

# Assessment of Different Traits to Evaluate Genetic Divergence in Some Wheat (*Triticum aestivum* L.) Genotypes under Late Sowing Condition

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## Abstract

The research work was undertaken to identify the extent of genetic diversity in different parameters of wheat related to heat tolerance mechanism. Performances of currently available 25 spring wheat genotypes were studied at the Regional Wheat Research Institute, Shyampur, Rajshahi during the winter season of 2016/2017. All these genotypes (25) were grouped into five clusters on the basis of non-hierarchical clustering parameters viz. cluster I (G2, G5, G6, G16, G20), II (G4, G7, G9, G11, G12, G17), III (G10, G24), IV (G1, G13, G19, G21) and V (G3, G8, G14, G15, G18, G22, G23, G25). These groups were arranged into five (5) pairs of clusters viz. cluster I and III; II and III; II and V; III and IV; IV and V considering their similar potentiality of different traits. Results revealed that the maximum number of genotypes (8) was found in cluster V while cluster III comprised minimum genotypes (2). The inter-cluster distance was higher than intra-cluster distances. The highest and second highest eigenvalues belonged to spike/m<sup>2</sup> (25.23%) and spikelets/spike (20.18%) respectively, along with positive canonical values in both the vectors 1 and 2 for these two traits identified them as major traits by exposing their highest potential toward genetic divergence. Cluster III produced the highest spike/m<sup>2</sup> (388.8), grain/spike (48.1), plant height (89.5 cm), SPAD (54.2), yield (2799 kg/ha) and biomass (7758.1 Kg/ha) with lowest heading days (64.7 days), maturity days (98.7 days), canopy temperature at vegetative stage (21.7°C) and canopy temperature at grain filling stage (22.4°C). In contrast, cluster V produced the lowest 1000-grain weight (30.4 g) and grain yield (2172 kg/ha) belonging to the highest canopy temperature at both stages

(23.8°C and 24.7°C). However, results suggested that the genotypes G10 and G24 under the cluster III, and genotypes G01, G13, G19 and G21 under the cluster IV could be considered as parents for future hybridization program, as well as the five pairs of clusters viz. cluster I and III; II and III; II and V; III and IV; IV and V might be matched as considered for getting more heterotic  $F_1$ . The results of the study would help to identify the divergent genotypes associate with heat tolerance and this might be helpful in designing future breeding program.

## Keywords

Genetic Divergence, Heat Tolerance, Assessment of Different Traits, Cluster Analysis, Principal Component Analysis, Selection of Genotype

## 1. Introduction

Bread wheat is widely adapted crop that can be grown under variable environments. Although it is best adapted to cool or temperate growing conditions, it is grown in many areas of the world where heat stress is a major yield-limiting factor, especially at the end of the season. Under the changing climatic conditions, heat stress is one of the major challenges for wheat production in Bangladesh.

Geographically Bangladesh is a sub-tropical country. Optimum time for sowing wheat is limited (15 - 30 Nov) here due to very short winter spell, about 60% of these are sown late (after 30<sup>th</sup> Nov) because of the delayed harvesting of the preceding crop. The temperature starts to increase sharply after February and thus reproductive stage of the late sown crop undergoes very high temperature of late March to mid-April [1].

Genetic diversity for heat tolerance in cultivated spring wheat is well established [2]. The success of breeding depends entirely upon the genetic diversity of desired traits. Genetic diversity is defined as the extent to which heritable materials differ within a group of plants as a result of evolutionary forces, including domestication and plant breeding [3].

One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to benefit transgressive segregation, genetic distance between parents is necessary [4]. The higher genetic distance between parents, the higher heterosis in progeny can be observed [5].

Wheat Research Centre, BARI now has a wide range of spring wheat germplasm collection from different sources. Most of these have collection from CIMMYT, Mexico and few from Nepal, India, Pakistan, Australia etc. It is important to evaluate the extent of diversity present in this germplasm collection and identify useful variation associated with heat tolerance.

The multivariate analysis has been established by several investigators for

measuring the degree of divergence and for ascertaining the relative contribution of different characters of the total divergence [6]. D<sup>2</sup> cluster and factor analysis have been proved to be useful in selecting genotypes for hybridization.

