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Selection parameters for grain yield and its components in bread wheat (*Triticum aestivum* L.)

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Abstract

Wheat (*Triticum aestivum* L.), a cereal grass of Graminae (Poaceae) family and of the genus *Triticum*, is the world's largest cereal crop. Selection parameters in bread wheat were studied in 28 F₁s developed by crossing of 8 genotype viz., HD 3171, WH 147, K-906, K 307, K 1006, K 7903, DBW 14 and PBW 502 in half diallel design to study the twelve quantitative characters. The analysis of variance revealed highly significant differences among the genotypes for all the 12 characters. In this study the high heritability (narrow sense) were recorded for plant height, days to maturity & number of spikelets per spike while moderate heritability were found for days to heading, tillers per plant & 1000 grain weight, whereas grains per spike showed low heritability. The estimate of genetic advance in percentage over mean ranged from 3.30 (biological yield per plant) to 32.90 (grain yield per plant) in F₁ generation. In F₁ generation in general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficient except number of grains per spike, suggesting therefore, a strong inherent relationship in different pairs of characters in wheat genotype. The most important character grain yield per plant had exhibited highly significant and positive phenotypic correlation with biological yield per plant (0.850), spike length (0.490), number of spikelets per spike (0.444) and plant height (0.442). The Path coefficient analysis was carried out at phenotypic and genotypic level to resolve direct and indirect effect of eleven characters on grain yield per plant.

Keywords: Heritability (narrow sense), genetic advance, correlation coefficients and Path coefficient.

Introduction

Wheat is one of the most staple food crop in the world. In pre-historic times it was grown in the ancient Persia, Egypt, Greece and Europe as early as 10,000 to 15,000 B.C. The evolution of bread wheat occurred by combining the tetraploid species *T. turgidum* var. *dicoccoides* (AABB) and diploid species *Aegilops squarosa* (DD) followed by doubling the chromosome number. The major wheat growing countries in the world are China, India, U.S.A., Russia, France, Canada, Germany, Turkey, Australia and Ukraine. Globally, wheat is being grown more than in 122 countries and occupies an area of 214.29 million hectares producing nearly 734.04 million tonnes and productivity is 3425 kilogram per hectare (FAO 2018). India stands second rank both in area and production next to China in the world. At national level area under wheat is 29.58 million ha with the production of 99.70 million tonnes with a productivity of 3371 kilogram per hectare (DACFW 2018). The India's share in world wheat area and production is about 13%. These studied the parental material by all means particularly in terms of selection parameter for different characters, heritability, genetic advance, correlation & path analysis for twelve important characters in bread wheat. Heritability is a good index of transmission of character from parents to offspring. Genetic advance is improvement in genotypic value of selected population in contrast to original population. High heritability coupled with high genetic advance helps in selection of elite genotypes. The correlation and path coefficients help us in understanding the relative important of various yield influencing characters so that the most important yield components can be identified.

Materials and methods

The present investigation entitled "Study of combining ability and heterosis in F₁ generation of bread wheat (*Triticum aestivum* L.)" was conducted at Crop Research Farm, Nawabganj, C. S. Azad University of Agriculture and Technology, Kanpur-208002 UP, during two rabi season as 2016-17 and 2017-18. The experimental material with the 28 F₁s developed by crossing 8 lines viz., HD3171, WH147, K906, K307, K1006, K7903, DBW14, and PBW502 following half diallel mating design. A total of 36 treatments (28 F₁'s and 8 parents) were used for the study of selection parameters. The genotypes under study were planted in a randomized complete block design (RCBD) with three replications per entry and one row (3m) per replication.

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The entries were sown in a single row plot of 3 m length with inter and intra-row spacing of 25 cm and 10 cm, respectively. Recommended agronomic practices were adopted to raise a good crop. The observations were recorded from the five randomly selected plants in parents and their F₁s for all the following traits viz. days to 75% heading, number of tillers/plant, plant height (cm), days to maturity, length of

spike (cm), number of spikelet/spike, number of grain/spike, grain yield/plant (g), weight of grain per spike (g), 1000 seed weight (g), biological yield/plant (g) and harvest index %. The material for the present investigation comprised of 8 strains/varieties of wheat (*Triticum aestivum* L.) selected on the basis of wide variability for various characters. The salient features of these parental lines are given in Table 1.

