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RESEARCH ARTICLE

CORRELATION, PATH CO-EFFICIENT ANALYSIS AND HERITABILITY ESTIMATES OF SOME METRICAL TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

The present research was conducted to estimate the association of yield contributing characters with grain yield and the estimation of heritability percentage in broad sense. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications at Latif Experimental Farm Sindh Agriculture University Tando Jam in Rabi season 2013-2014. Three wheat genotypes, i.e. TD-1, Kiran-95 and Sarsabz, were evaluated for seven quantitative traits viz. plant height, number of tillers per plant, spike length, number of spikelets spike⁻¹, number of grains spike⁻¹, seed index and grain yield plant⁻¹. All the traits differed significantly at $P \leq 0.01$ level. The variety Kiran-95 showed superiority in plant height (90.35cm), number of tillers (7.37), spikelets spike⁻¹(15.135), grains spike⁻¹(52.90) and grain yield plant⁻¹(22.23g). The results indicated that there was a positive and significant correlation between plant height and spike length, spikelets spike⁻¹ and grain yield plant⁻¹. There was a strong positive association between spikelets spike⁻¹ and grain yield plant⁻¹. Path analysis indicated that the direct effect of spike length, spikelets spike⁻¹, grains spike⁻¹, and seed index on grain yield was 0.470, 0.992, -0.677 and -0.026 which makes 111.81, 141.38, -140.3, and -8.36 % respectively of the total phenotypic correlation. Plant height and number of grains spike⁻¹ exhibited maximum genetic variances which was associated with highest heritability estimates in broad sense and genetic advance among the traits under the study.

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is the leading cereal providing 20 percent of the total energy requirement in human food (Shewry, 2009). It is used to make flour for leavened, flat and steamed breads and most of the baked foods and also for fermentation to make beer and alcohol (Tsenov et al., 2008). It belongs to the family poaceae, originally from the Levant region of the Near East and Ethiopian Highlands, but now cultivated worldwide (Belderok, 2000). Major cultivated species of wheat are; *Triticum aestivum*, which is a hexaploid species and is widely cultivated in the world. *Triticum durum*, the only tetraploid form of wheat widely used today, and the second most widely cultivated wheat is *Triticum monococcum*, a diploid species with wild and cultivated variants; *Triticum dicoccum*, a tetraploid species, cultivated in ancient times but no longer has widespread use and *Triticum spelta*, another hexaploid species is cultivated in limited quantities (Moon, 2008).

Wheat is most important food crop of Pakistan and its products are used in a number of ways. Being the staple diet most of the people, it dominates all crops in acreage and production. Wheat accounts for 9.9 percent of the value added in agriculture and 2.0 percent of GDP of Pakistan. During 2015-16, area under wheat cultivation has increased to 9260 thousand hectares from last year's area of 9204 thousand shows an increase of 0.6 percent. While production of wheat stood at 25.482 million tonnes during 2015-16, showing an increase of 1.6 percent over the last year's production of 25.086 million tonnes. The production increased as crop was sown at appropriate time and available moisture particularly in Barany Track supported germination/growth and availability and use of inputs remained adequate (GOP, 2016). Vavilov (1951) emphasized that correlation studies is an important phase of breeding which was started in the last decades of 19th century and the beginning of 20th century in order to simplify breeders work and easy handling of material. Such investigations have to be carried out in various types of crop plants. Vavilov

pleaded pleiotropic gene effects being major causes of genetic correlation as a number of characters are conditioned by the effect of single gene. It is well known fact that quantitative characters, depending on the nature of gene action, are differently influenced by environmental variation. Moreover, the extents of heritability of quantitative traits are negatively correlated with environment. Heritability of traits indicated greater influence of environmental factors over genetic makeup of traits (Ansari and Ansari 1996). High heritability values become a measure of the genetic relationship between parents and progeny. The heritability of a character depicts the degree to which it is transmitted from era to era. Information on heritability parameters, and the evaluation of the relationship between important quantitative traits, is very useful in determining effective wheat breeding program (Rajper *et al.*, 1996). The association between any two variables is known as simple correlation; it can be estimated from both unreplicated as well as replicated data. Simple correlation is of three types: (1) Phenotypic, (2) Genotypic and (3) Environmental. Phenotypic correlation is the observable correlation between two variables; it includes both genotypic and environmental effects. Genotypic correlation, on the other hand, is the inherent association between two variables; it may be either due to pleiotropic action of genes, linkages or more likely both. Similarly, environmental correlation is entirely due to environmental effects (Singh, 1993). Genotypic and phenotypic correlations are important breeding parameters used for determining the degree of association of various yield contributing parameters with grain yield (Ali *et al.* 2009). Significant and positive phenotypic correlation of plant height with spike length and negative correlation of plant height with grain yield has been reported by Akhtar and Chowdhary (2006); while at both phenotypic and genotypic levels, number of spikelets spike⁻¹ had significant positive correlation with grain yield (Aycecik and Yildirim, 2006). The correlation studies (Lad *et al.*, 2003) suggested that number of grains spike⁻¹ is the major trait that has significant contribution to yield. Since the correlation coefficients generally show relationships among independent variables and the degree of linear relations among the variables, they could not sufficiently describe the relationship when a clear cause-result relationship was found between the variables (Dokuyucu *et al.* 2002). Therefore, the correlations between yield and yield components should be known in breeding programs (Turk and Celik, 2006). For this aim, the correlation coefficient is used to determine the extent of relationship between yield contributing traits and grain yield ha⁻¹ (Kara and Akman, 2007). The present research was conducted to estimate association of yield contributing characters with grain yield and the estimation of heritability percentage in broad sense.

