Research Article

Assessment of genetic variability and character association for Morpho-Chemical traits in Bread Wheat (*Triticum aestivum* L.)

Gauravrajsinh K. Vaghela, J. M. Patel, Parthsinh Rahevar, Gokulakrishnan. M.

Authors:
G. K. Vaghela, P. Rahevar ✉,
Gokulakrishnan M.
Department of Genetics and Plant Breeding,
C. P. College of Agriculture, Sardarkrushinagar
Dantiwada Agricultural University,
Sardarkrushinagar- 385506, Gujarat, India

J. M. Patel
Wheat Research Station, Sardarkrushinagar
Dantiwada Agricultural University,
Vijapur- 384 570, Gujarat, India

✉ parthrahevar@gmail.com

Abstract

The present investigation was carried out at the Agronomy Instructional Farm, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar using forty-four diverse bread wheat genotypes. These were sown and evaluated under timely sown condition, in a randomized complete block design with four replications during *Rabi* 2019-2020. In the present investigation, 11 morphological and 2 biochemical traits were analyzed. The analysis of variance revealed significant variation among the genotypes for all the studied characters indicating the presence of adequate amount of variability among forty-four genotypes. High heritability associated with high genetic advance as percent of mean was found for the number of tillers per meter, the number of grains per spike, grain yield per plant, leaf area per plant, and peduncle length indicating the traits were simply inherited in nature. Higher values of genotypic correlations than their corresponding phenotypic correlations were recorded for all the studied characters. The path coefficient analysis revealed that the harvest index recorded the highest direct effect towards grain yield per plant, followed by plant height, the number of grain per spike, and protein content. It can be summarized that forimproving the grain yield in wheat; more attention should be given to harvest index, grain yield per spike, protein content, days to heading, and spike length while making the selection for developing high yielding wheat genotypes under timely sown condition.

Keywords correlation, genetic variability, path analysis, wheat

Introduction

India is the second-largest producer of wheat in the world; whereas, in India, it is the second most important cereal crop after rice. The area, production, and productivity of wheat in India in 2017-18 was 29.58 million ha, 99.7 million tons, and 3.37 ton/ha, respectively [1]. Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, West Bengal, Uttarakhand, and Himanchal Pradesh together contribute about 98% to the total wheat production of the country and play an important role in supplying carbohydrate and proteins [2]. While Gujarat occupies an area of 13.81 lac hectares with a production of 45.03 million tons and productivity of 3260.68 Kg/ha [1].

The study of various traits and their association with each other is an important strategy designed to break genetic barriers of yield. Though the correlation studies help in determining the composition of a complex trait

Table 1. List of the forty bread wheat genotypes along with source used for investigation

Genotypes	Source
VA 2018-23, VA 2018-22, VA 2018-27, VA 2018-25, VA 2018-30, VA 2018-05, VA 2018-07, VA 2018-29, VA 2018-24, VA 2018-21, VA 2018-26 VA 2018-28, VA 2018-11, VA 2018-10, VA 2018-12, VA 2018-16, VA 2018-19, VA 2018-06, VA 2018-18, VA 2018-13, VA 2018-03,VA 2018-09, VA 2018-04, VA 2018-14, VA 2018-17 VA 2018-08 VA 2018-20 VA 2018-15	SDAU, Vijapur, Gujarat
WH 1235, C 306	CCSHAU, Hissar, Haryana
JWS 810	JNKKV, Sagar, Madhya Pradesh
NIAW 3170	MPKV, Niphad, Maharashtra
DBW 93, DBW 166	IIWBR, Karnal, Haryana
MP 3288, MP 1331	JNKKV, Powerkheda, Madhya Pradesh
HI 1544, HI 1620	IARI, Indore, Madhya Pradesh
RW 5	SKRAU, Durgapura, Rajasthan
K 1317	CSAU&T, Kanpur
GW 173, GW 451, GW 496 and GW 477	SDAU, Vijapur, Gujarat

i.e. seed yield, they do not provide an exact magnitude of direct and indirect effect towards the yield. Therefore, path coefficient analysis is an important tool to partition the correlation coefficient into the direct and indirect effect of the independent variables on the dependent variables. This information may be useful to breeders in selecting high yielding genotypes in a particular crop. Some information on genetic variation and association studies for grain filling period, vegetative period, and other yield-related traits is available, but such information concerning a range of environments within crop season, at a single location, is very scanty. For several field crops, the studies related to the understanding and development of wheat are being directed by the regular analysis of the genetic polymorphism among the genotypes because grain yield is a compound trait and is highly affected by numerous genetic factors and environmental fluctuation [3]. The scarcity of soil moisture is one of the foremost abiotic stresses which affect germination and thereby productivity of wheat [4]. Therefore, in the present investigation comparative study of variability and heritability parameters, genetic advance, correlation, and path analysis has been planned using the genotypes belonging to various maturity groups.

