Short Communication

Evaluation of bread wheat (*Triticum aestivum* L.) for terminal heat tolerance

Stuti Krishna[#], Priyanka Upadhayay[#], Vinod Kumar Mishra*, Shubhra N. Kujur, Monu Kumar[1], Punam S. Yadav, Parvin Kumar Mahto[2], Prashant Singh, Ashutosh, Sandeep Sharma and Ramesh Chand[3]

Department of Genetics and Plant Breeding, [1]ICAR-Central Research Institute for Jute & Allied Fibre, Barrackpore; [2]Institute of Environmental and Sustainable Development, [3]Department of Mycology and Plant Pathology, BHU, Varanasi, U.P.

Abstract

Terminal heat tolerance of 34 wheat genotypes were analyzed for two years. Among 14 traits, canopy temperature, plot yield and days to heading were major components in clustering of genotypes. Three genotypes namely, DBW39, DBW16 and DBW14 had lowest heat susceptibility index (0.34-0.36) for plot yield and were considered as heat tolerant genotypes by both Hierarchical Cluster Analysis as well as Discriminant Analysis. These genotypes may serve as potential donors in wheat breeding to improve the terminal heat tolerance.

Key words: Canopy temperature, DA, HCA, HSI, terminal heat stress

High temperature induced heat stress is one of the major challenges for wheat production and optimal crop yield (IPCC 2007). It has been reported earlier that with 1ºC increase in temperature global wheat production is reduced by 6% (Asseng 2015). Effect of terminal heat stress in wheat is detrimental at reproductive and grain filling stages and leads to adverse effects on various parameters of grain development (Reynolds et al. 2012). The present study was undertaken to evaluate terminal heat tolerance in wheat by studying morpho-physiological parameters.

The experimental materials comprised of 34 diverse wheat genotypes sown during *rabi* season 2016-17 and 2017-18 at Agriculture Research Farm, Banaras Hindu University, Varanasi. The material was planted under timely sown (3rd week of November, control) and late sown (3rd week of December, heat stress) using Randomized Block Design with three replications. Five plants of each genotype from each replication were selected randomly for trait measurement. Fourteen morpho-physiological traits *viz.,* Days to heading (DH), NDVI, SPAD, canopy temperature (CT), plant height (PH), peduncle length (PL), No. of spikelet/spike (SPS), spike length (SL), plot yield (PY), biomass (BM), thousand grain weight (TGW), days to maturity (DM), grain filling days (GFD) and glaucousness index (GI) were recorded.

Multivariate analysis was performed as previously described by Yadav et al. (2004). Clustering and dendrograms were prepared using Wards' method of Hierarchical Cluster Analysis (HCA) (Shamim et al. 2014). Relative importance of traits in clustering was calculated using Principal Component Analysis (PCA). Cluster Score was calculated using weighted linear combination of morpho-physiological traits. Classification accuracy of Wards' method of HCA was tested by Discriminant Analysis (DA). These statistical analyses were carried out using SPSSv.16 software. Heat Susceptibility Index (HSI) was calculated for plot yield using formula by Fisher and Maurer (1978).

Thirty-four genotypes were classified into three different clusters using Ward's HCA method (Table 1). Genotypes in Cluster I had significantly higher

Table 1. Descriptive statistics of morpho-physiological traits of 34 genotypes under different clusters

Parameters	Cluster I		Cluster II		Cluster III		Total	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
DH	61.93	1.49	61.25	1.00	65.67	0.58	61.94	1.70
NDVI	0.53	0.03	0.47	0.04	0.51	0.10	0.50	0.05
SPAD	43.95	1.79	40.40	2.09	39.97	0.58	41.92	2.59
CT	18.47	0.59	21.16	1.16	21.69	0.28	20.02	1.66
PL	13.90	1.82	13.63	1.75	11.33	1.15	13.54	1.84
PH	86.14	2.33	78.33	4.48	77.33	2.52	81.69	5.29
SPS	15.13	1.23	14.43	1.54	14.22	0.69	14.72	1.37
SL	13.73	1.28	11.35	1.72	11.46	1.59	12.41	1.90
PY	307.50	29.39	142.38	29.63	201.78	16.66	220.47	84.93
BM	757.57	65.58	292.60	67.10	481.07	25.67	514.36	233.97
TGW	43.55	2.95	28.94	3.16	31.68	3.47	35.63	7.78
DM	91.22	1.79	84.13	3.52	84.00	1.73	87.25	4.48
GFD	29.29	1.80	22.88	3.83	18.33	1.15	25.30	4.75
GI	2.82	0.87	1.90	0.59	2.67	1.15	2.37	0.88

values for TGW (22.2%), PY (39.47%), BM (47.2%) and GFD (15.7%) than the mean value of respective traits of 34 genotypes.

