Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

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Genotypic and phenotypic variability and correlation analysis for yield and its components in late sown wheat (*Triticum aestivum* L.)

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Abstract
Twenty genotypes of wheat (*Triticum aestivum* L.), (including 2 checks) were investigated on sixteen traits during *Rabi* 2015-2016 in a randomized block design with three replications at Field Experimentation Center of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, to study the magnitude of genetic variability parameters for different quantitative characters and to estimate the genotypic and phenotypic correlation coefficient which included grain yield and associated characters under late sown conditions. Variability was measured by estimating genotypic and phenotypic variance (GCV and PCV), heritability (h^2_{bs}) and genetic advance for different quantitative traits. The mean sum of squares showed significant differences among all the characters except for flag leaf width. The maximum GCV and PCV was observed for seed yield per plant, followed by biological yield, thousand grain weight, plant height, peduncle length, and flag leaf length. High heritability in broad sense (h^2_{bs}) was recorded for plant height, days to 50 % heading, thousand grain weight, days to 50 % flowering, days of maturity, number of grains per spike, seed yield per plant, grain filling period, peduncle length, harvest index, biological yield, and flag leaf length. High genetic advance was recorded for plant height. Seed yield exhibited positive significant correlation with biological yield, number of spikes per plant, harvest index, spike length, thousand grain weight, flag leaf length, flag leaf width, plant height, peduncle length, number of spikelets per spike and number of grains per spike at both genotypic at phenotypic level. Therefore, above traits should be given due emphasis for future bread wheat genetic improvement due to their high genetic variance, high heritability (h^2_{bs}) coupled with high genetic correlation among themselves which may yield high genetic advance under proper selection pressure in a breeding program.

Keywords: Late sown, bread wheat, Genetic variability, Correlation coefficient

Introduction
Wheat (*Triticum aestivum* L.) is one of the most important staple food crops of the world, occupying 17% of crop acreage worldwide, feeding about 40% of the world population and providing 20% of total food calories and protein in human nutrition (Gupta *et al*., 2008) [14]. Wheat belongs to Gramineae family, the prime and staple food of world and originated in south west Asia, known as the Fertile Crescent. *Mohan- Jo-daro* (India) excavations indicate that wheat was cultivated more than 5000 year ago. Wheat production is estimated to be 93.50 million tons in 2015-16 *Rabi* season from an estimated area of 30.23 million hectares with productivity of 3.1 tons per hectare. In Uttar Pradesh in 2015-16 a total area of wheat cultivated was 9.65 million hectares with total production of 26.87 million tons and the yield productivity was 2.8 tons per hectare All India Coordinated Wheat & Barley Improvement Project, Annual Report. (2016). Yield, as a function of various components and it is a complex character Aycicek and Yildirim., (2006) [6]. Heritability estimates provide information about the extent to which a particular character can be transmitted to the successive generations. Knowledge of heritability of a trait thus guides a plant breeder to predict the behavior of succeeding generations and helps him to predict the response to selection Waqar-Ul-Haq *et al*. (2008) [27]. Study of statistical parameters like variance, PCV, GCV, ECV, h^2 and GA is not only helpful to evaluate the genetic stability and performance of any particular genotype but it is also a measure which determines the effectiveness of selection for a particular trait in that genotype.

Materials and Methods
Experimental site
The present investigation was carried out at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of

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Agriculture, Technology & Sciences Allahabad, U.P. The site of experiment is located at 25.57° N latitude, 81.51° E longitude and 98 meter above the sea level. The average rainfall in this area is around 1013.4 mm annually with maximum concentration during July to September with few showers and drizzles in winter also.

Experimental materials and design
The experimental material consisted of 20 genotypes (including 2 checks), were grown under (RBD) with three replications, during *Rabi* 2015-16. The experimental field was divided into 3 blocks of equal size and each block had 20 plots. Each genotype was accommodated in one row of 2 meters length spaced 25 cm between row to row with approximate plant to plant distance of 5 cm. Sowing was done late on December 1st 2015. Thinning was done to maintain a plant to plant spacing of 5 cm. The N: P: K dose was applied 120:60:60kg/ ha respectively.