Mahalanobis's [7] D<sup>2</sup> analysis has been successfully used in measuring the diversity in several crops. An understanding of nature and magnitude of variability among the existing wheat germplasm is a prerequisite for its improvement. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population of geographical level and to access in assessing relative contribution of different components to the total divergence both intra and inter cluster levels [8].

Estimation of genetic distance is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase [9].

Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parent for purposeful hybridization [10].

This study will help to determine the extent of genetic diversity for heat tolerant traits that present in the currently available breeding materials of the Wheat Research Centre, BARI, to classify them into group and to identify the appropriate germplasms.

Results of this study will also help in designing future improvement program for the development of heat tolerant varieties. The development of effective selection and breeding methodology is also important to develop heat tolerant varieties. The analysis of physiological determinants of yield responses to heat may help in breeding for both high yield and greater stability under heat stress conditions.

The objectives of this study were to assess the magnitude of diversity and classify them under different groups based on genetic divergence, identify the character contribution to genetic diversity and identify heat tolerant genotypes for hybridization program expecting to provide superior segregates. Therefore, it would be logical to undertake the present investigation.

## **2. Materials and Methods**

### **2.1. Locale of the Experiment**

The experiment was carried out at the field of the Regional Wheat Research Centre (RWRC), Shyampur, Rajshahi in the jurisdiction of Bangladesh Agricultural Research Institute (BARI) from the month of December, 2016 to April 2017 and thereafter. The location situated at 24°22' North latitude and 88°39' East longitude above 14 m sea level, and belongs to the Agro Ecological Zone of High Ganges River Floodplain (AEZ-11). The field soil of the experiment is silty clay which is Gangetic alluvial type, slightly alkaline with a pH of 7.1 to 8.5. The soil contains low organic matter, deficient in boron but high in iron content and poor fertility level.

## 2.2. Planting Materials

Wheat seeds of 25 different genotypes were used as planting materials in this study collected from the Regional Wheat Research Center (RWRC), Shyampur, Rajshahi and cultivated over there from December, 2016 to April, 2017. The used twenty five wheat genotypes (varieties/line) were G01 (BARI Gham 21) check, G02 (BARI Gham 21) check from BARI and the rest G03, G04, G 05, G06, G07, G08, G09, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G24 and G25 collected from CIMMYT (International Maize and Wheat Improvement Center).

## 2.3. Lay Out and Experimental Design

The experiment was laid out in Alpha Lattice Design with two replications. Recommended crop management practices were followed to cultivate the wheat crop. The seeds were sown by hands on the 22<sup>nd</sup> December, 2016 under irrigated late sowing (ILS) condition and the harvesting for the collection of yield data was completed by April 06, 2017.

## 2.4. Data Collection: Phonological, Physiological Parameters and Yield

Plant phenology is the scientific study of periodic biological phenomena of plant characters in relation to climatic conditions such as days to heading, days to maturity, days to anthesis, flag leaf senescence days and grain filling duration. Plant physiology concerned with the plant characters like canopy temperature, chlorophyll content, ground coverage, grain filling rate and biomass production.

Data were collected on different phenological, physiological and yield contributing parameters of selected wheat genotypes. Randomly selection of ten (10) plants from each plot for taking data at growing and post-harvest stages was completed. For statistical analysis the average values of ten plants for each character were used.

The traits such as days to heading, days to physiological maturity, canopy temperature were measured on the basis of whole plot, while spikelet/spike, grains/spike, 1000-grain weight and chlorophyll content of flag leaf were measured on the basis of an average of randomly selected plants. Heading days was calculated by counting the days from seeding to a stage at which 50% of the spikes came out fully from the leaf sheath. Maturity days were counted from the date of seeding to the date when 50% peduncle of 50% plants of each plot became yellow [11]. Plant height was measured from bottom to the top of the spike by a meter scale. The number of spike was counted in 1 m<sup>2</sup> area. Total number of spikelets was computed from ten selected spikes of each unit plot and the mean of them was used as number of spikelets/spike. Total number of grain was counted from the same spikes in the same way and was expressed as grains/spike. The canopy temperature (°C) at vegetative and grain filling stage was measured 2 times at 5 day interval by a infrared thermometer under bright

sunlight and less wind flow condition. The chlorophyll content of flag leaf at grain filling stage (SPAD) was determined by a Minolta SPAD meter. The harvested wheat crop with all spikes, leaves and stems were dried by the sun, then taken the weight and expressed as biomass in kg/ha. One thousand (1000) sun dried clean grains were randomly counted from each plot after harvest then weighed in gram (g) and finally converted the yield into kg/ha.

