



## Association studies for yield and yield attributing traits of bread wheat, *Triticum aestivum* L.

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Received : 17.10.2019 ; Revised : 15.07.2020 ; Accepted : 10.08.2020

DOI : <https://doi.org/10.22271/09746315.2020.v16.i2.1316>

### ABSTRACT

Forty-nine genotypes of bread wheat (*Triticum aestivum* L.) were screened at District farm, AB Block, B.C.K.V. situated at Kalyani in Nadia district of West Bengal during Rabi season for two years, i.e. 2015-2016 and 2018-2019 following Randomized Block Design. All the genotypes exhibited a considerable amount of variability for the parameters studied. PBW 744, UP 2940, DBW 187, HD 3219, K 1502 and WH 1201 were high yielding ones. A closer PCV & GCV was reported for all the characters except grain weight spike<sup>-1</sup>. High PCV, GCV, heritability, GA, GA % of mean was reported for the characters viz., days to heading, days to flowering, no of tillers plant<sup>-1</sup>, grain protein content and yield plant<sup>-1</sup>. The yield had a significant positive association with the number of tillers plant<sup>-1</sup>, number of grains spike<sup>-1</sup> and test weight. The selection of genotypes may be done with the help of identified traits like the number of tillers plant<sup>-1</sup> and test weight.

**Keywords:** Bread wheat, correlation analysis, path analysis and yield attributes

Wheat (*Triticum aestivum* L.) belongs to family Poaceae (Graminae), is a hexaploid species (2n = 42, AABBDD) and it contributes about 1/3rd of the total food grain production (Tandon, J.P.,2000). As wheat is a self-pollinated crop, pure line selection, mass selection, progeny selection, or hybridization followed by next-generation selection is effective for genetic improvement. A better understanding of the genetic basis of this variability and character association will improve the efficiency of wheat crop improvement. Genetic presumption provides information about how far a character can be passed down to successive generations. One of the effective plant improvement techniques is the availability of good knowledge about heredity and the genetic yields present in various yield parameters. Any breeding program eventually aims to increase yield. Yielding is a complex trait that depends on many factors. Therefore, related components should be dealt with simultaneously to improve this trait. Although correlation values explain the interrelationship between various characters, the path coefficient analysis as suggested by Dewey and Lu (1959) divides the amount of interrelationship into direct and indirect components as exercised by the dependent character.

### MATERIALS AND METHODS

The current experiment was performed at District Farm, AB Block, B.C.K.V. Kalyani Simanta of West Bengal, for 2 years during the Rabi season 2015-2016 and 2018-2019 in Randomised Block Design (RBD)

with two replications. Gangetic alluvial sandy loam in texture with soil pH 6.9 to 7.0 with good drainage facility was the experimental soil. The -blocks were taken as replicas and each block was split into forty-nine identical plots in turn. The research material comprised of 49 wheat genotypes (*Triticum aestivum* L.) including 4 check varieties (Table 1). Five randomly selected plants were taken per replication for individual genotype to record data for the characters viz. days to heading (DH), days to flowering (DF), the days to maturity (DM), plant height (PH)(cm), number of tillers plant<sup>-1</sup> (NTP), spike length (SL)(cm), number of spikelet spike<sup>-1</sup> (NSS), number of grains spike<sup>-1</sup> (NGS), grain weights spike<sup>-1</sup> (g) (GWS), test weight (g) (TW), Yield plant<sup>-1</sup> (YPP)(g) and grain protein per cent (GPP)(%). The Statistical analysis was performed with the assistance of SPAR-1 and STAR software.

### RESULTS AND DISCUSSION

Analysis of variance revealed significant variations between the genotypes against several of the studied traits. Comparing all the 49 genotypes, PBW 744, UP 2940, DBW 187, HD 3219, K 1502 and WH 1201 were high yielding ones (Table 2).