MATERIALS AND METHODS

A study was conducted during rabi season 2013-14 at Latif Experimental Farm, Sindh Agriculture University Tandojam, to work out correlation, and path co-efficient analysis of some metrical traits in bread wheat (*Triticum aestivum L.*). The correlation and path coefficients were calculated according to Dewey and Lu (1959), while heritability estimates was determined as adopted by Breese (1972). The experimental material was sown in randomized complete block design with three replications. The trial consisted of four rows of 320 cm length and 120 cm width for each genotype per replication. The sowing was done by dibbling, keeping 20 centimeters

space between plants and 30 cm between rows. Ten plants were randomly selected and tagged from each replication. After collecting necessary data under field conditions further observations were recorded at field and laboratory. The experimental material consisted of 3 parents which included (V1= TD-1, V2= Kiran-95 V3 = Sarsabz). All the recommended cultural practices were carried out at appropriate time. The data were recorded in the following manner.

Plant height (cm): At the season of development the tallness of each chose plant was measured in centimeters from the surface of soil to the tip of ear-head barring awns.

Number of tillers plant⁻¹: The tillers number produced by each chose plant were numbered at the season of development and replication insightful the information was recorded.

Spike length (cm): Length of the spike of fundamental tiller was measured in centimeters from the base of spike to the upper most spikelets barring awns.

Number of spikelets spike⁻¹

The quantity of spikelets in the essential tiller of each chose plant were checked and the information were recorded as spikelet spike⁻¹.

Number of grains spike⁻¹ The principle spike of essential tiller of each chose plant was sifted independently, number of grains was checked and replication savvy information were recorded.

Seed index (1000) grain weight (g): 100 grains were haphazardly taken from each chosen plant and were said something grams on electric equalization in laboratory.

Grain yield plant⁻¹ (g): Subsequent to reaping, each chose plant was shifted independently with single plant wheat thresher and cleaned in the research center. The grains were weighed on electric adjust and yield plant⁻¹ was recorded in grams. The gathered information were broke down through New Student Statistics Software SXW Package. The correlations were worked out between 21 characters of economical importance. Simple correlations (r) were calculated according to Snedecor and Cochran (1980) by using the following formula.

$$\text{Correlation Coefficient (r)} = \frac{\text{Covariance}}{\text{Geometric mean of covariances}}$$

$$\Sigma xy = \frac{\Sigma xy}{N}$$

$$\Sigma x^2 = \frac{\Sigma X^2 - (\Sigma X)^2}{N}$$

$$\Sigma y^2 = \frac{\Sigma Y^2 - (\Sigma Y)^2}{N}$$

Where as,

X = Independent variable

Y = Dependent variable

N = Number of observations recorded

Regression coefficient byx

$$by_x = \frac{\Sigma xy}{\Sigma x^2}$$

The heritability was calculated for variance components followed by Breese (1972) as under.

$$H^2 = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e_{lr}} \quad \text{Or} \quad \frac{\sigma^2 g}{\sigma^2 p}$$

$$\text{Coefficient of } H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

$$\text{Selection index} = K \sigma^2 p h$$

K = constant 2.06

HW = Heritability

$$\text{Genetic Advance (GA)} = K \times H^2 \times \sqrt{\sigma^2 p}$$

Where;

K = Constant for selection intensity at 10%

$\sqrt{\sigma^2 p}$ = Square root of phenotypic variance

The path coefficients were calculated through the solution of the following equations:

1. $P_{1y} = r_{11} P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + r_{14} P_{4y}$
2. $P_{2y} = r_{21} P_{1y} + r_{22} P_{2y} + r_{23} P_{3y} + r_{24} P_{4y}$
3. $P_{3y} = r_{31} P_{1y} + r_{32} P_{2y} + r_{33} P_{3y} + r_{34} P_{4y}$
4. $P_{4y} = r_{41} P_{1y} + r_{42} P_{2y} + r_{43} P_{3y} + r_{44} P_{4y}$
5. $P_{xy} =$
6. $1 - \frac{(P_{1y}^2 + P_{2y}^2 + P_{3y}^2 + P_{4y}^2 + 2P_{1y} P_{2y} r_{21} + 2P_{1y} P_{3y} r_{31} + 2P_{1y} P_{4y} r_{41} + 2P_{2y} P_{3y} r_{32} + 2P_{2y} P_{4y} r_{42} + 2P_{3y} P_{4y} r_{43})}{P_{xy}}$

