

# **Genetic Variability and Association of Morpho-physiological Traits in Bread Wheat (*Triticum aestivum* L.)**

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## **Authors' contributions**

*This work was carried out in collaboration among all authors. Author PK designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors YPSS and VS managed the analyses of the study. Author Kiran managed the literature searches. All authors read and approved the final manuscript.*

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## **ABSTRACT**

The experiment was conducted with 60 genotypes of bread wheat. These genotypes were grown in RBD using three replications during *Rabi* 2016-17 at Research Area of Wheat and Barley Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar. To study the variability, correlation and path analysis, data were recorded for yield and its component traits i.e. days to 50% heading, days to anthesis, grain growth rate at 14, 21, 28 days (mg/g/day), plant height (cm), number of effective tillers/meter, flag leaf length (cm), flag leaf width (cm), flag leaf area (cm<sup>2</sup>), spike length (cm), number of spikelets per spike, number of grains per spike, 1000 grain weight (g), grain yield per plot (g), biological yield/plot (g) and harvest index (%). ANOVA showed highly significant differences among the genotypes for all the traits indicating adequacy of material and the traits studied for further assessment of genetic variability parameters. High value of GCV and PCV was recorded for grain yield per plot, followed by biological yield, indicating greater amount of variability among the genotypes. Highest heritability was recorded for days to 50% heading, followed by days to anthesis. Highly significant and positive association was perceived between grain yield and tillers per meter, plant height, number of grains per spike, number of spikelets per spike, flag leaf area,

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grain growth rate at 14, 21 and 28 days after anthesis, spike length, 1000 grain weight, biological yield and harvest index. The high direct effects were recorded for biological yield, harvest index, flag leaf breadth, number of effective tillers per meter and 1000 grain weight, in order.

**Keywords:** Genetic variability; correlation; path analysis; wheat; morpho-physiological traits.

## 1. INTRODUCTION

Wheat (*Triticum aestivum* L.) belongs to the family *Poaceae*, earlier known as *Gramineae*, of tribe *Triticeae* [1] and is the most important cereal crop and staple food for nearly 35% of the world population. It covers 32 per cent of the world's total acreage under cereal crops. Worldwide India has the maximum area under wheat cultivation and is second largest producer after China in the world. It is the second most important food crop of India after rice, both in terms of area and production. It is grown in an area of 29.58 million ha in India and 2.55 million ha in Haryana with a production of 93.50 million tonne and 12.73 million tonnes, respectively [2]. As per UN projections world population is estimated to be 8.5 billion by 2030 and it will be around 9 billion till 2050 [3] To feed a growing world population, wheat grain production must increase 2 % annually. Sustainable solution to this problem is breeding high yielding wheat crop varieties.

Grain yield is complex character, which is influenced by a number of yields contributing characters. Hence, the selection for desirable genotypes should not only be based on yield alone as it is under polygenic control and the other yield components should also be considered. For effective utilization of the genetic stock in crop improvement, information of mutual association between yield and its contributing components is necessary. Thus, it becomes essential to know the correlation of various component characters with yield and among themselves. The correlation coefficients between yield and yield components usually show a complex chain of interacting relationship, it determines the relationship between them which can speed up the process of crop improvement [4,5]. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and illuminates the relationship in a more meaningful way [6].

The success of a breeding program depends largely upon the amount of genetic variability present in the populace and the extent to which the desired traits are hereditary [7]. Several genetic variability studies have been conducted

on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization [8]. Genetic improvement to develop varieties with high yield potential and resistance/tolerance to a biotic and abiotic stresses, with acceptable end-use quality, is the most viable and environment-friendly option to sustainably increase wheat yield. Such improvement of crops requires creation and introduction of genetic variation, selection, and extensive evaluation of breeding materials to identify adapted and stable genotypes with desirable agronomic traits. Therefore, the objective of present study is to evaluate the genetic variability present in experimental material and to find out the association of yield contributing characters among themselves and with yield.

