Environment & Ecology 35 (2B) : 1087—1092, April—June 2017
Website: environmentandecology.com ISSN 0970-0420

Genetic Parameters and Characters Association Analysis for Yield Components and Heat Tolerance in Bread Wheat (*Triticum aestivum* L.)

Ankit Kumar, Pradeep Kumar, Gyanendra Singh, Ravi Kumar, Sandeep Kumar

Received 11 July 2016; Accepted 4 August 2016; Published online 24 August 2016

Abstract This experiment was conducted under three temperature regimes in a randomized block design (RBD) with 20 diverse wheat genotypes under three microenvironments in *rabi* 2012-2013, In the present investigation, days to 50% flowering (gr=0.22** & Pr=0.33**), biological yield per plant (gr=0.85** & pr=0.84**) and harvest index (gr=0.82** & pr=0.48**) have highly significant and positive association with grain yield also have recorded maximum positive direct effect on grain yield by the same traits namely biological yield per plant (g=0.72 & p=1.62), harvest index (g=1.96 & p=0.45) and days to 50% flowering (g=0.21 & p=0.01), by pooled analysis at genotypic as well as phenotypic level indicating that we can improve grain yield per plant by improving these traits as well as emphasis should be given on these traits for the selection of elite genotypes from the segregating generation. The characters showed highest heritability with highest genetic advance namely plant height, peduncle length, harvest index, thousand kernel weight and grain yield also have highest PCV and GCV therefore, selection will be effective based on these traits for the improvement of wheat crop.

Keywords Characters associations, Genetic parameters, Bread wheat, Heat tolerance, Yield.

A. Kumar, R. Kumar, S. Kumar
Sardar Vallabhbhai Patel University of Agriculture & Technology,
Meerut 250110, (UP), India

P. Kumar*, G. Singh
Indian Institute of Wheat & Barley Research,
Karnal 132001, Haryana, India
e-mail : prodeeptaliyan231@gmail.com
*Correspondence

Introduction

India has been giving special emphasis to improve productivity of wheat under harsh environments viz. drought and high temperature at the time of maturity. At present global climate change is the burning issue which attracts wheat researchers to study about the interaction between genotype × environments. Heat stress affecting around 13.5 million ha area grown under wheat in India [1]. Terminal heat stress is responsible for decline in wheat production in 36 million ha of the world [2]. Wheat production can be enhanced through the development of new cultivals

Table 1. Pooled analysis of variance (ANOVA) for 13 yield components in breed wheat.

Characters	Replication (d f=2)	Environments (df=2	Interaction (d f=4)	Overall Sum (d f=8)	Treatments (d f=19)	Error (d f=152)
Days to maturity	1.072	17778.672**	0.372	4445.122**	6.777**	2.767
Days to 50% flowering	3.072	8655.672**	6.664	2168.018**	27.882**	7.989
Chlorophyll content	14.706	59.999**	9.069	23.211**	32.505**	8.800
Plant/height (cm)	0.300	13474.427**	1.307	3369.335**	344.568**	19.696
Peduncle length (cm)	0.310	1607.057**	1.111	402.397**	114.141**	4.158
Spike length (cm)	0.062	24.294**	0.051	6.115**	3.039**	0.402
Spikelets per spike	0.425	99.554**	0.226	25.108**	10.269**	0.888
Grain per spikelet	0.010	2.363**	0.030	0.608**	0.405**	0.037
Productive tillers	0.445	327.997**	0.528	82.375**	1.803**	0.853
Thousand grain weight (g)	0.069	265.897**	0.069	66.526**	52.652**	0.155
Biological yield (g)	6.796	8168.344**	10.718	2049.144**	49.113**	20.948
Harvest index (%)	13.243	2048.331**	5.029	517.908**	162.304**	15.060
Grain yield (g)	6.511	1994.230**	3.742	502.056**	22.761**	4.466

