Plant Archives Vol. 25, Supplement 2, 2025 pp.974-981 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-2.121

EXAMINING VARIABILITY AND COEFFICIENTS OF TRAIT ASSOCIATIONS AMONG WHEAT YIELD AND ITS ATTRIBUTES

Neha[1], Saurabh Singh[2] and Chetariya C.P.[1]*

[1]AIC-DAA, Dept. of Genetics and Plant Breeding, SAGR, Lovely Professional University,
Phagwara, Punjab-144411. India
[2]Department of Crop Physiology, Chandra Shekhar Azad University of Agriculture and Technology (CSAUAT),
Kanpur, Uttar Pradesh-208002, India
*Corresponding authors E-mail: chetariyachana89@gmail.com

(Date of Receiving : 21-03-2025; Date of Acceptance : 22-05-2025)

ABSTRACT

Wheat holds the mantle of being the paramount food crop across the globe. Approximately 40% of the population relies on it for sustenance, thereby constituting 20% of the daily dietary protein intake worldwide. Elevating the variability and yield potential through a consolidated breeding approach especially in self-pollinated crop emerges as the optimal strategy to meet burgeoning global food requisites. Considering these points, study was conducted at Rama University Kanpur (U.P.) with a total of 27 wheat genotypes in RBD to assess the variability and association among ten traits studied, aiming for accurate generation advancement selection. The ANOVA showed significant different among various traits studied. The trait NTPP showed moderate genotypic coefficient of variation and phenotypic coefficient of variation whereas other traits possessed low level of GCV and PCV. High estimates of h^2 (bs) (%) were observed for all the traits except for days to 50% flowering (DFPF), harvest index (HI), biological yield per plant (BYPP) and 1000 seeds weight (g) (TGW). The traits examined displayed minimal genetic advancement. High heritability coupled with high GAM was noted for the number of tillers per plant (NTPP), while spike length and the number of grains per spike exhibited high heritability with moderate GAM. Traits namely NTPP, BYPP and HI depicted positive and significant correlations plus has direct effect on grain yield per plant and early maturity (DM) could be emphasised while advancing parents and genotypes to next generations keeping breeding objective futuristic.

***Keywords* :** *Triticum aestivum*, GCV, PCV, Heritability, Genetic Advance.

Introduction

Wheat stands as a bountiful reservoir of vegetarian protein and carbohydrates; hence it garners widespread consumption amongst the global population. The ascendancy in yield and constituent attributes augments the efficacy of food crop productivity (Chaurasiya *et al.*, 2023). Approximately 40% of the population relies on it for sustenance, thereby constituting 20% of the daily dietary protein intake worldwide [LACC/IGW, (2018) and Chaurasiya *et al.*, (2023)]. It ranks as the second most abundant food crop, yielding 776.26 million tons globally, and boasts the largest cultivation expanse, spanning 220.95 million hectares worldwide (USDA-FAS, 2022). Wheat holds the mantle of being the paramount food crop across the globe. Amongst the seventeen distinct species of wheat, only three, namely *T. aestivum*, *T. durum*, and *T. dicoccum*, are under cultivation globally. *T. aestivum* (bread wheat) dominates over 90% of the cultivation area, trailed by *T. durum* (9 to 10%), while *T. dicoccum* occupies a minute fraction (Tarkeshwar *et al.*, 2020). The Ethiopian highlands provide a myriad of climatic conditions conducive to wheat cultivation, spanning latitudes from 6° to 16° N and longitudes ranging between 35° and 42° E, situated within the altitude range of 1500 to 3000 meters above sea level (Bakele *et al.*, 2000). Ensuring global food security necessitates a continuous influx of enhanced germplasm in response to global climate shifts, projected to elevate crop yields from 2.6 to 3.5 tons per hectare on average over the ensuing 25 years (Tubiello *et al.*, 2008). Elevating the yield potential through a consolidated breeding approach emerges as the optimal strategy to meet burgeoning global food requisites (CAS Secretariat, 2020).

The enhancement of quantitative traits *via* genetic augmentation hinges upon the intrinsic variability within the genetic reservoir and the heritability quotient of desirable traits (Tarkeshwar *et al.*, 2019). GY in wheat is a multifaceted attribute influenced by constituent traits, necessitating an exploration of the genetic variability for yield-associated attributes and quality features to genetically modulate grain production, quality, and ancillary characteristics (Chaudhary *et al.*, 2022). In order to modify yield, quality, and additional traits in wheat, breeders require a comprehension of the genetic variability related to yield, as well as its associated attributes and quality traits (Nageshwar *et al.*, 2023). The extent and characteristics of variability and heritability, alongside the quantum of hereditary variation, are pivotal components for efficacious breeding programs, facilitating the selection of genotypes imbued with desirable attributes (Dudley and Mall, 1969, and Majumder *et al.*, 2008). The genetic advance stands as another critical parameter for high genetic advance concomitant with heritability, prognosticating a more efficacious genotype selection for yield-associated traits (Hanson *et al.*, 1956).

Correlation analysis serves as a potent instrument to delineate the interrelation amongst disparate traits in genetically diverse strains, augmenting the crop amelioration endeavour (Schober *et al.*, 2018). It merely elucidates the degree of correlation between traits, although it fails to elucidate the causative factors behind the correlation (Desheva, 2016). Path coefficient analysis evaluates the relative contribution of direct and indirect effects of traits to yield by partitioning association coefficients (Verma *et al.*, 2019). The current study analyses breeding parameters and methodologies for the meticulous selection of diverse high-yielding genotypes, expediting wheat production and productivity.