## 2. MATERIALS AND METHODS

The seed material comprised of 60 bread wheat genotypes which were grown in a randomized block design (RBD) with three replications during *Rabi* 2016-17 at Research Area of the Wheat and Barley section Department of Genetics and Plant Breeding, CCS HAU, Hisar. Each plot comprised of 6-meter length with three rows and row to row distance was kept 20 cm in each replication. The recommended practices for raising a healthy crop was followed. All the cultural practices for growing crop were kept constant. Weeds were removed by hand as and when required. The data were recorded on three randomly selected plants from each genotype in each replication for days to 50% heading, days to anthesis, grain growth rate: 14, 21, 28 days (mg/gr/day), plant height (cm), number of effective tillers/meter, flag leaf length (cm), flag leaf width (cm), flag leaf area (cm<sup>2</sup>), spike length (cm), number of spikelets per spike, number of grains per spike, 1000 grain weight (g), grain yield per plot (g), biological yield/plot (g) and harvest index (%). These traits were measured by using visual observations, lab equipment's and simple statistical methods.

Mean data was subjected to analysis of variance to test the significance of difference among the genotypes for different character according to Panse and Sukhatme [9] at 1% levels of

significance. Genotypic and phenotypic coefficients of variation were estimated by the formula given by Burton [10] Heritability in broad sense was calculated according to method suggested by Hanson et al. [11]. The Genetic advance as in terms of percentage of means was estimated as described by Johnson et al. [12]. The methodology proposed by Dewey & Lu [13] was used to perform the path analysis for grain yield and its components keeping grain yield as resultant variable and its components as causal variables. Analysis of variance (ANOVA), coefficients of variation, path analysis and correlation analysis (at 1% and 5% levels of significance) were performed using OPSTAT software developed by CCSHAU Hisar.

### 3. RESULTS AND DISCUSSION

#### 3.1 Variability Parameters

The analysis of variance for different characters is presented in Table 1. The mean sums of squares due to genotypes were found to be highly significant for all the traits studied at 0.01 level of significance, indicating the presence of adequate genetic variability for all the character studied, which revealed the existence of substantial variation among the genotypes for all the characters observed. Mean values reveals that sufficient range of variation among the genotypes for each character, *i.e.*, wide range in values, was observed in the genotypes for all the characters. Bhutto et al. [14], Tahmasebi et al. [15] and Mollasadeghi et al. [16] also reported significant differences for all the characters studied.

The results of mean, range, GCV, PCV, heritability and genetic advance as percentage of mean for all characters are presented in Table 2, which revealed sufficient variation for genotypes under study. The heritable component can be assessed by studying phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percentage of mean.

Genotypic coefficient of variance ranges from 3.27 (days to anthesis) to 18.62 (grain yield per plot), while phenotypic coefficient of variance ranges from 3.46 (days to anthesis) to 20.73 (grain yield per plot) for the traits studied. All the traits under studies showed very less difference between phenotypic and genotypic coefficient of variation indicates less environmental influences and phenotypic selection will be effective for these traits. So, phenotypic expression would be

good indication of the genotypic potential [17]. Grain yield per plot exhibited higher GCV (18.62) and PCV (20.73) estimates followed by biological yield per plot, number of tillers per meter, seed density and harvest index indicating that greater amount of variability prevailed among the genotypes for these characters and selection for these traits will be effective. The higher PCV and GCV values for most of the characters could be evidence of a wide range of variation, which confirmed the finding of Choudhary et al. [18], Kalimullah et al. [19], Demelash et al. [20], Nukasani et al. [21], Singh et al. [22], Kumar et al. [23] for grain yield and number of tillers per meter. Low GCV and PCV were obtained for days to anthesis (3.27 and 3.46, respectively) followed by days to 50% heading, plant height and number of spikelets per spike. Almost similar findings were reported by Bilgin et al. [24] for days to 50% heading. However, GCV itself would not be a correct measure to know the heritable variations present and therefore, GCV should be considered together with heritability estimates to get the more reliable picture of the amount of the advance to be expected from the selections [10]. In the present study, the maximum heritability (broad sense) was found for days to 50% heading followed by days to anthesis and grain yield per plot. Moderate heritability was recorded for traits like spike length (cm), 1000 grain weight, plant height, biological yield and harvest index. Moderate heritability estimates suggested that selection should be delayed to more advance generation for these characters. Similar findings were also reported by Bilgin et al. [24], Tiwari [25], Singh et al. [22], Kalimullah et al. [19], Khan et al. [26], Salem et al. [27] and Haydar et al. [28] in wheat. Traits like number of effective tillers per meter, flag leaf area, number of spikelets per spike and number of grains per spike showed low heritability estimates.