having wide genetic base and better performance under various agro-climatic conditions. Wheat is grown in India under sub-tropical environment during mild winter warm up towards grain filing stages of the crop. Almost all the stages of wheat growth and development are adversely affected by heat stress. Wheat breeders are seeking to incorporate late heat tolerant in the wheat germplasm and to develop genotypes that are early in maturity in order to escape the terminal heat stress. Tolerance to heat stress is a complex phenomenon and controlled by multiples genes [3], no single trait fully explains why some varieties are able to give higher yield even whean they experirnce heat stress. The modern wheat breeding program focuses on the improvement of agronomic and grain quality traits with its adaptability to varied climatic condition. Grain yield is a complex trait and highly influenced by many environmental factors, biotic and abiotic stresses including water-logging, salinity and heat stress. Therefore correlation coeffi-

Table 2. Estimates of parameters of variability, heritability and genetic advance for 13 yield components in bread wheat. DTM-Days to maturity, DTF-Days to flowering, CC-Chlorophyll contain, PH-Plant height, PL-Peduncle length, SL-Spike length, SPS-Spikelets per spike, GPS-Grains per spikelet, PT-Productive tillers, TKW-Thousand kernel weight, BY-Biological yield, HI-Harvest index, GY-Grain yield, PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation, GA-Genetic advance.

Characters	Environment	Mean	Range		Coefficient of variation		Heritability broad sense	GA as % of mean
			Minimum	Maximum	GCV	PCV		
DTM	POOLED	119.83	117.88	121.44	0.55	1.49	13.87	0.42
DTF	POOLED	79.80	76.22	82.77	1.86	4.00	21.67	1.78
CC	POOLED	41.91	37.68	45.07	3.87	8.06	23.03	3.82
PH	POOLED	82.32	68.80	89.97	7.29	9.07	64.69	12.09
PL	POOLED	33.83	27.55	39.84	7.29	9.07	64.69	12.09
SL	POOLED	10.91	10.04	12.15	4.95	7.63	42.15	6.63
SPS	POOLED	17.30	15.40	19.20	5.89	8.02	54.00	8.9
GPS	POOLED	3.18	2.80	2.80	6.35	8.74	52.85	9.5
PT	POOLED	5.51	4.71	6.38	5.89	17.76	11.01	4.03
TKW	POOLED	39.20	34.15	44.35	6.16	6.24	97.41	12.52
BY	POOLED	25.52	21.52	30.70	6.93	19.22	12.99	5.14
HE	POOLED	39.65	31.95	50.19	10.20	14.13	52.06	15.16
GY	POOLED	10.57	8.04	13.79	13.48	24.11	31.27	15.53

Table 3. Genotypic and phenotypic correlation for 13 yield components and heat tolerance in bread wheat. *, ** : Significant at 5% and 1% probability levels, respectively.

Characters	r	DTM	DTF	CC	PH	PL	SL	SPS
DTM	P	1.000	0.128	-0.205**	0.150*	0.061	0.077	0.257**
	G	1.000	0.497**	-0.914**	0.389**	0.247**	0.134	0.504**
DTF	P		1.000	0.037	0.106	-0.048	0.101	0.387**
	G		1.000	-0.202**	0.038	-0.167*	-0.212**	0.379**
CC	P			1.000	0.108	-0.060	0.132	0.017
	G			1.000	0.119	-0.115	0.131	-0.027
PH	P				1.000	0.594**	0.361**	0.295**
	G				1.000	0.651**	0.417**	0.365**
PL	P					1.000	0.041	-0.127
	G					1.000	-0.098	-0.258**
SL	P						1.000	0.579**
	G						1.000	0.700**
SPS	P							1.000
	G							1.000
GPS	P							
	G							
P T	P							
	G							
T W	P							
	G							
BY	P							
	G							
HI	P							
	G							

Table 3. Continued.