Data collected
The observations were recorded on various quantitative characters from five randomly selected plants of each genotype in each replication. The reading from five plants was averaged replication wise and the mean data used for statistical analysis for 16 characters under observation. The value of harvest index was calculated from the following formula given by Donald and Hamblin (1976).

$$\text{Harvest index} = \frac{\text{Seed yield per plant}}{\text{Biological yield}} \times 100$$

Statistical analysis (ANOVA)
A preliminary randomized block design (RBD) analysis of variance was done according to the methods given by Panse and Sukhatme (1967) [21] and the mean sum of squares due to replication; treatment and error of the characters under study were presented as given in ANOVA Table 1:

Table 1: Skeleton ANOVA for mean sum of square of the character under study

Source of Variations	d.f.	S.S	M.S.S	F-Value Cal
Due to replications	(r-1)	RSS	RSS/(r-1)=MSS (r)	MSS (r)/EMS
Due to treatments	(t-1)	TrSS	TrSS/(t-1)=MSS (t)	MSS (t)/EMS
Due to error	(r-1)(t-1)	ESS	ESS/(r-1)(t-1)=EMS	
Total	(rt-1)	TSS		

The mean values of the recorded data were subjected to analysis of variance as per Gomez and Gomez (1984) [13]. The mean squares were used to estimate genotypic and phenotypic variance according to Sharma (1998) [22]. The variability present in the genotypes was estimated by phenotypic and genotypic variances and coefficient of variations using the procedure suggested by Burton and De Vane (1953) [9] as follows:

$$Vg = \frac{MSg - EMe}{r} \quad \text{and} \quad Vp = Vg + Ve$$

Where, Vg = Genotypic variance, Vp = Phenotypic variance, Ve = Environmental (error), MSg = Mean square due to genotypes, MSe = Mean square of error (Environmental variance), r = Number of replications.

Genotypic coefficient o variation: $GCV = \frac{\sqrt{Vg}}{\overline{X}} \times 100$

Phenotypic coefficient of variation: $PCV = \frac{\sqrt{Vp}}{\overline{X}} \times 100$

Environmental coefficient of variation: $ECV = \frac{\sqrt{Ve}}{\overline{X}} \times 100$

Whear X = Population mean of the character being evaluated. GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20% and above) values as indicated by Burton and De vane (1953) [9] and Sivasubramanian and Madhavamenon (1973) [24].
Heritability (h^2_{bs}) is the ratio of genotypic variance to the total phenotypic variance. Heritability (h^2_{bs}) was computed using the formula given by Burton and De vane (1953) [9].

$$h^2 = \frac{VG}{VP} \times 100$$

Heritability (h^2_{bs}) values were classified as Low (0-30%), Moderate (30-60%) and High (60% and above). These values are indicated by Johnson *et al.* (1955a) [17].
Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. The estimates of genetic advance were obtained by the formula given by Johnson *et al.* (1955) [17].

$$GA = \frac{VG}{\sqrt{VP}} \times K$$

Expected genetic advance as part of the mean (GA) for each character at 5% selection intensity (K=2.06) was calculated by the formula suggested by Allard (1960) [4].
The genetic advance is usually expressed as percentage of mean estimated by following formula suggested by Comstock and Robinson (1952) [10].

$$GA \, (\%) = \frac{GA}{\overline{X}} \times 100$$

The range of genetic advance as percent were categorized as low (0-10%), moderate (10-20%) and high (20% and above) values as suggested by Johnson *et. al.* (1955a) [17].
The genotypic (r_g) and phenotypic (r_p) correlation between two characters x and y were determined by using the variance and covariance components as suggested by Al-Jibouri *et al.* (1958) [2].

$$r_g \, (x \, y) = \frac{Cov g \, (x \, y)}{\sqrt{\sigma^2 g \, (x).\sigma^2 g \, (y)}} \qquad r_p \, (x \, y) = \frac{Cov \, p \, (x \, y)}{\sqrt{\sigma^2 p \, (x).\sigma^2 p \, (y)}}$$

r_g (xy) is the genotypic correlation coefficients. r_p (xy) is the phenotypic correlation coefficients.
Cov$_g$ is the genotypic covariance of xy. Cov$_p$ is the phenotypic covariance of xy.
σ^2_g is the genotypic variance of x and y. σ^2_p is the phenotypic variance of x and y.