#### *Genetic parameters for yield and its attributing characters*

The broad range in mean value was measured in DH, DF, DM, PH, NTP, NSS, TW, and YPP indicated variation present among different component characters

(Table 2). The value of the Phenotypic Coefficient of Variation (PCV) for all traits was stated to be higher than the genotypical coefficient of variation (GCV) (Table 3). A broad range of variation between GCV and PCV was reported in grain weight spike<sup>-1</sup>, thus the trait is largely affected by the environment. On the contrary, for the rest of the traits, a narrow difference between GCV and PCV was registered indicating that the environment plays very little role in the expression of such traits. A high value of GCV and PCV was documented for the YPP, NTP, DH, DF and GPP. There were little variability and scope for selection in the materials for the NSS, TW, DM, TW, SL, and PH having lower GCV and PCV. Very high heritability was observed for all the characters except for the NSS which showed high heritability. This finding corroborates the observation of Thapa *et al.* (2019).

The high heritability combined with high genetic advance were sown by the DH, DF, NTP, GPP, and YPP (Table 3). High heritability coupled with medium genetic advance was reported for the PH and NGS. High heritability with low genetic advance was observed in DM, SL, NSS and TW indicating the favourable

influence of the environment and therefore selection for these traits may not be rewarding. High PCV, GCV, heritability, and GA % of mean was observed in the characters *viz.*, DH, DF, NTP, GPP and YPP. It indicates that such characters demonstrated the predominance of the action of the additive gene. Thereby selection can be successful for these characters. Similar findings were also reported by Singh *et al.* (1999).

#### Character association

A significant positive correlation was sown by DH, DF, DM, PH and NSS at genotypic as well as phenotypic levels (Table 4). The DF showed a significant positive correlation with DM, PH, SL and NSS at genotypic and phenotypic levels. It showed a significant negative correlation with NGS and YPP at both the levels and with GWS at phenotypic levels. This finding was corroborated with Mohammadi *et al.* (2012); Zafarnaderi *et al.* (2013) and Shoran *et al.* (2005). The days to maturity (DM) were found to have a significant positive correlation with PH at the genotypic and phenotypic level and with NSS at a phenotypic level only. PH showed a significant positive correlation with NSS at genotypic as well as phenotypic levels. PH showed a significant

**Table 1: List of bread wheat genotypes used in the experiment**

Sl. No.	Genotypes	Sl. No.	Genotypes
1	UP 2936	26	HUW 802
2	HD 3218	27	DBW 194
3	DBW 189	28	WH 1203
4	HUW 801	29	RAJ 4465
5	JKW 230	30	UP 2940
6	WH 1200	31	RAJ 4462
7	DBW 190	32	HD 222
8	NW 6078	33	HD 1962
9	HD 3221	34	UP 2937
10	WH 1204	35	DBW 191
11	PBW 745	36	DBW 192
12	WH 1105 ©	37	K 1502
13	NW 6094	38	PBW 761
14	RAJ 4463	39	PBW 744
15	K 1501	40	DBW 187
16	DBW 193	41	PBW 746
17	DBW 88 ©	42	K 0307 ©
18	BRW 3785	43	DBW 188
19	WH 1202	44	HD 3223
20	UP 2939	45	UP 2938
21	RAJ 4464	46	WH 1201
22	BRW 3786	47	HD 3217
23	HD 2967 ©	48	K 1503
24	PBW 747	49	HD 3200
25	HD 3219		

© Check variety

Table 2: Mean performance of different characters among the bread wheat genotypes from pooled data analysis.

