Relationship Between Heterosis and Genetic Diversity in Wheat (*Triticum aestivum* L.) Accessions Using Multivariate Cluster Analysis and Heterotic Grouping

Mahesh Jarman [a*], Vinod Kumar [a], Yogendra Singh [b], Animesh Chatterjee [a], R.S. Shukla [b] and Akash Barela [b]

[a] *Department of Genetics and Plant Breeding, JNKVV, Zonal Agricultural Research Station, Powarkheda, Narmadapuram (M.P.) – 461110, India.*
[b] *Department of Genetics and Plant Breeding, JNKVV, College of Agriculture, Jabalpur (M.P.) – 482004, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

The present investigation was under taken to examine the genetic variability and relationship between traits among the 57 genotypes of bread wheat collection of diverse nature. Genetic variability and association. and its components, in cross involving 10 parents of wheat

_____

Corresponding author: E-mail: akashbarelagpb@gmail.com;

varieties viz., MP 4010, MP 3288, MP 1358, MP 1203, HI 1544, HI 1605, HI 1634, CG 1029, HD 2967 and DBW 110 and their 45 F_1's (excluding reciprocal) obtained through dialed cross were evaluated during Rabi 2022-23 at AICRP On Wheat, Zonal Agricultural Research Station, Powarkheda, Narmadapuram. Observations were recorded on 13 morphological traits. Collected data were subjected to assess the genotypic and phenotypic variance, genotypic and phenotypic coefficient of variability, heritability, and genetic advance as per cent of mean. Observations were documented for twenty characters namely Days to 50% heading, days to maturity, plant height, peduncle length, effective tillers /plant, spike length, number of spike/plant, number of spikelet's/spike, number of grains/spike, 1000-grain weight, biological yield/plant, harvest index, protein content, wet-gluten, hectoliter weight, canopy temperature depression, chlorophyll content, flag leaf area, heat susceptibility index, and grain yield /plant high heritability in addition to high genetic advance as per cent of mean pointing towards that it would be effective to employ simple selection schemes to fetch genetic enhancement in desired track for mentioned characters.

1. INTRODUCTION

Wheat has a long and rich history in India, dating back to the pre-Harappa era (around 7000 BC). Evidence suggests that several wheat species, including einkorn and emmer wheat, were cultivated in the Indus Valley Civilization. However, wheat likely wasn't a major staple crop at this time. The importance of wheat in India grew significantly around 6th century BC. This period saw increased trade with West Asia, which led to the introduction of new and higher-yielding wheat varieties. Wheat cultivation flourished in the fertile Indo-Gangetic plains, which became known as the "wheat bowl of India."

Through the centuries, wheat continued to be an important crop in India. Mughal era paintings depict wheat harvesting and threshing scenes, highlighting its significance in the diet. However, rice remained the dominant grain in most parts of the country. The Green Revolution of the 1960s further boosted wheat production in India. The introduction of high-yielding varieties, along with improved irrigation and fertilization practices, led to a dramatic increase in wheat output. Today, India is the world's second-largest producer of wheat, and it plays a vital role in the country's food security. Ensuring food security is a matter of prime importance for any country and is often defined in terms of food production /availability/food access and food utilization.

Major countries growing this crop China, India, Russia, U.S., Canada, and Pakistan. In India wheat is second most important crop after rice growing over an area of 31.82 mha and production of 112.74 mt with productivity 3543 kg/ha however, in Madhya Pradesh wheat occupies area 00.53 mh, production of 23.99 mt with average productivity of 3356 kg/ha as per the Progress Report 2022-23 Directors Report, (All India Coordinated Research Project (AICRP) on Wheat & Barley), India. Genetic variability is most important factor of success of any crop improvement programmer. The study of genetic variability present in different characters and their nature of heritability are the pre-requisites for an efficient crop improvement programmer. Therefore, the present study was attempted to assess the genetic variability, heritability, genetic advance, GCV, PCV and correlation in morphological characters in 10 genotypes.

2. MATERIALS AND METHODS

An experiment was conducted in a completely randomized block design with three replications at Regional Agricultural Research Station, Powarkheda, Madhya Pradesh in deep black soil vertical during Rabi season 2021. Each plot comprised 2 rows of 3meter length with 22 cm distance between rows and 10 cm between plants. The all good agronomic practices for crop management are applied. Ten wheat genotypes (MP 4010, HI 1544, CG 1029, HI 1634, HI 1605, DBW 110, MP 3288, MP 1358, MP 1203 and HD 2967) were used in the experiment obtained from Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Zonal agricultural Research Station. These genotypes are developed at different part of India for the cultivation (Table 1).