Methodology

Plant materials
The experimental material for the present study comprised of forty-four bread wheat genotypes; among them 28 were elite germplasm lines from Wheat Research station(WRS), Vijapur; 4 were released varieties of WRS, Vijapur and 12 genotypes were diverse genotypes belonging to different agroclimatic regions of India. (Table 1)

Field experiments
The experimental material consisting of forty-four genotypes of wheat were grown in a randomized block design (RBD) with four replications. The experimental material was planted in the field during *rabi* in the year 2019-20 at Agronomy Instruction Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Two rows of each genotype were sown having 3.0 m length with a spacing of 22.5 cm between two rows. Eleven agronomic traits *viz.*, days to heading, days to maturity, plant height, number of effective tillers per meter, number of grains per spike, spike length, peduncle length, 1000 seed weight, leaf area per plant harvest index, and grain yield per plant and two quality traits i.e. protein content, sedimentation value were studied.

Statistical analysis
The mean performance of each genotype was subjected to statistical analysis. Analysis of variance to test the significance for each character was carried out as per the methodology given by Panse and Sukhatme [5]. Genotypic and phenotypic correlation coefficients were calculated by standard procedures [6].

Table 2. GCV (%), PCV (%), broad sense heritability and genetic advance as percent of mean of 13 different traits of forty bread wheat genotypes.

S.N.	Characters	GCV (%)	PCV (%)	h²(b.s) (%)	GA (%)
1	Days to heading	8.68	10.38	69.89	14.95
2	Days to maturity	3.29	6.94	22.42	3.20
3	Plant height	9.03	13.99	41.63	12.00
4	Number of effective tillers per meter	13.07	15.33	72.74	22.97
5	Number of grains per spike	15.99	20.37	61.61	25.85
6	1000 seed weight	5.53	5.92	87.32	10.65
7	Leaf area per plant	16.45	16.79	95.93	33.19
8	Peduncle length	18.39	19.83	86.01	35.14
9	Spike length	10.51	13.02	65.16	17.48
10	Protein content	3.95	5.90	44.90	5.45
11	Sedimentation value	4.20	5.98	49.29	6.08
12	Harvest index	4.98	10.51	22.49	4.87
13	Gain yield per plant	16.10	19.99	64.85	26.71

Table 3. Genotypic correlation and phenotypic correlation coefficient for 13 different characters in bread wheat

		DH	DM	PH	TIL/M	GPS	TGW	LA	PL	SL	Pro	SV	HI	GY
DH	r_g	1	0.783**	0.614**	-0.155*	0.027	-0.273**	0.205**	-0.523**	0.275	-0.126	0.116	-0.351**	0.018
	r_p	1	0.543**	0.506**	-0.125	0.022	-0.183**	0.172*	-0.431**	0.232**	-0.058	0.048	-0.284**	0.018
DM	r_g		1	0.616**	-0.146	-0.003	-0.291**	0.115	-0.538**	0.246**	-0.189*	-0.142	-0.412**	-0.115
	r_p		1	0.476**	-0.116	0.002	-0.228**	0.094	-0.425**	0.196**	-0.097	-0.000	-0.314**	-0.055
PH	r_g			1	-0.105	0.133	-0.090	0.487**	-0.236**	0.364**	-0.212**	0.140	-0.304**	0.172*
	r_p			1	-0.099	0.131	-0.090	0.478**	-0.234**	0.359**	-0.134	0.085	-0.293**	0.161*
TIL/M	r_g				1	0.095	0.022	-0.130	0.225**	-0.183*	-0.219**	-0.404**	0.073	0.017
	r_p				1	0.093	0.005	-0.124	0.219**	-0.177*	-0.131	-0.276**	0.062	0.015
GPS	r_g					1	0.571**	0.316**	-0.155*	0.216**	-0.285**	-0.211**	0.472**	0.838**
	r_p					1	0.521**	0.309**	-0.155*	0.213**	-0.177*	-0.141	0.446**	0.780**
TGW	r_g						1	0.359**	0.082	0.085	-0.153*	-0.267**	0.903**	0.636**
	r_p						1	0.332**	0.079	0.079	-0.127	-0.179*	0.807**	0.563**
LA	r_g							1	-0.228**	0.497**	-0.196**	-0.095	0.347**	0.464**
	r_p							1	-0.225**	0.494**	-0.133	-0.061	0.332**	0.434**
PL	r_g								1	-0.341**	0.350**	0.002	0.104	-0.243**
	r_p								1	-0.338**	0.222**	-0.001	0.098	-0.229**
SL	r_g									1	-0.057	0.155*	0.184*	0.407**
	r_p									1	-0.040	0.107	0.177*	0.383**
Pro	r_g										1	0.514**	-0.049	-0.164*
	r_p										1	0.342**	-0.015	-0.104
SV	r_g											1	-0.029**	-0.095
	r_p											1	-0.205**	-0.043
HI	r_g												1	0.640**
	r_p												1	0.592**

