT
G 18	CIMMYT
G 19	CIMMYT
G 20	CIMMYT

genotypes (varieties/ lines) were used for conducting the study which are presented in the Table I.

Alpha Lattice Design was adopted for the experiment with two replications. The seeds were sown by hand continuously in lines (line to line distance was 20 cm) on 25 December 2019. Different intercultural operations were done timely. Data were collected on physiological and yield

component characters related to heat tolerance. The collected data were subjected to different biometrical analysis by using GENSTAT 5.13 and Microsoft Excel 2010 software to determine principal component analysis, principal coordinate analysis, cluster analysis and canonical vector analysis were done.

Results and discussion

Principal component analysis

The principal component analysis of principal component axes and percentage of total variation are presented in the Table 2. The principal component analysis produces thirteen values of principal component axes. The first axis accounted 32.51% of the total variation among the genotypes. The first two axes accounted 55.11% of the total variation. This result indicate that these components

Table 2. Eigen values and percent of variation of traits towards divergence in wheat genotypes

Principal component axes	Eigen values	Contribution (%)	Cumulative variation (%)
a	4.2266	32.51	32.51
b	2.9381	22.60	55.11
c	1.3698	10.54	65.65
d	1.2348	9.50	75.15
e	1.1075	8.52	83.67
f	0.5499	4.23	87.90
g	0.5302	4.08	91.98
h	0.4200	3.23	95.21
i	0.2939	2.26	97.47
j	0.1919	1.48	98.95
k	0.0867	0.67	99.62
l	0.0502	0.38	100
m	0.0003	0.00	100

were highly responsible for genetic divergence. Sharma (1998) reported that principal component analysis reflects the importance of the largest contributor towards the total variation.

Non-hierarchical clustering

The genotypes were significantly different from each other for grain yield, morphological and physiological traits. By using covariance matrix, the wheat genotypes were grouped into five clusters (Table 3). Cluster II had the maximum genotypes (9) followed by cluster V. Cluster I had the minimum number of genotypes (2) followed by cluster III and IV. Pattern of distribution of genotypes among various clusters reflected the genetic divergence present in the genotypes. This

Table 3. Distribution of 20 wheat genotypes in five clusters

Clusters	No. of genotypes	% of total entries	Genotypes
I	2	10	G 2, G 11
II	9	45	G 1, G 5, G 7, G 8, G 9, G 10, G 14, G 16, G 19
III	2	10	G 12, G 13
IV	2	10	G 3, G 4
V	5	25	G 6, G 15, G 17, G 18, G 20

genetic variability of the wheat genotypes may be due to their adaptation to specific environmental conditions. These results are agreed with that of Ferdous *et al.* (2011). They carried out an experiment with 24 genotypes of bread wheat and got similar results with five clusters. Arega *et al.* (2007) obtained the similar results on exotic and indigenous durum wheat genotypes in the northeast Ethiopia.

Canonical variate analysis

Canonical variate analysis was done to calculate the inter cluster distances. The intra and inter cluster distances are presented in Table 4. Genotypes of the same cluster are expected to be genetically similar than genotypes of different clusters.The intra-cluster distance varied from 2.08 to 0.95. The highest intra-cluster distance was observed in cluster II and the lowest one was found in cluster III. The highest inter-cluster distance was noted between clusters I and V (25.614) followed by between I and II (17.869) and between III and V (17.544). The maximum value of inter-cluster distance indicating genetic divergence among the genotypes of the cluster I and of cluster V. Similarly, the higher inter-cluster distance between clusters I, II and III and V indicated that these genotypes of each pair of clusters have wide range of diversity. The lowest distance (2.743) was found between the clusters III and IV followed by the distance (7.481)

Table 4. Average intra and inter cluster values for wheat genotypes

Cluster	I	II	III	IV	V
I	2.01				
II	17.869	2.08			
III	14.409	9.303	0.95		
IV	16.524	7.481	2.743	2.03	
V	25.614	8.583	17.544	15.256	2.06

between II and IV suggesting close relationship among the genotypes within these pairs and considered as less diverged. Ghaderi *et al.* (1984) and Diers *et al.* (1996) reported that parents for hybridization could be selected on the basis of large inter-clusters distance for the isolation of useful recombinants in the segregating generations. As a result diverse lines from different clusters

should be chosen for crossing in wheat breeding program. The average inter-cluster distances were higher than the average intra-cluster distances indicated wider range of genetic diversity among the genotypes. This results are in agreement with that of Choudhury *et al*. (2006).

Contribution of traits towards divergence

Contribution of characters towards divergence of the genotypes are presented in the Table 5. Jagadev and Samal (1991) reported that the trait contributing maximum to the divergence are used to give greater emphasis for deciding on the cluster for the purpose of further selection and in the choice of parents for hybridization. Negative values indicated lower contribution of the trait in the respective vector while positive values indicated higher contribution.