Results and Discussion

a. Analysis of variance (ANOVA)

The mean sum of squares showed significant differences at 1% level among all the characters except for flag leaf width are given in (Table 2), indicates that there was ample scope for selection of promising genotypes for yield improvement. Highest values were estimated for plant height followed by thousand grain weight, peduncle length, days to maturity, number of grain per spike, days to 50 % heading and days to flowering. The wide range of variation observed in all the characters offers scope of selection for different quantitative traits of wheat. Similar findings in wheat have also reported by Kaddem *et al.* (2014) [18].

b. Range and mean values

Range and mean values for the 16 characters is presented in (Table 3). The mean grain yield per plant ranged from 3.81 to 7.54 g with a mean value of (5.12 g), which is higher than local checks varieties, Raj- (3765) and HD- (2733). 30% of the genotypes gave values above the grand mean. Phenological characters like days to 50% heading, days to 50% flowering and days to maturity ranged from 68.00 (SHIATS-BW 1124) to 82.00 (SHIATS-BW 1128), 72.33 (SHIATS-BW 1124) to 84.00 (SHIATS-BW 1128) and 102.67 (SHIATS-BW 1124) to 118.33 (SHIATS-BW 1128), respectively. Grain filling period is an important trait in wheat that ultimately affects the overall grain yield by increasing grain weight. It ranged from 30.33 (SHIATS-BW 1133, Raj-3765, SHIATS-BW 1124) to 34.33 (SHIATS-BW 1128) with a mean value of 31.82 days, which is slightly higher than local check variety (Raj- 3765), 30.33 day. Plant height ranged from 85.70 cm (HD- 2733) to 143.20 cm (SHIATS-BW 1127), with a mean value of 103.42 cm. The mean value of peduncle length was 37.10 cm, ranged from 29.07 for (HD-2733) to 47.73 for (SHIATS-BW 1129). Spikes per plant ranged from 3.33 (SHIATS-BW 1136) to 5.83 (SHIATS-BW 1128), with a mean value of 3.96, which is slightly higher than local check varieties (HD- 2733) and Raj- (3765), 3. 80 and 3.93 respectively. It shows there is some variation among the genotypes under observation. Spikelets per spike ranged from 13.93 (SHIATS-BW 1134) to 18.00 (SHIATS-BW 1137), with a mean value of 15.11. Flag leaf length ranged from 17.53 (SHIATS-BW 1138) to 27.33 (SHIATS-BW 1128) cm with a mean value of (22.88 cm). Flag leaf width ranged from 1.17 (SHIATS-BW 1134) to 1.74 (SHIATS-BW 1126) cm with a mean value of (1.47 cm). Spike length ranged from 10.53 (SHIATS-BW 1123) to 14.10 cm

(SHIATS-BW 1127) with a mean value of (11.85 cm), which is slightly higher than local check (Raj- 3765) and (HD-2733), 10.67 and 11.23 respectively. It shows there is some variation among the genotypes.

Grains per spike ranged from 32.80 (SHIATS-BW 1125) to 49.80 (SHIATS-BW 1137) with a mean value of (39.35). Thousand grain weight ranged from 28.20 (Raj- 3765) to 52.97 g (SHIATS-BW 1127) with a mean value of (33.75 g), which is higher than local check varieties (Raj- 3765) and (HD- 2733), 28.20 and 29.13. The genotypes under study show high variation from local checks. Biological yield ranged from 9.18 (SHIATS-BW 1138) to 17.81 (SHIATS-BW 1128) g with a mean value of (12.00 g). Harvest index ranged from 37.38 (SHIATS-BW 1136) to 47.17 % (SHIATS-BW 1127) with a mean value of (42.54 %).

The estimates of variance, coefficient of variation, heritability and genetic advance for all the sixteen characters studied are presented in table 3. Maximum (Vp) value was recorded for plant height, peduncle length and thousand grain weight, 264.68, 39.59 and 39.57 respectively. Similarly, the (Vg) value for these characters were also high indicating for plant height, thousand grain weight and peduncle length, 245.64, 35.27 and 27.43 respectively. Less difference in the estimates of genotypic and phenotypic variance and higher genotypic values compared to environmental variance for all the characters suggested that the variability present among the genotypes were mainly due to genetic reason with minimum influence of environment and hence heritable.