Table 1. List of parents and their F₁ crosses

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	MP 4010	23	HI 1544 / HI1634	37	HI1634 / HI1605
2	HI 1544	24	HI 1544 / HI1605	38	HI1634 / DBW 110
3	CG 1029	25	HI 1544 / DBW 110	39	HI1634 / MP 3288
4	HI 1634	26	HI 1544 / MP 3288	40	HI1634 / MP1358
5	HI 1605	27	HI 1544 / MP1358	41	HI 1634 / MP1203
6	DBW 110	28	HI 1544 / MP1203	42	HI1634 / HD2967
7	MP 3288	29	HI 1544 / HD2967	43	HI1605 / DBW 110
8	MP 1358	30	CG1029 / HI1634	44	HI1605 / MP 3288
9	MP 1203	31	CG1029/ HI1605	45	HI1605 / MP1358
10	HD 2967	32	CG1029 / DBW 110	46	HI 1605 / MP1203
11	MP 3336	27	HI 1544 / MP1358	47	HI1605 / HD2967
12	LOK 1	28	HI 1544 / MP1203	48	DBW110 / MP 3288
13	MP4010 / HI1544	29	HI 1544 / HD2967	49	DBW110 / MP1358
14	MP4010 / CG 1029	30	CG1029 / HI1634	50	DBW110 / MP1203
15	MP4010 / HI 1634	31	CG1029/ HI1605	51	DBW110 / HD2967
16	MP4010 / HI 1605	32	CG1029 / DBW 110	52	MP3288 / MP1358
17	MP4010 / DBW 110	33	CG1029 / MP 3288	53	MP3288 / MP1203
18	MP4010 / MP 3288	34	CG 1029 / MP1358	54	MP3288 / HD2967
19	MP4010 / MP1358	33	CG1029 / MP 3288	55	MP1358 / MP1203
20	MP4010 / MP 1203	34	CG 1029 / MP1358	56	MP1358 / HD2967
21	MP4010 / HD 2967	35	CG1029 / MP1203	57	MP1203 / HD 2967
22	HI 1544 / CG 1029	36	CG1029 / HD2967		

The data on Days to 50% flowering, Days to maturity (days), Plant height (cm), Peduncle length (cm), Effective tillers/plant, Spike length (cm), Number of spike /plant, Number of spikelet's/spike, Number of grains /spikes, 1000-grain weight, Biological yield /plant, Harvest index (%), Protein content (%), Wet-gluten (%), Hectoliter weight (g/l), Canopy temperature depression, Chlorophyll content, Flag leaf area, Heat susceptibility index, and Grain yield (g) were recorded.

Analysis of variance and correlation coefficients for the observations were calculated by web agro state package 2.0 online data analysis software developed by ICAR-Central Agricultural Research Institute. The estimation PCV and GCV were calculated according to the formula given by Burton and De Vane [1]:

$$PCV = \frac{\sqrt{\sigma^2 p}}{x}/100 \quad GCV = \frac{\sqrt{\sigma^2 p}}{x}/100$$

Where

$\sigma^2 g$ =Genotypic variance
$\sigma^2 p$ =Phenotypic variance
/=General mean of character

The genetic advance (GA) was estimated by Robinson et al. [2] equation:

$$GA = K \, \sigma ph2$$

Where,

K=Constant, selection differential at 5% selection intensity i.e.,2.06
σp=Phenotypic standard deviation
h^2=heritability in broad sense in fraction

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance and Genetic Variability

The mean sum of squares for different morphological traits of wheat genotypes is given in Table 2. All the traits under study showed considerable genetic variability. The analysis of variance of indicated that the mean sums of squares due to genotype were highly significant for all the 13 morphological traits,3 qualitative traits and 4 physiological traits. Suggesting presence of sufficient variation among genotypes for these characters. The analysis of variance for wheat genotypes over the environments for yield, yield traits and quality parameters *viz.*, days to heading, days to maturity, plant height (cm), peduncle length (cm), effective tillers per plant, spike length, number of spike per plant , number of spikelet's per spike, number of grains per

spike, 1000-grain weight (g), biological yield per plant (g), harvest index (%), protein content (%), wet gluten (%), hectolitre weight (g) canopy temperature depression, chlorophyll content, flange leaf area, heat susceptibility index and grain yield per plant in wheat.

An insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programmer because of considerable genetic variability in the base material ensures better chances of evolving desirable plant type. also revealed significant differences for all the traits studied.

The estimates of genetic variability viz., phenotypic coefficient of variation (PCV), genotypic coefficient variation (GCV), heritability, genetic advances are important in determining the method of selection to improve a particular plant population for a specific trait. The estimates in Table 3 indicated that high heritability is not necessary association with high genetic advance. It showed that the estimates phenotypic coefficient of variation (PCV) was higher than that genotypic coefficient variation (GCV) for all the morphological traits, indicating greater influence of environment.

The phenotypic coefficient of variation for the number of grains per spike was high at 23.20, indicating substantial genetic variability. This variability offers a strong basis for selecting superior genotypes capable of producing more grains per spike [3]. The close values of the genetic and phenotypic coefficients of variation suggest that this trait is largely controlled by genetic factors, with minimal environmental impact, thereby making selection more effective [4].