Genotypes	DH	DF	DM	PH (cm)	NTP	SL (cm)	NSS	NGS	GWS (g)	TW (g)	GPP (%)	YPP (g)
UP 2936	72.5	78	111.25	76.23	7.2	11.64	21.05	47.72	1.45	38.47	11.17	13.4
HD 3218	74.75	80	116	89.8	5.63	8.88	18.85	35.37	1.14	34.17	11.68	6.83
DBW 189	84.5	88.25	111.75	85.13	6.37	10.96	18.12	39.12	1.14	37.58	12.12	9.47
HUW 801	70.25	77	112.75	85.97	6.81	10.18	16.91	38.62	1.3	38.08	9.14	10.01
JKW 230	82.25	88.25	111.75	89.69	6.97	10.68	19.93	39.42	1.04	35.05	8.52	9.59
WH 1200	70.75	75.5	112.5	86.18	5.88	9.57	16.44	34.39	0.87	35.25	13.14	7.17
DBW 190	82.25	87.5	116.25	89.58	4.83	12.44	21.16	42.34	1.77	43.11	13.35	9.1
NW 6078	75.25	81.5	112.25	93.57	5.2	12.21	20.2	43.95	1.5	37.38	9.25	8.79
HD 3221	82	87.75	112.25	93.25	10.05	11.39	19.92	35	0.96	32.86	9.13	11.61
WH 1204	71.5	77.25	108.25	90.32	5.92	10.48	19	40.26	1.38	34.8	10.49	8.29
PBW 745	60	67.75	102.25	80.78	5.81	11.35	17	41.2	1.23	39.88	13.03	9.64
WH 1105©	65.25	73.5	108.75	86.81	6.58	11.02	15.24	37.22	1.46	38.28	10.27	9.43
NW 6094	70.5	76.75	108	92.04	7.24	9.64	19.68	44.38	1.47	39.22	10.52	12.95
RAJ 4463	60.5	65	104.5	84.76	5.12	9.68	17.2	40.85	1.11	37.39	12.44	7.83
K 1501	74	61.75	112.25	100.43	5.8	10.14	19.06	47.29	1.67	34.44	10.93	9.67
DBW 193	88.5	92.5	128	91.04	5.09	10.16	19.53	36.91	0.99	40.06	13.18	7.53
DBW 88©	72.5	76.75	110.5	90.3	7.09	10.2	17.21	38.74	1.48	33.06	14.06	9.1
BRW 3785	70.25	76.75	108.75	93.95	6.92	9.39	16.24	45.35	1.28	34.54	14.39	10.75
WH 1202	66.75	75.75	110.25	88.68	7.22	9.98	17.15	37.78	1.23	38.96	14.04	10.81
UP 2939	76.5	83.25	115	86.15	6.38	10.57	20.56	45.37	1.22	31.88	11.23	9.12
RAJ 4464	76.5	82.25	117	92.18	5.31	9.58	19.92	32.39	0.98	34.48	11.41	5.91
BRW 3786	73.25	80	115.25	94.94	6.42	11.53	21.21	39.9	1.47	34.93	12.46	9.31
HD 2967©	74.75	79.75	116.5	91.98	6.17	10.67	18.24	40.72	1.28	39.89	11.31	10.31
PBW 747	78.75	86.25	111.5	85.06	5.74	10.34	21.45	38.24	0.92	30.58	10.56	6.68
HD 3219	58.5	64.25	102	84.39	6.56	10.89	17.33	48.81	1.68	40.94	13.64	13.47
HUW 802	77.25	80.75	116	96.22	5.83	10.35	19.16	40.91	1.11	38.48	11.71	9.19
DBW 194	78.5	85.75	116.5	92.14	5.47	10.39	18.57	37.79	1.03	36.92	11.83	7.66
WH 1203	58.75	62	104	88.35	5.8	9.66	18.73	41.68	1.13	33.08	11.9	8.2
RAJ 4465	84	88.25	116.75	100.32	5.98	11.24	20.6	40.3	1.3	35.14	10.55	8.41
UP 2940	67	72.5	109.75	90.1	6.43	10.72	18.03	52.95	1.43	43.96	11.71	14.97
RAJ 4462	66.25	74	114.25	92.12	7.59	11.17	16.11	31.25	1	36.92	12.44	8.7
HD 3222	70.5	76.5	114	95.15	6.34	9.33	17.99	33.02	0.94	37.37	12.41	7.83
HD 1962	85.75	90	117	96	5.67	10.35	19.29	44.5	1.1	38.04	10.48	9.62
UP 2937	85.25	88	116.5	94.99	5.43	10.86	20.07	37.13	0.91	40.32	10.3	8.38
DBW 191	66.25	73.75	110.5	88.3	5.43	9.45	18.7	41.75	1.38	34.18	11.17	7.73
DBW 192	64.5	71.25	111.75	89.12	6.23	11.32	18.44	42.7	1.4	35.59	12.19	9.51
K 1502	62.25	67.5	111	78.32	7.38	9.32	16.6	44.71	1.34	40.03	12.12	13.28

Contd.

Table 2 Contd.

