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Genetic variability, correlation and path analysis in bread wheat (*Triticum aestivum* L.) genotypes for yield and its attributing traits

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Abstract
Forty-five bread wheat genotypes were evaluated for genetic variability, correlation and path analysis to identify the traits associated with grain yield. The experimental material was sown in randomized block design (RBD) in three replications and studied fourteen different traits. Among all the traits, moderate values of GCV and PCV were recorded for number of spikelets per main spike and number of effective tillers per plant, whereas most of the traits observed with lower values of GCV and PCV. High heritability coupled with moderate genetic advance as percent mean was observed for days to 50% heading, days to maturity, plant height, number of effective tillers per plant, length of main spike, number of spikelets per main spike and grain yield per plant. Correlation and path analysis studies revealed that, four character like number of effective tillers per plant, biological yield per plant, harvest index and number of spikelets per main spike are the most important characters as these exhibited positive and strong association and maximum positive direct effects on grain yield.

Keywords: Heritability, genetic advance, correlation, path coefficient, bread wheat (*Triticum aestivum* L.)

Introduction

Wheat (*Triticum aestivum* L.) is a hexaploidy ($2n = 6x = 42$), belongs to the grass family *poaceae*. Wheat grain has a high nutritional value with 8 – 20% proteins, 70 – 75% starch, 2 – 3% non-starch polysaccharides, 2% lipids, 1.6% minerals, antioxidants *etc*. and it is world's most important crop that excels all other cereal crops both in production and area (Goesaert *et al.* 2005) [7]. The production of wheat must increase due to increasing population and their demand. In order to meet the population's rising need for food, breeders should focus on the potential to enhance the production of wheat by creating new varieties. (Nizamani *et al.* 2020) [13]. Wheat is self-pollinated crop with outcrossing ranging from 0.5 to 1.0 percent. The variability observed in the plant population of a species is because of the both heredity effects of concerned genes and the environment effect. Therefore, grain yield is very complex trait and it is influenced by so many genetic factor and environmental factors. Thus, successful breeding and selection of high yielding genotypes depends on information availability for genetic variability and the association of yield contributing traits with grain yield. Correlation gives idea about the magnitude and direction of the relationship between various yield attributing traits and yield. Direct and indirect effects facilitate the estimation of the contribution of each yield attributing traits to the grain yield.
Therefore, the efforts were made to study the genetic variability, heritability, correlation and path coefficient analysis to analyze grain yield and its attributing traits of wheat.

Materials and Methods

Experimental material consisting of forty five diverse wheat genotypes which were procured from wheat research stations, S. D. Agricultural University, Vijapur. These genotypes were grown in randomized block design (RBD) with three replications during *Rabi* 2019-20 at Agricultural Research Station, Anand Agricultural University, Sansoli-387130. Genotypes were grown in two rows of 2 meter row length with spacing of 20 cm between rows and 10 cm between plants in row. All the recommended agronomic practices ware followed as per standard practices. Five competitive plants were randomly selected from each entry of each replication in field experiment for recording the observation on plant height, number of effective tillers per plant, 1000 seed weight, length of main spike, number of spikelets per

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main spike, grain yield per plant, biological yield per plant, harvest index, starch content, protein content, wet gluten content, sedimentation value, *etc*. and the observation on days to maturity and days to 50% heading were recorded on plot basis. The analysis was carried out by adopting genetic parameters of variability, estimation of heritability and genetic advance were determined as per Johnson *et al*. (1955) [8]. Correlation studies are computed as per Panse and Sukhatame (1978) [14] whereas, path coefficient analysis is done as suggested by Dewey and Lu (1959) [5].

Results and Discussion
The analysis of variance depicting mean sum of squares for fourteen quantitative as well as qualitative traits are given in table no. 1.Analysis of variance revealed that the mean sum of squares due to genotypes was significant for all the characters under study *viz*., days to 50% heading, plant height, number of effective tillers per plant, length of main spike, days to maturity, number of spikelets per main spike, 1000 seed weight, grain yield per plant, biological yield per plant, harvest index, protein content, starch content, wet gluten content and sedimentation value which indicates presence of considerable amount of genetic variability among the studied genotypes.