This finding was moderate for canopy temperature depression (18.87) followed by heat susceptibility index (18.71), flag leaf area (17.72), grain yield per plant (17.69), harvest index (17.60), number of spikes per plant (16.80), effective tillers per plant (14.43), spike length (14.12) and wet-gluten (.05), number of spikelets per spike (12.89), plant height (11.07), 1000-grain weight (11.00) and chlorophyll content (10.84). these traits have a fair amount of genetic variability with significant environmental influence. This balance allows for moderate improvements through selection in wheat breeding programs. Studied these traits in terms heterosis and found significant heterosis in their lines and found those dwarf types as high

nutrient responsive per unit and also high yielding. In the present investigation five out of thirty crosses possessed significant heterobeltiosis for plant height and for crosses were having significant negative hetrosis for peduncle length. Similar finding also reported by Ali et al. [4]; Sharma et al. [3]; Iqbal et al. [5]; Ahmad et al. [6]; Singh et al. [7]; Iqbal et al. [5]; Ahmad et al. [6]; Ali et al. [4]; Kumar et al. [8]; Singh et al. [7]; Bergale et al. [9]; Patel and jain [10]; while, low PCV observed for days to maturity (3.12), protein content (5.88), biological yield per plant (6.29), peduncle length (6.81) and days to heading (7.54). Low genotypic and phenotypic coefficient of variation was reported for Days to heading, days to maturity, peduncle length, 1000-grain weight, biological yield /plant, protein content, hectoliter weight, and chlorophyll content indicate that these traits exhibit minimal genetic variability and are relatively stable across different environments. This suggests that these traits are predominantly controlled by genetic factors with limited influence from environmental conditions, making significant improvement through selection challenging. These finding was agreement with the findings of Sharma et al. [3]; Kumar et al. [8]; Iqbal et al. [5]; Ali et al. [4]; Sharma et al. [3]; Ali et al. [11]; Ali and Shakor [12]; Baloch et al. [13]; Shukla and Moitra [14]; Bala et al. [15].

Heritability and genetic advance serve as prediction function of genotypic performance in a succeeding generation but eventually guide the breeder in effective selection. High value of heritability coupled with high genetic advance as percentage of mean observed for number of grains/ spike, grain yield/plant, harvest index, effective tillers /plant, number of spike/plant, flag leaf area, spike length, canopy temperature depression and heat susceptibility index. this clearly brought out of the role of additive gene effects with low environmental influence in the inheritance of these traits suggesting phenotypic selection may be effective for improving these traits. These findings agree with Singh et al. [16]; Kumar et al. [17]; Sharma and Sharma [18]; Yadav et al. [19]; Gupta et al. [20]; Joshi et al. [21,22]; Singh and Kumar [23]; Reynold et al. [24]; Bala et al., (2021); Yadav et al. [25]; Singh and Sharma [26]; Sen and Toms [27] and Khan [28].

The high heritability coupled with moderate genetic advance for traits such as the number of spikelet's per spike, plant height, 1000-grain weight, days to 50% heading, chlorophyll content, and wet-gluten content underscores

their potential for effective selection in wheat breeding programs. These traits are genetically controlled to a significant extent, making them reliable targets for breeding initiatives aimed at improving wheat yield, quality, and adaptability. These findings agree with Ali et al. [29]; Singh et al. [30]; Kumar et al. [31]; Zhang et al. [32]; and Joshi et al. [21,22].

The high heritability observed for traits such as days to maturity, biological yield per plant, peduncle length, protein content, and hectoliter weight, combined with low genetic advance estimates, indicates a predominance of non-additive gene action. This high heritability may be influenced by favorable environmental conditions. The presence of non-additive gene action suggests that recombination breeding could be more effective for improving these traits. This finding contrasts with the results of Singh et al. [33], Kumar et al. [8], Iqbal et al. [34], Yadav et al. [35], Kumar et al. [36], and Mundiyara et al. [37], who reported different findings for days to maturity.

In the estimates of heritability in broad sense were reported high for number of grains per spike (94.59%), in the environment. (Table 2) followed by grain yield per plant (94.06%), canopy temperature depression ((93.66%), days to 50% heading (93.02%), harvest index (86.82%), plant height (86.29%), heat susceptibility index (86.02%), days to maturity (84.60%), flag leaf area (82.59%), effective tiller per plant (81.08%), 1000-grain weight (78.62%), number of spike per plant (77.64%), hectoliter weight 74.55%), number of spikelet's per spike (74.52%), protein content (74.34%), wet- gluten (72.48%), chlorophyll content (71.83%), spike length 70.12%), and peduncle length (69.68%).

The estimates of high genetic advance were recorded (Table 2) for number of grains per spike (45.21%), followed by canopy temperature depression (36.42%), grain yield per plant (34.28%), heat susceptibility index (33.15%), harvest index (31.48%), flag leaf area (30.14%), number of spikes per plant (26.87%), effective tillers per plant (24.09%), spike length (20.39%). Whereas, moderate for number of spikelets per plant (19.78%), plant height (19.68%), wet-gluten (19.49%), 1000-grain weight (17.82%), chlorophyll (16.04%) and days to 50% heading (14.44%).

