



E-ISSN: 2278-4136

P-ISSN: 2349-8234

JPP 2018; 7(1): 2114-2117

Received: 23-11-2017

Accepted: 24-12-2017

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Relationship between grain yield and other yield attributing characters in wheat under terminal heat stress

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Abstract

Wheat (*Triticum aestivum* L.) is an important cereal crop of cool climates, and plays a key role in the food and nutritional security of India. The objective of this study was to analyse the inter-relationship of various quantitative characters and their contribution on seed yield under terminal heat stress. Forty nine wheat entries / genotypes along with check varieties were studied for various characters contributed to yield under terminal heat stress at Barrister Thakur Chhedilal college of Agriculture and Research Station, Sarkanda Bilaspur, Chhattisgarh. Generally, the estimates of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for all the character combinations. Seed yield was significantly and positively associated with number of spikelets plant-1, followed by number of effective tillers and 1000-seed weight at both phenotypic and genotypic levels. Seed yield showed a significant negative association with number of seeds spikelet-1 at genotypic level. Among the significant inter-relationships, the association of days to 50 % spike emergence with days to maturity and 100-seed weight were significant and positive, but were negative and significantly associated with number of seeds spikelet-1 and number of grains spike-1. Similarly, the associations of spike length with number of seeds spikelet-1, and number of spikelets plant-1 and number of effective tillers were negative and significant. The association of number of spikelets plant-1 with number of effective tillers was also positive and highly significant.

Keywords: genotypic correlation, phenotypic correlation, CTD, *Triticum aestivum*

Introduction

Wheat (*Triticum aestivum* L.) is an important cereal crop of cool climates, and plays an important role in the food and nutritional security of India. In India, 86% of the cultivated area under wheat represents hexaploid spring type belonging to *Triticum aestivum* L. em. Theil., (Singh *et al.*, 2008) ^[1] more commonly called bread wheat. Wheat is widely grown the world-over and stands first among the cereals both in area and production. Most of the agronomic characters in crop plants are quantitative in nature. Yield is one such character that results due to the actions and interactions of various component characters (Grafius, 1960) ^[3]. It is also widely recognized that genetic architecture of yield can be resolved better by studying its component characters. This enables the plant breeder to breed for high yielding genotypes with desired combinations of traits. Linear correlation between yield and several of its components can present a confusing picture due to inter-relationships between component characters themselves. The objective of this study was to establish the inter-relationship of various wheat components among themselves and with seed yield.

Materials and Methods

Forty nine diverse wheat trial entries along with check varieties were used in this study. The trial was grown at the Research Farm of B.T.C. College of Agriculture and Research station, Sarkanda, Bilaspur, Chhattisgarh, India during *rabi* season of 2013-14. These lines were planted in a Randomised block design with two replications along with the check entries. In each replication, 49 treatments were grown in 6 m long rows and the spacing of 25 cm between rows. Initially, extra seed was planted which was later thinned to maintain an optimum population density. Ten randomly selected plants from each treatment were tagged for recording the observations on the following characters, viz., canopy temp depreciation (CTD) with the help of infra-red thermometer, chlorophyll index with the help of chlorophyll meter, days to 50% flowering, flag leaf length, spike length, peduncle length, plant height, tillers per meter, no of florets, grains per spike, 1000 seed weight, days to maturity and finally seed yield. Meteorological data of particular days when canopy temperature has taken

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is used to take out the canopy temperature depreciation (CTD) values. The data were analysed by windostat version 9.1 hyderabad for the estimation of correlation values. Genotypic correlations were computed using variance and co-variances as suggested by Johnson *et al.* (1955) [6].

Results & Discussion

Correlation coefficients at phenotypic and genotypic levels are presented in the Table 1. Significant ($P < 0.05$)*, highly significant ($P < 0.01$)***, ($P < 0.005$)** and very highly significant ($P < 0.001$ ****) are reported on the table. The shaded correlation matrix also signifies the extent of association with dark green colours. The phenotypic correlation is the sum total of phenotype and genotype ($P \text{ corr.} = G \text{ corr.} + E \text{ corr.}$). The results indicated that genotypic correlations estimates are higher than phenotypic correlations. The results are discussed serially.