Where $p_{ly} = b_i s_i$

and $b_4 = b_{4y}$

$$b_3 = B_{3y} - b_{34} b_4$$

$$b_2 = b_{2y} b_{23} b_3 - b_{24} b_4$$

$$b_1 = b_{1y} - b_{12} b_2 - b_{13} b_3 - b_{14} b_4$$

RESULTS

The experimental material consisted of three parents of bread wheat (*Triticum aestivum* L.) to determine some genetic parameters, such as correlation between yield and yield related components and heritability percentage in broad sense (h^2 % b.s). Genetic variance, selection index and genetic advance (GA) at 5% selection intensity for number of tiller plant⁻¹, plant height, spike length, number of spikelets spike⁻¹, number of grains spike⁻¹, seed index and grain yield plant⁻¹. The results are described as follows. The mean squares for all the growth and yield contributing traits are presented in Table-1, while the mean values corresponding to all the growth and yield contributing traits are given in Table-2. The results for correlation coefficients among traits of economic importance are shown in Table-3. The results for heritability estimates are shown in Table 5, while the Table-4 indicates the direct effects and alternate effects of various important traits on grain yield along with the total effect by regression analysis. It may be observed from the results presented in Table-1, that all the characters i.e, plant height, spike length, spikelets spike⁻¹, grains spike⁻¹, seed index and yield plant⁻¹ differed significantly ($p < 0.05$) among the varieties, whereas differences for number of tillers were non- significant.

Mean performance: The results of mean performance for different agronomic traits of wheat are presented in Table 2. It

reveals that variety Kiran-95 displayed maximum plant height (90.345 cm) among all the genotypes, followed by Sarsabz (78.93 cm), whereas minimum plant height was found in TD-1 variety (61.50 cm). Maximum tillers plant⁻¹ were also produced by Kiran-95 (7.366) followed by Sarsabz (7.133) again. The spike length was maximum for the variety TD-1 (12.47) followed by Kiran-95 (12.01), whereas Sarsabz produced minimum spike length (9.64). Maximum spikelets spike⁻¹ were produced by both Kiran-95 (15.13) and TD-1 (15.00). Kiran-95 revealed more grains spike⁻¹ (52.90) among all the genotypes followed by TD-1 (44.93). TD-1 again showed maximum seed index of (4.306 g) followed by Kiran-95 (3.934 g). Highest grain yield plant⁻¹ was produced by Kiran-95 (22.23 g) followed by TD-1 (20.79 g) respectively.

Correlation and regression analysis

Plant height V/S No. of tillers plant⁻¹: Plant height showed negative correlation with number of tillers but was non-significant ($r = -0.2655^{NS}$). This relationship reveals that if plant height increases, the number of tillers reduce to a negligible level.

Plant height V/S spike length: Association between plant height and spike length revealed negative and highly significant correlation ($r = -0.9192^{**}$), referring as plant height increases the spike length will also increase simultaneously at maximum level.

Plant height v/s spikelets spike⁻¹: The phenotypic correlation between plant height and spikelets Spike⁻¹ showed positive and significant relationship ($r = 0.7793^*$). This shows that the character spikelets spike⁻¹ is dependent on plant height, as the plant height increases spikelets spike⁻¹ also increases.

Plant height v/s Grain spike⁻¹: Interrelationship between these two traits showed positive and highly significant correlation ($r = 0.8064^{**}$), revealing that the grains spike⁻¹ is dependent on the character plant height.

Plant height V/S Seed index: Plant height and seed index interrelationship revealed positive and significant correlation ($r = 0.7117^*$), which influenced that seed index is dependent on the character plant height.

Plant height v/s yield plant⁻¹: Correlation between plant height and yield plant⁻¹ was positive and highly significant ($r = 0.7028^{**}$). This emphasized that as plant height increases yield also increases.

Number of tillers plant⁻¹ v/s spike length: Interrelation between number of tillers plant⁻¹ with spike length showed negative and significant correlation ($r = -0.6366^*$). It means, as the tillers increase, the spike length will reduce simultaneously.

Number of tillers v/s spikelets spike⁻¹: The data depicted in Table-3 reveals that correlation for number of tillers plant⁻¹ with spikelets spike⁻¹ was negative but non-significant ($r = -0.0727^{NS}$). This shows that both the characters are independent.

Number of tillers plant⁻¹ v/s grains spike⁻¹: The association of these two traits showed negative and non-significant correlation ($r = -0.4111^{NS}$). As the tillers increases, the grains spike⁻¹ will reduce in number but not to the significant level.

Table 1. Mean squares (ANOVA) for grain yield and its components of bread wheat

S.O.V	D.F	Plant height (cm)	Number of tillers plant ⁻¹	Spike length (cm)	Spikelets spike ⁻¹	No. of grains/spike ⁻¹	Seed index (g)	Grain Yield (g)
Replication	2	1.573	0.47544	0.3874	2.99778	17.7743	0.01723	3.1934
Genotypes	2	578.063*	0.65455 ns	5.92977*	2.38122*	63.8412*	0.20342*	10.9961*
Error	4	8.43	0.20789	0.27361	0.33288	4.0743	0.03002	1.3165

*Significant at P ≤ 0.05 level n.s Non significant

Table-2 Mean performance of grain yield and its components of bread wheat

Varieties	Plant height(cm)	Tillers plant ⁻¹	Spike length	Spikelets Spike ⁻¹	Grains spike ⁻¹	Seed index	Grain yield plant ⁻¹
TD-1	61.550c	6.5343	12.428a	15.012a	44.943a	4.3077a	20.778ab
Kiran-95	90.345a	7.3767	12.028a	15.135a	52.905b	3.9357ab	22.243a
Sarsabz	78.944b	7.1345	9.654b	13.605b	40.604a	3.7677b	18.437b