Genotypes	DH	DF	DM	PH (cm)	NTP	SL (cm)	NSS	NGS	GWS (g)	TW (g)	GPP (%)	YPP (g)
PBW 761	50.25	56.75	100.5	75.55	8.22	9.52	14.73	40.31	1.3	33.55	11.07	11.08
PBW 744	70.25	77.25	113.25	87.07	9.24	10.67	20.92	50.33	1.04	40.35	12.63	18.41
DBW 187	70.25	76	114.75	92.13	6.97	10.64	15.99	48.18	1.41	40.81	10.34	13.48
PBW 746	65	71.5	116.75	75.6	7.65	9.79	17.15	36.06	1.33	43.1	10.17	12.66
K 0307©	64	69	115.75	94.2	7.341	0.62	17.11	39.49	1.17	35.86	9.67	10.36
DBW 188	73.75	80.75	115	83.3	6.59	9.92	24.47	39.84	1.17	35.68	9.69	9.51
HD 3223	71.75	76.75	111.75	88.39	5.48	10.79	17.73	42.62	1.11	42.37	12.69	9.96
UP 2938	66.75	73.75	112.75	89.54	6.07	9.76	16.92	34.57	1.17	46.15	12.77	9.76
WH 1201	74	79.75	116	93.16	7.72	11.91	21.9	51.56	1.27	34.72	11.79	13.16
HD 3217	88.5	90.5	120.5	96.13	5.6	10.56	17.82	32.85	1.17	39.53	12.67	7.79
K 1503	84.75	89.75	111.75	94.86	5.75	10.46	20	43.03	0.92	36.9	10.71	9.17
HD 3200	69.75	76.25	115.75	94.58	6.12	9.55	18.37	37.74	1.22	35.4	11.97	7.67
GRAND MEAN	72.4	77.78	112.61	89.57	6.42	10.45	18.65	40.75	1.23	37.34	11.56	9.86
C.V.	1.71	1.72	1.01	0.42	4.67	2.26	1.97	1.24	8.63	1.55	2.03	4.45
<b>SEm (±)</b>	<b>1.24</b>	<b>1.34</b>	<b>1.14</b>	<b>0.39</b>	<b>0.3</b>	<b>0.23</b>	<b>0.37</b>	<b>0.51</b>	<b>0.1</b>	<b>0.58</b>	<b>0.23</b>	<b>0.44</b>
<b>LSD (0.05)</b>	<b>2.46</b>	<b>2.66</b>	<b>2.26</b>	<b>0.77</b>	<b>0.6</b>	<b>0.46</b>	<b>0.73</b>	<b>1.01</b>	<b>0.2</b>	<b>1.15</b>	<b>0.46</b>	<b>0.87</b>

Table 3: Genetic parameters for yield and its attributing characters of bread wheat estimated on pooled data

Characters	G.M	MSS	Range	G.C.V.	P.C.V.	Heritability (%)	G.A.	G.A. of Mean (%)
DH	72.4	1.22	50.25-88.50	11.69	11.82	97.9	17.26	23.84
DF	77.78	2.17	56.75-92.50	10.63	10.77	97.4	16.81	21.61
DM	112.61	1.94*	100.50-128.00	4.25	4.37	94.6	9.59	8.52
PH (cm)	89.57	21.73**	75.55-100.43	5.87	5.89	99.5	10.8	12.06
NTP	6.42	0.29**	4.83-10.05	15.66	16.34	91.8	1.98	30.84
SL (cm)	10.45	1.37**	8.88-12.44	5.21	5.67	84.2	1.03	9.86
NSS	18.65	13.11**	14.73-24.47	3.45	3.97	75.5	1.15	6.17
NGS	40.75	77.40**	31.25-52.95	6.01	6.14	95.9	4.94	12.12
GWS (g)	1.23	0.16**	0.87-1.77	6.64	10.89	50	0.145	8.13
TW (g)	37.34	36.84**	30.58-46.15	3.75	4.06	85.4	2.67	7.15
GPP(%)	11.56	0.46**	8.52-14.39	11.63	11.81	97	2.73	23.62
YPP (g)	9.86	8.10**	5.91-18.41	19.49	20	95	3.86	39.15