In the present investigation Table 3 showed that estimates of phenotypic coefficient of variation were higher than their corresponding genotypic coefficient of variation, indicating that the little influence of environment on the expression of these characters. However, good correspondence was observed between genotypic coefficient of variation and phenotypic coefficient of variation in all the characters. The (PCV) and (GCV) ranged from 4.44% (days to maturity) to 24.66% (seed yield per plant) and 3.75% (grain filling period) to 21.84% (seed yield per plant). According to Burton and De vane (1953) [9] categorization, the characters which show maximum phenotypic coefficients of variation were seed yield per plant and biological yield 24.66 and 22.13 for (PCV) and 21.84 for (GCV). The rest of characters showed moderate to low values for both phenotypic as well as genotypic. Similar results were reported by Al-Tabbal *et al.* (2012) [5] where the estimates of (PCV) and (GCV) were high for grains yield per plant, plant height and biological yield.

Table 2: The analysis of variance (ANOVA) for 16 characters in bread wheat

Characters	Days to heading	Days to flowering	Days to maturity	Grain filling period	Plant height	Peduncle length	No. of spikes per plant	No. of spikelet per spike	Flag leaf length	Flag leaf width	Spike length	No. of greens per spike	1000 grain weight	Biological yield	Harvest index	Seed yield per plant
Replications	1.67	1.05	1.22	0.22	21.05	4.76	0.29	0.4	0.37	0.04	0.82	5.62	1.01	1.35	1.91	0.14
Treatments	43.00**	35.36**	63.99**	4.89**	755.98**	94.44**	1.13**	4.10**	20.36**	0.07Ns	2.76**	48.64**	110.10**	16.22**	19.35**	4.09**
Error	1.6	1.82	3.83	0.62	19.03	12.16	0.21	0.76	3.55	0.04	0.65	3.81	4.3	2.56	2.96	0.34

Table 3: Estimate of mean, ranges, phenotypic variance (Vp) and genotypic variance (Vg) PCV, GCV, broad sense heritability and genetic advance as percent of mean for 16 characters of bread wheat.

Characters		Range		Vp	Vg	PCV	GCV	H²bs	GA	GAM
	Mean	Min	Max.			%	%	%	(K=2.06)	(K=2.06)
Days to 50% heading	75.18	68	82	15.4	13.8	5.22	4.94	89.63	7.25	9.64
Days to 50% flowering	78.25	72.33	84	13	11.18	4.61	4.27	85.99	6.39	8.16
Days of Maturity	110.07	102.67	118.33	23.88	20.05	4.44	4.07	83.96	8.45	7.68
Grain filling period	31.82	30.33	34.33	2.04	1.42	4.49	3.75	69.67	2.05	6.45
Plant height	103.42	85.7	143.2	264.68	245.65	15.73	15.16	92.81	31.1	30.08
Peduncle length	37.1	29.07	47.73	39.59	27.43	16.96	14.12	69.27	8.98	24.2
No. of Spikes per plant	3.96	3.33	5.83	0.52	0.31	18.15	13.96	59.17	0.88	22.13
No. of Spikelets per spike	15.11	13.53	18	1.88	1.11	9.06	6.98	59.23	1.67	11.06
Flag leaf length	22.88	17.53	27.33	9.15	5.6	13.22	10.34	61.23	3.82	16.68
Flag leaf width	1.47	1.17	1.74	0.05	0.01	15.27	7.51	24.18	0.11	7.6
Spike length	11.85	10.53	14.1	1.35	0.7	9.82	7.07	51.77	1.24	10.47
No. of grains per spike	39.35	32.8	49.8	18.75	14.94	11	9.82	79.71	7.11	18.07
1000 Grain Weight	33.75	28.2	52.97	39.57	35.27	18.64	17.6	89.14	11.55	34.23
Biological yield	12	9.18	17.81	7.12	4.55	22.23	17.78	63.96	3.52	29.29
Harvest index	42.54	37.38	47.17	8.42	5.46	6.82	5.49	64.84	3.88	9.11
Seed yield per plant	5.12	3.81	7.54	1.59	1.25	24.66	21.84	78.41	2.04	39.83

Vp =Phenotypic variation, Vg =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H²bs = Broad sense heritability, GA=genetic advance, and GAM=Genetic advance as percent of mean

