



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(2): 2522-2524
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www.thepharmajournal.com

Received: 21-12-2022

Accepted: 23-01-2023

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Evaluation of recombinant inbred lines for terminal heat stress tolerance in bread wheat (*Triticum aestivum* L. Em. Thell)

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Abstract

Wheat is third most important cereal crop grown worldwide and is staple source of diet for millions of people all over world. According to the sixth assessment report of the IPCC (2021), the temperature reaches the 1.5 °C warming limit, at least for some period of time in the middle of the 21st century. As a consequence of this, worldwide, wheat will be exposed to considerable variation in environmental conditions majorly heat stress which restricts wheat production and productivity during both germination as well as grain filling period. In the present investigation, the RILs population derived from crossing the two contrasting parents PBN51 and Raj 4014 were evaluated under late sown conditions (heat stress) at Pantnagar (2020-21) and were characterized for various morpho-physiological traits namely, days to 50% heading, Grain Filling Duration, relative chlorophyll content, Canopy Temperature Depression, plant height, days to maturity, TGW (Thousand Grain Weight) and grain yield per plot. The combined analysis of variance showed that the RILs differed significantly for the above recorded traits. The lines showed continuous variation with normal distribution and had negligible skewness and kurtosis. Broad sense heritability was found to be high for different morpho-physiological traits hence selection will be effective among these lines. Under heat stress, the lines 26, 32, 138, 189 and 15 were found to be top performing with higher grain yields. These lines can be used in further breeding programs for developing heat stress tolerance varieties in wheat.

Keywords: Wheat, RILs, heat stress, heritability, grain yield

Introduction

Wheat is the third most important cereal crop grown worldwide which provides 25%-50% calorific needs of growing human population and is the staple source of diet for millions of people all over the world (Dixon *et al.*, 2009) ^[1]. Worldwide, wheat is exposed to considerable variation in environmental conditions like rainfall distribution, temperature patterns, water availability, biotic and abiotic stresses. In case of wheat, heat stress is known to restrict the production and productivity during both seedling as well as grain filling period by reducing fertilization and grain development rate, size of head, number of spikelets per spike, number of grains per spike, photosynthate translocation and starch granule deposition within kernels (Mohammadi *et al.*, 2004; Bhullar and Jenner 1985) ^[2, 3]. Hence in the present investigation, the RILs of wheat were evaluated under heat stress at CRC, Pantnagar in 2020-21 for different morpho-physiological and yield traits. The lines that were found to be better performing were evaluated further in different environmental conditions and the stable lines thus obtained can be used in future breeding programs.

Material and Methods

For the present investigation, a set of 192 Recombinant inbred lines derived from the cross between PBN51 and Raj4014 were evaluated at Crop Research Centre, GBPUAT, Pantnagar under late sown conditions during rabi 2020-21. The experimental design followed was Augmented RCBD. The lines were sown in 8 blocks with three checks. The phenotypic data was recorded on days to 50% heading (DH), Grain Filling Duration (GFD), relative chlorophyll content (SPAD), Canopy Temperature Depression (CTD), plant height (PH), days to maturity (DM), TGW (Thousand Grain Weight) and grain yield per plot (YPP). The analysis was carried out in R using AugmentedRCBD bulk package. Genetic variability parameters, heritability, genetic advance over mean were determined. The data was also checked for its type of distribution.

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Results and Discussion

The Analysis of variance (Table 1) revealed the presence of significant difference among the genotypes for different morphs-physiological and yield traits. The coefficient of variation for different traits was obtained as follows. Days to heading, 1.52; grain filling duration, 2.26; relative chlorophyll content, 0.88; canopy temperature depression, 23.32; plant

height, 14.17; days to maturity, 1.04; TGW, 5.6 and grain yield per plot, 22.2. Overall adjusted mean for different traits were, 73.1 days for DH, 41.73 days for GFD, 429.05 micro moles per meter square for SPAD, 2.62 °C for CTD, 73.86cm for PH, 114.82 days for DM, 32.98g for TGW and 238.83g for YPP. Similar results were obtained by Pinto *et al.*, 2008, Gao *et al.*, 2016 and Liu *et al.*, 2019 [4, 5, 6].