Table-3. Correlation between various traits in bread wheat genotypes

Character studied	Plant height (cm)	No. of tiller plant-1	Spike Length (cm)	Number of spikelets per pike	Number of grain spike ⁻¹	Seed index (gm)	Grain yield per plant
Plant height	-	-	-	-	-	-	-
No. of tiller plant-1	-0.2655 NS	-	-	-	-	-	-
Spike length	-0.9192**	-0.6366*	--	-	-	-	-
Number of spikelets spike-1	0.7793*	-0.0727 NS	0.6485*	-	-	-	-
Number of grains spike ⁻¹	0.8064**	-0.4111NS	0.8523**	0.7781**	-	-	-
Seed index	0.7117*	-0.2516 NS	0.7303*	0.1872 NS	0.6011*	-	-
Grain yield pant ⁻¹	0.7028**	0.4312*	0.4221*	0.7191**	0.48309*	0.3308 NS	-

*Significant at 0.01 level **Significant at 0.05 level N.S, Non-significant

Table 4. Direct and alternate pathways influence of spike length, spikelets/spike, grains/spike, and seed index on grain yield/plant in wheat

Characters	Direct effect	%	Alternate effect	%	R
Spike length (p1y)	0.47082	111.80	-	-	-
Alternate path ways (a) spikelets/spike (p2y) (r12)	-	-	0.64455	129.31	-
(b) grains /spike (p3y) (r13)	-	-	-0.67758	-137.16	-
(c) seed index (p4y) (r14)	-	-	-0.01669	-3.95	-
Total effect	-	-	-	-	0.422
Spikelets /spike (p2y)	0.99298	141.37	-	-	-
(a) via spike length (p1y) (r12)	-	-	0.25819	36.75	-
(b) via grains /spike (p3y) (r23)	-	-	-0.62717	-75.05	-
(c) via seed index (p4y) (r24)	-	-	-0.02164	-3.08	-
Total effect	-	-	-	-	0.7191
Grains /spike (p3y)	-0.77762	-140.2	-	-	-
(a) via spike length (p1y) (r13)	-	-	0.40131	83.11	-
(b) via spikelets /spike (p2y) (r23)	-	-	0.77254	159.8	-
(c) via seed index (p4y) (r34)	-	-	-0.01325	-2.75	-
Total effect	-	-	-	-	0.48309
Seed index (p4y)	-0.02647	-8.35	-	-	-
(a) via spike length (p1y) (r14)	-	-	0.39668	125.32	-
(b) via spikelets /spike (p2y) (r24)	-	-	0.28577	90.28	-
(c) via grains /spike (p3y) (r34)	-	-	-0.33947	-107.25	-
Total effect	-	-	-	-	0.3308
Residual effect	-	-	-	-	0.81735

Table-5. Phenotypic and genotypic variance, heritability %, Genetic advance for yield and yield components of bread wheat.

Character studied	Phenotypic variance (Vp)	Genetic variance (Vg)	Heritability (hw)	Genetic Advance
Plant height	192.68	189.86	0.97	35.36
Tillers per plant	0.174	0.114	0.76	0.79
Spike length	1.5	1.87	0.94	3.44
No. of spikelets spike-1	0.78	0.79	0.85	1.97
No. of grains spike ⁻¹	21.28	19.91	0.92	11.2
Seed index	0.7	0.6	0.84	0.62
Grain yield	3.64	3.21	0.87	4.34

Number of tillers v/s seed index: Number of tillers plant⁻¹ had negative but non-significant correlation with seed index ($r = -0.2516^{NS}$), showing that as tillers increased, seed index reduced ultimately to some extent.

Number of tillers plant⁻¹v/s yield plant⁻¹: Number of tillers showed positive and significant correlation with yield plant⁻¹ ($r = 0.4312^*$). This shows that any increase in number of tillers will result in proportionate increase in yield plant⁻¹.

Spike length v/s spikelets spike-1: Association between spike length and spikelets spike-1 is given in Table-3.

The association revealed positive and significant correlation between both characters ($r = 0.6485^*$). It shows that with every unit increase in spike length, yield will also increase proportionately.

Spike length V/S grains spike⁻¹: These two traits were positive and highly significantly correlated to each other ($r = 0.8523^{**}$), showing that as spike length increases, the grains spike⁻¹ will increase ultimately.

Spike length v/s seed index: Correlation between spike length and seed index (Table-3) was positive and significant. (r

=0.7303*). This association reveals that as spike length increases, seed index will also increase simultaneously.

Spike length V/S grain yield plant⁻¹: The Table-3 indicates that Spike length was positively but significantly correlated with yield plant⁻¹ ($r = 0.4221^*$). It indicates that spike length increases, the grain yield plant⁻¹ also increases significantly.

Spikelets spike⁻¹ v/s grains spike⁻¹: The spikelets spike⁻¹ and grain spike⁻¹ revealed positive and highly significant correlation with each other ($r=0.7781^{**}$), emphasizing that as the spikelets spike⁻¹ are increased, the grains spike⁻¹ will increase also.