The estimates of different variability parameters are presented in table no.2. Among all the traits under study, number of spikelets per main spike and number of effective tillers per plant shows moderate value for GCV and PCV, indicating moderate level of genetic variability is present in this trait. The traits like length of main spike, harvest index and grain yield per plant shows low magnitude of GCV and moderate magnitude of PCV. The similar findings for this character were reported by Abinasa *et al*. (2011) [1] and Korkut *et al*. (2001) [9]. Low magnitude of GCV and PCV were observed for traits like days to 50% heading, days to maturity, plant height, 1000 seed weight, biological yield per plant, protein content, starch content, wet gluten content, sedimentation value which indicates the variation among the lines was not only due to their genotypes but also due to influence of environment. These results were accordance with Meles *et al*. (2017) [11], Fikre *et al*. (2015) [6], Naik *et al*. (2015) [12], Bhushan *et al*. (2013) [4] and Baranwal *et al*. (2012) [3].

In present investigation the values of phenotypic coefficient of variation were found higher than the genotypic coefficient of variation for all the studied traits which show the expression of these characters highly influenced by environment, thus selection for such characters sometimes might be misleading breeder. However close affinity between GCV and PCV for the traits *viz*., days to 50% heading, days to maturity, 1000 seed weight, starch content, wet gluten content and sedimentation value suggesting the environmental influence was narrow for the expression of these traits.

Heritability indicates proportion of total variability that is due to genetic causes and it is a good index of the transmission of traits from parents to their offspring. Among all traits, highest heritability was observed for the traits *viz*., days to 50% heading, days to maturity, plant height, number of effective

tillers per plant, length of main spike, number of spikelets per main spike, 1000 seed weight, protein content, sedimentation value, grain yield per plant suggested that heritability may be due to higher contribution of genotypic component in these characters. Similar results were observed by Meles *et al*. (2017) [11], Rahman *et al*. (2016) [15], Fikre *et al*. (2015) [6], Bhushan *et al*. (2013) [4], Baranwal *et al*. (2012) [3] and Korkut *et al*. (2001) [9]. While traits like biological yield per plant, harvest index, starch content and wet gluten content reported moderate heritability, indicating that these characters were less influenced by environment and direct selection for these components would be effective for further improvement in grain yield.

High heritability coupled with moderate genetic advance as percent mean was observed for days to 50% heading, days to maturity, plant height, number of effective tillers per plant, length of main spike, number of spikelets per main spike and grain yield per plant. Whereas high heritability coupled with low genetic advance as percent mean was observed for 1000 seed weight and sedimentation value. Moderate heritability coupled with low genetic advance as percent mean was observed for character *viz*., biological yield per plant, starch content and wet gluten content.

Correlation Coefficients
Correlation study gives an idea about magnitude and direction of traits with grain yield which is useful for selection of elite genotypes from population. Genotypic and phenotypic correlation coefficient among grain yield per plant and its contributing traits are presented in table 3 and table 4.In the present investigation, grain yield per plant was found positive and significantly correlated with number of effective tillers per plant, biological yield per plant harvest index and number of spikelets per main spike at both genotypic and phenotypic level this indicates that selection for these characters would be effective in improve yield per plant in wheat. Similar results were reported by Sourour *et al*. (2018) [16], Mecha *et al*. (2017) [10] and Azimi *et al*. (2017) [2]. In most of the cases, it was observed that the genotypic correlations were higher in magnitude than the phenotypic correlations, suggesting strong and inherent correlation between pair characters.

Path coefficient analysis
Partitioning of total correlation into direct and indirect effects provide a direct and indirect contribution of characters to grain yield and thus form the basis for selection to improve the yield. The path coefficient analysis reveals (table 5) in partitioning the contribution of different characters towards yield through direct and indirect effects. The path coefficient analysis revealed that number of effective tillers per plant, biological yield per plant, harvest index and number of spikelets per main spike had exhibited positive direct effect and significant positive genotypic correlation with grain yield per plant. Therefore, direct selection for these characters would be easy and would be rewarding improvement in yield of wheat.

Table 1: Analysis of variance for yield and yield contributing characters in forty five genotypes of wheat

Sr. no	Characters	Mean sum of square		
	Degree of freedom	Replication	Treatment	Error
1	Days to 50% heading	0.096	51.767**	3.740
2	Days to maturity	2.422	114.296**	6.566
3	Plant height (cm)	20.239	112.370**	16.372
4	Number of effctive tillers per pant	0.107	4.163**	0.528
5	Length of main spike (cm)	0.518	2.570**	0.401
6	Number of spikelets per main spike	0.347	9.670**	1.206
7	1000 seed weight (g)	0.251	9.447**	0.816
8	Biological yield per plant (g)	2.746	4.947**	1.633
9	Harvest index (%)	1.969	48.021**	11.138
10	Protein content (%)	0.342	0.940**	0.164
11	Starch content (%)	0.451	0.798**	0.169
12	Wet gluten content (%)	0.079	0.864**	0.182
13	Sedimentation value (zeleny)	3.201	10.076**	1.240
14	Grain yield per plant (g)	0.498	2.081**	0.356