Table 1: ANOVA for different morpho-physiological and yield traits under Augmented RCBD.

Source	Df	CTD	DH	DM	GFD	PH	SPAD	TGW	YPP
Treatment (ignoring Blocks)	194	1.33 *	12.55 **	7.32 *	14.71 **	386.16 *	321 **	35.12 **	14339.41 *
Treatment: Check	2	2.89 *	192.52 **	100 **	546.39 **	1130.64 *	862.89 **	387.55 **	189135.84 **
Treatment: Test vs. Check	1	0.47 ns	11.58 *	1.59 ns	6.88 *	8.95 ns	302.55 **	13.68 ns	7164.29 ns
Treatment: Test	191	1.32 *	11.61 **	6.87 *	11.97 **	384.23 *	318.26 **	33.39 **	13461.81 *
Block (eliminating Treatments)	7	1.14 ns	3.62 ns	8.29 *	4.85 *	135.99 ns	42.87 ns	7.37 ns	5451.73 ns
Residuals	14	0.37	1.23	1.43	0.89	109.35	14.32	3.42	2845.18

DH varied in the range of 64.22-85.72 days, had normal distribution with a mean of 73.1 days and standard error of 0.26. GFD varied in the range of 29.41-49.91 days, had normal distribution with a mean of 41.73 days and standard error of 0.28. SPAD varied in the range of 392.03-468.03 µmol/m², had significant kurtosis with a mean of 429.05 µmol/m² and standard error of 1.31. CTD varied in the range of 0.27-7.22 °C, had significant skewness with a mean of 2.62 °C and standard error of 0.09. PH varied in the range of 34.34-128.59cm, had significant skewness with a mean of 73.86cm and standard error of 1.48. DM varied in the range of 108.5-123 days, had significant skewness with a mean of 114.82 days and standard error of 0.23. TGW varied in the range of 20.06-56.29g, had significant skewness and kurtosis with a mean of 32.98g and standard error of 0.44. YPP varied in the range of 130-718.13g, had significant skewness and kurtosis with a mean of 338.86g and standard error of 4.75. Similar results were obtained by Sharma *et al.*, 2020, Paliwal *et al.* 2012, Tiwari *et al.*, 2013 [7, 8, 9].

The genetic variability analysis (Figure 1 and 2) revealed the presence of high broad sense heritability for different traits.

DH had low phenotypic and genotypic coefficient of variation and low genetic advance over mean. Hence selection will be ineffective. GFD had low phenotypic and genotypic coefficient of variation and medium genetic advance over mean. Hence selection will be ineffective. SPAD had low phenotypic and genotypic coefficient of variation and low genetic advance over mean. Hence selection will be ineffective. CTD had high phenotypic and genotypic coefficient of variation and high genetic advance over mean. Hence selection will be effective. PH had high phenotypic and genotypic coefficient of variation and high genetic advance over mean. Hence selection will be effective. DM had low phenotypic and genotypic coefficient of variation and low genetic advance over mean. Hence selection will be ineffective. TGW had medium phenotypic and genotypic coefficient of variation and high genetic advance over mean. Hence selection will be effective. YPP had high phenotypic and genotypic coefficient of variation and high genetic advance over mean. Hence selection will be effective. Similar results were obtained by Schmidt *et al.*, 2020, Erena *et al.*, 2021, Speilmeyer *et al.*, 2007 [10, 11, 12].