1. Seed yield plot / kg was positively correlated with peduncle length, 1000 seed weight followed by tillers per meter at phenotypic level suggesting that plants with more tillers with high peduncle length bear plenty of spikelets plant-1 and produce higher seed yield. The results are in tune with earlier reports (Kashif and Khaliq, 2004; Aycicek and Yildirim, 2006; Akram *et al.*, 2008; Khan & Dar, 2010; Zafarnaderi N. *et al.*, 2013) [13, 1, 10].
2. Canopy Temperature Depreciation has significant positive correlation with peduncle length whereas it had significant negative correlation with chlorophyll index, tillers per meter, days to maturity and seed yield for both phenotypic and genotypic estimates, while significant negative genotypic correlation for plant height. Cooler Canopy Temperature is positively associated with yield under heat and drought stress and both physiological (Lopes and Reynolds, 2010) [8].
3. Chlorophyll index has Significant positive correlation with days to 50 % flowering and significant negative correlation for peduncle length for both phenotypic and genotypic estimates, while significant negative genotypic correlation for flag leaf length. (Guendouz, A. *et al.*, 2012) [4] reported positive correlation with days to 50% flowering, whereas a significant negative correlation is found between chlorophyll content and average senescence signifies that genotypes having high chlorophyll index takes more days to complete flower.
4. No. of Spikelet has highly significant positive correlation days to 50 % flowering and showed very highly significant positive correlation with grains per spike and no. of florets for both phenotypic and genotypic estimates, while significant negative genotypic correlation for peduncle length. The results are in tune with (Veselinka Zečević *et al.*, 2009) [12] for florets and grain per spike and (Yagdi *et al.*, 2007) for grain per spike.
5. Spike length showed significant positive correlation with peduncle length where as highly significant positive correlation with flag leaf length and no. of florets and showed very highly significant positive correlation with grains per spike and plant height for both phenotypic and

genotypic estimates, while significant negative genotypic correlation for days to maturity. The results are in tune with (Yagdi *et al.*, 2007) for plant height and (Iftikhar *et al.*, 2012) [5] for grains per spike

6. Flag leaf length showed highly significant positive correlation with peduncle length, 1000 seed wt. while it showed very highly significant positive correlation with plant height whereas it had significant negative correlation with no of floret and grain per spike for both phenotypic and genotypic estimates, while significant positive genotypic correlation for seed yield. The results are in tune with (Zafarnaderi N. *et al.*, 2013) [13] for negative correlations with grain per spike and positive genotypic correlation for seed yield (Iftikhar *et al.*, 2012) [5].
7. Peduncle length showed significant positive correlation with plant height and seed yield while it showed highly significant positive correlation for 1000 seed weight for both phenotypic and genotypic estimates, while highly significant negative genotypic and phenotypic correlation for no of florets and days to 50% flowering. The results are in tune with (Zafarnaderi N. *et al.*, 2013) [13] for plant height, grain yield and 1000 grain weight.
8. Plant height showed very highly significant positive correlation with flag leaf length followed by spike length for both phenotypic and genotypic estimates. The results are in tune with (Gelalcha and Hanchinal, 2013) for spike length and peduncle length.
9. Tillers per meter showed significant positive correlation with days to 50 % flowering and seed yield for both phenotypic and genotypic estimates, while significant positive genotypic correlation for days to 50 % flowering. The results are in tune with (Khan & Dar, 2010) [10] for seed yield.
10. No. of florets showed highly significant positive correlation with spike length, days to 50% flowering followed by grains per spike and significant negative correlation for days to maturity and 1000 seed weight for both phenotypic and genotypic estimates.
11. Grains per spike showed significant positive correlation with days to 50 % flowering and significant negative correlation for days to maturity and 1000 seed weight for both phenotypic and genotypic estimates.
12. 1000 seed weight showed significant positive correlation with seed yield and significant negative correlation with days to 50% flowering for both phenotypic and genotypic estimates. The results are in tune with (Zafarnaderi N. *et al.*, 2013) [13].
13. Days to 50 % flowering has significant positive correlation with days to maturity and significant negative correlation with seed yield for both phenotypic and genotypic estimates. The results are in tune with (Gelalcha and Hanchinal, 2013)
14. Days to maturity was found to positively correlated with grains per spike and days to 50 % flowering while it is negatively correlated with CTD, spike length, no. of florets. Similar finding of maturity with 50 % flowering correlation was reported by (Khan A.A. *et al.*, 2013).