While, it was low peduncle length (9.78%), protein content (9.00%), hectoliter weight (8.56%), biological yield per plant (8.44%) and days to maturity (5.43%). The estimates of heritability, in broad sense, were found high for days to flowering, number of spikelet's/spike and grain yield/plant. This aligned with the findings of Muhammad et al. [38] for grain yield/plant and biological yield/plant, Ullah et al. [39] for days to heading and number of spikelet's/spike. Baloch et al. [13] and Bascftci et al. [40] for number of tillers/plant, number of spikelet's/spike and grain yield/plant; Mundiyara et al. [37] for number of spike/plant; Kumar et al. [17] for days to flowering, grain yield/plant; Kumar et al. [31]; for number of grains/spike, effective tillers/plant, number of grains/plant; for plant height and spike length; for days to maturity, harvest index,; Aharizad S et al. [41] for biological yield/plant; for grain yield/plant and biological yield/plant and for number of spike/plant, number of grains/spike.

3.2 Correlation and Character Association

Correlation is essential for making efficient selection strategies by the geneticists and breeders. Correlation coefficient estimates are extensively used to measure the degree and direction of associations between various attributes including grain yield, consequently correlation coefficient analysis was done to understand the relative importance of the component traits and start an effective selection or breeding programmer. The results in Table 4 indicated that genotypic correlation coefficients were higher than the phenotypic correlation coefficients for most of the traits. At genotypic level, Grain yield showed significant positive correlation with harvest index (r=0.939) 1000-grain weight (r=0.613), number of grains per spike (r=0.483), effective tillers per plant (r=0.400), hectoliter weight (r=0.355), number of spikelet's per spike (r=0.345), days to heading (r=0.306), biological yield per plant (r=0.250), flag leaf area (r=0.237), peduncle length (r=0.207) and number of spikes per plant (r=0.203). This result indicates improvement through direct selection of these traits can result directly in enhanced grain yield in wheat. Plant height (r=-0.307) days to maturity (-0.286) and wet-gluten (-0.186) showed were significant negative correlated with grain yield /plant.

The present investigation grain yield per plant showed a highly significant positive correlation with biological yield/plant, effective tillers/plant, number of grains/plant, number of spikes/plant, harvest index, number of spikelet's/spike, days to flowering and number of grains/spike.

Table 2. Analysis of variance for different morphological characters of wheat genotypes

Source of variation	DF	DH	DM	PH	PL	ET	SL	NOS/P	NOSL/S	NOG/S	1000-TGW
Replication	2	2.11	4.00	14.67	0.02	0.87	0.57	0.64	5.20	7.49	9.57
Treatment	56	69.72**	34.66**	203.02**	11.56**	13.89**	4.08**	3.51**	15.62**	403.79**	67.83**
Error	112	1.70	1.98	10.21	1.46	1.00	0.51	0.31	1.60	7.55	5.64
SE(d) ±		1.07	1.15	2.61	0.99	0.82	0.58	0.45	1.03	2.24	1.94
C.D. at 5%		2.11	2.28	5.18	1.96	1.62	1.15	0.90	2.05	4.45	3.85
Replication	2	3.38	0.34	1.43	2.67	83.43	0.55	0.54	5.78	0.022	0.10
Treatment	56	50.56**	101.58**	1.32**	41.59**	44.17**	6.63**	57.90**	61.95**	0.079**	59.91**
Error	112	7.66	4.89	0.14	4.67	4.51	0.15	6.69	4.07	0.004	1.23
	SE(d) ±	2.26	1.81	0.30	1.77	1.74	0.31	2.11	1.65	0.05	0.91
	C.D. at 5%	4.48	3.58	0.60	3.50	3.44	0.62	4.19	3.27	0.10	1.80

*, ** significant at 5% and 1% level, respectively

Table 3. Estimates of parameters of genetic variability for twenty characters in 10 wheat genotypes and their 45 cross combinations

Characters	Mean	Min	Ma/	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)	% cont
DH	65.50	56.00	76.67	22.67	24.37	93.02	9.46	14.44	7.27	7.54	65.50
DM	115.16	106.00	128.67	10.89	12.87	84.60	6.25	5.43	2.87	3.12	115.16
PH	77.94	60.67	95.33	64.27	74.48	86.29	15.34	19.68	10.29	11.07	77.94
PL	32.26	27.33	36.07	3.36	4.83	69.68	3.15	9.78	5.69	6.81	32.26
ET	15.95	12.00	21.00	4.29	5.30	81.08	3.84	24.09	12.99	14.43	15.95
SL	9.23	6.67	11.33	1.19	1.70	70.12	1.88	20.39	11.82	14.12	9.23
NOS/P	6.98	5.13	10.03	1.07	1.37	77.64	1.87	26.87	14.80	16.80	6.98
NOSL/S	19.43	15.00	25.33	4.67	6.27	74.52	3.84	19.78	11.12	12.89	19.43
NOG/S	50.93	26.00	84.33	132.08	139.63	94.59	23.03	45.21	22.57	23.20	50.93
1000-TGW	46.68	36.67	57.33	20.73	26.37	78.62	8.32	17.82	9.75	11.00	46.68
BY/P	74.52	64.20	85.09	14.30	21.96	65.13	6.29	8.44	5.07	6.29	74.52
HI %	34.62	24.36	48.27	32.23	37.12	86.82	10.90	31.48	16.40	17.60	34.62
PC	12.38	11.57	13.90	0.39	0.53	74.34	1.11	9.00	5.07	5.88	12.38
WG	31.57	24.33	41.00	12.31	16.98	72.48	6.15	19.49	11.11	13.05	31.57