## 2.5. Data Analysis through Multivariate Analysis (D<sup>2</sup> Statistics)

The data collected on different yield contributing, phenological and physiological traits were subjected to analyze applying different biometrical methods under Multivariate analysis (D<sup>2</sup> statistics). Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz. cluster analysis, principal component analysis, principal coordinate analysis and canonical vector analysis.

### 2.5.1. Cluster Analysis (CA)

Cluster analysis was performed by D<sup>2</sup> analysis (originally outlined by Mahalanobis, 1928 [12] and 1936 [13] and extended by Rao, 1952 [14], which divides the genotypes based on the data set into more or less homogenous groups. D<sup>2</sup> is the sum of squares of differences between any two populations for each of the uncorrelated variables (obtained by transforming correlated variables through Pivotal condensation method). Clustering was done by using non-hierarchical and hierarchical classification. D<sup>2</sup> statistic is defined by:

$$D_x^2 = \sum_{k=1}^p (\lambda^{ij}) d_i d_j \quad (1)$$

where,  $X$  = Number of metric in point,

$P$  = Number of populations or genotypes,

$\lambda^{ij}$  = The matrix reciprocal to the common dispersion matrix,

$d_i d_j$  = The differences between the mean values of the two genotypes for the  $i^{\text{th}}$  and  $j^{\text{th}}$  traits respectively.

In simpler form, D<sup>2</sup> statistic is defined by the following formula:

$$D^2 = \sum_{i=1 \text{ to } x}^p d_i^2 = \sum_{i=1 \text{ to } x}^p (y_i^j - y_i^k)(j \neq k) \quad (2)$$

where,  $y$  = Uncorrelated variable which varies from  $i = 1$  to  $X$ .

$X$  = Number of traits.

Superscripts  $j$  and  $k$  to  $y$  = a pair of any two genotypes.

Cluster analysis was performed by computer software GENSTAT 5.13, which used to search for optimal values of the chosen criterion. The algorithm did some initial classification of the genotypes into required number of groups and then repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer could be found to improve the criterion, the algorithm switched to a second stage, which examined the effect of swooping of two genotypes of different groups, and so on.

### 2.5.2. Principal Component Analysis (PCA)

The technique PCA was used to examine the inter relationships among quantitative traits. The principal component was computed from the correlation matrix (obtained from sum of squares and products matrix of the traits) and genotype scores (obtained from the first component and the succeeding component with latent roots greater than unity). The latent roots are called 'Eigen values'. The first component has the property of accounting for maximum variance. The PCA displays most of the original variability in a smaller number of dimension, since it finds linear combination of a set of variate that maximize the variation contained within them. Contributions of the different traits towards divergence are discussed from the latent vectors of the first two principal components.

### 2.5.3. Principal Coordinate Analysis (PCA)

Principal coordinate analysis was used to calculate the inter genotype distance and give the minimum distance between each pair of the N points using similarity matrix through the use of all dimensions of P [15].

### 2.5.4. Canonical Vector Analysis (CVA)

Canonical vector analysis (CVA) complementary to  $D^2$  statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes are respectively derived. Canonical vector analysis finds linear combination of original variability that maximize the ratio between groups to within groups variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation sequentially maximize the ratio among groups to within group variation.

### 2.5.5. Computation of Average Intra-Cluster Distance

The average intra-cluster distance for each cluster was calculated by taking all possible  $D^2$  values within the members of a cluster obtained from Principal coordinate analysis. The formula used to measure the average intra-cluster distance was:

$$\text{Intra-cluster distance} = \frac{\sum D^2}{n} \quad (3)$$

where,  $\sum D^2$  = The sum of distances between all possible combinations ( $n$ ) of the genotypes included in a cluster.

$n$  = Number of all possible combination.

