



## Genetic analysis of grain yield and its contributing traits for their implications in improvement of bread wheat cultivars

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**Abstract:** Genetic analysis was carried out in 55 genotypes (10 parents and 45 F<sub>1</sub>s) through diallel mating design excluding reciprocals in bread wheat. Analysis of variance showed appreciable variability among the breeding material for almost all the traits under study. The highest value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was found for flag leaf area (PCV=18.82, GCV=17.74), biological yield (PCV=12.98, GCV=11.70), grain yield (PCV=11.90, GCV=10.39) and harvest index (PCV=10.39, GCV=10.05). Highest heritability with highest genetic advance was estimated for flag leaf area ( $h^2=52.24$ , GA=34.64), biological yield ( $h^2=15.04$ , GA=21.71), harvest index ( $h^2=18.19$ , GA=20.01), peduncle length ( $h^2=31.72$ , GA=15.96) and spikelets per spike ( $h^2=34.92$ , GA=12.96), therefore selection will be effective based on these traits. Grain yield was found significantly correlated (at <1% level of significance) with productive tillers ( $gr=0.3283^{**}$ ,  $pr=0.4347^{**}$ ), spike length ( $gr=0.1959^{**}$ ,  $pr=0.2203^{**}$ ), spikelets per spike ( $gr=0.4342^{**}$ ,  $pr=0.3813^{**}$ ), grains per spike ( $gr=0.7188^{**}$ ,  $pr=0.4918^{**}$ ), biological yield ( $gr=0.6101^{**}$ ,  $pr=0.6616^{**}$ ), harvest index ( $gr=0.3518^{**}$ ,  $pr=0.3227^{**}$ ) and thousand grain weight ( $gr=0.5232^{**}$ ,  $pr=0.3673^{**}$ ). Similarly path coefficient analysis estimates for biological yield ( $g=1.0524$ ,  $p=1.0554$ ), harvesting index ( $g=0.8862$ ,  $p=0.8291$ ), thousand grain weight ( $g=0.0588$ ,  $p=0.0269$ ), grains per spike ( $g=0.0496$ ,  $p=0.0074$ ), spike length ( $g=0.0209$ ,  $p=0.0289$ ), days to maturity ( $g=0.0142$ ,  $p=0.0127$ ), productive tillers ( $g=0.0186$ ,  $p=0.0147$ ), peduncle length ( $g=0.0123$ ,  $p=0.0157$ ), days to 50% flowering ( $g=0.0093$ ,  $p=0.0072$ ) and plant height ( $g=0.0042$ ,  $p=0.0020$ ) showed high positive direct effects on grain yield indicating that due importance should be given to these traits during selection for high yield.

**Keywords:** Bread wheat, Correlation, Diallel analysis, Heritability and Path coefficient

### INTRODUCTION

Wheat (*Triticum aestivum* L.) is the largest grown cereal in the world and it supplements around 19 percent of our total calories. It is one of the principal crops cultivated in India as a staple food commodity for a majority of Indians that also contributes to the overall food security of country. India holds the prestigious position of being second largest wheat producing country for many years and has it a share of about 36 percent to the country's total food grains production (Anonymous 2014, Sharma *et al.*, 2013). The major wheat producing countries are China, India, USA, France, Russia, Canada, Australia, Pakistan, Turkey, UK, Argentina, Iran and Italy. These countries contribute about 76 % of the total world wheat production. India holds second position in terms of both in area and production after china. At global level, India's share in world wheat area is about 12.5%, whereas it occupies 12 % in total world wheat production (<http://Directorate of Wheat Research 2013-2014>). Genetic analysis in wheat for yield improvement had shown

that grain yield is determined by several component traits and it is a highly complex character as reported by Sajjad, *et al.* (2011). They observed that these component traits affect the grain either directly or indirectly. Development of high yielding varieties is a major objective of any breeding programme for but success depends upon the presence of genetic variability in germplasm, extent of transmissibility of characters under consideration and traits associations with grain yield and among themselves. The genotypic and phenotypic coefficient of variation is helpful in understanding the clear cut picture of existing variability in the material. Several researchers have reported genetic variations for different yield contributing traits in wheat genotypes (Dhananjay *et al.*, 2012, Kumar *et al.*, 2013; Bhushan *et al.*, 2013; Singh *et al.*, 2013). Correlation coefficient is a measure of relationship between any two characters but that does not indicate anything about the cause and effect relationship. Yield is the most economic trait which is the result of overall contribution of several characters from the beginning of germination to the final development of the crop.