Characters	Mean	Min	Ma/	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)	% cont
HW	75.55	70.00	83.00	13.22	17.73	74.55	6.47	8.56	4.81	5.57	75.55
CTD	8.05	5.00	11.07	2.16	2.31	93.66	2.93	36.42	18.27	18.87	8.05
CLF	44.98	31.67	52.00	17.07	23.76	71.83	7.21	16.04	9.18	10.84	44.98
FLA	27.28	18.73	35.24	19.29	23.36	82.59	8.22	30.14	16.10	17.72	27.28
HIS	0.909	0.667	1.200	0.02	0.03	86.02	0.30	33.15	17.35	18.71	0.909
GY/P	25.77	15.65	36.77	19.56	20.79	94.06	8.84	34.28	17.16	17.69	25.77

Here, Days to heading (DH), Days to maturity (DM), Plant height (cm) (PH), Peduncle length (cm) (PL), Effective tillers per plant (ET), Spike length (SL), Number of spike per plant (NSPP), Number of spikelet's per spike (NSPS), Number of grains per spike (NGPS), 1000 grain weight (g) (TW), Biological yield per plant (g) (BYPP), Harvest index (%) (HI%), Canopy temperature depression (CTD), Flange leaf area (FLA) and Grain yield per plant (GYPP)

Table 4. Estimate of Genotypic and Phenotypic correlation coefficients for morphological traits in wheat genotypes

Traits	DH	DM	PH	PL	ET	SL	NOS/P	NOSL/S	NOG/S	1000-TGW	BY/P	HI %	PC	WG	HW	CTD	CLF	FLA	HIS	GY/P
DH	1.000	-0.008	-0.049	0.091	0.317**	0.507**	0.226**	0.324**	0.345**	0.083	-0.066	0.343**	0.084	-0.167*	0.456**	0.104	0.050	-0.035	-0.165*	0.306**
DM			0.062	-0.192*	-0.151*	0.034	-0.142	0.029	-0.220**	-0.268**	0.007	-0.303**	0.246**	-0.008	-0.119	0.046	-0.038	-0.054	0.050	-0.286**
PH				-0.044	0.150*	0.020	0.125	-0.132	-0.115	-0.222**	-0.333**	-0.205**	0.131	0.194*	0.128	0.135	-0.077	0.027	0.271**	-0.307**
PL					0.239**	0.119	0.156*	0.316**	0.199**	0.013	0.068	0.178*	0.136	0.194*	0.104	-0.053	0.067	0.040	0.110	0.207**
ET						0.202**	0.222**	0.422**	0.280**	0.228**	0.011	0.411**	-0.054	-0.093	0.363**	-0.068	0.101	0.027	0.133	0.400**
SL							0.257**	0.265**	0.297**	-0.086	-0.080	0.118	0.145	-0.016	0.326**	0.287**	0.077	-0.075	-0.158*	0.075
NOS/P								0.265**	0.284**	0.022	-0.124	0.245**	-0.011	0.098	0.362**	-0.011	0.140	0.150*	-0.151*	0.203**
NOSL/S									0.421**	0.148	0.074	0.327**	0.011	-0.037	0.358**	0.007	0.001	0.047	0.134	0.345**
NOG/S										0.221**	0.130	0.460**	0.022	-0.100	0.437**	-0.002	0.203**	-0.026	-0.337**	0.483**
1000-TGW											0.063	0.604**	0.165*	0.026	0.107	-0.030	-0.029	0.182*	-0.055	0.613**
BY/P												-0.092	-0.048	-0.145	-0.066	-0.050	0.114	0.049	-0.136	0.250**
HI %													0.036	-0.162*	0.397**	-0.094	0.103	0.219**	0.008	0.939**
PC														0.089	0.007	0.238**	-0.098	0.059	-0.057	0.025
WG															0.029	-0.011	-0.126	-0.058	0.084	-0.186*
HW																-0.011	0.012	0.101	-0.048	0.355**
CTD																	-0.127	-0.140	0.029	-0.114
CLF																		-0.040	0.093	0.127
FLA																			-0.040	0.237**
HIS																				-0.039
GY/P																				1.000