High expected genetic advance as percent of mean was observed on grain yield per plot, biological yield and grain growth rate at 14 days, which confirmed the finding of Dhanda et al. [29] and Kalimullah et al. [19] in wheat. Low genetic advance as per cent of mean was obtained for flag leaf length (6.03) followed days to anthesis (6.39), number of spikelets per spike (6.92), plant height (7.12), days to 50% heading (7.38), number of grains per spike (9.25) and 1000 grains weight (10.75). Low genetic advance as per cent of mean indicates slight changes of improvement of these characters in subsequent generations as discussed by Teich [30], Chaturvedi and Gupta [31].

**Table 1. Analysis of variance (ANOVA) for various traits in sixty genotypes of wheat**

Source of variation (SV)	Degree of freedom (df)	Mean sum of squares														
		Days to 50% heading	Days to anthesis	Grain growth rate (14)	Grain growth rate (21)	Grain growth rate (28)	Plant height (cm)	No. of effective tillers/m	Flag leaf length (cm)	Flag leaf breadth (cm)	Flag leaf area (cm <sup>2</sup> )	Spike length (cm)	Spikelets/ Spike	No. of grains /spike (g)	1000 grain weight (g)	Grain yield/plot
Replication	2	1.09	5.32	0.07	0.29	0.03	107.62	261.94	15.83	0.04	52.82	9.90	18.25	40.19	8.28	16097.22
Genotypes	59	36.88	33.59	0.49	0.26	0.22	86.96	604.56	8.27	0.04	47.29	2.47	4.14	76.25	23.57	403064.74
Error	118	1.24	1.23	0.05	0.08	0.02	15.48	174.57	2.65	0.01	14.85	0.25	1.18	24.24	3.34	29783.66

\*\* Significant at p= 0.01

**Table 2. Estimates of mean performance, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA%) means for physio-morphological traits in sixty genotypes of wheat**

Traits*	Mean ± S.E (m)	Range		GCV	PCV	h <sup>2</sup> (bs)	GA (%)
		Minimum	Maximum				
DH	91.63±0.91	83.33	104.33	3.76	3.95	90.58	7.38
DA	100.33±0.91	92.33	113.67	3.27	3.46	89.76	6.39
GGR14	2.26±0.14	1.52	3.23	13.31	15.32	75.51	23.82
GGR21	2.20±0.19	1.70	2.88	8.91	13.65	42.60	11.98
GGR28	1.88±0.10	1.40	2.41	10.98	12.61	75.85	19.70
PH	110.03±3.21	91.52	121.38	4.44	5.70	60.61	7.12
T/M	113.94±10.79	85.33	147.00	10.51	15.65	45.09	14.53
FLL	30.05±1.33	25.80	33.03	4.55	7.08	41.34	6.03
FLB	2.11±0.08	1.90	2.36	5.01	6.77	54.89	7.65
FLA	47.53±3.15	37.65	55.10	6.92	10.66	42.13	9.25
SL	12.07±0.41	9.71	13.75	7.12	8.24	74.75	12.69
S/S	19.96±0.89	17.45	22.34	4.98	7.37	45.62	6.92
G/S	59.64±4.02	48.00	72.33	6.98	10.81	41.70	9.29
TGW	40.68±1.49	35.06	47.08	6.38	7.81	66.87	10.75
GY	1894.72±140.91	1016.67	2766.67	18.62	20.73	80.69	34.45
BY	5653.33±464.61	3833.33	7766.67	14.75	17.86	68.24	25.11
HI	33.50±1.83	25.43	41.57	9.64	11.73	67.57	16.33