Spikelets spike⁻¹ v/s seed index: Spikelets spike⁻¹ showed positive and non-significant correlation with seed index ($r = 0.1872^{NS}$) showing that as spikelets spike⁻¹ would increase the seed index will also increase but negligibly.

Spikelets spike⁻¹ v/s grain yield plant⁻¹: Association between spikelets spike⁻¹ with yield plant⁻¹ was positive and revealed highly significant correlation with each other ($r = 0.7191^{**}$) indicating that grain yield plant⁻¹ is also dependant on spikelets spike⁻¹.

Grain spike⁻¹ v/s seed index: Grain spike⁻¹ had positive and significant correlation with seed index ($r=-0.6011^*$). This association shows that as grains spike⁻¹ increases, the seed index will also increase considerably.

Grain spike⁻¹ v/s grain yield plant⁻¹: Interrelationship between grain spike⁻¹ and yield plant⁻¹ had positive and significant correlation ($r = 0.48309^*$) It states that grain spike⁻¹ increases, the grain yield plant⁻¹ also increase at large scale

Seed index v/s grain yield plant⁻¹: The data revealed that seed index relationship with yield was positive and non-significantly correlated with each other ($r = 0.3308^{NS}$).

Path coefficient: Further information on the interrelationship among the grain yield and yield components are obtained by path coefficient analysis of phenotypic correlation coefficient. This was accomplished by assessing the direct and indirect effects of the yield components as their contribution to the total grain yield. Grain yield plant⁻¹ was considered as the resultant variable whereas, spike length, number of spikelets spike⁻¹, number of grains spike⁻¹ and seed index the causal variables. The residual 'X' was assumed to be independent of other variables and infers the failure of these four yield components to account for grain yield. Each yield component had a direct effect acting alone and an influence of acting in combination with the other variables with which it was correlated. The amount of variation in the dependent variable (grain yield plant⁻¹) which is accounted for by path coefficient analysis can be determined as $1-R^2$, where 'R' is path coefficient of the residual. The results of path coefficient analysis are given in Table-5. Where 'P' represents the direct effect (path coefficient), 'R' as residual effect and 'r' denotes the phenotypic correlation between the characters involved in the analysis.

Spike length: The direct effect of spike length on seed yield plant⁻¹ was 0.47 formed about 111.80% of the total phenotypic correlation in positive direction. The alternate effect via spikelets spike⁻¹ 0.64 gave positive direction which makes

129.31%, those through grains spike⁻¹ and seed index showed negative effects -0.67 and -0.01 which made -137.16% and -3.95% contribution towards seed yield per plant. The phenotypic interrelationship between spike length and number of grains spike⁻¹ has been estimated as 0.422.

Spikelets spike⁻¹: The direct effect of spikelets spike⁻¹ towards seed yield plant⁻¹ has been estimated as 0.99, which shows 141.37% through contribution of spikelets spike⁻¹ to seed yield plant⁻¹ in positive direction. The alternate effect through spike length was in positive direction 0.25 which is 36.75%, through grains spike⁻¹ -0.62 was in negative direction forming -75.05% and through seed index it was -0.02 in negative direction with -3.08% contribution towards the seed yield per plant. The phenotypic interrelationship between spikelets spike⁻¹ and grain yield plant⁻¹ was estimated as 0.71.

Number of Grains spike⁻¹: The direct effect of number of grains spike⁻¹ on seed yield plant⁻¹ was -0.77 in negative direction which formed about -140.2% of phenotypic correlation. Its alternate effect through spike length was 0.40 in positive direction which formed 83.11% of seed yield. Its alternate effect through spikelets spike⁻¹ was 0.77 in positive direction which formed 159.8%, and through seed index was -0.01 in negative direction with -2.75% effect on the seed yield per plant. The phenotypic interrelationship between number of grains spike⁻¹ and grain yield plant⁻¹ was estimated as 0.48.

Seed index: It was assessed that the direct effect of seed index on grain yield plant⁻¹ -0.02 was in negative direction -8.35%. Its alternate effect via spike length was in positive direction 0.39 and formed of 125.32%, through spikelets spike⁻¹ 0.28 was in positive direction and formed 90.28% and through grains spike⁻¹ -0.33 it was in negative direction and formed -107.25%. The phenotypic interrelationship between seed index and grain yield plant⁻¹ was estimated as 0.33. The residual effect (Pxy) was estimated as 0.81 in present studies and suggested that the path coefficient obtained within the control of the construct did not reflect the influence of the second order components.

Heritability: The heritability (H^2 b.s) estimates in broad sense, genetic variance (δ^2_g), phenotypic variance (δ^2_{ph}), selection index and genetic advance (GA) from variance components for various traits studied are depicted in Table-5 and explained here under;

Plant height: Plant height manifested lower genetic variance ($\delta^2_g = 189.86$) than its phenotypic variance ($\delta^2_P = 192.68$) and high heritability estimates ($h^2 = 98.54\%$), which was associated with high genetic advance (GA=35.36), which indicated that plant height is more influenced by genetic factors.

Tillers plant⁻¹: Tillers plant⁻¹ were little affected by environment because genetic variance ($\delta^2_g = 0.114$) and phenotypic variance ($\delta^2_P = 0.174$) showed high heritability estimates ($h^2 = 65.71\%$) but showed low GA = (0.79 for tillers per plant).