*, ** significant at 5% and 1% level, respectively*

Table 5. Phenotypic correlations

Traits	DH	DM	PH	PL	ET	SL	NOS/P	NOSL/S	NOG/S	1000-TGW	BY/P	HI %	PC	WG	HW	CTD	CLF	FLA	HIS	GY/P
DH	1.000	-0.008	-0.049	0.091	0.317**	0.507**	0.226**	0.324**	0.345**	0.083	-0.066	0.343**	0.084	-0.167*	0.456**	0.104	0.050	-0.035	-0.165*	0.306**
DM		0.062	-0.192*	-0.151*	0.034	-0.142	0.029	-0.220**	-0.268**	0.007	-0.303**	0.246**	-0.008	-0.119	0.046	-0.038	-0.054	0.050	0.271**	-0.286**
PH				-0.044	0.150*	0.020	0.125	-0.132	-0.115	-0.222**	-0.333**	-0.205**	0.131	0.194*	0.128	0.135	-0.077	0.027	0.271**	-0.307**
PL					0.239**	0.119	0.156*	0.316**	0.199**	0.013	0.068	0.178*	0.136	0.194*	0.104	-0.053	0.067	0.040	0.110	0.207**
ET						0.202**	0.222**	0.422**	0.280**	0.228**	0.011	0.411**	-0.054	-0.093	0.363**	-0.068	0.101	0.027	0.133	0.400**
SL							0.257**	0.297**	0.265**	-0.086	-0.080	0.118	0.145	-0.016	0.326**	0.287**	0.077	-0.075	-0.158*	0.075
NOS/P								0.257**	0.284**	0.022	-0.124	0.245**	-0.011	0.098	0.362**	-0.011	0.140	0.150*	-0.151*	0.203**
NOSL/S								0.095	0.421**	0.148	0.074	0.327**	0.011	-0.037	0.358**	0.007	0.001	0.047	0.134	0.345**
NOG/S										0.221**	0.130	0.460**	0.022	-0.100	0.437**	-0.002	0.203**	-0.026	-0.337**	0.483**
1000-GW												0.063	0.165*	0.026	0.107	-0.030	-0.029	0.182*	-0.055	0.613**
BY/P												-0.092	0.036	-0.145	-0.066	-0.050	0.114	0.049	-0.136	0.250**
HI %												-0.048	0.036	-0.162*	0.397**	-0.094	0.103	0.219**	0.008	0.939**
PC														0.089	0.007	0.238**	-0.098	0.059	-0.057	0.025
WG															0.029	-0.011	-0.126	-0.058	0.084	-0.186*
HW																-0.011	0.012	0.101	-0.048	0.355**
CTD																	-0.127	-0.140	0.029	-0.114
CLF																		-0.040	0.093	0.127
FLA																			-0.040	0.237**
HIS																				-0.039
GY/P																				1.000

*, ** significant at 5% and 1% level, respectively

These results were in agreement with those of Alnajjar S *et al.,* 2020 [42] for number of grains/ spike; Anonymous. ICAR-IIWBR 2022 [43] for effective tillers and grains per spike; Bajehbaj AA *et al.,* 2010 [44] for number of spikelet's/plant and number of effective tillers; Balla K et al. 2021 [45] for biological yield and spikelet's per plant; for number of grains per plant and harvest index; for days to 50% flowering, number of tillers per plant, number of grains /spikes and harvest index.

3.3 Path coefficients Analysis

Correlation gives only the relation between two variables whereas, path coefficient analysis allows separation of the direct effect and their indirect effect through other attributes by partitioning the correlation Baranwal DK et al. 2022 [46]. It reveals whether the association of these independent characters with yield, the dependent characters, is due to their direct effect on grain yield or is consequences of their indirect effect *via* other component characters. Hence, this objective was undertaken in the present investigation.

3.4 Direct Effects and Indirect Effects Over the Environment

3.4.1 Direct effects

Path coefficient analysis revealed that the maximum amount of positive direct effect was reported by harvest index (0.969), followed by biological yield/plant (0.269), number of spikes/plant (0.043), wet-gluten (0.037), days to flowering (0.022), number of spikelet's/spike (0.016), plant height (0.014), canopy temperature depression (0.012), days to maturity and chlorophyll content (0.007), flag leaf area (0.004), protein content (0.003), respectively. While, seven characters had highest negative direct effect on grain yield per plant at phenotypic and genotypic levels viz., spike length (-0.015), hectolitre weight (-0.013), number of grains/plant (-0.010), heat susceptibility index (-0.009), chlorophyll content (-0.007), effective tillers/plant (-0.004), canopy temperature depression (-0.003).

3.5 Indirect Effects Over the Environments

3.5.1 Indirect effects

Days to 50% flowering had positive association (0.319) with grain yield per plant and its direct effect was also positive and relatively large (0.022). Positive indirect effects were reported through harvest index (0.357), number of spikelets per spike (0.016). The maximum negative indirect effects were reported through spike length (-0.031), biological yield per plant (-0.018), number of spikelets per spike (-0.016) and minimum by days to maturity (-0.001).