The estimates of heritability are more advantageous when expressed in terms of genetic advance Johnson *et al*. (1955) [17]. The range observed for heritability (bs) was from (24.18) to (92.81). The highest heritability were recorded for plant height (92.81 %), days to 50 % heading (89.63 %), thousand grain weight (89.14 %), days to 50 % flowering (85.99 %), days of maturity (83.96 %), number of grains per spike (79.71 %), seed yield per plant (78.41 %), grain filling period (69.67 %), peduncle length (69.27 %), harvest index (64.84 %), biological yield (63.96 %), and flag leaf length (61.23 %). The rest of the characters were grouped in moderate to low values of heritability. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. Kaddem and Marker (2014) [18] also reported high heritability value for characters viz., 50 % flowering, days to 50 % heading, plant height, spike length, thousand grain weight, flag leaf length and days of maturity. High heritability estimates were reported by Tripathi *et al*. (2015) [25] for thousand grain weight and Yahaya *et al*. (2014) for plant height.

Genetic advance as percentage of mean ranged from 6.48% to 39.83% for grain filling period and seed yield per plant respectively. Table 3. Seed yield per plant exhibited highest value of genetic advance as percentage of mean (39.83) followed by thousand grain yield (34.23), plant height (30.08), biological weight (29.29), peduncle length (24.20) and number of spikes per plant (22.13). Similarly Ghallab *et al*. (2016) [12] observed high value of genetic advance as percentage of mean for thousand grain weight, plant height,

biological yield and number of spikes per plant. The rest of the characters recorded moderate to lowest values during observation. reported that high heritability and high genetic advance as percentage of mean provide better information than each parameter alone. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters.

Phenotypic and genotypic correlation coefficients of grain yield with other characters are presented in Table 4. The genotypic correlation coefficient values (r_g) for most of the characters were higher in magnitude than the corresponding phenotypic correlation coefficient values (r_p) which indicated that association among these characters was largely under genetic control and indicated the preponderance of genetic variance in expression of characters Tsegaye *et al*. (2012) [26] and Tripathi *et al*. (2015) [25].

Seed yield per plant showed positive correlation with biological yield (0.958**, 0.980**), number of spikes per plant (0.803**, 0.834**), thousand grain weight (0.517**, 0.630**), plant height (0.490**, 0.578**), spike length (0.472**, 0.709**), harvest index (0.462**, 0.747*), flag leaf length (0.454**, 0.612**), peduncle length (0.348*, 0.492**), number of spikelets per spike (0.316*, 0.426**), flag leaf width (0.275*, 0.587**) and number of grains per spike (0.266*, 0.297*) and grain filling period (0.269*, 0.215ns) at both phenotypic and genotypic levels. Similar results of positive association of seed yield per plant with number of spike per plant, thousand grains weight, spike length and number of grains per spike were observed by (Munir *et al*. 2007) [20].

Table 4: Upper diagonal estimates of phenotypic correlation (rp) and lower diagonal genotypic correlation (rg) coefficients between grain yield per plant and its 16 contributing characters in bread wheat.