Spike length: For spike length genotypic variance was very close to ($\delta^2_g = 1.87$) phenotypic variance ($\delta^2_P = 1.97$) and manifested highest heritability ($h^2 = 95.91$), whereas it revealed low genetic advance (GA=3.44).

Spikelets spike⁻¹: However, number of spikelets spike⁻¹ also showed close genetic variance ($\delta^2_g = 0.79$) and phenotypic

variance ($\delta^2_p = 0.78$) resultant high heritability ($h^2 = 86.07\%$) and a fair amount of genetic advance ($GA = 1.97$).

Number of grain spike⁻¹: For number of grains spike⁻¹ genetic variance ($\delta^2_g = 19.91$) was lower than its phenotypic variance ($\delta^2_p = 21.28$). High heritability estimates ($h^2 = 93.64\%$) and lower genetic advance ($GA = 11.20$) demonstrated that number of grains spike⁻¹ is significantly affected by environmental factors.

Seed Index: Genetic variance ($\delta^2_g = 0.05$) was smaller than its phenotypic variance ($\delta^2_p = 0.06$) and high heritability estimates ($h^2 = 84.33\%$), with low genetic advance ($GA = 0.62$) was shown for this trait.

Grain yield: Grain yield had more genetic variance as compared to environmental factors. Although genetic variance ($\delta^2_g = 3.21$) was equal to its phenotypic variance ($\delta^2_p = 3.64$) with very little difference between them. Highest heritability estimates ($h^2 = 88.21\%$), and fair amount of genetic advance ($GA = 4.34$) were obtained for grain yield per plant.

DISCUSSION

Genetic variability and heritability estimates are considered as very important parameters for the improvement of any quantitative trait. The mean performance, genetic and phenotypic variances, correlation coefficients, and heritability estimates were worked out for three varieties of bread wheat.

The results shown in Table-1 indicated significant differences in the mean squares from analysis of variance at $P \leq 0.01$ level for seven quantitative traits viz, plant height, number of tillers per plant, spike length, number of spikelets spike, number of grains spike⁻¹, seed index and grain yield per plant. The mean performance shown in Table-2 reveals that maximum plant height was produced by Kiran-95 (90.30 cm), whereas minimum plant height was produced by TD-1 (61.50 cm). Maximum tillers plant⁻¹ was produced by Kiran-95 (7.36 cm), followed by Sarsabz (7.13). TD-1 and Kiran-95 revealed maximum spike length of (12.41) and (12.01 cm) respectively, and produced more spikelets spike⁻¹ of (15.00) and (15.13) respectively. Again TD-1 and Kiran-95 gained more grains spike⁻¹ (44.93) and (52.90), seed index (4.30) and (3.93) and more grain yield plant⁻¹ (20.79g) and (22.23g). Correlation coefficients between yield and other traits are shown in Table-3. Plant height had negative and non significant association with number of fertile tillers plant⁻¹ ($r = -0.2655$ NS) revealing that plant height had no influence on number of fertile tillers per plant. Spike length had negative but significant correlation with number of fertile tillers plant⁻¹ and negative and highly significant interrelationship with plant height ($r = -0.6366^*$ and $r = -0.9192^{**}$), respectively. These results showed that as spike length increases significantly, the number of fertile tillers plant⁻¹ decreases, and spike length increases significantly as plant height increase and vice versa. Our results are in conformity with Safeer-ul-Hussain et al. (2004), Gul et al. (2004) and Chandra et al. (2004), who reported similar findings in bread wheat (*Triticum aestivum L.*) for above traits. Number of spikelets spike⁻¹ had got negative and non-significant association with number of fertile tiller plant⁻¹ ($r = -0.727$ NS), positive but non-significant correlation with plant height (0.7793*NS) and positive but still non-significant association with spike length ($r = 0.6485^*$ NS). These results suggested that number of spikelets spike⁻¹ were not correlated with number of tillers per plant, plant height and spike length, these traits were

more influenced by the environmental factors. Number of grains spike⁻¹ were positive but had non significant correlation with number of fertile tillers plant⁻¹ plant height, spike length and number of spikelets spike⁻¹ ($r = -0.4111$ NS, 0.08064 NS, 0.8523** NS and 0.7781** NS respectively). These results showed that when number of grains spike⁻¹ increase, it would not significantly increase the number of tillers plant⁻¹, plant height, spike length and number of spikelets spike⁻¹. Seed index had positive but significant correlation with plant height, spike length Number of spikelets spike and grains spike ($r = -0.7117^*$, 0.7303*, 0.1872 and 0.6011ns) respectively, and negative association with number of tillers plant⁻¹ (-0.2516 NS) These results suggested that with increase in seed index, plant height increases, significantly and in the same way it will result in significant increase in spike length, number of grains spike⁻¹ respectively. Similar findings were reported by Biju and Malik (2006), Singh et al. (2005), Safeer-ul-Hassan et al. (2004), Singh and Singh (2001) and Mishra et al. (2001). They reported that seed index had the highest positive correlation with grain yield ($r = 0.9271$). Grain yield plant⁻¹ had the positive significant correlation with number of fertile tillers plant⁻¹ ($r = 0.4312^*$) and positive and significant association with spike length, number of grains/spike and seed index ($r = 0.4221^*$, 0.48309 NS 0.3308 NS respectively). These results suggested that grain yield has positive and significant correlation with number of fertile tillers per plant, spike length, number of grains spike and seed index which are major yield contributing traits. Moreover, any increase in these traits significantly increases the grain yield per plant. Our findings are in conformity with Fida et al. (2006), Kumar et al. (2005), Kumar et al. (2002), Mishra (1999) and Sinha et al. (1999) who reported that grain yield plant⁻¹ was significantly and positively correlated with number of tillers plant⁻¹ and seed index. In the view of above results, it can be suggested that number of tiller plant⁻¹, plant height, spike length and seed index are major contributors for increasing the grain yield plant⁻¹ and selection could be more effective for these traits.