Characters	r	GPS	PT	TW	BY	HE	GY
DTM	P	-0.010	-0.006	0.060	0.066	0.116	0.144
	G	-0.029	0.124	0.149*	0.241**	0.335**	0.370**
DTF	P	0.074	0.156*	0.003	0.365**	0.008	0.337**
	G	0.415**	-0.279**	0.041	0.094	0.302**	0.227**
CC	P	0.006	0.026	-0.073	0.054	-0.059	0.017
	G	0.269**	-0.326**	-0.160*	-0.255**	0.013	-0.179*
PH	P	-0.045	0.018	0.157*	0.141	0.066	0.171*
	G	-0.147*	0.296**	0.210**	0.369**	0.176*	0.340**
PL	P	-0.177*	0.154*	-0.073	0.094	-0.173*	0.020
	G	-0.335**	0.676**	-0.086	0.430**	-0.341**	0.068
SL	P	0.060	0.049	0.179*	0.092	0.366**	0.286**
	G	0.153*	-0.077	0.278**	0.033	0.602**	0.391**
SPS	P	0.239**	0.065	0.263**	0.247**	0.605**	0.551**
	G	0.417**	-0.060	0.375**	0.259**	0.872**	0.693**
GPS	P	1.000	-0.003	0.205**	0.130	0.649**	0.358**
	G	1.000	-0.183**	0.266**	0.440**	0.678**	0.611**
P T	P		1.000	-0.029	0.819**	0.059	0.750**
	G		1.000	-0.128	0.750**	-0.193*	0.419**
T W	P			1.000	0.148	0.533**	0.339**
	G			1.000	0.398**	0.713**	0.586**
BY	P				1.000	0.006	0.847**
	G				1.000	0.449**	0.858**
HI	P					1.000	0.480**
	G					1.000	0.829**

cient provides a better understanding the association of different traits with grain yield and provides useful information to the breeders in selecting the desirable genotypes. The main objective of this study was to analyze the genetic parameters and characters association for grain yield and its contributing traits and their implication in selection of heat tolerance wheat genotype.

Materials and Methods

Field experiment was conducted during crop season (*rabi*), 2012–2013 at Crop Research Center , Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (UP). The experimental materials comprised of twenty genotypes and/or elite lines of wheat namely K 910-4, K 612, K 910-30, SVPW-1, K 512, K 607, K 911, HUW 648, AAI 11, AAI 12, AAI 13, AAI 16, NW 4035, NW 4081, NW 6007, HUW 658, K 307, NW 1014, HD 2733 and K 9162. These twenty genotypes and/or elite lines were sown and evaluated in a randomized block design with three replications in three different dates of sowing. Each genotype was shown on three different dates 25th November, 2012 (Environment first-Timely sown). 24th December, 2012 (Environment second-Late sown) and 15th January 2013, (Environment third-Vary late sown). Plot size was kept at four rows of 2 m length with row to row distance of 23 cm and plant to plant distance of 10 cm. All the recommended agronomical practices and plant protection measures were adopted to raise the good crop. Plant were scored for grain yield and its components namely days to maturity, days to 50% flowering, chlorophyll content (%), plant height (cm), peduncle length (cm), spike length (cm), number of spikelets per spike, number of grains per spikelet, tillers per plant, thousand kernel weight (g), biological yield per plant (g), harvest index (%) and grain yield per plant (g). Phenological traits were recorded at 50% of the crop stage. All other traits were recorded on five randomly selected plants from each genotype in each replication. The mean values of each genotype in each replication were subjected to statistical analysis using SAS and CROPSTAT computer software. The data were analyzed to test the significance differences between the genotypic means for various characters as per procedure out lined earlier [4]. The correlations at genotypic, phenotypic and environmental levels were estimated from the analysis of variance and covariance as suggested by Searle [5]. The path coefficients were calculated by employing the method suggested by Dewey and Lu [6]. Both PCV and GCV were calculated as per the method suggested by Burton [7]. Heritability in broad sense and genetic advance was calculated with the formula as suggested by Johanson et al. [8].