Notes : \*\*significant at 1%, \*significant at 5% (DH- days to heading, DF-days to flowering, DM-days to maturity, PH- plant height, NTP-number of tillers plant<sup>-1</sup>, SL-siliqua length, NSS-number of spikelet spike<sup>-1</sup>, NGS- number of grains spike<sup>-1</sup>, GWS-grain weight spike<sup>-1</sup>, TW- test weight, GPP-grain protein per cent, YPP-yield plant<sup>-1</sup>)

Table 4: Genotypic (G) and Phenotypic (P) correlation among yield and its attributing characters estimated on pooled data

Characters	DH	DF	DM	PH (cm)	NTP	SL (cm)	NSS	NGS	GWS (g)	TW (g)	GPP (%)	YPP (g)
DH	G 1	0.944**	0.720**	0.577**	-0.488**	0.413**	0.603**	-0.646**	-0.855**	-0.312*	-0.398**	-0.371**
DF	P 1	0.931**	0.710**	0.570**	-0.278	0.376**	1.366**	-0.340*	-0.440**	-0.111	-0.19	-0.362*
DM	G 1	0.693**	0.685**	0.445**	-0.219	0.447**	0.541**	-0.521**	-0.024	-0.061	-0.184	-0.360*
PH (cm)	P 1	0.685**	0.685**	0.440**	-0.213	0.409**	1.309**	-0.505**	-0.620**	-0.065	-0.18	-0.350*
NTP	G 1	0.489**	1	0.489**	-0.207	0.173	0.095	-0.766**	-0.889**	0.156	-0.492**	-0.317*
SL (cm)	P 1	0.476**	1	0.476**	-0.196	0.155	0.920**	-0.535**	-0.428**	0.129	-0.085	-0.300*
NSS	G 1	0.476**	1	0.476**	-0.281	0.178	0.406**	-0.358*	-0.225	-0.414**	-0.075	-0.451**
NGS	P 1	0.476**	1	0.476**	-0.27	0.165	0.351*	-0.348*	-0.136	-0.382**	-0.074	-0.439**
GWS (g)	G 1	0.476**	1	0.476**	1	0.156	-0.419**	0.224	-0.091	-0.2	-0.169	0.803**
TW (g)	P 1	0.476**	1	0.476**	1	0.133	-0.352*	0.206	-0.068	-0.158	-0.16	0.803**
GPP (%)	G 1	0.476**	1	0.476**	1	1	0.659**	0.263	0.737**	0.318*	-0.172	0.184
YPP (g)	P 1	0.476**	1	0.476**	1	1	0.521**	0.235	0.403**	0.247	-0.164	0.155
	G 1	0.476**	1	0.476**	1	1	1	-0.880**	-0.579**	-0.648**	-0.608**	-0.825**
	P 1	0.476**	1	0.476**	1	1	1	-0.715**	-0.914**	-0.752**	-0.695**	-0.685**
	G 1	0.476**	1	0.476**	1	1	1	0.407**	0.407**	0.871**	-0.059	0.828**
	P 1	0.476**	1	0.476**	1	1	1	0.281	0.281	0.802**	-0.063	0.803**
	G 1	0.476**	1	0.476**	1	1	1	1	1	0.244	0.202	0.244
	P 1	0.476**	1	0.476**	1	1	1	1	1	0.243	0.111	0.181
	G 1	0.476**	1	0.476**	1	1	1	1	1	1	0.650**	0.325*
	P 1	0.476**	1	0.476**	1	1	1	1	1	1	0.582**	0.333*
	G 1	0.476**	1	0.476**	1	1	1	1	1	1	1	0.008
	P 1	0.476**	1	0.476**	1	1	1	1	1	1	1	0.003
	G 1	0.476**	1	0.476**	1	1	1	1	1	1	1	1
	P 1	0.476**	1	0.476**	1	1	1	1	1	1	1	1

Notes : \*\*significant at 1%, \*significant at 5%

**Table 5: Genotypic path coefficient analysis showing direct (bold) and indirect effects estimated on pooled data of yield attributing traits on yield.**