Thus yield is primarily a dependent character wherein many other characters show association with grain yield. Thus in order to determine contribution of various characters towards yield, it is necessary that the relationship between yield and its component characters undergoes partitioning into a series of direct and indirect effects revealing specific forces which are acting to build up a given correlation. The estimates of heritability and genetic advance provide the indices of transmissibility of characters while correlation coefficient and path analysis gives the information about the characters association and relative contribution of both direct and indirect effects of components traits on grain yield. The direct selection based on just yield cannot be effective, but selection via yield and its components traits has been more efficient. For effective selection, information on nature and magnitude of variability in population, association of characters with yield and among themselves are necessary. Therefore the main objective of the present investigation was to study the genetic variability, heritability, genetic advance and characters association of grain yield and other important agro-morphological traits in wheat through half diallel mating design.

## MATERIALS AND METHODS

Ten genotypes of bread wheat namely, Raj 3765, K 9162, PBW 373, K 9423, K 7903, Unnat-Halna, NW 1014, HUW 560, NW 1076 and UP 2425 were sown during *rabi* 2011-2012 for attempting crossing programme in a 10 x 10 diallel fashion excluding reciprocals. In the next crop season *rabi* 2012-2013, experimental material consisted 55 genotypes (10 parents and 45 F<sub>1</sub>S) was sown in a randomized block design with three replications. Each of the parental lines and crosses were sown by dibbling of seeds in two row plot of 2 meter length at spacing of 10 cm between plants within a row keeping row to row spacing at 23cm. All the standard agronomical practices (dose of fertilizer, irrigation at all critical stages) were followed to raise normal crop from sowing to till harvest of crop. Observations were recorded on five randomly selected plants in each replication for fourteen characteristics namely; days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, flag leaf area (cm<sup>2</sup>), spike length (cm), number of spikelets per

spike, number of grains per spike, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%) and gluten content (%). For flag leaf area (cm<sup>2</sup>), length and the maximum width of flag leaf was measured and the area was calculated using the following formula suggested by Muller (1991) as Flag leaf area = leaf length × maximum leaf width × correction factor (0.74). The analysis of variance was based on the model suggested by Panse and Sukhatme, (1967). Coefficient of heritability (in narrow sense) in F<sub>1</sub>S generation based on component analysis was calculated as proposed by Crumpacker and Allard, (1962). The genetic advance was worked out by the formula proposed by Robinson *et al.* (1949). Genotypic and phenotypic coefficient of variation was calculated by the formula given by Burton and De vane (1953). The genotypic and phenotypic correlation coefficients were calculated as suggested by Al-Jibouri *et al.* (1958). In path analysis; direct and indirect as well as residual effects were calculated. All the analysis work was done in Microsoft Excel as per the procedure given by Singh and Chaudhary, (1985).

## RESULTS AND DISCUSSION

**Analysis of variance:** The presence of sufficient genetic variability among the parental lines is essential for planning a successful breeding programme. Analysis of variance for parents and their F<sub>1</sub>S crosses showed highly significant differences (at 1% level of significance) among all the 55 treatments for the traits except days to 50 % flowering in parents and grains per spike in parents and F<sub>1</sub>S revealing existence of variability for the traits namely; flag leaf area, productive tillers per plant, spike length, number of spikelets per spike, peduncle length, plant height, thousand grain weight, harvest index, biological yield and days to maturity. Similar findings on the presence of variability were reported by Singh *et al.* (2012), Bhushan *et al.* (2013), Singh *et al.* (2013), Kumar *et al.* (2014), Ramesh *et al.* (2015) and Kumar *et al.* (2015) for different agro morphological traits in wheat crop at different locations in India.