Results and Discussion

Pooled analysis of variance showed highly significant differences (at 1% level of significance) among all the genotypes, environments and overall sum (Table 1), indicating the presence of genetic and environmental variability among the studied genotypes, for all the 13 characters namely plant height, harvest index, peduncle length, thousand grain weight, biological yield, chlorophyll content, days to 50% flowering, grain yield, spikelets per spike, days to maturity, spike length, tillers per plant and grains per spikelet. Similar findings on variability were also reported earlier [9, 10] for various yield components in wheat. The result of the present investigation showed that in general, the material under study had wide range of variability for all the traits. Phenotypic coefficients of variation (PCV) were higher than their corresponding genotypic coefficients of variation (GCV) (Table 2) for all the traits among the genotypes by pooled analysis. The highest PCV and GCV (>10%) were recorded for grain yield (24.11 and 13.48) and harvest index (14.13 and 10.20) respectively. High PCV and GCV for grain yield per plant were also reported earlier [9—12] under normal condition Kumar et al. [13]. also reported high PCV and GCV under normal as well as stress condition for grain yield and harvest index which is similar to the findings of the present investigation. Low PCV and GCV were recorded for days to flowering, days to maturity and plant height by Dhakar et al. [11] as supported to the result of present investigation under normal and late sowing condition. Higher values of PCV than GCV indicated that the variation in the expression of the character was not only due to genotypes alone but also due to varying influence of environment.

The estimates of high heritability (broad sense) coupled with high genetic advance (as % of mean)

Table 4. Genotypic and phenotypic path coefficient analysis for 13 yield components and heat tolerance in bread wheat.

Chara-cters	r	DTM	DTF	CC	PH	PL	SL	SPS	GPS	PT	TGW	BY	HI	GY
DTM	P	**0.018**	0.002	-0.004	0.003	0.001	0.001	0.005	0.000	0.000	0.001	0.001	0.002	0.144
	G	**-0.081**	-0.040	0.074	-0.032	-0.020	-0.011	-0.041	0.002	-0.010	-0.012	-0.020	-0.027	0.370**
DTF	P	0.002	**0.012**	0.000	-0.001	-0.001	0.001	0.005	0.001	0.002	0.000	0.004	0.000	0.337**
	G	0.108	**0.217**	-0.044	0.008	-0.036	-0.046	0.082	0.090	-0.061	0.009	0.020	0.065	0.227**
CC	P	-0.001	0.000	**0.005**	0.001	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.017
	G	0.131	-0.029	**0.143**	0.017	-0.016	0.019	-0.004	0.038	-0.047	-0.023	-0.036	0.002	-0.179*
PH	P	-0.001	-0.001	-0.001	**-0.007**	-0.004	-0.003	-0.002	0.000	0.000	-0.001	-0.001	0.000	0.171*
	G	-0.117	-0.012	-0.036	-0.300	-0.195	-0.125	-0.109	0.044	-0.089	-0.063	-0.111	-0.053	0.340**
PL	P	0.001	-0.001	-0.001	0.012	**0.020**	0.001	-0.003	-0.004	0.003	-0.001	0.002	-0.003	0.020
	G	0.030	-0.020	-0.014	0.080	**0.122**	-0.012	-0.032	-0.041	0.083	-0.010	-0.053	-0.042	0.068
SL	P	-0.001	-0.001	-0.001	-0.004	0.000	**-0.010**	-0.006	-0.001	0.000	-0.002	-0.001	-0.004	0.286**
	G	0.024	-0.038	0.023	0.075	-0.018	**0.179**	0.125	0.027	-0.014	0.050	0.006	0.108	0.391**
SPS	P	0.028	0.043	0.002	0.032	-0.014	0.064	**0.110**	0.026	0.007	0.029	0.027	0.066	0.551**
	G	-0.329	-0.248	0.018	-0.238	0.169	-0.457	**-0.653**	-0.273	0.039	-0.245	-0.169	-0.569	0.693**
GPS	P	0.000	-0.003	0.000	0.002	0.008	-0.003	-0.011	**-0.047**	0.000	-0.010	-0.006	-0.031	0.358**
	G	0.035	-0.496	-0.321	0.175	0.401	-0.183	-0.499	**-1.196**	0.218	-0.318	-0.526	-0.811	0.611**
PT	P	-0.001	0.018	0.003	0.002	0.018	0.006	0.008	0.000	**0.116**	-0.003	0.095	0.007	0.750**
	G	-0.082	0.184	0.216	-0.196	-0.447	0.051	0.040	0.121	**-0.661**	0.085	-0.495	0.127	0.419**
TGW	P	-0.001	0.000	0.002	-0.003	0.001	-0.004	-0.005	-0.004	0.001	**-0.021**	-0.003	-0.011	0.339**
	G	-0.139	-0.038	0.150	-0.196	0.080	-0.260	-0.351	-0.249	0.120	**-0.936**	-0.372	-0.668	0.586**
BY	P	0.048	0.265	0.039	0.102	0.068	0.066	0.180	0.094	0.595	0.107	**0.726**	0.004	0.847**
	G	0.392	0.153	-0.414	0.600	0.700	0.053	0.420	0.714	1.218	0.647	**1.625**	0.730	0.858**
HI	P	0.052	0.003	-0.027	0.030	-0.078	0.165	0.272	0.292	0.027	0.240	0.002	**0.450**	0.480**
	G	0.660	0.593	0.026	0.346	-0.671	1.184	1.714	1.332	-0.379	1.402	0.883	**1.966**	0.829**