\* DH-Days to Heading, DA-Days to anthesis, GGR14-Grain growth rate at 14 day(mg/grain/day), GGR21-Grain growth rate at 21 day(mg/grain/day), GGR28-Grain growth rate at 28 day(mg/grain/day), PH- Plant height (cm), T/m-Tillers per meter, FLL-Flag leaf length(cm), FLB-Flag leaf breadth (cm), FLA-Flag leaf area (cm<sup>2</sup>), SL-Spike length(cm), S/S-Number of spikelets per spike, G/S- Number of grains per spike, TGW- 1000 grain weight(g), GY- Grain yield per plot (g), BY- Biological Yield/plot(g), HI-Harvest index (%)

The high heritability estimates would be helpful for breeding superior genotypes on the basis of phenotypic performance of quantitative characters. However, Johnson et al. [12] and Johnson and Hernandez [32] reported that that high GCV along with high heritability and genetic gain provide better estimate than each parameter alone. Panse [33] further elaborated that high heritability together with high genetic advance was an indication of dominance and epistatic effects. In the present study biological yield and grain yield shows high PCV and GCV with moderately high heritability and genetic advance as percent of mean. These characters could be taken as useful basis for selection. Similar results were also observed by Degewione et al. [34]. Days to anthesis and days to 50% heading have low genetic advance as per cent of mean along with high heritability.

### 3.2 Correlation Coefficient Analysis

Correlation studies were conducted to find out association at phenotypic level among different characters and it was observed that only a few of them exhibited a significant correlation coefficient at 0.01 or 0.05 level of significance. The values for correlation among different characters have been presented in Table 3. Grain yield per plot was positively and significantly correlated with grain growth at 14 days after anthesis (0.160\*), grain growth at 21 days after anthesis (0.240\*\*), grain growth at 28 days after anthesis (0.211\*\*), plant height (0.214\*\*), effective tillers per meter (0.453\*\*), flag leaf area (0.153\*), spike length (0.212\*\*), spikelets per spike (0.199\*\*), number of grains per spike (0.227\*\*) and 1000 grain weight (0.355\*\*), biological yield per plot (0.826\*\*) and harvest index (0.571\*\*). Days to 50% heading exhibited positive and significant correlation with days to anthesis (0.916\*\*), while negative and significant correlation of this character was observed with grain growth rate at 28 days after anthesis (-0.324\*\*), 1000 grains weight (-0.375\*\*), biological yield per plot (-0.180\*), harvest index (-0.276\*\*) and grain yield per plot (-0.293\*\*). Similarly, the association of grain yield with either one or more than one trait has also been reported by Zeeshan et al. [35], Degewione et al. [34] for number of tillers per meter in wheat. Kumar et al. [23], Suleiman et al. [36] and Desheva [37] for 1000 grains weight. Yani and Rashidi [38] for flag leaf area in wheat. Days to 50% heading was positively and significantly correlated with days to anthesis, whereas, negative correlation 1000 grains weight, biological yield per plot, harvest index and grain

yield per plot. Days to anthesis was significantly correlated with plant height, whereas, negatively associated with grain growth rate at 28 days after anthesis, flag leaf length, 1000 grains weight, biological yield per plot and harvest index. Grain growth rate at 14 days after anthesis showed positive and significant correlation with grain growth rate at 21 days after anthesis, grain growth rate at 28 days after anthesis, plant height, flag leaf breadth, flag leaf area and grain yield per plot. Plant height showed positive and significant correlation with flag leaf length, flag leaf breadth, flag leaf area, 1000 grains weight, and biological yield per plot. Number of effective tillers per meter was positively and significantly correlated with biological yield per plot and grain yield per plot. Flag leaf area was positively correlated with spike length, number of number of spikelets per spike, number of grains per spike, 1000 grains weight, and biological yield per plot. Spike length was positively correlated with number of number of spikelets per spike, number of grains per spike, and biological yield per plot. Number of number of spikelets per spike exhibited positive and significant correlation with number of grains per spike, biological yield per plot. Number of grains per spike positively associated with biological yield per. 1000 grains weight was positively correlated with biological yield per plot, harvest index and grain yield per plot. Singh et al. [39], Ali et al. [40], Bilgin et al. [24], Demelash et al. [20], Zarei et al. [41], Haydar et al. [28] and Baye et al. [42] have recorded almost similar patterns of positive correlations in bread wheat. The negative correlation of some important characters with yield may lead to some undesirable selection depending on whether negative association is due to linkage or pleiotropic effect. To improve yield components with negative association with other, suitable recombination may be obtained through biparental mating, mutation breeding or diallel selective mating by breaking undesirable linkages.