The effectiveness of any selection scheme depends upon the presence of genetic variability among the genotypes. The understanding of variability and genetic architecture of population is essential for the im-

**Table 1.** Pedigree and other available details of the parental lines used in crossing programme.

Genotype	Species	Parentage	Centre developed
Raj 3765	<i>T. aestivum</i>	HD 2402/VL639	R.A.U. Rajasthan
K 9162	<i>T. aestivum</i>	K 7827/HD 2204	C.S.A.U. Kanpur
PBW 373	<i>T. aestivum</i>	ND/VG1944//KAL/BB/3/YACO`S`/4/VEE#5`S`	P.A.U. Ludhiana
K 9423	<i>T. aestivum</i>	HP 1533/Kalyan Sona/UP 262	C.S.A.U. Kanpur
K 7903	<i>T. aestivum</i>	HP 1982/K 816	C.S.A.U. Kanpur
Unnat-Halna	<i>T. aestivum</i>	-	C.S.A.U. Kanpur
NW 1014	<i>T. aestivum</i>	HAHN`S`	N.D.U. A.T. Faizabad
HUW 560	<i>T. aestivum</i>	-	B.H.U. Banaras
NW 1076	<i>T. aestivum</i>	OPATA/KILL	N.D.U.A.T. Faizabad
UP 2425	<i>T. aestivum</i>	HD 2320/UP 2263	G.B.P.U.A.T. Pantnagar

**Table 2.** Analysis of variance for different agro-morphological characters and grain yield in bread wheat (*T. aestivum* L.).

SOV	Mean Sum of Square													
	DF	DTF	DTM	PH	PL	FLA	PT	SL	SPS	GPS	BY	HI	TGW	GY
Replication	02	0.16	1.76	15.68*	0.75	4.12	0.14	0.28	2.17	14.98	11.18	0.67	0.31	1.12
Treatments	54	40.69**	13.73**	72.93**	23.17**	123.54**	0.48**	0.80**	10.94**	51.26**	104.14**	68.34**	13.43**	18.30**
Parents	09	16.51	5.20**	129.42**	30.85**	58.79**	0.66**	1.29**	4.95*	28.11	98.83**	140.49**	8.62**	17.57**
F <sub>1s</sub>	44	46.39**	15.26**	58.09**	21.17**	139.02**	0.35**	0.58**	7.84**	17.45	81.65**	49.39**	10.94**	6.16**
Parents Vs F <sub>1s</sub>	01	7.77*	23.28**	217.37**	42.37**	25.24*	4.28**	5.93**	201.21**	1747.15**	1141.02**	252.55**	166.44**	559.01**
Error	108	1.61	0.82	4.44	0.99	4.48	0.07	0.20	2.26	18.21	7.47	1.53	2.20	1.72

DTF- Days to 50 % Flowering, DTM- Days to Maturity, PH- Plant Height, PL- Peduncle Length, FLA- Flag Leaf Area, PT - Productive Tillers, SL- Spike Length, SPS- Spikes Per Spike, GPS- Grams Per Spike, BY- Biological Yield, GY- Grain Yield, HI- Harvest Index, TGW -Thousand Grain Weight. \*, \*\* Significant at 5 % and 1 % probability level, respectively.

**Table 3.** Estimates of genotypic and phenotypic correlation coefficients for different characters in Bread wheat (*T. aestivum* L.).