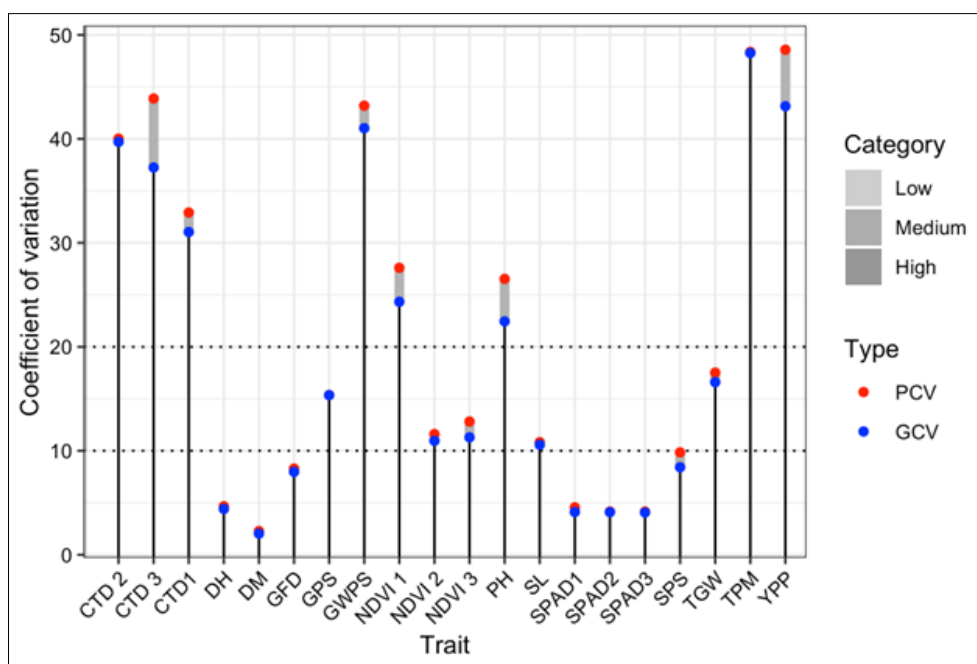


Fig 1: Genetic variability parameters for different morphs-physiological and yield traits

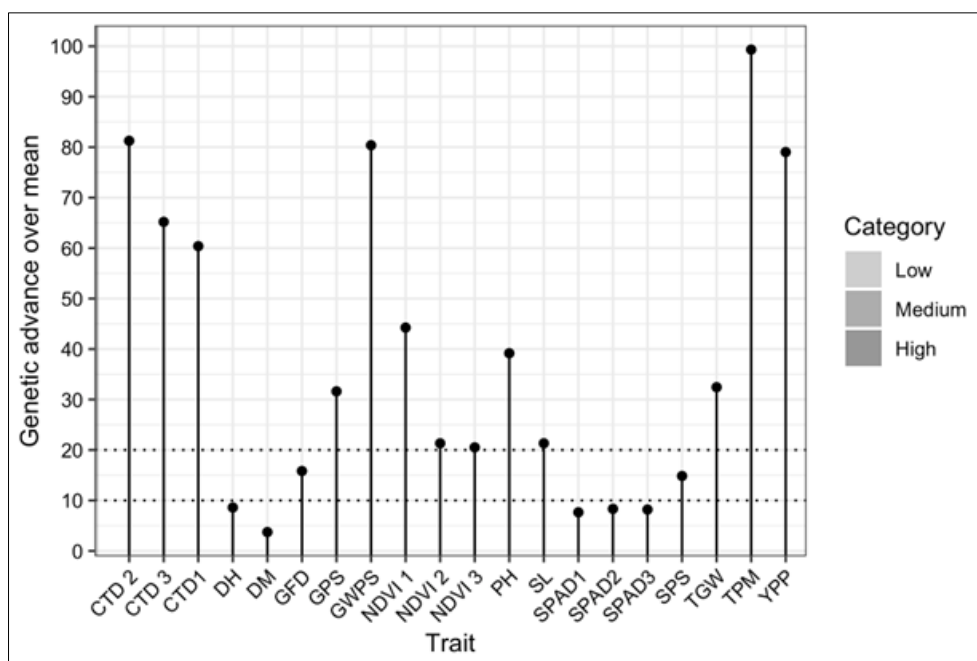


Fig 2: Genetic advance over mean for different morpho-physiological and yield traits.