### 3.3 Path Coefficient Analysis

The path coefficient analysis takes into account the cause and effect relationship between the variables which is unique in partitioning the associations into direct and indirect effects through other dependent variables. The path analysis helps to resolve the correlations further and provides a clear picture in which component traits contribute towards dependent variable.

**Table 3. Phenotypic correlation coefficients among various traits of wheat genotypes**

	DH	DA	GGR14	GGR21	GGR28	PH	T/M	FLL	FLB	FLA	SL	S/S	G/S	TGW	GY	BY	HI
<b>DH</b>																	
<b>DA</b>	0.916**																
<b>GGR14</b>	0.13	0.143															
<b>GGR21</b>	-0.043	-0.044	0.377**														
<b>GGR28</b>	-0.324**	-0.312**	0.327**	0.560**													
<b>PH</b>	0.186*	0.181*	0.203**	0.251**	0.213**												
<b>T/M</b>	0.051	0.049	0.095	0.05	-0.099	-0.006											
<b>FLL</b>	-0.141	-0.166*	0.053	0.07	0.183*	0.158*	-0.072										
<b>FLB</b>	0.0001	-0.006	0.210**	0.170*	0.199**	0.226**	-0.067	0.222**									
<b>FLA</b>	-0.096	-0.116	0.161*	0.151*	0.249**	0.248**	-0.086	0.789**	0.772**								
<b>SL</b>	-0.135	-0.102	0.145	0.06	0.071	0.111	-0.127	0.179*	0.410**	0.371**							
<b>S/S</b>	0.072	0.055	0.101	-0.105	-0.081	0.008	0.079	0.170*	0.269**	0.276**	0.260**						
<b>G/S</b>	-0.08	-0.108	-0.044	-0.081	0.033	0.095	-0.035	0.072	0.189*	0.172*	0.226**	0.231**					
<b>TGW</b>	-0.375**	-0.392**	0.143	0.226**	0.372**	0.177*	-0.081	0.290**	0.091	0.250**	0.135	0.007	0.123				
<b>GY</b>	-0.293**	-0.298**	0.160*	0.240**	0.211**	0.214**	0.453**	0.057	0.187*	0.153*	0.212**	0.199**	0.227**	0.355**			
<b>BY</b>	-0.180*	-0.173*	0.13	0.188*	0.200**	0.287**	0.470**	0.078	0.243**	0.203**	0.183*	0.266**	0.197**	0.275**	0.826**		
<b>HI</b>	-0.276**	-0.299**	0.087	0.142	0.124	-0.048	0.104	0.006	-0.021	-0.012	0.08	-0.048	0.138	0.228**	0.571**	0.023	

\*Significant at  $p=0.05$ , \*\* Significant at  $p=0.01$ 

DH-Days to 50% Heading, DA-Days to anthesis, GGR14-Grain growth rate at 14day(mg/grain/day), GGR21-Grain growth rate at 21day(mg/grain/day), GGR28-Grain growth rate at 28day(mg/grain/day), PH- Plant height (cm), T/m- Tillers per meter, FLL-Flag leaf length(cm), FLB-Flag leaf breadth (cm), FLA-Flag leaf area (cm<sup>2</sup>), SL-Spike length(cm), S/S-Number of spikelets per spike, G/S- Number of grains per spike, TGW-1000 grain weight (g), GY-Grain yield per plot (g), BY-Biological Yield/plot(g), HI-Harvest index (%)