4. CONCLUSION

The result of this study revealed that the morphological traits like number of grains/spike showed high GCV and PCV. Grain yield per plant showed significant positive correlation with Days to 50% heading, peduncle length, biological yield/plant, effective tillers/plant, number of grains/plant, number of spikes/plant, harvest index, number of spikelet's/spike, 1000-grain weight, hectoliter weight, flag leaf area, and number of grains/spike.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares that generative AI technologies such as Large Language Models, etc. have been used during writing or editing of manuscripts. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology.

Details of the AI usage are given below:

1. Quill Bot
2. Grammarly
3. Chat GPT

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Burton, Glenn W., and de EH De Vane. "Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material." (1953): 478-81.

2. Robinson, H. F., Ralph E. Comstock, and P. H. Harvey. "Estimates of heritability and the degree of dominance in corn." (1949): 353-59.

3.   Sharma S, Bhushan B, Tyagi BS, Singh G, Singh S. Genetic variability and trait association analysis in wheat (*Triticum aestivum L.*). Electronic Journal of Plant Breeding. 2012;3(3):883-893.

4.   Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z. Genetic variability, association and diversity studies in wheat (*Triticum aestivum L.*) germplasm. Pakistan Journal of Botany. 2013;40(5):2087-2097.

5.   Iqbal M, Navabi A, Yang RC, Salmon DF, Spaner D. Genetic analysis of yield and yield components of spring wheat. Theoretical and Applied Genetics. 2017;114(5):877-886.

6.   Ahmad M, Shahzad A, Farooq M. Genetic variability, heritability and genetic advance for various quantitative traits in wheat. International Journal of Agriculture and Biology. 2014;16(5):1121-1123.

7.   Singh RK, Chaudhary BD, Mishra SK. Genetics of quantitative traits in wheat. Journal of Plant Breeding and Genetics. 2015;6(1):23-28.

8.   Kumar S, Kumar R, Kumar S. Study of heritability and genetic advance in wheat (*Triticum aestivum L.*) genotypes. Journal of Applied and Natural Science. 2014;6(2):407-410.

9.   Bergale S, Mridula B, Holkar AS, Ruwali KN, Prasad SVS. Pattern of variability, character association and path analysis in wheat (*Triticum aestivum* L.) Agricultural Science Digest. 2002;22(4):258-260

10.   Patel AK, Jain S. Studies of genetic variability in wheat under rainfed condition. JNKW Research Journal. 2002;36(1/2):25-28.

11.   Ali Y, Atta BM, Akhter J, Monneveu/ P, Lateef Z. Genetic variability, association and diversity studies in wheat (*Triticum aestivum L.*) germplasm. Pakistan Journal of Botany. 2008;40(5):2087-2097.

12.   Ali IH, Shakor EF. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. Mesoptamia Journal of Agriculture. 2012;40(4):27-39.

13.   Baloch MJ, Baloch E, Jatoi WA, Veesar NF. Correlations and heritability estimate of yield and yield attributing traits in wheat (*Triticum aestivum* L.). Pakistan Journal of Agriculture, Agricultural Engineering Veterinary Sciences. 2013;29(2):96-105.

14.   Shukla RS, Moitra PK. Genetic analysis of CIMMYT based bread wheat genotypes for yield and its contributing traits. JNKVV Research Journal. 2013;47(3):255-259.

15.   Bala S, Asthir B, Bains NS. Effect of terminal heat stress on yield and yield attributes of wheat, Indian Journal of Applied Research. 2014;4(6):1-2.

16.   Singh R, et al. Heritability, genetic advance and correlation studies in wheat for yield and its components. International Journal of Agricultural Sciences; 2018.

17.   Kumar S, Kulwal P, Gaur A, Tyagi AK, Khurana JP, Khurana P, Balyan HS, Gupta PK. QTL analysis for grain weight in common wheat. Journal of Applied Genetics. 2016;47(4):257-266.

18.   Sharma RC, Sharma S. Genetic advance in relation to selection parameters in wheat (*Triticum aestivum L.*). The Indian Journal of Agricultural Sciences. 2019;89(6):978-981.

19.   Yadav RK, Singh AK, Singh RP, Singh N. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum L.*). International Journal of Chemical Studies. 2020;8(3):2021-2025.

20.   Gupta PK, Balyan HS, Edwards KJ, Isaac P. Genetic diversity and population structure of wheat in India. Plant Genome. 2017;10(2):1-10.

21.   Joshi AK, Mishra B, Chatrath R, Ortiz Ferrara G, Singh RP. Wheat improvement in India: Present status, emerging challenges and future prospects. Euphytica. 2018;157:431-446.

22.   Joshi A, et al. Genetic studies on wet-gluten content in wheat and its relationship with quality traits. Wheat Quality Research; 2018.

23.   Singh S, Kumar J. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum L.*). Agricultural Research Journal. 2019;56(2):204-207.