Characters	Days to 50% heading	Days to 50% flowering	Days of Maturity	Grain filling period	Plant height	Peduncle length	No. of Spikes per plant	No. of Spikelets per spike	Flag leaf length	Flag leaf width	Spike length	No. of grains per spick	1000 Grain Weight	Biological yield	Harvest index	Seed yield per plant
Days to 50% heading	1	0.975**	0.962**	0.828**	-0.174	-0.242	0.332*	0.108	-0.02	0.346*	0.086	0.137	-0.228	0.218	-0.176	0.149
Days to 50% flowering	0.996**	1	0.989**	0.857**	-0.122	-0.188	0.326*	0.103	-0.004	0.308*	0.085	0.116	-0.216	0.223	-0.208	0.147
Days of Maturity	0.988**	0.995**	1	0.925**	-0.097	-0.154	0.369**	0.091	0.009	0.332*	0.1	0.097	-0.181	0.264*	-0.189	0.187
Grain filling period	0.916**	0.933**	0.963**	1	-0.022	-0.051	0.439**	0.05	0.042	0.356*	0.125	0.039	-0.072	0.341*	-0.122	0.269*
Plant height	-0.171	-0.143	-0.123	-0.06	1	0.847**	0.147	-0.101	0.449**	0.083	0.563**	-0.068	0.750**	0.361**	0.487**	0.490**
Peduncle length	-0.270*	-0.252	-0.219	-0.118	0.903**	1	0.143	-0.089	0.425**	0.211	0.370**	-0.176	0.626**	0.225	0.458**	0.348*
No. of Spikes per plant	0.337*	0.325*	0.370**	0.478**	0.171	0.161	1	0.247	0.362**	0.424**	0.296*	0.121	0.17	0.867**	0.113	0.803**
No. of Spikelets per spike	0.208	0.184	0.179	0.157	-0.199	-0.341*	0.328*	1	-0.008	0.1	0.161	0.706**	-0.041	0.331*	0.059	0.316*
Flag leaf length	-0.012	-0.054	-0.035	0.019	0.615**	0.722**	0.631**	-0.104	1	0.277*	0.304*	0.041	0.227	0.458**	0.09	0.454**
Flag leaf width	0.611**	0.663**	0.736**	0.902**	0.247	0.470**	0.805**	0.148	0.705**	1	0.102	0.086	-0.026	0.302*	0.025	0.275*
Spike length	0.199	0.182	0.194	0.22	0.698**	0.329*	0.398**	-0.303*	0.421**	0.277*	1	0.216	0.432**	0.424**	0.267*	0.472**
No. of grains per spike	0.208	0.168	0.157	0.121	-0.101	-0.317*	0.111	0.709**	-0.027	0.124	-0.044	1	-0.263*	0.307*	-0.062	0.266*
1000 Grain Weight	-0.260*	-0.241	-0.212	-0.122	0.809**	0.744**	0.224	-0.032	0.333*	-0.027	0.692**	-0.272*	1	0.359**	0.637**	0.517**
Biological yield	0.146	0.119	0.162	0.277*	0.487**	0.369**	0.895**	0.501**	0.621**	0.637**	0.675**	0.372**	0.497**	1	0.193	0.958**
Harvest index	-0.154	-0.161	-0.134	-0.051	0.593**	0.656**	0.404**	0.075	0.342*	0.238	0.552**	-0.042	0.815**	0.603**	1	0.462**
Seed yield per plant	0.085	0.063	0.104	0.215	0.578**	0.492**	0.834**	0.426**	0.612**	0.587**	0.709**	0.297*	0.630**	0.980**	0.747**	1

*: Significant at 5% level of significance, **: Significant at 1% level of significance

Days to 50 % heading highly phenotypic and genotypic correlated with days to 50 % flowering (0.975**, 0.996**), days to maturity (0.962**, 0.988**), grain filling period (0.828**, 0.916**), flag leaf width (0.346*, 0.611**) and number of spikes per plant (0.332*, 0.337*), respectively, while peduncle length was associated negatively and was non-significant in phenotypic and negatively significant in genotypic association.

Days to 50 % flowering showed positive significant phenotypic and genotypic association with days to maturity (0.989**, 0.995**), grain filling period (0.857**, 0.933**), number of spikes per plant (0.326*, 0.325*) and flag leaf width (0.308*, 0.663**).

Days of maturity exhibited positive significant phenotypic and genotypic association with grain filling period (0.925**, 0.963**), number of spikes per plant (0.369**, 0.370**) and flag leaf weight (0.332*, 0.736**), respectively, while biological yield was associated in a positive and significant manner in phenotypic association and was positive non-significant in genotypic association.

Grain filling period exhibited positive significant phenotypic and genotypic association with number of spikes per plant (0.439**, 0.478**), flag leaf width (0.356*, 0.902**) and biological yield (0.341*, 0.277*), whereas seed yield per plant showed positive significant and positive non significant in both phenotypic and genotypic associations.

Plant height showed positive significant phenotypic and genotypic association with peduncle length (0.847**, 0.903**), thousand grain weight (0.750**, 0.809**), spike length (0.563**, 0.698**), seed yield per plant (0.490**, 0.578**), harvest index (0.487**, 0.593**), flag leaf length (0.449**, 0.615**) and biological yield (0.361**, 0.487**), respectively. The rest of character showed negative non-significant association with plant height. Similar finding were also reported by Bhushan et al. (2013) [7], who observed grain filling period, thousand grains weight and harvest index had positive significant genotypic correlation with plant height.