Path co-efficient: The path co-efficient analysis in the present study indicated that the direct effect of spike length was in positive direction (0.47) and formed 111.80 percent of phenotypic correlation among all genotypes. The indirect effect through spikelets spike⁻¹ was positive whereas that of grains spike⁻¹ and seed index was recorded negative. This shows that spike length had maximum direct effect on increasing grain yield. The total correlation co-efficient in genotypes was mainly due to direct effect of spike length and indirect effect through spikelets spike⁻¹. These traits were considered as reliable variables for further genetic improvement in wheat. Bergale et al. (2002) studied the characteristics of 50 bread wheat genotypes using variability, correlation and path analysis. The number of spikes plant⁻¹, grains spike⁻¹, and plant height showed a significant positive correlation with grain yield, whereas, spikes plant⁻¹ and grain spikes⁻¹ showed high positive direct effect on grain yield. The results further revealed that direct effect of spikelets spike⁻¹ was positive (0.990 and formed 141.37 percent of total phenotypic correlation on genotypes. Its indirect effect through spike length was also in positive direction, but its indirect effect via grains spike⁻¹ and seed index was negative. Therefore, spikelets spike⁻¹ can be used as a reliable character in selection of high yielding wheat cultivars. These results are further supported by Gul et al. (2004) who recorded data on spikes, 1000 grain weight, grains spike⁻¹ and grain yield. The genotypes were huge for spikes plant⁻¹, and grains spike⁻¹ and Safeer-ul-Hassan et al. (2004)

recorded and dissected information on days to heading, days to maturity, plant stature, spike length, number of spikelets spike⁻¹, number of grains spike⁻¹, grain weight spike⁻¹, 1000-grain weight and yield plant⁻¹. Their ascertained connection coefficients showed that number of spikelets spike⁻¹, days to development and plant stature were essentially and absolutely related with grain yield per plot, while a small relationship was seen between grain yield plot⁻¹ and number of grains plot⁻¹, days to heading, grain weight spike⁻¹, 1000-grain weight and spike length. The impact of spikelets spike⁻¹ with other yield donors, for example, plant tallness, grains spike⁻¹ and organic yield plant⁻¹ was additionally recorded positive in all genotypes. This demonstrates spikelets spike⁻¹ had direct impact on expanding grain yield. The aggregate connection coefficient in genotypes was predominantly because of aberrant impact of plant stature, number of grains spike⁻¹ and natural yield plant⁻¹. The aberrant impact of spikelets spike⁻¹ with plant tallness 13.09 percent was in positive heading furthermore had positive circuitous impact with grains spike⁻¹ 40.05 percent with natural yield plant⁻¹ 4.23 percent reported in all genotypes. It was further observed that direct effect of grains spike⁻¹ was negative -0.77 and formed -140.2 percent of total phenotypic correlation among the varieties. Whereas, indirect effect through spike length and spikelets spike⁻¹ was also recorded positive but through seed index it was negative. This shows that grains spike⁻¹ had no direct effect on increasing grain yield. The total correlation coefficient in genotypes was mainly due to indirect effect of spike length and spikelets spike⁻¹. These results are further supported by Soomro *et al.* (2001), who studied phenotypic correlations between number of spikes per plant, number of spikelets spike⁻¹, harvest index and yield per plant. Correlation coefficients were significant either at 0.01 or 0.05 level of probability in all character combinations. Further partitioning of correlation coefficients into direct and indirect pathway influences on yield showed major direct effect of number of grains spike⁻¹ followed by number of spikelets spike⁻¹. The direct effect of seed index on grain yield plant⁻¹ was negative and negligible, which formed only 8.36% total correlation. However its indirect effect via spike length and spikelets spike⁻¹ was positive and formed 125.32% and 90.28% of total correlation, respectively. That it had significant negative effect via grains spike⁻¹ which formed 107.26% of total correlation in negative direction. This study shows that spike length and spikelets spike⁻¹ were the major contributors towards grain yield and should be given due preference; this reflects for higher grain yield in these genotypes.

Heritability: The genetic variability that is transferable to the progeny referred to as heritability is also of great importance in improving any quantitative trait. It is again divided into two types, viz heritability in broad sense and heritability in narrow sense. The results regarding heritability estimates in broad sense (h^2) for various quantitative traits studied are presented in Table-4. Plant height influenced directly on grain yield because dwarf wheat varieties were more lodging resistant as compared to tall varieties and tall varieties took more time in vegetative growth which affected the reproductive phase resulting in low grain yield. The predicted genetic variance ($\delta^2g=189.86$) was lower than phenotypic variance ($\delta^2p=192.68$), which was associated with high heritability estimates ($h^2=98.54\%$) and high genetic advance (GA=35.36). These results suggested that genetic variance was maximum than environmental variance. Furthermore, it suggested that improvement with more efforts is also possible in plant height. Similar results are also reported by Fida Mohammed *et al.* (2006) and Jedy and Ski (2001).