Table 1: details of genotypes in this following table.

| S. No. | Genotype | Species | Pedigree | Place of origin |
|--------|----------|--------------------|-----------------------------------------|-----------------|
| 1 | HD 3171 | <i>T. aestivum</i> | PBW 343/HD 2879 | IARI, New Delhi |
| 2 | WH 147 | <i>T. aestivum</i> | PJSIB/P14/KT54B/3/C286/C273/4/S339/PV18 | HAU, Haryana |
| 3 | K 906 | <i>T. aestivum</i> | UP2338/PBW373 | CSA, Kanpur |
| 4 | K 307 | <i>T. aestivum</i> | K 9321/UP 2003 | CSA, Kanpur |
| 5 | K 1006 | <i>T. aestivum</i> | PBW 343/HP 1731 | CSA, Kanpur |
| 6 | K 7903 | <i>T. aestivum</i> | HD 1982/K 816 | CSA, Kanpur |
| 7 | DBW 14 | <i>T. aestivum</i> | RAJ 3765/PBW 343 | IWBR, Karnal |
| 8 | PBW 502 | <i>T. aestivum</i> | W 485/PBW 343//RAJ 1482 | PAU, Panjab |

Estimation of coefficient of variability: The genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) were computed following Burton and de Vane (1953) ^[1].

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100 \quad \text{Or} \quad \frac{\sigma_g}{\bar{x}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100 \quad \text{Or} \quad \frac{\sigma_p}{\bar{x}} \times 100$$

Estimation of selection parameters as Heritability in narrow sense (h²_{ns}) and broad sense (bs) was calculated as suggested by Crumpacker and Allard, (1962) ^[2].

Heritability

$$\text{Heritability } (\hat{h}^2) = \frac{\frac{1}{4}\hat{D}}{\frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 + E_1 - \frac{1}{4}F}$$

$$H(\text{bs}) = \frac{\frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 - \frac{1}{4}F}{\frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 + E_1 - \frac{1}{4}F}$$

$$E_1 = \left(\frac{E_{\text{parent}}}{n} \right) + (n-1) \frac{E_{F1}}{n}$$

Where,

\hat{D} = Component of variation due to additive effects of genes.

\hat{H}_1 = Component of variation due to dominance effects of gene.

\hat{F} = The mean of F_r over arrays, where F_r is the covariance of additive and dominance effects in a single array.

\hat{E}_1 = The expected environmental component of variation.

Genetic advance: The genetic advance was calculated as per formula given by Robinson *et al.* (1949) ^[20].

Genetic Advance = (σ_{ph}) × (K) × (h² bs)

Genetic advance in per cent of mean of the character

$$G.A. (\%) = \frac{\sigma_{ph} \times K \times h^2}{\bar{X}} \times 100$$

Where,

G. A. = Estimate of genetic advance

K = Selection differential at 5% selection intensity (K = 2.06)

h² = Heritability coefficient in broad sense.

σ_{ph} = Phenotypic standard deviation.

\bar{X} = Mean value of the character concerned

Correlation Coefficients: The following formulae were used for calculating the genotypic and phenotypic coefficient of correlations in both the experiments as suggested by Al-Jibouri *et al.* (1958).

Genotypic correlation [r_{xy}(g)] = Cov._{xy}(g) / [V_x(g).V_y(g)]^{0.5}

Where,

Cov._{xy}(g) = genotypic covariance between characters x and y, and this was obtained as follows:

Cov._{xy}(g) = [Cov._{xy}(p) - Cov._{xy}(e)]

$$\text{Cov.}_{xy}(g) = \frac{\text{Treatment MSP} - \text{Error MSP}}{r}$$

V_x(g) and V_y(g) = genotypic variances for the characters x and y, respectively

r = number of replications

Phenotypic correlation [r_{xy}(p)] = [Cov._{xy}(p)] / [V_x(p).V_y(p)]^{0.5}

Where,

Cov._{xy}(p) = phenotypic covariance between the characters x and y, and this was obtained as follows:

Cov._{xy}(p) = Cov._{xy}(g) + Cov._{xy}(e)

V_x (p) and V_y (p) = phenotypic variance for the characters x and y respectively,

Path analysis: The concept of path coefficient analysis was originally developed by Wright in 1921, but the technique was first used for plant selection by Dewey and Lu 1959 [3]. Path coefficient analysis is simply standardized partial regression coefficient which split the simple correlation into the measures of direct and indirect effects and it measures the direct and indirect contribution of each independent variable on the dependent variable. If "Y" is dependent (causal) characters by X_1, X_2, X_3 ----- independent characters and some undefined factors designated by R, this relation can be represented by

$$Y = X_1 + X_2 + X_3 + \dots + R$$

Path analysis reveals whether the association is due to their direct effect or is a consequence of their indirect effects *viz.*, other component characters. Correlation between cause (X_1) and effect (Y_1) is partitioned into the direct effects and indirect effects via other characters.