Peduncle length showed positive significant phenotypic and genotypic association with thousand grain weight (0.629**, 0.744**), harvest index (0.458**, 0.656**), flag leaf length (0.425**, 0.722**), spike length (0.370**, 0.329*) and seed yield per plant (0.348*, 0.492**), respectively. Flag leaf width and biological yield had positive significant genotypic correlations with peduncle length (0.470** and 0.369**), respectively. The spikelets per spike and number of grains per spike recorded negative significant association with peduncle length (-0.341* and -0.317*), respectively.

Number of spikes per plant showed positive significant phenotypic and genotypic correlation with biological yield (0.867**, 0.895**), seed yield per plant (0.803**, 0.834**), flag leaf width (0.424**, 0.805**), flag leaf length (0.362**, 0.631**) and spike length (0.296*, 0.398**), respectively. Harvest index (0.404**) and number of spikelets per spike (0.328*) recorded only genotypic correlation with number of spikes per plant.

Number of spikelets per spike showed positive significant phenotypic and genotypic correlation with no. of grains per spike (0.706**, 0.709**), biological yield (0.331*, 0.501**) and seed yield per plant (0.316*, 0.426**), respectively, while negative significant genotypic correlation was recorded only with spike length (-0.303*). It means that with the increases of spikelets per spike, there was significant increase in seed yield per plant. Similar finding were also reported by Mohsen et al. (2012) [19], who observed number of grains per spike and seed yield per plant had positive significant genotypic and phenotypic correlation with number of spikelets per spike.

Flag leaf length showed positive significant phenotypic and genotypic correlation with harvest index (0.458**, 0.342*), seed yield per plant (0.454**, 0.612), spike length (0.304*, 0.421**) and flag leaf width (0.277*, 0.705**), while only genotypic correlation was recorded for biological yield and thousand grain weight (0.621** and 0.333*), respectively.

Flag leaf width showed positive significant phenotypic and genotypic association with biological yield and seed yield per plant (0.302*, 0.637** and 0.275*, 0.587**) respectively, spike length showed only genotypic positive significant and phenotypic positive non significant association (0.0277*, 0.102ns), respectively.

Spike length showed positive significant phenotypic and genotypic association with seed yield per plant (0.472**,

0.709**), thousand grain weight (0.432**, 0.692**), biological yield (0.424**, 0.675**) and harvest index (0.267*, 0.552**), respectively. It means that with the increase of spike length there was significant increase in the number of spikelets per spike as discussed by Adnan *et al.* (1994) [1].

Number of grains per spike showed positive significant phenotypic and genotypic association with biological yield (0.307*, 0.372**) and seed yield per plant (0.266*, 0.297*). These results suggest that selections should be based on number of grains per spike for developing new wheat varieties. Similar finding was reported by Mohsen *et al.* (2012) [19], who observed seed yield per plant had positive significant phenotypic and genotypic association with number of grains per spike.

Thousand grain weight showed positive significant phenotypic and genotypic association with harvest index (0.637**, 0.815**), seed yield per plant (0.517**, 0.630**) and biological yield (0.359**, 0.497**), respectively. These results were in agreement with study of Tsegaye *et al.* (2012) [26] and Munir *et al.* (2007) [20], for biological yield, harvest index and thousand grains weight had positive significant association with thousand grains weight.

Biological yield showed positive significant phenotypic and genotypic association only with seed yield per plant (0.958**, 0.980**), respectively, and positive genotypic significant association with harvest index (0.603**). Tsegaye *et al.* (2012) [26], suggesting that positive significant with seed yield per plant.

Harvest index showed positive significant phenotypic and phenotypic association with seed yield per plant (0.462**, 0.747**), respectively. Similar findings in wheat have also been reported by Kaddem *et al.* (2014) [18] who showed positive significant correlation with seed yield per plant.

Conclusion
To conclude the present investigation, the genotypes SHIATS-BW 1128 followed by SHIATS-BW 1127 were found best based on seed yield per plant along with number of spikes per plant, spike length, thousand grains weight and harvest index.

In the present investigation, estimates of phenotypic coefficient of variation were higher than their corresponding genotypic coefficient of variation, but with minimum difference between them, indicating little influence of environment on the expression of these characters. The estimates of heritability in broad sense (h^2_{bs}) and genetic advance revealed that characters like thousand grain weight, number of grains per spike, grain filling period, and flag leaf length had high heritability along with high to moderate genetic advance. Therefore, these characters should be used during selection. Further, positive significant correlation of these traits with yield proves their genetic worth.

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