Characters	DH	DF	DM	PH (cm)	NTP	SL (cm)	NSS	NGS	GWS (g)	TW (g)	GPP (%)	YPP (g)
DH	<b>0.199</b>	-0.437	-0.043	0.022	-0.216	0.036	0.1	-0.104	0.106	-0.033	-0.001	-0.371**
DF	0.188	<b>-0.463</b>	-0.041	0.017	-0.164	0.039	0.096	-0.156	0.144	-0.018	-0.001	-0.360*
DM	0.143	-0.321	<b>-0.059</b>	0.019	-0.155	0.015	0.068	-0.17	0.097	0.046	0	-0.317*
PH (cm)	0.115	-0.206	-0.029	<b>0.038</b>	-0.211	0.015	0.025	-0.107	0.032	-0.122	0	-0.451**
NTP	-0.057	0.101	0.012	-0.011	<b>0.751</b>	0.013	-0.026	0.067	0.013	-0.059	-0.001	0.803**
SL (cm)	0.082	-0.207	-0.01	0.007	0.117	<b>0.086</b>	0.041	0.079	-0.103	0.094	-0.001	0.184
NSS	0.319	-0.713	-0.065	0.015	-0.315	0.057	<b>0.062</b>	-0.264	0.362	-0.281	-0.004	-0.825**
NGS	-0.069	0.241	0.033	-0.014	0.168	0.023	-0.055	<b>0.3</b>	-0.057	0.258	0	0.828**
GWS (g)	-0.15	0.474	0.041	-0.009	-0.068	0.063	-0.161	0.122	<b>-0.14</b>	0.072	0.001	0.244
TW (g)	-0.022	0.028	-0.009	-0.016	-0.15	0.027	-0.059	0.261	-0.034	<b>0.296</b>	0.003	0.325*
GPP (%)	-0.039	0.085	0.005	-0.003	-0.127	-0.015	-0.05	-0.018	-0.028	0.192	<b>0.005</b>	0.008

Notes : RESIDUAL= 0.0286\*\*Significant at 1%, \*Significant at 5%

(DH- days to heading, DF-days to flowering, DM-days to maturity, PH- plant height, NTP-number of tillers per plant, SL-siliqua length, NSS-number of spikelet spike<sup>-1</sup>, NGS- number of grains spike<sup>-1</sup>, GWS-grain weight spike<sup>-1</sup>, TW- test weight, GPP-grain protein percent, YPP-yield plant<sup>-1</sup>)

**Table 6: Phenotypic path coefficient analysis showing direct (bold) and indirect effects estimated on pooled data of yield attributing traits on yield**

Characters	DH	DF	DM	PH (cm)	NTP	SL (cm)	NSS	NGS	GWS (g)	TW (g)	GPP (%)	YPP (g)
DH	<b>0.498</b>	0.093	-0.21	0.001	-0.258	-0.131	-0.23	-0.036	-0.079	-0.064	0.054	-0.362*
DF	0.464	<b>0.1</b>	-0.203	0	-0.197	-0.142	-0.22	-0.054	-0.112	-0.037	0.051	-0.350*
DM	0.353	0.068	<b>-0.296</b>	0.001	-0.182	-0.054	-0.155	-0.057	-0.077	0.074	0.024	-0.300*
PH (cm)	0.284	0.044	-0.141	<b>0.001</b>	-0.251	-0.057	-0.059	-0.037	-0.024	-0.219	0.021	-0.439**
NTP	-0.138	-0.021	0.058	0	<b>0.927</b>	-0.046	0.059	0.022	-0.012	-0.091	0.045	0.803**
SL (cm)	0.187	0.041	-0.046	0	0.123	-0.348	-0.088	0.025	0.073	0.142	0.046	0.155
NSS	0.68	0.131	-0.272	0	-0.327	-0.181	<b>-0.168</b>	-0.076	-0.236	-0.431	0.196	-0.685**
NGS	-0.169	-0.05	0.158	0	0.191	-0.082	0.12	<b>0.107</b>	0.051	0.46	0.018	0.803**
GWS (g)	-0.219	-0.062	0.127	0	-0.063	-0.14	0.221	0.03	<b>0.18</b>	0.14	-0.031	0.181
TW (g)	-0.055	-0.007	-0.038	0	-0.146	-0.086	0.126	0.086	0.044	<b>0.574</b>	-0.164	0.333*
GPP (%)	-0.095	-0.018	0.025	0	-0.148	0.057	0.117	-0.007	0.02	0.334	<b>-0.282</b>	0.003