### 2.5.6. Cluster Diagram

A cluster diagram was drawn using the values of inter and intra cluster distances. The diagram represented the pattern of diversity among the genotypes and relationships between different genotypes included in the clusters.

### 2.5.7. Selection of Germplasm for Future Hybridization Program

Divergence analysis is usually performed to identify the diverse genotypes for

hybridization purposes. The genotypes grouped together are less divergent among themselves than those of others, which fall into different clusters. Clusters separated by the largest statistical distances ( $D^2$ ) express the maximum divergence among the genotypes included into different clusters.

Singh and Chaudhury [16] stated the following points to be considered while selecting genotypes for hybridization:

- 1) Choice of cluster from which genotypes are selected for the use as parent (s);
- 2) Selection of particular genotype (s) from the selected cluster (s);
- 3) Relative combination of the traits to the total divergence;
- 4) Other important traits of the genotypes (as for performance).

### 3. Results

The extent of genetic diversity present in a germplasm collection of a crop plant is an index of its genetic dynamism. The experimental data were collected and analyzed to study the performance of wheat genotype under late sowing condition and clustering the genotypes into several clusters those were similar to each other.

#### 3.1. Multivariate Analysis ( $D^2$ Statistics)

This technique is helpful to describe phenotypic variation among the genotypes. Cluster analysis, principal component analysis (PCA), principal coordinate analysis and canonical vector analysis were used to analyze 12 traits of twenty five (25) wheat genotypes in this study.

##### 3.1.1. Non-Hierarchical Clustering

Non-hierarchical clustering using Mahalanobis  $D^2$  statistics and Tocher's method, grouped 25 wheat genotypes into five different clusters. These results were in conformity with the clustering pattern of the genotypes obtained through principal component analysis. The pattern of distribution of genotypes into various clusters is shown in **Table 1**. The distribution pattern indicated that the maximum number of genotypes (8) was obtained in cluster V followed by cluster II (6), cluster I (5), cluster IV (4) and cluster III (2).

**Table 1.** Distribution of 25 wheat genotypes into five clusters based on Mahalanobis  $D^2$  Values.

Clusters	No. of genotypes	Total entries (%)	Genotypes
I	5	20	G2, G5, G6, G16, G20
II	6	24	G4, G7, G9, G11, G12, G17
III	2	08	G10, G24
IV	4	16	G1, G13, G19, G21
V	8	32	G3, G8, G14, G15, G18, G22, G23, G25

### 3.1.2. Canonical Vector Analysis

Canonical vector analysis was done to compute the intra (bold) and inter-cluster distances ( $D^2$  statistics) presented in **Table 2**. The highest intra-cluster distance was observed in cluster IV (1.17) and the lowest was in cluster III (0.19). The longest inter-cluster distance was obtained in between cluster III and IV (23.06) followed by the distance between clusters II and III (19.06) and then between clusters I and III (15.94). Alternatively, the distance between cluster II and IV was the shortest (4.55) followed by the distance between clusters I and II (5.03).

### 3.1.3. Principal Component Analysis

The eigenvalues and variance percentage about principal components for twenty five (25) agronomic traits are presented in **Table 3**. The principal component analysis is used to compress and classify the data.

The main purpose is to reduce the dimensionality of a data set to interpret the data in a more meaningful way. However, the number of variables is reduced to

**Table 2.** Average matrix of intra (bold) and inter cluster distances ( $D^2$  statistics) among 12 traits of 25 wheat genotypes

Cluster number	I	II	III	IV	V
I	<b>0.72</b>				
II	5.03	<b>0.76</b>			
III	15.94	19.06	<b>0.19</b>		
IV	8.34	4.55	23.06	<b>1.17</b>	
V	7.02	10.44	9.39	14.48	<b>0.61</b>

**Table 3.** Eigenvalues and variance percentage (%) of 12 agronomic traits towards divergence in 25 wheat genotypes.

Principal components	Eigenvalues	% Variance	Cumulative variance %
Spike/m <sup>2</sup>	3.028	25.23	25.23
Spikelets/Spike	2.422	20.18	45.41
Grain/Spike	1.788	14.90	60.31
1000-grain weight	1.324	11.03	71.34
Heading days	0.880	7.33	78.67
Maturity days	0.656	5.47	84.14
Plant height (cm)	0.558	4.65	88.79
Canopy tem.Vg	0.488	4.06	92.85
Canopy tem.Gf	0.366	3.05	95.90
SPAD	0.238	1.98	97.88
Yield	0.181	1.51	99.39
Biomass	0.071	0.59	99.98

Canopy tem.Vg = Canopy temperature at vegetative stage, Canopy tem. Gf = Canopy temperature at grain filling stage and SPAD = Chlorophyll content of flag leaf at grain filling stage.

a few and more easily interpretable linear combinations of data. This each new linear combination is known as principal component.