*, ** Significant at P = 0.05 and P = 0.01 levels of probability, respectively

Table 2: Genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as percent of mean for yield and yield contributing characters in 45 genotypes of wheat

Sr. No.	Characters	σ^2_g	σ^2_p	GCV (%)	PCV (%)	H^2 (%)	GA	GA (%)
1	Days to 50% heading	16.009	19.749	6.848	7.606	81.061	7.421	12.701
2	Days to maturity	35.910	42.476	5.828	6.339	84.542	11.350	11.039
3	Plant height (cm)	31.999	48.371	7.193	8.844	66.136	9.478	12.050
4	Number of effctive tillers per pant	1.212	1.740	10.515	12.602	69.616	1.892	18.073
5	Length of main spike (cm)	0.723	1.124	8.619	10.750	64.290	1.404	14.237
6	Number of spikelets per main spike	2.821	4.028	11.327	13.534	70.048	2.896	19.530
7	1000 seed weight (g)	2.877	3.693	4.037	4.574	77.898	3.084	7.339
8	Biological yield per plant (g)	1.105	2.737	5.644	8.884	40.361	1.376	7.386
9	Harvest index (%)	12.295	23.433	7.261	10.024	52.468	5.232	10.835
10	Protein content (%)	0.259	0.423	4.209	5.382	61.163	0.819	6.781
11	Starch content (%)	0.210	0.378	0.733	0.984	55.370	0.702	1.123
12	Wet gluten content (%)	0.228	0.409	1.702	2.283	55.615	0.733	2.615
13	Sedimentation value (zeleny)	2.945	4.186	4.460	5.317	70.364	2.966	7.707
14	Grain yield per plant (g)	0.575	0.932	8.460	10.766	61.739	1.228	13.693

Table 3: Genotypic correlation coefficient for different characters in wheat

Characters	DH	DM	PH	NTP	LS	NSS	TW	BY	HI	PC	SC	WG	SV	GY
DH	1	0.749**	0.169	0.09	-0.045	-0.018	-0.244	0.088	-0.088	-0.117	-0.078	-0.143	0.215	-0.02
DM		1	0.121	-0.025	-0.204	0.137	-0.02	-0.182	0.028	0.045	-0.242	-0.001	0.165	-0.101
PH			1	0.046	0.217	0.236	-0.380*	0.244	-0.184	0.140	-0.029	-0.002	0.141	0.008
NTP				1	0.008	0.106	0.028	0.471**	0.696**	-0.164	-0.06	-0.171	0.056	0.931**
LS					1	0.581**	-0.123	0.205	0.026	-0.011	0.139	-0.092	-0.14	0.181
NSS						1	-0.076	0.142	0.293	-0.314*	0.167	-0.271	-0.063	0.343*
TW							1	-0.067	0.301*	0.011	0.037	0.123	-0.186	0.233
BY								1	-0.167	0.265	-0.195	0.168	0.109	0.514**
HI									1	-0.346	0.126	-0.315*	-0.042	0.758**
PC										1	-0.888**	0.99**	0.561**	-0.097
SC											1	-0.582**	-0.551**	-0.023
WG												1	0.292	-0.14
SV													1	0.029
GY														1

** - Significant at p = 0.01 * - Significant at p = 0. 05

DH- Days to 50% heading, DM- Days to maturity, PH- Plant height, NTP- No. of tillers per plant, LS- Length of main spike, NSS - Number of spikelets per main spike, TW- 1000 seed weight, BY- Biological yield per plant, HI- Harvest index, PC- Protein content, SC- Starch content, WG- Wet gluten content, SV- Sedimentation value and GY- Grain yield per plant

Table 4: Phenotypic correlation coefficient for different characters in wheat

Characters	DH	DM	PH	NTP	LS	NSS	TW	BY	HI	PC	SC	WG	SV	GY
DH	1	0.634**	0.145	0.078	-0.027	0.033	-0.201*	0.038	-0.023	-0.039	-0.064	-0.055	0.122	0.005
DM		1	0.094	-0.023	-0.148	0.116	-0.003	-0.116	0.042	0.056	-0.148	0.029	0.114	-0.062
PH			1	0.074	0.049	0.165	-0.218*	0.145	-0.051	0.167	-0.047	0.02	0.061	0.07
NTP				1	-0.015	0.07	-0.009	0.285**	0.386**	-0.081	-0.042	-0.091	0.089	0.612**
LS					1	0.362**	-0.076	0.063	0.023	0.027	0.103	-0.1	-0.16	0.086
NSS						1	-0.115	0.127	0.163	-0.197*	0.102	-0.197*	-0.048	0.249**
TW							1	0.029	0.132	-0.046	0.086	0.099	-0.126	0.154
BY								1	-0.364**	0.053	-0.111	0.093	0.095	0.485**
HI									1	-0.12	-0.018	-0.128	-0.057	0.634**
PC										1	-0.403**	0.485**	0.273**	-0.059
SC											1	-0.530**	-0.417**	-0.115
WG												1	0.282**	-0.031
SV													1	0.031
GY														1