Trait	DTM	PH	PL	LA	PT	SL	SL	GPS	BY	HI	TGW	G	GY
DTF	G	-0.3251	0.3513	0.2795	0.0446	-0.1022	-0.1959	0.0282	0.1660	-0.3001	-0.0847	-0.3137	-0.0853
	P	-0.2512**	0.3117**	0.2562**	0.0493	-0.1016	-0.1369	0.0131	0.1339	-0.2671**	-0.0843	-0.1665*	-0.0757
DTM	G		-0.2780	-0.2461	-0.1073	0.0014	0.2099	-0.1023	0.1355	0.1697	-0.3608	0.0559	0.1358
	P		-0.2199**	-0.2166**	-0.0798	-0.0308	0.0803	-0.1059	0.0591	0.1442	-0.2987	0.0243	0.0834
PH	G			0.2277	0.1737	-0.0512	-0.3094	0.0003	0.0600	-0.3321	0.0610	-0.3350	-0.2291*
	P			0.2197**	0.2164**	-0.0627	-0.2341**	-0.0415	0.0665	-0.3039**	0.0261	-0.1414	-0.1795*
PL	G				0.3495	-0.0454	-3.505	-0.2793	-0.4429	-0.2638	0.0090	-0.4273	-0.2725**
	P				0.3294**	-0.0350	-0.2336**	-0.1888*	-0.2523**	-0.0317	-0.0099	-0.1656*	-0.2058**
FLA	G					0.3727	0.1416	0.1782	0.0073	-0.1843	0.1203	-0.0877	-0.0506
	P					0.2867**	0.0913	0.1133	-0.0098	-0.1772*	0.0650	-0.0867	-0.0279
PT	G						0.6130	0.7352	0.6545	0.2817	0.5439	0.2723	0.3283**
	P						0.3804**	0.4750**	0.3549**	0.2169**	0.3672**	0.0567	0.4347**
SL	G							0.4665	0.3381	0.2580	0.4247	0.5927	0.1959**
	P							0.6478**	0.6236**	0.1877*	0.2550**	0.0620	0.2203**
SPS	G								0.7807	0.0593	0.7267	0.4397	0.4342**
	P								0.8663**	0.0583	0.4742**	0.0260	0.3813**
GPS	G									0.1901	0.6876	0.6011	0.7188**
	P									0.1301	0.3700**	0.0436	0.4918**
BY	G										0.3790	0.3452	0.6101**
	P										-0.5237	0.1517	0.6616**
HI	G											0.0786	0.3518**
	P											0.0465	0.3227**
TGW	G												0.1380
	P												0.5232**
GY	G												0.1768*
	P												0.3494
													0.1115

\*, \*\* Significant at 5 % and 1 % probability level, respectively.

**Table 4.** Estimates of direct (diagonal) and indirect effects of different characters on grain yield per plant in Bread wheat (*T. aestivum* L.).

Trait	DTF	DTM	PH	PL	FLA	PT	SL	SPS	GPS	BY	HI	TGW	GY
DTF	G	0.0093	-0.0030	0.0033	0.0026	0.0004	-0.0010	0.0003	0.0004	0.0015	-0.0028	-0.0008	-0.0853
	P	0.0072	-0.0018	0.0022	0.0018	0.0004	-0.0007	0.0001	0.0002	0.0010	-0.0019	-0.0006	-0.0757
DTM	G	-0.0046	0.0142	-0.0039	-0.0035	-0.0015	0.0000	-0.0014	0.0019	-0.0004	0.0024	-0.0051	0.1358
	P	-0.0032	0.0127	-0.0028	-0.0027	-0.0010	-0.0004	-0.0013	0.0007	-0.0005	0.0018	-0.0038	0.0834
PH	G	0.0015	-0.0012	0.0042	0.0010	0.0007	-0.0002	0.0000	-0.0002	0.0003	-0.0014	0.0003	-0.2291
	P	0.0006	-0.0004	0.0020	0.0004	0.0004	-0.0001	-0.0005	-0.0002	0.0001	-0.0006	0.0001	-0.1795*
PL	G	0.0034	-0.0030	0.0028	0.0123	0.0043	-0.0006	-0.0034	-0.0055	-0.0005	-0.0033	0.0001	-0.2725
	P	0.0040	-0.0034	0.0035	0.0157	0.0052	-0.0006	-0.0030	-0.0040	-0.0005	-0.0036	-0.0002	-0.2058**
FLA	G	0.0000	-0.0001	0.0001	0.0002	0.0006	0.0002	0.0001	0.0000	0.0000	-0.0001	0.0001	-0.0506
	P	0.0006	-0.0010	0.0027	0.0042	0.0126	0.0036	0.0014	-0.0001	0.0011	-0.0022	0.0008	-0.0279
PT	G	0.0019	0.0000	0.0010	0.0008	-0.0069	-0.0186	-0.0114	-0.0122	-0.0005	-0.0053	-0.0101	0.3283
	P	-0.0015	-0.0005	-0.0009	-0.0005	0.0042	0.0147	0.0056	0.0052	0.0030	0.0032	0.0054	0.4347**
SL	G	-0.0041	0.0044	-0.0065	-0.0073	0.0030	0.0128	0.0209	0.0070	-0.0016	0.0054	0.0089	0.1959
	P	-0.0040	0.0023	-0.0068	-0.0068	0.0026	0.0110	0.0289	0.0180	0.0007	0.0054	0.0074	0.2203**
SPS	G	-0.0009	0.0034	0.0000	0.0094	-0.0060	-0.0247	-0.0157	-0.0262	-0.0109	-0.0020	-0.0244	0.4342
	P	-0.0001	0.0010	0.0004	0.0018	-0.0011	-0.0045	-0.0061	-0.0081	-0.0027	-0.0005	-0.0044	0.3813**
GPS	G	0.0021	0.0067	-0.0025	-0.0220	0.0004	0.0325	0.0168	0.0496	0.0238	0.0094	0.0341	0.7188
	P	0.0002	0.0004	-0.0006	-0.0019	-0.0001	0.0026	0.0046	0.0074	0.0025	0.0010	0.0027	0.4918**
BY	G	0.1747	-0.0286	0.0632	-0.0438	0.0826	0.0267	-0.0784	0.3406	0.5047	-0.5511	0.3989	0.6101
	P	0.1413	-0.0390	0.0702	-0.0334	0.0891	0.2173	0.0259	0.2987	0.3545	-0.5130	0.2978	0.6616**
HI	G	-0.2660	0.1504	-0.2943	-0.2338	-0.1634	0.2497	0.2286	0.1685	-0.4641	0.8862	0.0697	0.3518
	P	-0.2215	0.1196	-0.2520	-0.1879	-0.1469	0.1798	0.1556	0.1079	-0.4030	0.8291	0.0386	0.3227**
TGW	G	-0.0050	-0.0212	0.0036	0.0005	0.0071	0.0320	0.0250	0.0404	0.0223	0.0046	0.0588	0.5232
	P	-0.0023	-0.0080	0.0007	-0.0003	0.0017	0.0099	0.0127	0.0099	0.0076	0.0013	0.0269	0.3673**