Table 1: Phenotypic and Genotypic Correlation Matrix for wheat characters

Upper Phenotypic Corr.	Canoy Temp.	Chl. Index	No. Of Spikelets	Spike length (cm)	Flag Leaf Lth.(cm)	Peduncle Lth. (cm)	Plant ht. (cm)	Tillers/ Meter	No. of Florets	Grain/ spike	1000 Seed wt. (gms)	Days to 50 % Flower.	Days to Maturity	Seed yield(kg)/plot
Lower Genotypic Corr.														
Canoy Temp.	1.000	-0.215*	-0.108	0.085	0.140	0.208*	-0.186	-0.224*	0.033	0.062	0.080	-0.101	-0.224*	-0.249*

Chl. Index	-0.269**	1.000	0.155	-0.108	0.184	-0.237*	0.112	-0.020	0.158	0.104	-0.061	0.233*	0.065	-0.083
No. Of Spikelets	-0.092	0.147	1.000	0.125	-0.122	-0.186	0.040	-0.004	0.415***	0.382***	-0.094	0.263**	-0.060	0.049
Spike length (cm)	0.127	-0.184	0.095	1.000	0.287**	0.254*	0.352***	0.167	0.296**	0.336***	-0.104	-0.014	-0.209*	0.067
Flag Leaf Lth.(cm)	0.169	0.201*	-0.184	0.312**	1.000	0.304**	0.391***	-0.041	-0.317**	-0.258*	0.287**	-0.151	0.171	0.041
PeduncleLth. (cm)	0.232*	-0.265**	-0.250*	0.293**	0.326**	1.000	0.255*	0.056	-0.219*	-0.119	0.362***	-0.538***	-0.047	0.246*
Plant ht. (cm)	-0.216*	0.128	0.032	0.433***	0.406***	0.285**	1.000	0.100	-0.161	-0.106	-0.043	-0.008	0.065	0.167
Tillers/ Meter	-0.218*	-0.035	-0.111	0.100	-0.069	0.075	0.091	1.000	-0.025	0.116	-0.150	0.258*	0.138	0.207*
No. of Florets	0.072	0.149	0.499***	0.348***	-0.369***	-0.241*	-0.172	-0.079	1.000	0.834***	-0.399***	0.280**	-0.317**	-0.065
Grain/ spike	0.119	0.084	0.421***	0.370***	-0.290**	-0.134	-0.106	0.070	0.892***	1.000	-0.455***	0.232*	-0.382***	-0.002
1000 Seed wt. (gms)	0.100	-0.074	-0.096	-0.138	0.329***	0.393***	-0.040	-0.182	0.440***	0.489***	1.000	-0.470***	0.166	0.243*
Days to 50 % Flower.	-0.103	0.255*	0.335***	-0.025	-0.157	-0.558***	-0.009	0.323**	0.313**	0.256*	-0.504***	1.000	0.296**	-0.261**
Days to Maturity	-0.260**	0.050	-0.089	-0.232*	0.185	-0.039	0.084	0.183	0.357***	0.449***	0.193	0.306**	1.000	0.080
Seed yield(kg)/plot	-0.320**	-0.127	-0.011	0.016	0.462***	0.361***	0.185	0.161	-0.125	-0.065	0.337***	-0.324**	0.125	1.000
Significance Levels	0.05	0.01	0.005	0.001	* Upper Diagonal values indicates the Phenotypic Correlations									
If correlation $r \Rightarrow$	0.198	0.259	0.281	0.327	* Lower Diagonal values indicates the Genotypic Correlations									
Star values	*	**	**	***										