PCA showed that the CT, DH, PY and biomass had maximum contribution in grouping of clusters. Heat tolerance level of genotypes under different clusters were identified by summation of linear combination of selected traits under heat stress and, thus, the total score of each cluster was calculated. Based on the score values, cluster I genotypes were identified as tolerant (1268.98), Cluster II as sensitive (683.91) and cluster III as intermediate (901.31) for terminal heat stress.

Dendrogram analysis revealed group II as the largest with 16 genotypes followed by group I with 15 genotypes. Group III had only 3 genotypes. DA showed that there were significant covariance matrix differences between the clusters (p<0.01) (Table 2). In present analysis, a canonical correlation for function 1 was 0.988. Wilk's lambda indicated the significance of the discriminant function. Eigen values for the discriminant functions were computed where function 1 (39.26) explained 94.9 % variance for selected traits. However, function 2 contributed to only 5.1% of the total phenotypic variance. The DA predictions showed consistency with HCA, which suggests the use of DA in screening large number of genotypes for heat tolerance. HSI was analyzed to evaluate heat stress tolerance (Tiwari et al. 2013). Based on HSI score,

Table 2. Summary of discriminant analysis of various traits under different clusters

Box's M	F	Degree of Freedom 1	Degree of Freedom 2	SIG
Box's test of equality of covariance matrices				
251.009	1.383	91	2611	0.01
Function	Eigen value	% of variance	cumulative %	canonical correlation
1	39.26	94.9	94.9	0.988
2	2.13	5.1	100	0.825
Test of function	Wilk's Lambda	Chi Square	DF	SIG
Wilk's Lambda 1 through 2	0.008	120.89	26	0

wheat genotypes were classified into three groups- tolerant (HSI<0.5), sensitive (HSI>1.0) and intermediate (HSI= 0.5-1.0). DBW16, DBW14 and DBW39 showed least values of HSI, indicating that they were heat tolerant.

Experiment was repeated in the next year (2017-18). Similar results were obtained as the first year clearly suggested reproducibility of the data set. Taken together, DBW16, DBW14 and DBW39 were identified as heat tolerant genotypes that may be used as parents/donor in future breeding program to enhance heat tolerance of wheat.

Authors' contribution

Conceptualization of research (VKM, RC); Designing of the experiments (VKM, PSY); Contribution of experimental materials (VKM); Execution of field/lab experiments and data collection (SK, PU, AM, PKM, PS); Analysis of data and interpretation (SK, SNK, MK, PS, A, SS); Preparation of the manuscript (SK, SNK, MK, SS, VKM).

Declaration

The authors declare no conflict of interest.

References

Asseng S. 2015. Rising temperatures reduce global wheat production. Nat. Clim. Change., **5**: 143-147.

Fisher R. A. and Maurer R. 1978. Drought resistance in spring wheat cultivars I. Grain yield responses. Aust. J. Agric. Res., **29**(5): 897-912.

IPCC. 2007. Intergovernmental Panel on Climate Change fourth assessment report: Climate change. Synthesis Report. *World Meteorological Organization,* Geneva, Switzerland.

Reynolds M., Foulkes J., Furbank R., Griffiths S., King J., Murchie E., Parry M. and Slafer G. 2012. Achieving yield gains in wheat. Plant Cell Environ., **35**: 1799-1823.

Shamim F., Saqlan S. M., Athar H. and Waheed A. 2014. Screening and selection of tomato genotypes/ cultivars for drought tolerance using multivariate analysis. Pak. J. Bot., **46**(4): 1165-1178.

Tiwari C., Wallwork H., Kumar U., Dhari R., Arun B., Mishra V. K., Reynolds M. P. and Joshi A. K. 2013. Molecular mapping of high temperature tolerance in bread wheat adapted to the eastern Gangetic Plain of India. Field Crop Res., **154**: 201-210.

Yadav R., Grewal R. P. S. and Pahuja S. K. 2004. Multivariate analyses in forage sorghum [*Sorghum bicolor* (L.) Moench]. Indian J. Genet., **64**(1): 39-45.