*, ** significant at 0.05% and 0.01% level of significance, respectively

Whereas, heritability in a broad sense (h²) and genetic advance were estimated using the formula given by Allard [7]. Correlation and path coefficients were worked out as per the method suggested by Al-Jibouri et al., [8] and Dewey and Lu [9] respectively.

Results and Discussion

A wide range of variation was observed among the genotypes for most of the morphological characters. Analysis of variance revealed significant differences among the genotypes for all the studied traits indicating the presence of sufficient genetic variability in the germplasm, and considerable scope for their improvement and utilization in future breeding programs.
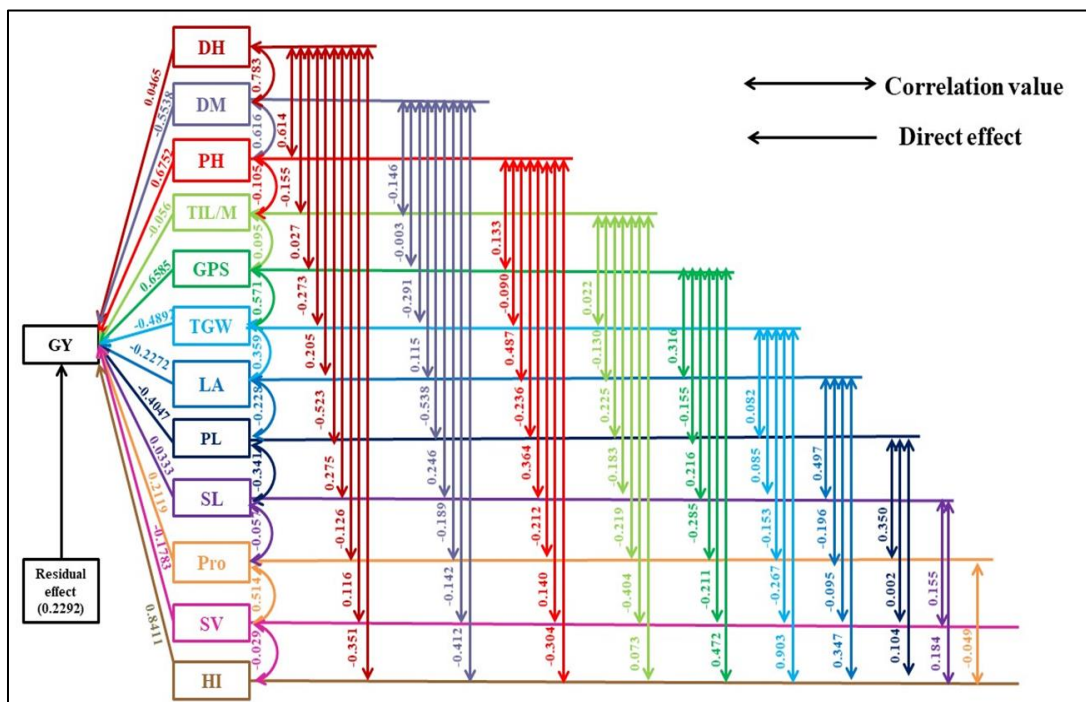

Figure 1. Diagrammatic representation of genotypic path analysis in bread wheat

Genotypic and Phenotypic coefficient of variation (GCV and PCV)