Results explored that the parameter spike/m<sup>2</sup> showed its highest (25.23%) genetic variation among all the traits and genotypes, followed by spikelets/spike as the second highest trait (20.18%). The individual value of the first four traits were greater than one (>1) and accounted for total of 71.34% variation among 12 traits whereas the first two accounted for a maximum value of 45.41% as illustrating different traits of 25 wheat genotypes.

### 3.1.4. Contribution of Traits towards Divergence

Contribution of different traits toward genetic divergence obtained from canonical vector analysis is presented in **Table 4**. The important traits spike/m<sup>2</sup>, spikelets/spike, maturity days, plant height and yield were showed as positive values in vector 1. In vector 2, spike/m<sup>2</sup>, spikelets/spike, 1000-grain weight, heading days, plant height and biomass were marked as positive values.

Results revealed from the canonical vector analysis that both the vectors 1 and 2 had positive values for spike/m<sup>2</sup>, spikelets/spike and plant height. On the other hand, the grain/spike, heading days, canopy temperature at vegetative stage, canopy temperature at grain filling stage and SPAD had negative values in both vectors.

### 3.1.5. Intra-Cluster Mean

Intra-cluster means for 12 traits are presented in **Table 5** exposed distinguishing potentiality for most of the traits which indicated their proper clustering capacity. Cluster III provided the highest spike/m<sup>2</sup> (388.8), grain/spike (48.1), plant height (89.5 cm), SPAD (54.2), yield (2799 kg/ha) and biomass (7758.1 Kg/ha) belonging to the lowest heading days (64.7 days), maturity days (98.7 days),

**Table 4.** Latent vectors for 12 traits in 25 wheat genotypes

Traits	Vector 1	Vector 2
Spike/m <sup>2</sup>	0.0072	0.0447
Spikelets/spike	0.5870	0.5895
Grain/spike	-0.1090	-0.3582
1000-grain weight	-0.1062	0.1918
Heading days	-0.0516	0.4630
Maturity days	0.0563	-1.3146
Plant height (cm)	0.0034	0.1669
Canopy temp.vg	-0.0035	-0.3643
Canopy temp.gf	-0.0846	-0.4327
SPAD	-0.0032	-0.1713
Yield	0.0280	-0.0070
Biomass	-0.2438	1.2618

**Table 5.** Cluster means for the 12 traits of 25 wheat genotypes.

Traits	Cluster mean				
	I	II	III	IV	V
Spike/m <sup>2</sup>	334.7	331.2	388.8	353.9	350.2
Spikelets/spike	16.8	16.4	17.8	18.0	17.5
Grain/spike	45.6	43.2	48.1	42.1	43.2
1000-grain weight	34.1	33.0	31.8	35.1	30.4
Heading days	66.3	67.7	64.7	66.6	66.5
Maturity days	100.4	99.6	98.7	99.1	100.6
Plant height (cm)	84.9	83.9	89.5	85.6	86.5
Canopy tem. vg	23.7	22.5	21.7	22.0	23.8
Canopy tem. gf	24.0	24.5	22.4	24.0	24.7
SPAD	50.3	48.1	54.2	49.9	51.2
Yield	2301	2400	2799	2502	2172
Biomass	6227.5	4601.9	7758.1	5401.9	6809.0

Canopy tem. Vg = Canopy temperature at vegetative stage, Canopy tem. Gf = Canopy temperature at grain filling stage and SPAD = Chlorophyll content of flag leaf at grain filling stage.

canopy temperature at vegetative stage (21.7°C) and canopy temperature at grain filling stage (22.4°C). The cluster IV had the highest spikelets/spike (18.0) and 1000-grain weight (35.1 g), the second highest spike/m<sup>2</sup> (353.9) and yield (2502 kg/ha) with lower canopy temperature at vegetative (22.0°C) and grain filling (24.0°C) stages.