Number of fertile tillers plant⁻¹ is a yield contributing trait in wheat, because more the tillering to set more number of spikes and more yield per plant. The genetic variance was ($\delta^2g=0.114$) was very close to phenotypic variance ($\delta^2p=0.174$) and demonstrated highest heritability estimates ($h^2=65.71\%$) which were associated with a low amount of genetic advance (GA = 0.79). Although the number of tillers plant⁻¹ is controlled by genetic variance yet a significant improvement is possible for improving the number of tillers plant⁻¹ in wheat. Similar results were obtained by Kumar *et al.* (2002), Chandra *et al.* (2004) and Safeer-ul-Hassan *et al.* (2004). They reported high heritability estimates for number of tillers plant⁻¹. Spike length had positive strong correlation with grain yield. It depends upon number of spikelets spike⁻¹ and number of grains spike⁻¹. The low genetic variance ($\delta^2g=1.87$) as well as phenotypic variance ($\delta^2p=1.5$) was observed. Maximum heritability ($h^2=95.91$) which was associated with equal amount of genetic advance (GA = 3.44) was estimated for spike length. These results suggested that spike length was influenced by the environment, yet significant improvement is possible in spike length. Camargo (1999), Narwal *et al.* (1999) and Korkut *et al.* (2001), and had also reported maximum heritability estimates for spike length in bread wheat.

Grain yield is positively correlated with number of spikelets spike⁻¹ as increase in spikelets spike⁻¹ also increased grain yield. Genetic variance ($\delta^2g=0.79$) which was coupled with low phenotypic variance ($\delta^2p=0.78$), consequently high heritability estimates ($h^2=86.07\%$) was observed which were associated with a fair amount of genetic advance (GA=1.97). It revealed that environment had little impact on number of spikelets spike⁻¹, which implied that significant improvement can be expected from selection in early generations. In agreement to our results Gul *et al.* (2004), Kumar *et al.* (2005) and Muhemmed *et al.* (2006), reported high heritability estimates for number of spikelets spike⁻¹ in wheat genotypes. Number of grains spike⁻¹ had linear positive correlation with grain yield maximum number of grains spike⁻¹ gave maximum grain yield. The predicted genetic variance ($\delta^2g=19.91$) was lower than its phenotypic variance ($\delta^2p=21.28$) showing high heritability estimates ($h^2=93.64\%$) with fair amount of genetic advance (GA=11.2). The results suggested that number of grains spike⁻¹ was significantly affected by the environmental factors, hence improvement with more efforts is also possible in number of grains spike⁻¹. Similar results were obtained by Humaira Gul *et al.* (2004), who reported moderate heritability estimates (62.00%) for number of grains spike⁻¹ in hexaploid wheat. Other researchers like Kumar *et al.* (2002), Khan *et al.* (2003) and Chandra *et al.* (2004) have also reported moderate heritability estimates for number of grains spike⁻¹ in bread wheat. Seed index was obtained by weight of 100 grains in grams. Seed index was not affected by the environmental factors because genetic variance ($\delta^2g=0.6$) was at par to the phenotypic variance ($\delta^2p=0.7$) and resulted in maximum heritability estimates ($h^2=84.33\%$) with (0.620) low genetic advance. These results suggested that improvement in seed index could be possible through selection in early generations. Fida *et al.* (2006) noted moderate heritability estimates ($h^2=64.00\%$) for seed index in hexaploid wheat. Other researchers like Kumar *et al.* (2002) and Safeer-ul-Hassan *et al.* (2003) have also reported maximum heritability estimates for seed index in bread wheat. Grain yield is dependent trait among the other traits, it depends upon number of tillers per plant, spike length, number of spikelets spike⁻¹, number of grains spike⁻¹ and

seed index. The data regarding grain yield plant⁻¹ revealed that environmental factors has less impact on grain yield, predicted genetic variance ($\delta^2_g = 3.21$) was smaller than its phenotypic variance ($\delta^2_p = 3.64$) and demonstrated high heritability estimates ($h^2=88.21\%$) and a fair amount of genetic advance (GA=4.34). These results suggested that improvement in grain yield could be possible through selection parameters in early generations of wheat cultivars. Our results are in conformity with Jedy and Ski (2001), Kumar *et al.* (2002), Chandra *et al.* (2004), Gul *et al.* (2004) and Safeer-ul-Hassan *et al.* (2004).

Conclusion

Keeping in view the findings of the current investigation it is concluded that all the traits showed significant differences at $P \leq 0.01$ level. The variety Kiran-95 produced highest grain yield plant⁻¹ followed by TD-1. Plant height, spike length, spikelets spike-land number of grains spike-1 were positively and significantly correlated with grain yield. Plant height showed highest heritability estimates in broad sense which was associated with maximum genetic advance. Selection of genotypes may be made on the basis of spike length and spikelets spike⁻¹, for high grain yield plant⁻¹ production in wheat genotypes.

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