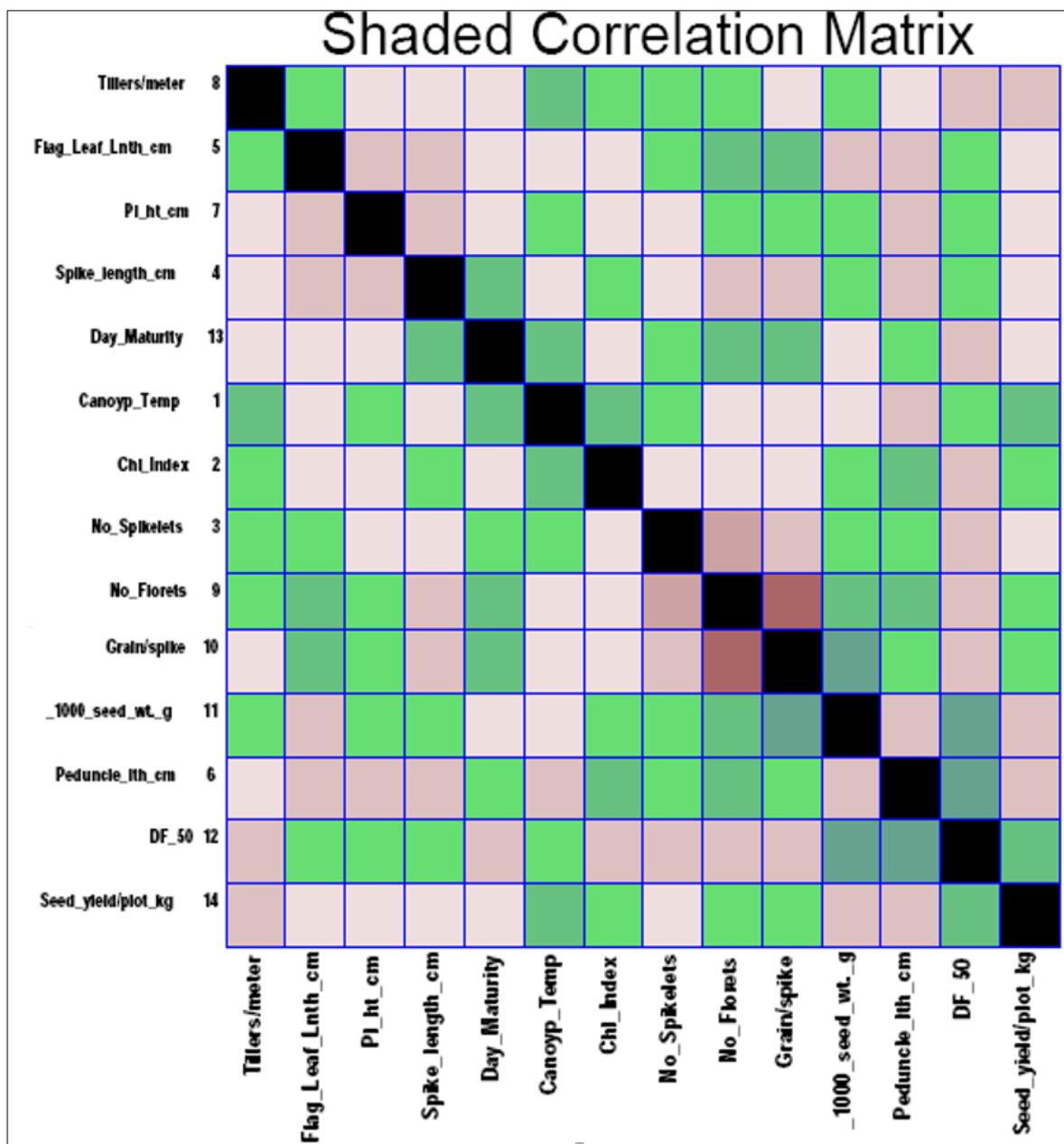


Fig 1
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