Alternatively, the lowest 1000-grain weight (30.4 g) and grain yield (2172 kg/ha) belonging to the highest canopy temperature at both stages (23.8°C and 24.7°C) were found in cluster V. Furthermore, the cluster II derived the lowest spike/m<sup>2</sup> (331.2), spikelets/spike (16.4), plant height (83.9), SPAD (48.1) and biomass (4601.9 Kg/ha) with largest heading days (67.7).

**Yield rank:** Cluster III > Cluster IV > Cluster II > Cluster I > Cluster V.

#### 4. Discussion

The investigation was undertaken to identify the extent of genetic diversity considering 12 traits of 25 wheat genotypes in heat tolerance condition. Upon taking in account non-hierarchical parameters these genotypes were classified into five clusters from which the cluster V comprised maximum eight (8) genotypes. The pattern of distribution of genotypes among various cluster groups reflected the considerable genetic variability existed in the genotypes and this wider genetic variability might be due to the adaptation of these genotypes to specific environmental conditions. In some cases, effect of geographical origin influenced clustering, though geographic distribution was not the sole criterion of genetic diversity. This suggested that it is not necessary to choose diverse parent from diverse geographic regions for hybridization [17].

The results in **Table 2** showed that the inter-cluster distances were longer than those of intra-cluster distances. Choudhury *et al.* [18] obtained similar results getting larger inter-cluster distances than the intra cluster distance in a multivariate analysis in wheat genotypes. The highest inter-cluster distance was observed in between cluster III and IV (23.06) followed by cluster II and III (19.06), which indicated higher degree of genetic diversity and thus it might be recommended to utilize in inter varietal hybridization program. It was also reported that genotypes within the clusters with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance [19]. The highest intra cluster distance was found within the genotypes of cluster IV (1.17). The greater inter-cluster and intra-cluster distances indicated greater genetic variability among accession between and within clusters respectively.

The more diversity of parents indicated the greater chance of obtaining higher degree of heterosis [20]. Parent for hybridization could be selected on the basis of large inter-cluster distance and cluster mean for isolating useful recombination in segregating generations [21]. In contrast, the lowest intra cluster distance was observed within the genotypes of cluster III (0.19) followed by cluster V (0.61), which exposed less genetic diversity and thus these might be utilized for population improvement of wheat genotypes.

The maximum eigenvalues those had the values greater than one (>1) were found in first four components viz. spike/m<sup>2</sup> (3.028; variance: 25.23%), spikelets/spike (2.422; variance: 20.18%), grain/spike (1.788; variance: 14.90%) and 1000-grain weight (1.324; variance: 11.03%) contributed the maximum variance (71.34%) for these agronomic traits (**Table 3**). Therefore, these factors/traits are responsible for major variation toward genetic divergence for 25 wheat genotypes in the experiment.

The results of canonical vector analysis in **Table 4** revealed that both the vectors 1 and 2 had positive values for spike/m<sup>2</sup> (0.0072 and 0.0447), spikelet/spike (0.5870 and 0.5895) and plant height (0.0034 and 0.1669) among 12 traits. Such positive results indicated that these traits had the highest contribution capacity toward the divergence among 25 wheat genotypes. Positive values for traits in any of the vectors indicating higher contribution of the trait in that respective vector while negative values indicated lower contribution. Therefore, the divergence in the present materials due to these traits will offer a good scope for improvement heat tolerance through selection of parents. The trait contributing maximum to the divergence were used to give greater emphasis for deciding on the cluster for the purpose of further selection and in the choice of parents for hybridization [22]. The attributes grain/spike (−0.1090 and −0.3582), canopy temperature at both stages (−0.0035 & −0.3643 and −0.0846 & −0.4327), and SPAD (−0.0032 and −0.1713) showed negative values in both vectors, and the rest traits exposed positive and negative values simultaneously indicated their lower potentiality for total genetic divergence.

