Short Communication



Genetic analysis for identification of terminal heat tolerant genotypes in wheat

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(Received: May 2016; Revised: December 2016; Accepted: December 2016)

Abstract

A study was conducted to analyze divergence in 49 genotypes of bread wheat (*Triticum aestivum* L.) under terminal heat stress environment. The results indicated a good amount of genetic divergence among the wheat genotypes under heat stress. The genotypes were grouped into five clusters with maximum intra cluster distance of 70.392 (Cluster V) and maximum inter cluster distance was recorded between clusters III and V (72.11). Principal component analysis extracted seven principal components accounting 80.9% of total genetic variation. The identification of genotypes displaying heat stress tolerance may be useful in breeding.

Key words: Wheat, D² statistics, PCA, terminal heat stress

In West Bengal, wheat is sown generally in mid December after AMAN paddy. Therefore, wheat is often affected due to sudden rise in temperature resulting in the initiation of reproductive phase even before completion of the required period for vegetative growth. As wheat is an autogamous crop, hybridization followed by subsequent selection is a major breeding approach. In order to benefit transgressive segregation, genetic distance between parents is necessary (Joshi et al. 2004). Principal component analysis (PCA) is a multivariate analysis method that aims to explain the correlation between a large set of variables in terms of a small number of underlying independent factors (Beheshtizadeh et al. 2013). Genotypic variation for normalized difference vegetation index and its relationship with grain yield in wheat under terminal heat stress is an important factor for consideration in breeding for heat stress tolerance (Ramya et al. 2015). Thus the choice of parents is the crucial step so as to combine heat tolerant traits as well as greater grain yield

Seeds of 44 genotypes and 5 checks *viz.*, DBW 14, RAJ 3765, HALNA, HD 2285 and SONALIKA of bread wheat (Table 1) were procured from Indian Institute of Wheat and Barley Research (IIWBR), Karnal. Seeds were sown on 15th December 2014 and 16th December 2015 in the field of AB block, Kalyani, Nadia, West Bengal following randomized block design with 2 replications. Each plot consisted of five rows of 1.5 meter length with a spacing of 50cm x 25cm. Data were recorded on five randomly and competitive plants of each genotype in consecutive seasons and were pooled over. The D² statistics and PCA were done according to Rao (1952) and Harman (1976) respectively. PCA was performed using MINITAB version 17 software.

All the genotypes were clustered into five groups (Table 1). The intra cluster heterogeneity of cluster number V (70.392) might serve as guideline to select desirable parents for recombination breeding programme even from the same cluster (Table 2). Cluster III showed high mean values for number of tillers plant⁻¹, number of spikes plant⁻¹, spike length, number of spikelets spike⁻¹, number of florets spike⁻¹, number of grains spike⁻¹, floret fertility, grain weight spike⁻¹, yield plant⁻¹. Cluster V had highest days to maturity, flag leaf area, proline content, 1000

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Published by the Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012 Online management by indianjournals.com; http://epubs.icar.org.in/journal/index.php/IJGPB

| 1 | 6 | 1 |
|---|---|---|
| | | |

| Cluster no. | No. of genotypes | Genotypes |
|----------------|------------------|---|
| I | 15 | AKAW 4498, AKAW 4702, WSM 135, DBW 74, DBW 113, DBW 118, DBW 125, WSM 131,DL 1058, GW 2008-153, GW 2008- 161, GW 2010-321, GW 2011-398, GW 2011-399, GW 2011-403 |
| II | 2 | GW 2012-474, DBW 14 $^{\odot}$ |
| III | 2 | GW 2012-475, RAJ 4360 |
| IV | 27 | GW 2011-404, GW 2012-471, GW 2012-472, GW 2012-473, VW 964, GW 2012-476, GW 2012-477, NIAW 2302, NIAW 2415, NIAW 2421, NWL-9-3, NWL-9-5, RAJ 4274, RAJ 4314, VL 946, J-07-47, RAJ 4318, RAJ 4358, RAJ 4359, RAJ 4361, RAJ 4362, RWP 2009- 05, RWP 2011-15, RWP 2011-17, RWP 2011-18, UP 2783, RAJ 3765 [©] |
| V | 3 | Halna [©] , HD 2285 [©] , Sonalika [©] |