Direct effects: Path coefficient is ratio of standard deviation of the effect due to given cause to the standard deviation of effect i.e. (X_1/y). This gives the direct effect of cause on yield.

$$r(x,y) = a + r(x_1, x_2) b + r(x_1, x_3) (\dots)$$

Here,

$r(x, y)$ = correlation coefficient between cause (x_1) and yield (effect) a, b, c is path coefficient (direct effects) of causal characters x_1, x_2, x_3 respectively.

$r(x_1, x_2)$ = Correlation coefficient between cause x_1 and x_2

$r(x_1, x_3)$ = Correlation coefficient between cause x_1 and x_3

Indirect effect: Indirect effect of x_1 via x_2 on $y = r(x_1, x_2) b$ Similarly, direct and indirect effects of all possible combinations were calculated for all component characters.

Result and discussion

The analysis of variance for all the twelve characters was given in table-2. The treatments showed highly significant differences for all the characters and highest value was estimated for biological yield followed by plant height and days to heading while, grain weight per spike was low. Selections of genotypes were genetically variable and considerable amount of variability existed among them.

The genotypic (GCV) and phenotypic (PCV) coefficients of variation were observed in the experimental material for all the characters studied (table 3). The higher magnitudes of GCV and PCV were recorded for biological yield, grain yield per plant, spike length (cm) and grain weight per spike. However, number of tiller per plant, harvest index, number of spikelets per spike, plant height, number of grain per spike, days to heading, one thousand grain weight and days to maturity exhibited least genotypic and phenotypic coefficient of variation. On an average the higher magnitude of GCA and PCV were recorded for biological yield (14.11 and 14.48), grain yield per plant (13.71 and 15.08), spike length (10.62 and 10.94) and grain weight per spike (10.25 and 13.54), respectively, suggesting sufficient variability are available and thus exhibited scope for genetic improvement through selection for all these traits.

Among the selection parameters the heritability and genetic advance are the most important direct selection parameters. In view of this, the heritability (in narrow sense) and genetic advance in % for the twenty eight crosses have been furnished

in Table-3. Generally the estimates of heritability and genetic advance were arbitrarily categorized in three by Robinson (1966) as under.

1. High (above 30%),
2. Moderate (above 10% & below 30%)
3. Low (below 10%)

Heritability (in narrow sense) in F_1 generation was calculated by the method proposed by Crumpacker and Allard, (1962). Accordingly, high estimates of heritability were observed for spike length (72.7), biological yield per plant (59.1), plant height (54.6), grain yield (49.3), days to maturity (43.1) and number of spikelets per spike (36.7) in F_1 generation. The moderate heritability estimates were found for days to heading (29.0), 1000 grain weight (27.7), number of tiller per plant (27.0), grain weight per spike (26.3) and harvest index (19.1). The low heritability estimate was found only for number of grains per spike (8.0).

Genetic advance, though not an independent identity, has an added advantage over heritability as a guiding factor to the breeders in selection Programme. Johnson *et al.*, (1955) [11] stated that without genetic advance, estimates of the heritability would not be of practical importance based on phenotypic expression and emphasized the concurrent use of genetic advance along with heritability. The estimates of genetic advance in percent over mean of characters ranged from 3.30 (biological yield) to 32.90 (grains yield per plant). The high genetic advance in percent over mean was observed in grains yield per plant (32.90), while spike length (27.33), grains weight per spike (20.51), harvest index (20.43), number of tiller per plant (19.97), spikelets per spike (15.45), plant height (14.15), number of grains per spike (13.98) and days to heading (11.46) showed moderate whereas days to maturity (6.90), 1000-grains weight (6.38) and biological yield per plant (3.30) were observed low genetic advance in percent over mean. Heritability and genetics advance are two complementary concepts. Based on this consideration, high heritability coupled with high genetic advance as percent of mean were registered for grain yield per plant indicated predominance of additive gene action in the expression of this trait. High heritability coupled with moderate genetics advance was observed for spike length, plant height and number of spikelets per spike. Same thing was observed by Dhananjay *et al.* (2012) Kumar *et al.* (2013) [13, 14], Navin Kumar *et al.* (2014) [16], Pradeep *et al.* (2016).