\*, \*\* Significant at 5 % and 1 % probability level, respectively.

**Table 5.** Mean, range, PCV, GCV, heritability and genetic advance for 13 characters in bread wheat.

Trait	Mean		Range		PCV	GCV	Heritability h <sup>2</sup> (ns)	GA as % of mean
	Parents	F <sub>1</sub> s	Parents	F <sub>1</sub> s				
DTF	92.23	91.77	89.00 - 95.67	86.66 - 98.33	4.16	3.93	5.81	7.63
DTM	139.50	140.47	137.00 - 141.00	136.00 - 144.66	1.61	1.48	10.80	2.79
PH	94.38	91.40	86.07 - 106.93	84.83 - 105.20	5.68	5.20	26.31	9.79
PL	34.03	32.72	28.86 - 39.60	28.13 - 40.10	8.79	8.25	31.72	15.96
FLA	34.68	35.69	27.90 - 42.66	25.60 - 49.40	18.82	17.74	52.24	34.64
PT	6.79	7.21	6.10 - 7.43	6.60 - 8.13	6.46	5.14	51.30	8.44
SL	9.97	10.46	8.87 - 11.15	9.84 - 11.36	6.10	4.32	50.30	6.29
SPS	17.89	20.76	16.08 - 19.86	17.29 - 24.42	11.22	8.40	34.92	12.96
GPS	50.57	59.01	44.88 - 55.26	53.62 - 63.66	9.41	5.77	17.94	7.30
BY	42.94	49.76	37.25 - 50.99	41.72 - 61.43	12.98	11.70	15.04	21.71
HI	44.35	47.56	34.71 - 59.71	39.87 - 57.50	10.39	10.05	18.19	20.01
TGW	39.84	42.45	37.38 - 43.02	38.87 - 45.55	5.81	4.61	20.73	7.54
GY	18.72	23.49	15.99 - 22.97	20.63 - 26.59	11.90	10.39	3.78	18.68

\*, \*\* Significant at 5 % and 1 % probability level, respectively.

plementation of systematic breeding method. The general mean of F<sub>1</sub> crosses were greater than their corresponding parents for all the characters except days to 50% flowering, plant height and peduncle length. The range of variability of F<sub>1</sub>s cross combinations was also greater than their corresponding parents for all the traits under study except plant height, spike length and grains per spike.