The values of GCV and PCV were presented in Table 2. A perusal of the data revealed that the magnitude of PCV was higher than GCV for all the characters suggesting the influence of the environment in the expression of the traits. GCV was recorded highest for peduncle length (18.39%) followed by leaf area per plant (16.45%) and grain yield per plant (16.10%) suggested that adequate variation is there for these traits and hence, there is a scope for employing suitable breeding programs for bringing about genetic improvement in these agronomic traits. Whereas, comparatively very low in protein content (3.95%) and days to maturity (3.29%). PCV was recorded the highest for the number of grains per spike (20.37%). The highest GCV for peduncle length was also observed by Devesh et al., [10].

Heritability (broad-sense heritability)

The estimates of broad-sense heritability in percent have been presented in Table 2. Higher heritability was observed for leaf area per plant (95.93%) followed by 1000 seed weight (87.32%), peduncle length (86.01%), and the number of effective tillers per meter (72.74%) suggesting a direct selection of these traits and their improvement will be rewarded. Similar results for heritability were observed by Kumar et al., [11].

Genetic advance as percent of mean

The estimates of genetic advance as percent of the mean are presented in Table 2. It revealed that the highest genetic advance as percent of mean was recorded for peduncle length (35.14%) followed by leaf area per plant (33.19%), grain yield per plant (26.71%), and the number of grains per spike (25.85%). Similarly, the high genetic advance for leaf area per plant was observed by Kalariya and Monpara [12] and

Imran et al., [13]. For days to heading, genetic advance as percent of mean was comparatively moderate (14.95%) coupled with high heritability (69.89%). High heritability coupled with high genetic advance as percent of mean, was reported by Nukasani et al., [14] and Wolde et al., [15] for the number of effective tillers per meter. Tabassum et al., [16] detected a high estimate of heritability coupled with moderate genetic advance for the number of grains per spike. High heritability for 1000 seed weight was in accordance with the findings of Bhanu et al., [17].

Correlation coefficients

In plant breeding, various yield attributing traits are handled together by the plant breeders, because most of the traits are correlated with each other. Economic yield or grain yield, in most of the crops, is referred to as a major trait that results from either additive action or the multiplicative interactions of several component traits that are termed as yield components (Table 3). In the present investigation, a non-significant and positive correlation between the number of tillers per meter and grain yield ($r_g = 0.017$ and $r_p = 0.015$) was observed. A similar result was recorded by Singh and Singh (1999) [18] and Khan et al., [19]. Correlation analysis showed that the character number of grains per spike had a positive and highly significant association with grain yield per plant ($r_g = 0.838$ and $r_p = 0.780$). A positive and significant correlation for number of 1000 seed weight ($r_g = 0.636$ and $r_p = 0.563$), harvest index ($r_g = 0.640$ and $r_p = 0.592$), leaf area

Table 4. Direct and indirect effects of yield component traits on grain yield in Bread wheat

S.N.	Character	DH	DM	PH	TIL/M	GPS	TGW	LA	PL	SL	Pro	SV	HI	Genotypic correlation with GY
1	DH	**0.046**	-0.433	0.414	0.008	0.017	-0.133	0.046	0.211	-0.009	0.026	-0.020	-0.295	**0.018**
2	DM	0.036	**-0.553**	0.415	0.008	-0.002	0.142	-0.026	0.217	0.008	-0.040	0.025	-0.346	**-0.115**
3	PH	0.028	-0.340	**0.675**	0.005	0.087	0.044	-0.110	0.095	0.012	-0.044	-0.025	-0.255	**0.171**
4	TIL/M	-0.007	0.080	-0.070	**-0.056**	0.062	-0.011	0.029	-0.091	-0.006	-0.046	0.072	0.061	**0.017**
5	GPS	0.001	0.001	0.089	-0.005	**0.658**	-0.279	-0.071	0.062	0.007	-0.060	0.037	0.396	**0.838**
6	TGW	-0.012	0.160	-0.060	-0.001	0.376	**-0.489**	-0.081	-0.033	0.002	-0.032	0.047	0.759	**0.635**
7	LA	0.009	-0.063	0.328	0.007	0.207	-0.175	**-0.227**	0.092	0.016	-0.041	0.017	0.292	**0.463**
8	PL	-0.024	0.298	-0.159	-0.012	-0.101	-0.040	0.051	**-0.404**	-0.011	0.074	-0.000	0.087	**-0.243**
9	SL	0.012	-0.136	0.246	0.010	0.142	-0.041	-0.112	0.138	**0.033**	-0.012	-0.027	0.154	**0.406**
10	Pro	-0.005	0.104	-0.142	0.012	-0.187	0.074	0.044	-0.141	-0.001	**0.211**	-0.091	-0.041	**-0.164**
11	SV	0.005	0.078	0.094	0.022	-0.138	0.130	0.021	-0.001	0.005	0.108	**-0.178**	-0.244	**-0.095**
12	HI	-0.016	0.228	-0.205	-0.004	0.310	-0.441	-0.078	-0.042	0.006	-0.010	0.051	**0.841**	**0.6395**