The phenotypic and genotypic correlation coefficient of F_1 generation computed among the twelve characters under study has been presented in Table-4. The correlation coefficient highest direct genotypic and phenotypic correlation with grain yield was observed in the biological yield (0.888, 0.850), spike length (0.549, 0.490), number of spikelets per spike (0.551, 0.444), plant height (0.538, 0.442) and harvest index (0.236, 0.222). Harvest index negative correlation with the biological yield. Biological yield was positive correlate with spike length, plant height, number of spikelets per spike and days to maturity. Grain weight was positive correlate with plant height while, 1000 grain weight and days to maturity showed negative significant. In 1000 grain weight was negative correlate with spike length. Spike length was positive correlate with plant height, number of spikelets per spike and days to heading while, negative correlate with number of tiller per plant. Number of spikelets per spike positive significant correlate with plant height. Days to maturity and plant height was positive significant correlating with days to heading. These components of

character on which selection can be used for genetics improvement in yield. The breeder is always concerned for the selection of superior genotype on the basis of phenotypic expression. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficient which might be due to marking on modifying effect of environment at both genotypic and phenotypic levels, same things was observed by Chaitali and Bini (2007), Yousaf *et al.* (2008) and El-Mohsen *et al.* (2012)^[5]. Kumar *et al.* (2013)^[13, 14]. Path analysis for determination of relationship between yield and yield components in bread wheat Mohammadi M, Sharifi P and Karimizadeh R. (2014)

^[17]. As it is more precise and accurate to estimate path coefficient based on genotypic correlation in Table -5. Path biological yield per plant (0.795) had highest direct positive effect on grain yield followed by grain weight per spike (0.713), spike length (0.428), harvest index (0.423), days to maturity (0.427), 1000 grain weight (0.368), number of spikelets per spike (0.181), number of grain per spike (0.006) and number of tiller per plant (0.006). However, plant height (-0.064) and days to heading (-0.148) had direct negative effect on grain yield per plant. This type of relationship is due to manifold effect of different genes.

Table 2: Analysis of variance (ANOVA) for twelve characters in bread wheat

| Source of variance | DF | DH | PH | DM | NT/P | NS/S | SL | NG/S | OTGW | GWS | BY/P | GY/P | HI |
|--------------------|----|---------|---------|---------|--------|--------|--------|---------|---------|--------|----------|---------|---------|
| Replications | 2 | 0.67 | 7.52 | 0.39 | 1.34 | 0.78 | 0.06 | 1.00 | 0.73 | 0.02 | 5.71 | 5.88 | 2.15 |
| Treatments | 35 | 44.60** | 89.06** | 33.72** | 6.34** | 5.01** | 3.05** | 26.73** | 17.61** | 0.16** | 216.70** | 32.76** | 32.64** |
| Error | 70 | 2.76 | 5.90 | 0.69 | 0.93 | 0.41 | 0.06 | 1.54 | 6.05 | 0.03 | 3.79 | 2.14 | 1.37 |

**Significant at 1% level, Where, DF: Degree of freedom, DH: Days to Heading, DM: Days to maturity, NT/P: Number of tillers per plant, PH: Plant height (cm), SL: Spike length (cm), NS/S: Number of spelets per spike, NG/S: Number of grains per spike, GWS: Grain weight /spike (g), OTGW: One thousand grain weight (g), GY/P: Grain yield per plant (g), BY/P: Biological yield per plant(g), HI: Harvest index %.