**Estimation of coefficient of variation:** The results indicated that the estimates of PCV were slightly greater than GCV for all the characters which exhibited role of environment in the expression of these traits. High estimates of GCV and PCV were recorded for the traits namely, flag leaf area (17.74% and 18.82%), biological yield (11.70 % and 12.98%), grain yield (10.39% and 11.90%) and harvest index (10.05% and 10.39%), which comes under the category of moderate type of GCV and PCV (10 - 25%). Similar findings for high PCV and GCV in wheat crop at different location of India have been reported by Kumar *et al.* (2013) for harvest index; Bhushan *et al.* (2013) for biological yield, Singh *et al.* (2013) for grain yield, Kumar *et al.* (2014) for biological yield, grain yield and harvest yield, Ramesh *et al.* (2015) for grain yield. The results of the present study indicated that useful variability in progenies may be utilized while making selection of suitable genotypes on the basis of different genetic parameters to improve yield in wheat.

**Heritability and genetic advance:** Both heritability and genetic advance are two important direct selection parameters independently but estimates of high heritability coupled with high genetic advance in a character are more effective for making selection due to the fact that expression of these traits is controlled by additive gene action. In the present study, highest value of heritability in narrow sense (more than 10 %) was observed for flag leaf area (52.24%) followed by productive tillers per plant (51.30%), spike length (50.30%), number of spikelets per spike (43.92%), peduncle length (31.72%), plant height (26.31%), 1000 grain weight (20.73%), harvest index (18.19%), grains per

spike (17.94%), biological yield (15.04%) and days to maturity (10.80%). Similar results on heritability were reported by Tazeen *et al.* (2009) for peduncle length; Singh *et al.* (2012) for productive tillers, plant height, grains per spike; Kumar *et al.* (2010) for flag leaf area in wheat crop at different locations in India.

In the present study, high genetic advance (more than 10 %) was observed for flag leaf area (34.64%), biological yield (21.71%), harvest index (20.01%), grain yield (18.68%), peduncle length (15.96%) and spikelets per spike (12.96%). Similar results on genetic advance have been reported by Prasad *et al.* (2006) for flag leaf area; Dhananjay *et al.* (2012) for harvest index, Singh *et al.* (2012) for spikelets per spike, Bhushan *et al.* (2013) for biological yield and grain yield, Kumar *et al.* (2015) for biological yield, grain yield and harvest index in wheat crop at different location of India.

It is well recognized that estimates of genetic advance are not effective without the estimates of heritability and thus knowledge of heritability and genetic advance existing in different yield parameters is a prerequisite for effective plant improvement programme. High heritability with high genetic advance was found for flag leaf area followed by biological yield, harvest index, peduncle length and spikelets per spike that indicated presence of additive and additive x additive type of gene effects in the expression of these traits. This also means that for improvement of these traits any type of selection scheme aimed at exploiting additive genetic variance would be helpful. Genetic advance has an added advantage over heritability as a guiding factor to the plant breeder during selection programme, where the character is to be improved through the series of selections in segregating generations.

**Correlation coefficient:** In the present study all possible phenotypic and genotypic correlations were worked out in all possible combinations involving 13 traits with grain yield. Grain yield is a very complex and highly variable trait and is a result of cumulative

effects of all its component traits and therefore, direct selection for grain yield may not be very effective. Moreover, all yield components may not be always be independent in their action but may be correlated. Therefore selection should be made for a particular trait that may also bring simultaneous change in other trait which may or may not be desirable. In all the cases, genetic correlations were similar in direction and magnitude than phenotypic correlations. It was also revealed that significant phenotypic association between attributes which primarily may be due to genetic cause could lead to pleiotropic effects and linkages. There shortlisting or identification of useful yield components and information about their association with each other would be of practical value in exerting selection pressure for the improvement of these component traits. It may also be associated with yield in desirable direction and be useful in developing the elite genotype resulting in to higher productivity. In the present investigation, all possible genotypic and phenotypic correlation coefficients were estimated to know the degree of association among 13 traits. A close relationship appeared between genotypic and phenotypic correlations in most of the traits thereby indicating low environmental effects on the degree of association between various traits.