In vector I obtained from Principal Component Analysis, the important traits responsible for genetic divergence were harvest index (420.50), canopy temperature at vegetative stage(0.40), grains spike^{-1}(0.27) and chlorophyll content of flag leaf (0.21) at grain filling stage. In vector II heading days (2.55), canopy temperature (2.32) at grain filling stage, 1000-grain weight (0.46) and plant height (0.18) were the important characters because of positive signs. Canonical Variate

Table 5. Latent vectors for thirteen characters in wheat genotypes

Traits	Vector I	Vector II
Plant height (cm)	-0.07	0.18
Spike m^{-2} (no.)	0.00	-0.07
Grain spike^{-1} (no.)	0.27	-0.37
Spikelets spike^{-1} (no.)	0.39	2.25
1000-grain weight (g)	-0.31	0.46
Yield (kg/ha)	-0.06	0.04
Biomass (kg/ha)	0.03	-0.01
Heading days	-0.14	2.55
Maturity days	-1.35	-3.15
CT vegetative stage (°C)	0.40	-2.54
CT vegetative stage (°C)	-0.53	2.32
CCFL at grain filling stage	0.21	-1.00
Harvest index	420.50	-285.35

CT= Canopy temperature, CCFL= Chlorophyll content of flag leaves

Analysis results revealed that spikelet's spike^{-1} had the positive values for both the vectors having higher contribution to the genetic divergence among genotypes studied. However, only maturity days had negative values in both the vectors indicated that this trait had lowest contribution to the total divergence. This results indicated the highest contribution towards the divergence among wheat genotypes. So, the divergence in the present materials in respect of spikelet's spike^{-1} will be a good scope for the improvement of heat tolerance through selection of parents. Choudhury *et al*. (2006) studied genetic diversity in 37 spring wheat genotypes. They observed that spike length and

grain spike^{-1} were found to have the highest contribution towards total divergence. Zaman *et al.* (2010) conducted an experiment on genetic diversity of wheat and noted that days to maturity and 1000-grain weight were found to have highest contribution towards total divergence.

Intra-cluster mean

Mean performance clusters for thirteen traits are presented in the Table 6. Different clusters remarkably distinguished for most of the traits indicating proper clustering. Mean values for harvest index was same for all the clusters among the characters studied. The highest grains spike^{-1}, spikelets spike^{-1}, 1000-grain weight, grain yield and biomass were found in cluster V. The lowest canopy temperature was noted at vegetative stage and also the grain filling stagein this cluster also. So, it has ability to maintain cooler canopy at vegetative as well as grain filling stage. This feature might have played a key role for all the positive attributes. The lowest grain yield was observed in cluster I. This cluster had the lowest spikes m^{-2}, grains per spike^{-1}, biomass, and chlorophyll content of flag leaf at grain filling stage. This cluster had the 2nd highest heading days, maturity days and canopy temperature at vegetative stage. The highest heading days, maturity days and plant height were reported in cluster III. It also had the highest spikes m^{-2} and 2nd highest spikelets spike^{-1} and chlorophyll content of flag leaf at grain filling stage and the lowest canopy temperature at grain filling stage and 2nd lowest grain yield and canopy temperature at grain filling stage. These results were not enough to ensure higher yield because of some undesirable values of desirable traits. Cluster II had 2nd highest grain yield as it had highest 1000-grain weight, 2nd highest grains spike^{-1} and biomass and lowest heading days and maturity days. Although it had lowest spikelets spike^{-1} but it was not affecting the grain yield so much.

Table 6. Mean performance of clusters for thirteen characters in wheat genotypes

Traits	Cluster mean				
	I	II	III	IV	V
Plant height (cm)	88.7	88.8	93.7	81.0	89.9
Spike m^{-2} (no.)	325.3	354.8	372.8	356.3	354.2
Grain spike^{-1} (no.)	31.6	36.4	34.5	32.5	42.6
Spikelets spike^{-1} (no.)	17.4	17.2	17.6	17.4	18.2
1000-grain weight (g)	24.9	29.0	23.4	25.0	29.0
Yield (kg ha^{-1})	1959.4	2979.3	2375.0	2444.0	3550.4
Biomass (kgha^{-1})	5401.9	7758.1	6227.5	6809.0	9067.8
Heading days	62.5	60.1	63.0	61.7	61.7
Maturity days	86.5	85.5	87.0	86.0	86.4
CT vegetative stage (°C)	21.0	20.9	20.5	21.6	20.2
CT at grain filling stage (°C)	28.1	28.5	27.3	28.7	27.6
CCFL at grain filling stage	32.1	36.8	38.8	41.3	38.6
Harvest index	0.4	0.4	0.4	0.4	0.4

CT= Canopy temperature, CCFL= Chlorophyll content of flag leaves

Selection of genotypes for future hybridization program

Generally, crosses should be made among the parents having the most divergent clusters for obtaining maximum heterosis and wide range of variability. It is at par with Sectharaman *et al.,* (1988). They suggested that genotypes among the clusters separated by D^2 values could be used in hybridization program for obtaining wide range of variability among the segregates.The higher inter cluster distances were noted between I and V. To select the clusters for more heterotic F_1, five pairs of clusters (I and V, I and II, I and IV, III and V and IV and V) to be considered for this purpose. Considering the distances of cluster and cluster mean, the genotypes of cluster I and genotypes of cluster V may be considered as parents for future hybridization program for obtaining heat tolerant lines for better yield.

Conclusion

D^2 statistics divided 20 wheat genotypes into five clusters where inter-cluster distances were higher than the intra-cluster distances.Among studied traits, spikelets spike^{-1}had a positive role towards genetic divergence. Selection of parents for this trait offers good scope to get wide range of segregates.Five pairs of clusters (I and V, I and II, I and IV, III and V and IV and V) may be considered for obtaining more heteroticF_1. It may be concluded that the genotypes of cluster I and the genotypes of cluster V may be considered as parents for future hybridization program to get better result in heat stress condition.

Acknowledgement

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