Table 3: Grand mean, PCV, GCV, heritability (narrow sense), genetic advance & genetic advance % over mean in twelve characters of bread wheat

| Characters | Grand mean | Range | GCV | PCV | Narrow sense heritability [(h ²) %] | Genetic advance | Genetic advance over % mean |
|---------------------------|------------|---------------|-------|-------|-------------------------------------------------|-----------------|-----------------------------|
| Days to heading | 78.60 | 66.33-86.33 | 4.75 | 5.20 | 29.0 | 9.00 | 11.46 |
| Plant height (cm) | 89.18 | 78.20-98.20 | 5.90 | 6.50 | 54.6 | 12.62 | 14.15 |
| Days to maturity | 123.03 | 114.33-128.33 | 2.69 | 2.78 | 43.1 | 8.49 | 6.90 |
| No. of tillers/plant | 14.41 | 11.26-17.13 | 9.31 | 11.47 | 27.0 | 2.87 | 19.97 |
| No. of spikelets /spike | 18.73 | 16.40-23.36 | 6.60 | 7.45 | 36.7 | 2.89 | 15.45 |
| Spike length(cm) | 9.39 | 7.66-10.83 | 10.62 | 10.94 | 72.7 | 2.55 | 27.23 |
| No. of grains / spike | 50.26 | 46.00-57.03 | 5.76 | 6.27 | 8.8 | 7.02 | 13.98 |
| 1000 grain weight(g) | 50.55 | 45.90-56.56 | 3.88 | 6.22 | 27.7 | 3.22 | 6.38 |
| Grain weight/spike (g) | 2.05 | 1.50-2.38 | 10.25 | 13.54 | 26.3 | 0.42 | 20.51 |
| Biological yield/plant(g) | 59.68 | 43.60-78.40 | 14.11 | 14.48 | 59.1 | 21.66 | 3.30 |
| Grain yield / plant(g) | 23.29 | 16.86-30.29 | 13.71 | 15.08 | 49.3 | 7.66 | 32.90 |
| Harvest index (%) | 39.20 | 31.94-47.12 | 8.23 | 8.76 | 19.1 | 8.01 | 20.43 |

*Significant at 5% level; **Significant at 1% level

Table 4: Phenotypic & Genotypic correlation for twelve characters in a set of diallel crosses.

| Attributes | Days to Heading | Plant height (cm) | Days to maturity | No. of tillers /plant | No. of spelets /spike | Spike length (cm) | No. of grains /spike | 1000 grain weight (g) | Grain weight /spike (g) | Biological yield (g)/plant | Harvest index % | Grain yield/ plant (g) |
|-----------------------|-----------------|-------------------|------------------|-----------------------|-----------------------|-------------------|----------------------|-----------------------|-------------------------|----------------------------|------------------|------------------------|
| Days to 75% Heading | 1.000 | 0.289** (0.328) | 0.249** (0.273) | -0.069 (-0.124) | 0.187 (0.271) | 0.383** (0.425) | -0.028 (-0.049) | -0.030 (-0.002) | -0.015 (0.008) | 0.032 (-0.003) | 0.059 (0.069) | 0.078 (0.035) |
| Plant height (cm) | | 1.000 | -0.016 (-0.024) | 0.184 (-0.295) | 0.427** (0.539) | 0.653** (0.768) | 0.101 (0.088) | -0.120 (-0.196) | 0.249** (0.381) | 0.470** (0.533) | 0.009 (0.034) | 0.442** (0.538) |
| Days to maturity | | | 1.000 | -0.006 (-0.019) | -0.034 (-0.051) | 0.188 (0.204) | -0.158 (-0.185) | 0.090 (0.221) | -0.521** (-0.730) | 0.193* (0.201) | 0.015 (0.025) | 0.186 (0.193) |
| No. of tiller/plant | | | | 1.000 | 0.058 (0.042) | -0.276** (-0.339) | -0.114 (-0.148) | 0.115 (0.181) | -0.093 (-0.125) | 0.080 (0.080) | 0.017 (0.085) | 0.113 (0.094) |
| No. of spelets /spike | | | | | 1.000 | 0.531** (0.599) | 0.005 (0.017) | -0.162 (-0.265) | 0.131 (0.112) | 0.436** (0.507) | 0.091 (0.106) | 0.444** (0.551) |
| Spike length (cm) | | | | | | 1.000 | -0.104 (-0.118) | -0.241* (-0.388) | 0.076 (0.094) | 0.529** (0.560) | 0.025 (-0.029) | 0.490** (0.549) |
| No. of grains/spike | | | | | | | 1.000 | 0.046 (0.053) | 0.124 (0.227) | 0.111 (0.115) | -0.137 (-0.136) | 0.059 (0.064) |
| 1000 grain weight (g) | | | | | | | | 1.000 | -0.277** (-0.549) | -0.114 (-0.160) | 0.037 (0.011) | -0.100 (-0.175) |
| Grain weight/spike(g) | | | | | | | | | 1.000 | 0.073 (0.100) | 0.057 (0.010) | 0.071 (0.170) |
| Biological yield (g) | | | | | | | | | | 1.000 | -0.201* (-0.233) | 0.850** (0.888) |
| Harvest index % | | | | | | | | | | | 1.000 | 0.222** (0.236) |

Genotypic correlation is given under parenthesis. *Significant at 5% level, ** Significant at 1% level.