Notes : RESIDUAL= 0.0131, \*\*Significant at 1%, \*Significant at 5%

(DH- days to heading, DF-days to flowering, DM-days to maturity, PH- plant height, NTP-number of tillers per plant<sup>-1</sup>, SL-siliqua length, NSS-number of spikelet spike<sup>-1</sup>, NGS- number of grains spike<sup>-1</sup>, GWS-grain weight spike<sup>-1</sup>, TW- test weight, GPP-grain protein percent, YPP-yield plant<sup>-1</sup>)



negative correlation with TW, NGS and YPP at both levels. The NTP showed a highly significant positive association with YPP at genotypic as well as phenotypic levels. The present findings confirmed with Burio *et al.* (2004) and Sharma *et al.* (2006). The NSS was reported to be highly significant negatively correlated with the NGS, GWS, TW, YPP and GPP (%) at both the levels. The NGS explained a highly significant positive correlation with TW and YPP at genotypic and phenotypic levels and with GWS at a genotypic level only. A highly significant positive correlation was found between GWS with SL at both genotypic and phenotypic levels. It showed a significant negative correlation at both the levels with DH, DM, PH, and NSS. The TW showed a significant positive correlation with grain YPP and GPP (%). This finding of the present study was similar to the report of Khan *et al.* (2005); Muhammad *et al.* (2007) and Yagdi *et al.* (2009).

A significant positive correlation was also reported between GPP (%) with the TW at both levels. In the present investigation, YPP (g) was observed to have a significant positive correlation with the NTP, the NGS and TW (g) in both genotypic and phenotypic levels. This was in accord with the NTP showing coincidence with Gelalcha and Hanchinal (2013). Positive but non-significant associations were observed between YPP and other characters like GWS, SL at both genotypic and phenotypic levels. It showed a significant negative correlation at both levels with DH, DF, DM, PH and the NSS.

#### **Path coefficient analysis**

The correlation coefficient of each independent quantitative character was segmented into a direct and indirect effect on grain yield. The residual effect was found low (0.0286 and 0.0131 for genotypic and phenotypic paths respectively) estimated on pooled data, which suggested that the number of characters chosen in the investigation was appropriate for yield determination of bread wheat (Table 5 and 6). The genotypic path has been discussed in detail. NTP imparted the maximum positive direct effect (0.751) on grain yield followed by the NGS, TW, DH, SL, NSS, PH and GPP (%) respectively. The DF imparted a maximum negative direct effect on grain yield followed by the GWS and DM. The NTP had imparted maximum positive direct effect along with a significant positive correlation with yield. DH indicated a high positive direct effect whereas it showed a significant negative correlation with yield. The NGS had a high positive direct effect along with a significant positive correlation with yield. So, we can go for direct selection for these traits for yield improvement.

The PH indicated positive direct effect but reported to have a significant negative correlation with yield. DF, DM, NTP, NGS, and TW were the causes of negative correlation. Indirect selection through such traits will be effective in yield improvement. GPP (%) was reported to have a positive direct effect and positive correlation with YPP. The GWS showed a negative direct effect but a positive correlation with YPP. DF, DM, NTP, SL, NGS, TW and GPP (%) were the causes of positive correlation. TW indicated a direct positive effect and reported to have a positive correlation with yield. Similar kinds of results were also reported by Singh *et al.* (2000) and Rajput (2019).

Thus, in the present investigation, the genotypic correlation coefficients obtained were reported to be higher than phenotypic correlation coefficients for almost all the characters under study. The days to heading (days), days to flowering (days), days to maturity (days), plant height (cm) and the number of spikelets spike<sup>-1</sup> attained a significant negative correlation with yield plant<sup>-1</sup> (g) at both the levels. The number of tillers plant<sup>-1</sup> and test weight is mentioned as selection criteria as these traits possessed higher direct effects as well as significant positive correlations with yield plant<sup>-1</sup> (g).

#### **ACKNOWLEDGMENT**

Authors are thankful to the Directorate of Wheat Research, Karnal for providing the experimental seed materials.

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