 Table 1. Grouping of 49 genotypes of wheat (Triticum aestivum L.) into 5 clusters

grain weight and amylose content but least value recorded for days to heading and days to flowering. The inter cluster distance was high explaining the presence of a greater diversity among them. Yield

Table 2. Average inter and intra cluster distances (D)

| Clusters | I | II | III | IV | V |
|----------|--------|--------|--------|--------|--------|
| I | 51.168 | 51.926 | 48.572 | 54.971 | 63.971 |
| II | | 18.481 | 51.553 | 58.334 | 70.753 |
| III | | | 20.976 | 52.366 | 72.11 |
| IV | | | | 60.247 | 67.101 |
| V | | | | | 70.392 |

plant⁻¹ followed by 1000 grain weight, number of grains spike⁻¹ and amylose content were also found to be the highest contributors towards total divergence. Therefore, the genotypes of cluster V *viz.*, Halna, HD 2285 and Sonalika and the genotypes of cluster III (GW 2012-475 and RAJ 4360) were found diverse and could be utilized as parents for hybridization programme to obtain maximum heterosis.

Seven principal components having Eigen values greater than one were extracted from the original data accounting 80.905% of total variation amongst the wheat genotypes assessed for twenty one quantitative traits. The first principal component (PC1), which accounted for about 24.172% of the variation, was strongly associated with number of grains spike⁻¹, yield plant⁻¹, grain weight spike⁻¹, number of florets spike⁻¹, floret fertility, spike length, number of spikelets spike⁻¹, plant height and amylose content with



Fig. 1. Score plot of 49 genotypes of wheat (Triticum aestivum L.)



Fig. 2. Loading plot of 49 genotypes of wheat (*Triticum aestivum* L.)

desirable direction. This component was regarded as a yield plant⁻¹ component since it included several traits, which were associated with yield plant⁻¹. Beheshtizadeh et al. (2013) also named PC1 as spike yield component. The PC2 explaining 18.058% of the total variation had highly positive scores from of chlorophyll-a, chlorophyll-b and total chlorophyll content, but showed negative loadings of grain yield plant⁻¹. High contribution of first few PCs in total variability based on various plant traits has already been reported in the literature by Khodadadi et al. (2011) and Shefazadeh et al. (2012). Spike length, number of spikelets spike⁻¹ and number of florets spike⁻¹ may be taken as direct selection criteria of bread wheat genotypes under terminal heat stress as they possessed high positive scores in the major components i.e., PC1, PC2 and PC3 explaining 56.778% variability. Loading plot (Fig. 2) depicted the direction of the variables as per the sign of score coefficients. Chlorophyll-a, chlorophyll-b, total chlorophyll, gluten content, and proline content aligned in opposite direction to the other characters signifying negative correlation with yield plant⁻¹. From the score plot (Fig. 1) it was visualized that, high yielding genotypes J-07-47 and GW 2011-403 that were identified from present research were distantly related with GW 2012-474, HALNA[©]. RWP 2011-15, VW 964 and RAJ 4362 also maintained a gap from GW 2011-404. These diverse genotypes may be selected as parents for hybridization programme.

Diversity analysis based on D^2 statistics and principal component analysis suggested the genotypes that could be utilized in designing a breeding program which directly indicate the possibility to get maximum heterosis as well as to combine heat tolerance with high yield. The genotypes could also be exploited for testing under various agro-climatic zones for expanding wheat into nontraditional areas of India.

Authors' contribution

Conceptualization of research (SM*, SM); Designing of the experiments (SM*, SM, APD, ABM); Contribution of experimental materials (SM);

Execution of field/lab experiments and data collection (SM*, SM, APD); Analysis of data and interpretation (SM*, SM, APD, ABM); Preparation of manuscript (SM*, SM).

Declaration

The authors declare no conflict of interest.

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