Table 5: Direct and indirect effects of twelve characters on grain yield of bread wheat as independent variable at genotype level.

| Attribute | Days to 75 % Heading | Plant height (cm) | Days to maturity | No. of tillers /plant | No. of spikelets /spike | Spike length (cm) | No. of grains/ spike | 1000 grain weight (g) | Grain weight / spike (g) | Biological yield (g)/plant | Harvest index % | Grain yield/plant (g) |
|------------------------|----------------------|-------------------|------------------|-----------------------|-------------------------|-------------------|----------------------|-----------------------|--------------------------|----------------------------|-----------------|-----------------------|
| Days to 75% Heading | -0.148 | -0.452 | -0.053 | 0.024 | -0.052 | -0.082 | 0.009 | 0.000 | -0.001 | 0.000 | -0.013 | 0.538** |
| Plant height (cm) | -0.194 | -0.064 | 0.011 | 0.133 | -0.244 | -0.347 | -0.039 | 0.089 | -0.172 | -0.241 | -0.015 | 0.035 |
| Days to maturity | 0.116 | -0.010 | 0.427 | -0.008 | -0.021 | 0.087 | -0.079 | 0.094 | -0.311 | 0.085 | 0.010 | 0.193 |
| No. of tillers /plant | -0.000 | -0.001 | -0.000 | 0.006 | 0.000 | -0.002 | -0.000 | 0.001 | -0.000 | 0.000 | 0.000 | 0.094 |
| No. of spikelets/spike | 0.049 | 0.097 | -0.009 | 0.007 | 0.181 | 0.108 | 0.003 | -0.048 | 0.020 | 0.091 | 0.019 | 0.551** |
| Spike length (cm) | 0.182 | 0.329 | 0.087 | -0.145 | 0.256 | 0.428 | -0.050 | -0.166 | 0.040 | 0.240 | -0.012 | 0.549** |
| No. of grains/ spike | -0.000 | 0.000 | -0.001 | -0.000 | 0.000 | -0.000 | 0.006 | 0.000 | 0.001 | 0.000 | -0.000 | 0.064 |
| 1000 grain weight (g) | -0.001 | -0.072 | 0.081 | 0.066 | -0.097 | -0.142 | 0.019 | 0.368 | -0.202 | -0.059 | 0.004 | -0.175 |
| Grain weight spike(g) | 0.005 | 0.272 | -0.520 | -0.089 | 0.080 | 0.067 | 0.162 | -0.391 | 0.713 | 0.071 | 0.007 | 0.170 |
| Biological yield (g) | -0.002 | 0.424 | 0.160 | 0.064 | 0.403 | 0.446 | 0.092 | -0.127 | 0.079 | 0.795 | -0.185 | 0.888** |
| Harvest index % | 0.029 | 0.014 | 0.010 | 0.036 | 0.045 | -0.012 | -0.057 | 0.004 | 0.004 | -0.098 | 0.423 | 0.236* |

*Significant at 5% level, ** Significant at 1% level

Conclusion

Correlation study revealed that plant height; number of spikelets per spike, spike length and biological yield per plant are major yield contributing traits in this investigation. High heritability and high or moderate genetic advance for a character spike length and grain yield per plant, respectively indicated that the characters will be responsible for selection and selection will be profitable. Studies revealed that the grain yield per plant with high heritability and high genetic advance followed by days to 75% heading, plant height, number of tillers per plant, number of spikelets per spike, spike length and harvest index were the major yield attributing traits coupled with moderate genetic advance, so due consideration should be given for these traits at the time of simple selection therefore, it is important to establish the genetic basis of correlation before initiating breeding programme aimed at yield improvement through component characters. Path coefficient analysis is however, more useful for partitioning of direct and indirect causes of correlation and also enables breeders to compare the component factors on the basis of their relative contributors. So these characters may be used as selection indices for yield improvement in wheat.

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Conflict of interest

Authors would hereby like to declare that there is no conflict of interests that could possibly arise.

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