Grain yield had positive and significant correlation (at 1% level of significant) with productive tillers per plant, spike length, spikelets per spike, grains per spike, biological yield, harvest index and thousand grain weight at both genotypic and phenotypic level. This reflected that by improving these traits, grain yield could be improved. However, it showed significant and negative correlation (at 5% level of significant) with plant height and peduncle length. Similar results on association between yield and its contributing traits in wheat were also reported by Yao *et al.* (2014) for productive tillers per plant and grains per spike in China; Singh *et al.* (2012) for biological yield, thousand grain weight and harvest index; Kumar *et al.* (2012) for spikelets per spike; Kumar *et al.* (2014) for harvest index and thousand grains weight, Das (2014) for spike length, grains per spike, thousand grains weight, harvest index, Avinashe *et al.* (2015) for spike length, thousand grains weight, harvest index, biological yield, Ramesh *et al.* (2015) for grains per spike, spike length, Bhattarai *et al.* (2015) for 1000-grain weight and spike length whereas negative association was also reported by Bhushan *et al.* (2013) for plant height in wheat at different locations of India. This also indicated that selection for short stature may be effective for high grain yield. However positive association between grain yield and plant height in wheat were also reported by Bhattarai *et al.* (2015) in Nepal which is contrary to the result of present study.

In the present study, genotypic correlation coefficients were higher than phenotypic correlation coefficients for the traits namely, spikelets per spike, grains per

spike, harvest index and 1000-grain weight and revealed inherent association among traits. In any breeding programme, simultaneous improvement for many characters would only be useful if positive correlation among them is in desirable direction. In the present study, the characters namely, productive tillers per plant, spike length, spikelets per spike, grains per spike, biological yield, harvest index and thousand grain weight exhibited positive correlation among these and directly related with grain yield which may be considered as most important characters for grain yield improvement in bread wheat through selection.

**Path coefficient:** Correlation coefficient provides measures of relationship between any two characters but they do not say anything about the cause and effect relationship. Yield is the most economic trait which is the result of overall contribution of several characters from the beginning of germination to the final development of the crop. Thus yield is a dependent character and many other characters show association with yield. Thus in order to determine how much contribution of various characters towards yield, it is necessary that the relationship between yield and its component characters undergoes partitioning into a series of direct and indirect effects revealing specific forces which are acting to build up a given correlation.

Only direct yield contributing traits should be used for yield improvement by path analysis. In the present study 11 traits namely, biological yield, harvest index, thousand grain weight, grains per spike, spike length, days to maturity, productive tillers per plant, peduncle length, days to 50% flowering, plant height and flag leaf area showed positive direct effects on grain yield whereas, negative direct effect was observed for rest of the traits. The present results on path coefficient analysis in wheat crop are similar to the earlier findings of Singh *et al.* (2012) for spike length; Bhushan *et al.* (2013) for productive tillers per plant, 1000 grain weight, biological yield and harvest index; Kumar *et al.* (2014) for spike length, thousand grain weight, harvest index, biological yield, Das *et al.* (2014) for 1000-grain weight, harvest index, grains per spike, Avinashe *et al.* (2015) for spike length, thousand grains weight, harvest index, biological yield, days to maturity at different locations of India and Sobia *et al.* (2014) for flag leaf area. Hence, these traits should be considered while exercising selection procedures for improvement in grain yield. All the characters have direct and indirect effects on grain yield through several other characters. Therefore, traits which showed positive direct and indirect effects on grain yield except days to flowering, plant height and days to maturity (where negative effects is desired) should also be used for the improvement of grain yield. It means these are the best characters by which we improved the grain yield per plant by improving these characters, because these traits have positive direct and indirect effect on grain yield with positive and significant correlation coefficient. The

findings of the present study were in accordance to the findings of Singh et al. (2012) in wheat crop in India.

## Conclusion

The traits namely flag leaf area, biological yield and harvest index showed highest heritability coupled with highest genetic advance and also highest PCV and GCV therefore selection will be effective based on these traits due to the maximum contribution of additive gene action. The traits such as productive tillers per plant, spike length, grains per spike, biological yield, harvest index, and 1000 grain weight showed positive and significant correlation coefficient and also have high direct effects on grain yield at both genotypic and phenotypic level, indicated that we might improve grain yield by improving these traits and thus emphasis should be given on these traits for the selection of elite genotypes from the segregating generations. It is evident that genotypes developed might serve as good source of material for further breeding programme. Therefore information generated on genetic parameters namely; coefficient of variation, heritability, genetic advance, correlation coefficient and path coefficient analysis could help the breeders to develop suitable cultivars within a short time.

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