indicate additive gene and improvement in these traits could be possible by direct selection. In the present study, high heritability coupled with high genetic advance was not observed in pooled analysis but high heritability coupled with moderate genetic advance were recorded for plant height (64.69 and 12.09), peduncle length (64.69 and 12.09) and thousand kernel weight (97.41 and 12.52) whereas moderate heritability with moderate genetic advance were recorded for harvest index (52.06 and 15.16) and grain yield (31.27 and 15.53) respectively by pooled analysis. High heritability with moderate genetic advance for plant height whereas high heritability with low genetic advance for days to maturity under normal as well as heat stresses condition were reported earlier [13]. Highest heritability with highest genetic advance were recorded for plant height, thousand grain weight, peduncle length, grain yield per plant and harvest index by pooled analysis, indicated the involvement of additive genetic components in the inheritance of these traits. For plant height, high heritability with high genetic advance earlier reported by [14]. High heritability along with high genetic advance and high coefficient of variability (PCV and GCV) for grain yield showed high scope for improvement following selection. However, the traits namely days to maturity, days to flowering, chlorophyll contain, thousand grain weight, spike length and spikelets per spike showed high to moderate heritability but moderate to low genetic advance, which may be due to non-additive gene action and presence of G × E interaction, simple selection may not rewarding. In such cases, hybridization followed by selecting, desirable transgressive segregants will be better options.

The genotypic and phenotypic correlations among different pairs of characters are presented in (Table 3). Genotypic correlation were higher in magnitude than their corresponding phenotypic correlation for almost all the traits, indicating strong inherent association between various pairs of traits as was also reported earlier [10—15]. In the present investigation, days to 50% flowering (gr=0.227 and pr=0.337), spike length (gr=0.391 and pr=0.286), spikelets per spike (gr=0.693 and pr=0.551), grains per spikelet (gr=0.611 and pr=0.358), productive tillers per plant (gr=0.419 and pr=0.750), thousand grain weight (gr=0.586 and pr=0.339), biological yield per plant (gr=0.858 and pr=0.847) and harvest index (gr=0.829 and pr=0.480) have highly significant and positive association with grain yield by pooled analysis at genotypic as well as phenotypic level. Positive significant association of grain yield with productive tillers, biological yield and harvest index was also reported earlier [10] under normal condition in wheat. Positive correlation between grain yield and thousand grain weights were given by Oguz et al. [14]. Grain yield was positively and significantly correlated with plant height, thousand grain weight and spike length wheraas, negatively correlated with days to 50% flowering as reported by Oguz et al. [14]. In the present investigation, only three characters productive tillers per plant, biological yield per plant and harvest index can be used as selection criteria in any of the three environments used presently, indicating that these three traits were main yield contributing traits. The lower degree of associations between two traits at phenotypic level might due to the masking and/or modifying effects of environment on the association of characters.

