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Research Article

Genetic divergence analysis for morpho-physiological traits, under timely and late sown condition in bread wheat (*Triticum aestivum L.*)

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Abstract

Fifty bread wheat genotypes were evaluated during *rabi* crop season, over the two years (2007/08 and 2008/09), to work out the genetic divergence for yield and morpho-physiological traits under normal and heat-stress environmental conditions. Significant differences were observed for genotypes in respect to all traits under both environments. Fifty genotypes were grouped into 10 diverse clusters under both normal and heat-stress environment. Most of the genotypes (9) were grouped in cluster I and 7 genotypes in cluster I and II under normal and heat- stress conditions. Maximum divergence was observed in cluster II and IX under normal conditions and cluster VI and VIII under heat-stress conditions. Therefore, genotypes of these cluster showed more divergence, then genotypes from cluster II, IX, VI and VIII can be used to produce superior hybrids for terminal heat-stress conditions.

Keywords: Bread wheat, genetic divergence, clustering, CTD, CMTS, terminal heat-stress

1. Introduction

India achieved remarkable progress in wheat production during the last four decades and is the second largest wheat producer in the world with the production touching a record level of 95.91 million tons during 2013-14 (Anonymous 2014). Food security worldwide is major challenged by increasing food demand and threatened by global climatic changes, as drought, temperature, salinity and nutrient imbalance and others (Trethowan and Kazi, 2008).

Terminal heat stress during crop growth is a main environmental factor that reduces the grain yield (Fischer, 1983), because of early senescence and acceleration of grain filling activities in wheat (Paulsen, 1994), and also shortening grain filling duration along with constriction of carbon assimilation (Stone, 2001). Stone and Nicolas (1994) have reported that losses in kernel weight (23%) occurred when the temperature was increased from 20°C to 15°C (day/night) to 40°C to 15° C on the third day after anthesis.

Obtaining accurate estimates of the genetic diversity among the germplasm sources may increase the efficiency of plant breeding (Barrett and Kidwell, 1998). Studying variation among the germplasm lines of known potentialities can generate information helpful to the breeders to choose suitable parents for purposeful hybridization (Sharma, 2008). Improving the productivity of wheat under heat-stress is one of the primary goals of the wheat breeding programmes in India.

Thus present study was undertaken to clustering the genotypes, based on inter and intra cluster distances along with heat-stress adapted traits and select suitable genotypes that can be recommended for further wheat breeding programmes for the development of high yielding and heat tolerant genotypes.

2. Materials and methods

Field experiments were conducted at the Amar Singh College, Lakhaoti, Bulanshahar, Uttar Pradesh, India during two growing *rabi* seasons (2007-08 and 2008-09) followed by randomized complete block design with three replications and two dates of sowing as 15th November as timely sown and 15th December as late sown, where timely sown conditions was considered as normal environment and late sown conditions as heat-stress environment. All the genotypes were sown in one row plot of 3.0 m length with 23 cm row to row distance. The standard agronomical practices were done for wheat under normal and heat-stress conditions.

Observations were recorded on 14 morpho-physiological traits as, days to 50% heading, days to maturity, grain filling duration, plant height (cm), number of tillers/plant, number of tillers/m, number of spikelets/spike, number of seeds/spike, 1000 grain weight (g), biological yield (g/plot), harvest index (%), canopy temperature depression, cell membrane thermo stability and grain yield (g/plot) from each plot. The canopy temperature depression was measured at crop growth particular at anthesis stage using a portable infrared thermometer (Model AG-42) with a view of 2.5° under both normal and heat-stress environment. Membrane thermal stability was estimated using procedures as described by Blum and Ebercon (1981). Cluster analysis was carried out using statistical softwareas SAS version 9.2 (2008). Possibly also include the name of clustering method with reference.

3. Results and discussion

Analysis of variance: All the traits studied showed significant variation in respect of the genotypes under the present investigation. This was apparent from the significant to highly significant values (F-calculated values) under timely sown conditions of year 2007-08 and 2008-09 and late sown conditions of the year 2007/08 and 2008/09. There was also significant differences exist at genotypic level under normal and heat-stress environments. Cluster analysis was done by using the data of normal and heat-stress environment and analyzed results are presented in table 1 and 2.

Table 1. Distribution of fifty genotypes of bread wheat into different clusters under normal and heat-stress environmental conditions.

Clusters	Environment	Number of genotypes	Name of genotypes included in different clusters
I	Normal	9	PBW502, BL1724, PBW175, GW322, HI1500, HUW510, HW2045, DWR195 and HP1744
	Heat-stress	7	DBW14, GW173, HD2009, HD2643, RAJ3765, HW2045 and UP2425
II	Normal	4	PBW343, WH542, HD2687 and HD 2733
	Heat-stress	7	K9107, VL738, K9006, RAJ4037, GW190, PBW550 and HI1077
III	Normal	7	PBW443, DL788-2, DBW14, HD2009, RAJ4037, PBW550 and HI1077
	Heat-stress	5	DBW17, PBW502, PBW175, PBW343 and HD2824
IV	Normal	7	UP2338, HUW468, GW273, WH157, NW1012, K9107 and UP2565
	Heat-stress	6	HD2687, HI977, HI1500, NW1014, CPAN3004 and HD2781
V	Normal	7	DBW17, HI977, HUW533, HUW234, NW1014, PBW299and PBW226
	Heat-stress	5	HUW510, HUW533, HP1744, HUW213 and PBW299
VI	Normal	2	GW173 and CPAN3004
	Heat-stress	2	C306 and DWR195
VII	Normal	5	HW2004, VL738, K9006, C306 and HD2781
	Heat-stress	6	WH542, WH157, BL1724, NW1012, HD2329 and PBW226
VIII	Normal	1	PBW373
	Heat-stress	3	PBW343, UP2338 and UP2565
IX	Normal	5	MP4010, HD2643, RAJ3765, UP2425 and HUW213
	Heat-stress	7	HD2733, HUW468, GW273, GW322, MP4010, DL788-2 and HUW234
X	Normal	3	HD2824, GW190 and HD2329
	Heat-stress	2	HW2004 and PBW373

Table 2. Estimates of average intra and inter cluster distances D^2 Values for ten clusters constructed from fifty genotypes of wheat under normal and heat-stress environment.