per plant ($r_g = 0.464$ and $r_p = 0.434$), and spike length ($r_g = 0.407$ and $r_p = 0.383$) with grain yield was observed. Similar findings were reported by Dabi et al., [20] and Males et al., [21]. Peduncle length ($r_g = -0.243$ and $r_p = -0.229$), Protein ($r_g = -0.164$) and sedimentation value ($r_g = -0.095$ and $r_p = -0.043$) showed a significant and negative correlation with grain yield per plant. These results are in accordance with the findings of different researchers [21, 22-23] and Rathod et al., [24] who also reported a negative correlation of peduncle length and protein content with grain yield per plant.

Path coefficient analysis

Two characters may demonstrate correlation as they are associated with a common third one. Thus, it is essential to employ a method that considers the true relationship between the variables. In addition to the extent of such relationships, path coefficient analysis estimates the direct effect of one variable upon the other and allows separation of correlation coefficients into components of direct and indirect effects. Partitioning of correlations provides a direct and indirect involvement of characters on dependent attribute and thus form the basis for upgrading in plant breeding.

The residual effect (0.229) in path coefficient analysis was considerably low indicating a sound explanation of the characters under study and a high contribution of independent traits to the dependent trait (grain yield) as shown in Table 4, Figure 1. Harvest index (0.841) had the highest direct contribution towards grain yield per plant followed by plant height (0.675), number of grains per spike (0.658) and

protein content (0.211). Days to heading had a poor direct effect (-0.553) on grain yield but a moderate indirect effect *via* plant height (0.415) and peduncle length (0.217). These findings are in agreement with Pooja et al., [25] for days to heading. The number of effective tillers per meter had a poor direct effect (-0.056) and a medium indirect effect *via* leaf area per plant (0.029) and harvest index (0.061). 1000 grain weight had a poor direct effect (-0.489) on grain yield but a moderate indirect effect *via* sedimentation value (0.037) and harvest index (0.759) Pooja et al., [25] reported a negative direct effect on grain yield. Leaf area per plant had a poor direct effect (-0.227) on grain yield and a medium indirect effect *via* plant height (0.298) and harvest index (0.292). Ayer et al., [26] reported contradictory results than current findings for leaf area per plant. Peduncle length had a poor indirect effect (-0.404) on grain yield but a moderate indirect effect via days to maturity (0.298) and harvest index (0.087). Sedimentation value had a poor indirect effect (-0.178) and a moderate indirect effect *via* 1000 grain weight (0.130) and protein content (0.108) on grain yield.

The analysis of variance revealed highly significant differences among the mean square of genotypes studied indicating the presence of sufficient variability and ample scope for selection. High heritability associated with high genetic advance as percent of mean was found for the characters *viz.*, number of tillers per meter, number of grains per spike, and grain yield per plant which indicated the dominance of additive genes, and therefore selection would be rewarded for improvement of these characters. Association studies showed that plant height, the number of grains per spike, 1000 seed weight, leaf area per plant, spike length, and harvest index were significantly and positively correlated with grain yield at both phenotypic and genotypic levels. Correlation studies exhibited that quality traits and yield were negatively correlated suggesting a need for different programs for quality and agronomic improvement of wheat. Path analysis revealed the highest positive and direct effect towards grain yield per plant from harvest index followed by plant height, the number of grains per spike, protein content, days to heading, and spike length, whereas days to maturity had the highest negative and direct effect on grain yield per plant followed by peduncle length, leaf area per plant, and sedimentation value. Hence, harvest index, plant height, number of grains per spike, protein content, days to heading, and spike length may be given due importance in the selection program to improve the grain yield in bread wheat.

Acknowledgments

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