Maximum positive direct effect on grain yield was recorded for biological yield per plant, harvest index, peduncle length, days to flowering and chlorophyll content by pooled analysis. The path coefficient analysis also indicated that out of the above three characters only biological yield per plant and harvest index contributed directly to grain yield and therefore, can be used directly as a basis of selection Kumar et al. (Table 4) [10] also reported highest positive direct effects of harvest index and biological yield on grain yield in wheat crop under normal condition. The information generated by this research will be helpful for the breeders in selecting high yielding genotypes which possess some specific traits under normal as well as heat stress condition or have a significant scope for improving grain yield through hybridization and selection to future breeding program.

References

1. Joshi AK, Mishra B, Chatrath R, Ferrara GO, Singh RP (2007) Wheat improvement in India: Present status, emerging challenges and future prospects. Euphytica 157 : 431—446.
2. Hays DB, Do JH, Mason RE, Morgan G, Finlayson SA (2007) Heat stress induced ethylene production in developing wheat grains induces kernel abortion and increased maturation in a susceptible cultivar. Pl Sci 172 : 1113—1123.
3. Barnabas B, Jager K, Feher A (2008) The effect of drought and heat stress on reproductive processes in cereals. Pl Cell and Environ 31 : 11—38.
4. Panse VG, Sukhatme PV (1967) Statistical methods of agricultural workers. 2nd edn. ICAR Publ, New Delhi, pp 381.
5. Searle SR (1961) Phenotypic, genotypic and environmental correlations. Biomet 47 : 474—480.
6. Dewey DR, Lu KH (1959) A correlation and path coefficient analysis components of crested wheat grass. Agron J 51 : 515—518.
7. Burton GN (1952) Quantitative inheritance in grasses. Proc of 6th. Int Grassl Cong 1 : 277—283.
8. Johanson HW, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in soybean. Agron J 47 : 314—318.
9. Singh BN, Soni SK, Srivastava A, Yadav VK (2012) Selection of parameters for architecturing model plant type in bread wheat (*Triticum aestivum*) in saline soil. Environ Ecol 30 : 110—113.
10. Kumar R, Gupta RK, Visistha NK, Singh MK (2013) Character association and path analysis for quantitative traits in bread wheat (*Triticum aestivum* L.). Environ Ecol 31 : 393—398.
11. Dhakar MR, Jat BL, Bairwa LN, Gupta JK (2012) Genetic variability, heritability, genetic advance and genetic divergence in wheat (*Triticum* spp.). Environ Ecol 30 : 1474—1480.
12. Das B (2015) Genetic diversity, variability and correlation studies of spike characters in bread wheat under boron deficient soil condition. Elect J Pl Breed 5 : 77—81.
13. Kumar R, Prasad BK, Singh MK, Verma A, Tyagi BS (2014) Genetic analysis for phenological and physiological traits in wheat (*Triticum aestivum* L.) under heat stress environment. Ind J Agric Res 48 : 62—66.
14. Oguz B, Kayihan Z, Korkut, Ismet B, Orhan D, Irfan O, Turhan K, Balkan A (2011) Genetic variation and inter-relationship of some morpho-physiological traits in Durum wheat (*Triticum durum* L.). Pak J Bot 43 : 253—260.
15. Tambe A, Mehta DR, Chovatia VP, Bhatiya VJ (2013) Genetic variability, character association and path coefficient analysis in Durum wheat (*Triticum durum* Desf.). Elect J Pl Breed 4 : 1303—1308.