Cluster	Environment	I	II	III	IV	V	VI	VII	VIII	IX	X
I	Normal	**2.21**	6.37	2.26	3.15	2.33	5.12	3.29	5.75	3.29	5.86
	Heat-stress	**2.47**	4.33	3.33	3.97	4.03	5.49	4.55	5.27	2.94	5.09
II	Normal		**2.12**	6.16	4.46	5.84	4.64	6.19	6.18	7.13	3.69
	Heat-stress		**2.35**	3.52	2.68	4.70	3.71	4.43	4.69	3.62	3.42
III	Normal			**1.79**	3.20	3.31	5.27	3.78	5.58	4.02	5.37
	Heat-stress			**2.60**	3.49	4.76	6.01	4.06	4.61	3.78	4.71
IV	Normal				**2.49**	3.52	4.54	2.89	4.25	3.98	4.76
	Heat-stress				**2.08**	4.11	3.78	3.18	3.92	3.22	4.42
V	Normal					**2.21**	4.08	4.03	5.51	3.36	5.41
	Heat-stress					**2.68**	4.52	4.21	5.38	3.69	5.68
VI	Normal						**1.88**	5.73	4.42	5.16	3.93
	Heat-stress						**1.97**	5.31	6.73	4.39	5.34
VII	Normal							**2.79**	4.87	4.95	5.67
	Heat-stress							**2.47**	3.57	3.35	5.82
VIII	Normal								**1.12**	6.51	5.67
	Heat-stress								**2.47**	4.15	4.59
IX	Normal									**2.02**	6.35
	Heat-stress									**2.32**	4.37
X	Normal										1.93
	Heat-stress										1.29

Bold values denote intra cluster distances for Normal and Heat stress environments.

Cluster analysis

Divergence analysis of 50 bread wheat genotypes was carried out and results with respect to normal and heat-stress environments are presented in the Tables 1-2. In any crop improvement programme, genetic diversity has been considered as an important factor which is also an essential prerequisite for hybridization programme for obtaining high yielding progenies or genotypes. Direct group constellation was formed using the D^2 values for each of the traits. All the fifty bread wheat genotypes were grouped into ten clusters in both normal and heat-stress environmental conditions and details of each of the cluster is presented in the table 1. Under normal environmental conditions, among the ten clusters, cluster I contained the maximum number of genotypes (9) followed by cluster III, IV and V with 7 genotypes. Under heat-stress environmental conditions, cluster I and II contained the maximum number of genotype (7) followed by cluster IV and VII (6), cluster III and V (5), cluster VIII (3), cluster VI and X (2) as exhibited by table 1.

D^2 analysis also used to identify the diverse and desirable genotypes on the basis of intra and inter-cluster distances and cluster mean performance respectively. The intra and inter cluster distances from the normal and heat-stress environmental conditions are presented in table 2. Under normal sown environmental conditions, maximum intra-cluster distance was observed in cluster VII, while maximum inter-cluster distances were observed between cluster II and IX (7.13) followed by cluster VIII and IX (6.51), cluster I and II (6.37), cluster IX and X (6.35), cluster II and VII (6.19), cluster II and VIII (6.18) and cluster II and III (6.16). The minimum inter-cluster distances were recorded between cluster I and III (2.26) as presented in table 2. Therefore genotypes of cluster II and IX exhibited maximum divergence and indicated that genotypes PBW343, WH542, HD2687 and HD2733 (cluster II) and genotypes MP4010, HD2643, RAJ3765, UP2425 and HUW213 (cluster IX) showed more divergence, these genotypes may be used to produce the superior hybrids and transgressive segregants.

Under heat-stress environmental conditions, the maximum intra-cluster distance was observed in cluster

V (2.68), while maximum inter-cluster distances were observed between clusters VI and VIII (6.73) followed by cluster III and VI (6.01), cluster VII and X (5.82) and cluster VI and VII (5.31). The minimum inter cluster distances were observed between cluster I and IX (2.94) as sown in table 2. The genotypes of cluster VI and VIII exhibited maximum divergence and indicated that the genotypes C306 and DWR195 (cluster VI) and genotypes PBW343, UP2338 and UP2565 (cluster VIII) showed more divergence, these genotypes may be used to produce superior hybrids. Similar results have been reported by Jag Shoran and Tandon (1995) and Kant *et al*., (1999).

One of the important aspects of the present investigation was to classify 50 genotypes into different clusters based on the genetic distances. This aspect is important in sense that in long run, it may be help full to avoid repetition of genetically similar genotypes in hybridization. This has been achieved by resorting to assignment of these genotypes into different groups and studying their inter- and intra-group distances. In our study D^2 analysis led to the formation of ten groups under both normal and heat-stress conditions.

A close view of 50 genotypes revealed that some genotypes were belonging to different eco-geographical areas, but they included in the same cluster. This indicated that there is no association between clustering pattern and eco-geographical distribution of the genotypes. Also, the clustering of genotypes from different eco-geographical locations into one cluster could be attributed to make possible free exchange of breeding material from one place to other (Sharma & Hore 1997). This may also be due to the fact that the unidirectional selection may helpful for a particular trait at several place which produced similar phenotypes and which were aggregated in one cluster irrespective of their distant geographical origin.

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