In clustering technique genotypes were splitted into various groups on the basis of their performances which are displayed in **Table 5**. This table based on the phenological, physiological, yield and yield attributing traits of 25 different wheat genotypes was constructed. Considering the similarity percentage and related characters five clusters were formed. Clustering these genotypes can be useful in identify accessions with similar traits, which can be useful in breeding programs. It is important that genotypes belonged to respective cluster could be used in crop improvement program for respective character. Crossing genotypes belonging to different clusters could maximize the opportunities for transgressive segregation as there is a higher probability that unrelated genotypes would contribute unique desirable alleles at different loci [23].

Among 12 traits, plant height and spike/m<sup>2</sup> were major traits that contributed mostly toward divergence. The Cluster III had the highest spike/m<sup>2</sup>, grains/spike, plant height, SPAD, yield and biomass with lowest canopy temperature at vegetative and grain filling stage and heading days and maturity days. This cluster also had the 2<sup>nd</sup> highest spikelets/spike. The highest spikelets/spike and 1000-grain weight, the second highest spike/m<sup>2</sup> and yield with lesser canopy temperature at vegetative and grain filling stages were belonged to the cluster IV. Cluster V produced the lowest 1000-grain weight and grain yield along with the highest canopy temperature at both stages. Likewise, the lowest spike/m<sup>2</sup>, spikelets/spike, plant height, SPAD and biomass with largest heading days were obtained from the cluster II. To select the clusters for more heterotic F1, five pairs of clusters to be considered for this purposes viz. Cluster III and IV, II and III, I and III, IV and V, II and V considered as a tools of hybridization program.

## 5. Conclusions

The potential genotypes for valuable traits found in different clusters. There were high degrees of diversity existed among the studied wheat genotypes which can be utilized in different varietal improvement program in future. Performances of 25 spring wheat genotypes were examined during the winter season of 2016/2017 to identify the extent of genetic diversity in different traits related to heat tolerance mechanism. On the basis of non-hierarchical clustering parameters all these genotypes were classified into five clusters viz. cluster I, II, III, IV and V and these groups were arranged in five (5) pairs of clusters viz. cluster I and III; II and III; II and V; III and IV; IV and V considering their similar potentiality of different traits. Maximum number of genotypes (8) was found in cluster V and minimum in cluster III (2). The longest inter cluster distance (23.06) was observed in between cluster III and IV, and the shortest (4.55) was in between cluster II and IV.

The highest eigenvalue was obtained in the parameter spike/m<sup>2</sup> (25.23%) and the second highest was in spikelets/spike (20.18%). These two parameters exposed positive canonical values both in the vectors 1 and 2 for which these traits can be recommended as major traits for exploring their highest potential toward

genetic divergence. Selection of parents considering these two traits had good scope to get broad spectrum of segregates. The highest spike/m<sup>2</sup> (388.8), grain/spike (48.1), plant height (89.5 cm), SPAD (54.2), yield (2799 kg/ha) and biomass (7758.1 Kg/ha) with lowest heading days (64.7 days), maturity days (98.7 days), canopy temperature at vegetative stage (21.7°C) and canopy temperature at grain filling stage (22.4°C) were found in Cluster III. Likewise, the highest spikelets/spike (18.0) and 1000-grain weight (35.1 g), the second highest yield (2502 Kg/ha) and spike/m<sup>2</sup> (353.9) along with lower canopy temperature at vegetative and grain filling stages (22.0°C and 24.0°C) were obtained in cluster IV. On the other hand, cluster V was exposed as the lowest producer of 1000-grain weight (30.4 g) and grain yield (2172 kg/ha) along with the highest canopy temperature at both stages (23.8°C and 24.7°C).

The traits spike/m<sup>2</sup> and spikelets/spike contributed mostly toward genetic divergence. Selection of parents for these two traits has good scope to get broad spectrum of segregates. Considering magnitude of genetic distance, contribution of different traits toward the total divergence, magnitude of cluster mean, the genotypes G10 and G24 under cluster III and genotypes G01, G13, G19 and G21 under the cluster IV might be considered as parents for future hybridization program. Therefore, this study can help breeders to increase genetic diversity by selecting materials of divergent parentage for crosses, thereby reducing vulnerability to diseases and climate changes.

### Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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