**Table 4. Direct (diagonal) & indirect (off-diagonal) effects of morpho-physiological traits on grain yield per plot**

	DH	DA	GGR14	GGR21	GGR28	PH	T/M	FLL	FLB	FLA	SL	S/S	G/S	TGW	BY	HI	GY(rg)
<b>DH</b>	-0.0114	0.0027	-0.0001	-0.0010	0.0113	0.0027	0.0013	-0.0172	0.0000	0.0205	-0.0033	0.0008	0.0008	-0.0079	-0.1417	-0.1500	-0.293**
<b>DA</b>	-0.0104	0.0030	-0.0001	-0.0011	0.0109	0.0027	0.0012	-0.0202	-0.0008	0.0246	-0.0025	0.0006	0.0011	-0.0082	-0.1366	-0.1625	-0.298**
<b>GGR14</b>	-0.0015	0.0004	-0.0007	0.0091	-0.0114	0.0030	0.0024	0.0065	0.0278	-0.0342	0.0035	0.0011	0.0004	0.0030	0.1027	0.0473	0.160*
<b>GGR21</b>	0.0005	-0.0001	-0.0003	0.0242	-0.0195	0.0037	0.0013	0.0085	0.0225	-0.0320	0.0015	-0.0012	0.0008	0.0047	0.1480	0.0774	0.240**
<b>GGR28</b>	0.0037	-0.0009	-0.0002	0.0135	-0.0347	0.0031	-0.0025	0.0223	0.0263	-0.0528	0.0017	-0.0009	-0.0003	0.0078	0.1578	0.0673	0.211**
<b>PH</b>	-0.0021	0.0005	-0.0001	0.0061	-0.0074	0.0147	-0.0002	0.0192	0.0299	-0.0526	0.0027	0.0001	-0.0009	0.0037	0.2265	-0.0263	0.214**
<b>T/M</b>	-0.0006	0.0001	-0.0001	0.0012	0.0034	-0.0001	0.0251	-0.0088	-0.0089	0.0183	-0.0031	0.0009	0.0004	-0.0017	0.3703	0.0564	0.453**
<b>FLL</b>	0.0016	-0.0005	0.0000	0.0017	-0.0064	0.0023	-0.0018	0.1219	0.0294	-0.1676	0.0044	0.0019	-0.0007	0.0061	0.0614	0.0033	0.057*
<b>FLB</b>	0.0000	0.0000	-0.0001	0.0041	-0.0069	0.0033	-0.0017	0.0271	0.1323	-0.1639	0.0101	0.0030	-0.0018	0.0019	0.1916	-0.0116	0.187*
<b>FLA</b>	0.0011	-0.0003	-0.0001	0.0036	-0.0086	0.0037	-0.0022	0.0962	0.1022	-0.2123	0.0091	0.0031	-0.0017	0.0053	0.1602	-0.0066	0.153*
<b>SL</b>	0.0015	-0.0003	-0.0001	0.0015	-0.0025	0.0016	-0.0032	0.0218	0.0543	-0.0788	0.0245	0.0029	-0.0022	0.0028	0.1446	0.0434	0.212**
<b>S/S</b>	-0.0008	0.0002	-0.0001	-0.0025	0.0028	0.0001	0.0020	0.0207	0.0356	-0.0586	0.0064	0.0111	-0.0023	0.0002	0.2102	-0.0260	0.199**
<b>G/S</b>	0.0009	-0.0003	0.0000	-0.0020	-0.0011	0.0014	-0.0009	0.0088	0.0250	-0.0366	0.0055	0.0026	-0.0097	0.0026	0.1557	0.0753	0.227**
<b>TGW</b>	0.0043	-0.0012	-0.0001	0.0055	-0.0129	0.0026	-0.0020	0.0354	0.0121	-0.0531	0.0033	0.0001	-0.0012	0.0210	0.2173	0.1238	0.355**
<b>BY</b>	0.0021	-0.0005	-0.0001	0.0045	-0.0070	0.0042	0.0118	0.0095	0.0322	-0.0431	0.0045	0.0030	-0.0019	0.0058	0.7887	0.0126	0.826**
<b>HI</b>	0.0032	-0.0009	-0.0001	0.0034	-0.0043	-0.0007	0.0026	0.0007	-0.0028	0.0026	0.0020	-0.0005	-0.0014	0.0048	0.0183	0.5438	0.571**