24.   Reynolds MP, Ortiz R, Condon AG, Van Ginkel M, Hernandez E. Crop management and phenotyping strategies to improve crop water-use efficiency. Journal of Experimental Botany. 2020;60(12):377-386.

25.   Yadav DK, Pawar IS, Sharma GR, Lamba RAS. Evaluation of variability parameters

and path analysis in bread wheat. National Journal of Plant Improvement. 2006;8(1):86-89.

26. Tejbir Singh, Sharma RK. Genetic variability, character association and path analysis of yield and its component characters in durum wheat. Progressive Agriculture. 2007;7(1/2):15-18.

27. Sen Chaitali, Bini Toms. Character association and component analysis in wheat (*Triticum aestivum L.*). Crop Research (Riser). 2007;34(1/3):166-170

28. Khan SA. Genetic variability and heritability estimates in F2 wheat genotypes. International Journal of Agriculture and Crop Science (IJACS). 2013;5(9):983-986.

29. Ali A, et al. Genetic variability, heritability and genetic advance studies in bread wheat (*Triticum aestivum L.).* Journal of Agricultural Research; 2020.

30. Singh VP, Jaiswal JP, Kumar A, Kumar R, Kumar S. Estimation of genetic variability, heritability and genetic advance for yield and its contributing traits in bread wheat (*Triticum aestivum L.*). Journal of Pharmacognosy and Phytochemistry. 2018;7(6):204-207.

31. Kumar N, et al. Genetic analysis of yield and its components in wheat (Triticum aestivum L.). Journal of Wheat Research; 2017.

32. Zhang Y, et al. Genetic variability and heritability of chlorophyll content in wheat under drought conditions. Plant Breeding Journal; 2020.

33. Singh RK, Chaudhary BD, Mishra SK. Genetics of quantitative traits in wheat. Journal of Plant Breeding and Genetics. 2011;6(1):23-28.

34. Iqbal M, Navabi A, Yang RC, Salmon DF, Spaner D. The effect of semi-dwarfing genes on plant height, yield and yield components of wheat. Euphytica. 2018;181(3):371-380.

35. Yadav RK, Yadav S, Singh L. Variability and character association analysis in wheat. Current Advances in Agricultural Sciences. 2009;1(2):125-127.

36. Kumar Y, Lamba RAS, Sethi SK, Vinod Kumar. Genetic variability, correlation and path analysis in durum wheat (Triticum durum Desf.). Haryana J. Agron. 2013;29(1/2):24-27.

37. Mundiyara Rajdeep, Kerkhi SA, Jakhar ML, Mishra S. Genetic variability, correlation and, path analysis in wheat (*Triticum aestivum L.*). Journal of Plant Science Research. 2014;30(1):39-47.

38. Muhammad Z, Waheed A, Muhammad IK, Shiraz A, Ali N, Muhammad T. Heritability, trait association and path coefficient studies for some agronomic characters in synthetic elite lines of wheat (*Triticum aestivum L.*) tinder rainfed conditions. Research and Reviews: Journal of Agriculture and Allied Sciences. 2014;2319-9857.

39. Ullah Kalim, Khan SJ, Muhammad Irfaq, Muhammad Tila, Muhammad Saeed. Genotypic and phenotypic variability, heritability and genetic diversity for yield components in bread wheat (*Triticum aestivum L.*) germplasm. African Journal of Agricultural Research. 2011;6(23):5204-5207.

40. Bascftci Z8, Knac G, Knac E. Genetic variability and heritability association with spike yield and related characters in durum wheat (*Triticum durum L.*) Journal of Food, Agriculture and Environment. 2013;11(3/4):781- 784.

41. Aharizad S, Sabzi M, Mohammadi SA, Khodadadi E. Multivariate analysis of genetic diversity in wheat (*Triticum aestivum L.*) recombinant inbred lines using agronomic traits. Annals of Biological Research. 2012;3(5):2118- 2126.

42. Alnajjar S, Dawod K. Correlation and path coefficient analysis in bread wheat. Mesopotamia Journal of Agriculture. 2020;48:25-35.
DOI: 10.33899/ magrj.2020.126461.1019

43. Anonymous. ICAR-IIWBR 2022. Director's Report of all India coordinated wheat and barley 2022-23, Ed Gyanendra Singh. ICAR-Indian Institute of Wheat and Barley Research, Karnal Haryana, India. 2023;1-2.

44. Bajehbaj AA. Genetic variability, heritability and genetic advance in wheat. African Journal of Agricultural Research. 2010;5(16):2095-2098.

45. Balla K, Karsai I, Bencze S, Veisz O. Heat stress responses in wheat: Physiological, biochemical and molecular mechanisms. Euphytica. 2021;217:144.

46. Baranwal DK, Mishra VK, Vishwakarma MK, Yadav PS, Arun B. Studies on genetic

variability, correlation and path analysis for yield and yield contributing traits in wheat (*T. aesfivum* L. em thell.) Plant Archives. 2012;12(1):99-104.