** - Significant at p = 0.01 * - Significant at p = 0. 05

DH- Days to 50% heading, DM- Days to maturity, PH- Plant height, NTP- No. of tillers per plant, LS- Length of main spike, NSS - Number of spikelets per main spike, TW- 1000 seed weight, BY- Biological yield per plant, HI- Harvest index, PC- Protein content, SC- Starch content, WG- Wet gluten content, SV- Sedimentation value and GY- Grain yield per plant

Table 5: Genotypic path coefficient analysis showing direct and indirect effects of thirteen causal variables on grain yield per plant in 45 genotypes of wheat

Character	DH	DM	PH	NTP	LS	NSS	TW	BY	HI	PC	SC	WG	SV	GY
DH	0.017	-0.031	0.004	0.022	-0.003	-0.001	-0.019	0.042	-0.057	0.014	0.004	-0.017	0.005	-0.020
DM	0.013	-0.042	0.003	-0.006	-0.012	0.005	-0.002	-0.088	0.018	-0.005	0.012	0.000	0.004	-0.101
PH	0.003	-0.005	0.021	0.011	0.013	0.009	-0.030	0.117	-0.118	-0.017	0.001	0.000	0.003	0.008
NTP	0.002	0.001	0.001	0.243	0.001	0.004	0.002	0.227	0.447	0.020	0.003	-0.020	0.001	0.931**
LS	-0.001	0.009	0.005	0.002	0.060	0.021	-0.010	0.099	0.017	0.001	-0.007	-0.011	-0.003	0.181
NSS	0.000	-0.006	0.005	0.026	0.035	0.036	-0.006	0.069	0.188	0.038	-0.008	-0.031	-0.002	0.343*
TW	-0.004	0.001	-0.008	0.007	-0.007	-0.003	0.080	-0.032	0.193	-0.001	-0.002	0.014	-0.004	0.233
BY	0.002	0.008	0.005	0.115	0.012	0.005	-0.005	0.482	-0.107	-0.032	0.009	0.019	0.003	0.514**
HI	-0.002	-0.001	-0.004	0.169	0.002	0.011	0.024	-0.081	0.642	0.042	-0.006	-0.036	-0.001	0.758**
PC	-0.002	-0.002	0.003	-0.040	-0.001	-0.011	0.001	0.128	-0.222	-0.121	0.043	0.114	0.013	-0.097
SC	-0.001	0.010	-0.001	-0.015	0.008	0.006	0.003	-0.094	0.081	0.107	-0.048	-0.067	-0.013	-0.023
WG	-0.002	0.000	0.000	-0.042	-0.006	-0.010	0.010	0.081	-0.202	-0.119	0.028	0.115	0.007	-0.140
SV	0.004	-0.007	0.003	0.014	-0.008	-0.002	-0.015	0.052	-0.027	-0.068	0.026	0.034	0.023	0.029

** - Significant at p = 0.01 * - Significant at p = 0. 05 Residual effect = -0.0034

DH- Days to 50% heading, DM- Days to maturity, PH- Plant height, NTP- No. of tillers per plant, LS- Length of main spike, NSS - Number of spikelets per main spike, TW- 1000 seed weight, BY- Biological yield per plant, HI- Harvest index, PC- Protein content, SC- Starch content, WG- Wet gluten content, SV- Sedimentation value and GY- Grain yield per plant

Conclusion

High heritability coupled with moderate genetic advance as percent mean was reported by, days to 50% heading, days to maturity, plant height, number of effective tillers per plant, length of main spike, number of spikelets per main spike and grain yield per plant indicating that selection might be effective for improvement of these characters. Correlation and path coefficient studies revealed that genotypes with more number of effective tillers per plant, higher biological yield per plant, higher harvest index and more number of spikelets per main spike play an important role in improvement of grain yield as they exhibited significant results in desirable direction. Therefore, direct selection for these characters would be easy and rewarding improvement in yield of wheat.

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