Among the 192 RILs evaluated for different traits, the lines 26, 32, 138, 189 and 15 were found to be top performing with higher grain yields under terminal heat stressed conditions. These lines can be further evaluated under multiple locations for determining their stability and validating their performance and thus be used in further breeding programs for developing heat stress tolerance varieties in wheat.

References

- Dixon J, Braun HJ, Crouch JH. Overview: Transitioning wheat research to serve the future needs of the developing world. In: J. Dixon, H.-J. Braun, P. Kosina and J.H. Crouch (eds.), *Wheat facts and figures 2009*. CIMMYT, Mexico, DF; c2009. p. 1-25.
- Mohammadi V, Ghannadha MR, Zali AA, Yazdi-Samadi B. Effect of post anthesis heat stress on head traits of wheat. *Intrnl. J. Agril. Biology*. 2004;6(1):42-44.
- Bhullar SS, Jenner CF. Differential responses to high temperature of starch and nitrogen accumulation in the grain of four cultivars of wheat. *Australian J. Plant Physiol*. 1985;12(4):363-375.
- Pinto RS, Chapman SC, McIntyre CL, Shorter R, Reynold MP. QTL for canopy temperature response related to yield in both heat and drought environments. In: R. Appels, R. Eastwood, E. Lagudah, P. Langridge M.M. Lynne (eds.), *Proceedings of the 11th International Wheat Genetic Symposium, Brisbane, Australia*; c2008.
- Gao F, Liu J, Yang L, Wu X, Xiao Y, Xia X, *et al*. Genome-wide linkage mapping of QTL for physiological traits in a Chinese wheat population using the 90K SNP array, *Euphytica*; c2016. DOI 10.1007/s10681-016-1682-6.
- Liu C, Sukumaran S, Claverie E, Sansaloni C, Dreisigacker S, Reynolds M.) Genetic dissection of heat and drought stress QTLs in phenology-controlled synthetic-derived recombinant inbred lines in spring wheat. *Mol Breeding*. 2019;39:34. <https://doi.org/10.1007/s11032-019-0938-y>.
- Sharma D, Jaiswal JP, Gahtyari NC, Chauhan A, Chhabra R, Saripalli G, Singh NK. Population structure, marker-trait association and identification of candidate genes for terminal heat stress relevant traits in bread wheat (*Triticum aestivum* L. em Thell). *Plant Genetic Resources: Characterization and Utilization*; c2020. Doi: 10.1017/S1479262120000131
- Paliwal R, Roder MS, Kumar U, Srivastava JP, Joshi AK. QTL mapping of terminal heat tolerance in hexaploid wheat (*Triticum aestivum* L.). *Theoretical and applied genetics*. 2012;125:561-575.
- Tiwari C, Walkwork H, Kumar A, Dhari R, Arun B, Mishra VK, *et al*. Molecular mapping of high temperature tolerance in bread wheat adapted the Eastern Gangetic Plain region of India. *Field crops research*. 2013;145:201-210.
- Schmidt J, Tricker PJ, Eckermann P, Kalambettu P, Garcia M, Fleury D. Novel Alleles for Combined Drought and Heat Stress Tolerance in Wheat. *Front. Plant Sci*. 2020;10:1800. Doi: 10.3389/fpls.2019.01800.
- Erena MF, Lohraseb I, Munoz-Santa I, Taylor JD, Emebiri LC, Collins NC. The Wtms DW Locus on Wheat Chromosome 2B Controls Major Natural Variation for Floret Sterility Responses to Heat Stress at Booting Stage. *Front. Plant Sci*. 2021;12:635397. Doi: 10.3389/fpls.2021.635397
- Spielmeyer W, Hyles J, Joaquim P, Azaña F, Bonnet D, Ellis ME, *et al*. A QTL on chromosome 6A in bread wheat (*Triticum aestivum*) is associated with longer coleoptiles, greater seedling vigour and final plant height. *Theor. Appl. Genet*. 2007;115:59-66.