Residual are 0.01087

DH- Days to Heading, DA- Days to anthesis, GGR14-Grain growth rate at 14 days (mg/grain/day), GGR21-Grain growth rate at 21 days (mg/grain/day), GGR28-Grain growth rate at 28 days (mg/grain/day), PH- Plant height (cm), FLL- T/m- tillers per meter, FLL-Flag leaf length (cm), FLB-Flag leaf breadth (cm), FLA-Flag leaf area (cm<sup>2</sup>), SL-Spike length(cm), S/S-Number of spikelets per spike, TGW- Thousand Grain weight(gm), GY- Grain yield per plot (gm), BY- Biological Yield/plot (gm), HI-Harvest index (%)

The Path analysis revealed that biological yield, harvest index, flag leaf breadth, number of effective tillers per meter and 1000 grain weight found to be more important as these traits had high direct contribution and also exhibited substantially indirect contribution to the gross correlation of other traits with grain yield (Table 4). Selection of above traits can be used for improving grain yield. This agrees with the findings of Izzat et al. [43], Subhani et al. [44], Tripathi et al. [45], Fallahi et al. [46], Phaugat et al. [47] and Baye et al. [42] in wheat. Days to 50% heading showed negative direct effect while positive indirect effects *via* plant height on grain yield per plot. Plant height showed positive direct effect on grain yield per plot and indirect effect *via* biological yield. Similar observations were also reported by other workers Aycicek and Yildirim [48] and Cifci [49]. Number of tillers per meter and number of spikelets per spike had direct effect on grain yield per plot and their indirect effects *via* spike length, 1000 grains weight and biological yield was also positive. Similar results have been reported by Aycicek and Yildirim [48]. Ali et al. [40], Subhashchandra et al. [50], Khan et al. [51] and Lone et al. [52] reported positive direct effect of tiller number per meter on grain yield.

The present study has led to improve the understanding of many interrelated processes involved in the genetic control of variation in the grain yield per plot in bread wheat. The results, thus, observed in the present study would provide some guidelines in the selection of parents and in the prediction of possible merits for genetic recombination and would also be of value in formulating model plant type for selection in segregating generations.

#### 4. CONCLUSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters, indicating a wide range of variability prevailing for all the traits studied for further selection and improvement. The present investigation concluded that high value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for grain yield per plot, followed by biological yield per plot, indicating that greater amount of variability existing among the genotypes for these characters. Grain growth rate at 14 days after anthesis and grain yield

exhibited high genetic advance as per cent of mean along with high heritability estimates revealed the opportunity of further improvement for these traits by selection. Positive and significant correlations of grain yield were recorded with tillers per meter, plant height, number of grains per spike, number of spikelets per spike, flag leaf area, grain growth rate at 14, 21 and 28 days after anthesis, spike length, 1000 grain weight, biological yield and harvest index. Strong correlation of these traits revealed that the selection based on these traits would ultimately improve grain yield and it is also suggested that hybridization of genotypes possessing combination of above characters is most useful for obtaining desirable high yielding segregants. Path coefficient analysis revealed that the characters viz., biological yield, harvest index, flag leaf breadth, number of effective tillers per meter, 1000 grains weight had positive and direct effects on grain yield per plot, while the characters, days to 50% heading, grain growth rate at 28 days after anthesis, flag leaf area and number of grains per spike showed direct negative effects. Hence, it would be rewarding to lay stress on these characters for the improvement of yield.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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