Materials and Methods

Located in the central region of Uttar Pradesh, Kanpur sits at an elevation of 126.49 meters above mean sea level within the Gangetic plain. It lies between the latitudes and longitudes of 26°33'0" north and 80°13'28" east, respectively. The experimental material for the present study comprises 18 F_1 crosses obtained by crossing 9 parents in a line x tester mating design configuration. The parents include six lines: RUJ 4037, DBW107, WH703, PBW 677, DBW 110, and DBW 93; and three testers: PBW343, MP3336, and MP3382. The parents were sourced from the GS available at the Faculty of Agriculture Sciences and Allied Industries, Rama University, Mandhana, Kanpur (refer to Table 1). Thus, 27 genotypes in total, comprising parental and cross materials, were utilized for the present investigation. These genotypes were sown in a RBD with 3 replications in the experimental field. Consisting of 2 rows in each plot, with a spacing of 20 x 5 cm. Fertilizer was applied at the rate of 120 kg nitrogen, 60 kg phosphorous, and 40 kg potassium. During the rabi season of 2021-22 The crosses were made, and these accessions, along with their parents, were cultivated following recommended packages and practices during the Rabi season of 2022-23 to ensure the growth of a healthy crop.

Table 1: List of parental materials and their source of collection used in the experiment

Sr. No.	Parents	Pedigree (Origin)
	Lines	
1	RUJ 4037	Oswal Seeds
2	DBW107	IIWBR (earlier DWR), Karnal.
3	WH703	-
4	PBW 677	PAU, Ludhiana, Punjab
5	DBW 110	IIWBR (DWR), Karnal.
6	DBW 93	IIWBR (DWR), Karnal.
	Testers	
1	PBW343	PAU, Ludhiana, Punjab
2	MP3336	IARI, New Delhi
3	MP3382	IARI, New Delhi

Data recorded and statistical analysis

Observations were made on 10 quantitative characters, as abbreviated and namely days to 50% flowering (DFPF), days to maturity (DM), numbers of tillers per plant (NTPP), plant height (PH) (cm), SL (cm), numbers of grains per spike (NGPS), biological yield per plant (BYPP) (g), 1000 grain weight (g) (TGW), harvest index (%) (HI) and grain yield per plant (GYPP) (g), to evaluate the variability and association coefficient among wheat genotypes. The computed mean data measurements of 10 characters across a total of 27 wheat genotypes were then subjected to various statistical analyses including analysis of variance (ANOVA) (Panse and Sukhatme, 1967), Heritability in broad sense (Hanson, 1963), genetic advance (GA) and genetic advance as percentage of mean (GAM) (Johnson *et al.*, 1955), correlation coefficient (Searle, 1961), and path coefficient analysis (Dewey and Lu, 1959).

Results and Discussion

Analysis of Variance (ANOVA)

The diversity within the germplasm offers breeders the chance to develop new and enhanced cultivars. The ANOVA revealed that the variance due to genotypes was significant for all the traits investigated *i.e.*, DFPF (9.15), DM (23.33), PH (cm) (26.19), NPT (3.31), SL (cm) (6.89), NGPE (33.80), 1000 seed weight (4.82), BYPP (14.94), HI (18.51) and GYPP (8.86) (Table 2). This implies the presence of considerable genetic variability among the varieties for these traits. Likewise, numerous other researchers have reported notable variability among wheat varieties for the examined traits, Kotal *et al.* (2010), Tarkeshwar *et al.* (2019), Chaudhary *et al.* (2022) and Chaurasia *et al.* (2023).

Table 2: Analysis of variance for the design of experiment of wheat

Characters	**Replication**	**Genotypes**	**Error**
df	**2**	**26**	**52**
Days to 50% flowering (DFPF)	2.75	9.15**	1.93
Days to maturity (DM)	1.12	23.33**	2.05
Plant height (cm) (PH)	1.81	26.19**	1.88
Numbers of tillers per plant (NTPP)	0.37	3.31**	0.37
Spike length (cm) (SL)	0.63	6.89**	0.34
No. of grains per spike (NGPS)	3.37	33.80**	3.92
1000 seed weight (Test weight) (TGW)	0.87	4.82**	0.96
Biological yield per plant (BYPP)	3.23	14.94**	6.06
Harvest Index (HI)	9.89	18.51**	3.72
Grain yield per plant (g) (GYPP)	1.8	8.86**	0.85

*,**Significant at 5 and 1% level of probability.

Mean performance analysis of genotypes

The performance of genotypes, along with the range and grand mean for all the studied traits, is presented in Table 3& 4. The mean DFPF ranged from 78.33 to 84.67 days. Seventeen of the genotypes took a greater number of days to heading than the overall mean 81.98 days. The mean DM ranged from 118.67 to 128.67. In general, it was observed that the all the parents used for crossing were the latest for 50% heading and days to maturity. Contrary to this, new hybrids/segregants developed through crossing had early days to heading and maturity, which is of importance for developing early maturing varieties. About sixteen of the genotypes took higher days in maturing over the grand mean 123.90 days. The mean Plant height (cm) ranged from 92.02 to 101.91 cm. Fifteen of the genotypes showed more height above the grand mean of 98.38 cm. The mean NTPP ranged from 5 to 8.43 tillers. It showed a grand mean 6.40 tillers per plant and eleven genotypes showed a greater number of tillers than grand mean. Compared to the parental materials developed genotypes had tall PH and more NTPP.

The grand mean for Spike length (cm) (SL) was 17.14 cm and it ranged from 14.84 to 20.02 cm. About nine of the genotypes showed a greater SL than the grand mean. The mean range of NGPS, 47.33 to 58.00 with a grand mean of 50.93 and nine of the total genotypes contained a greater number of grains than mean value. The mean 1000 seed weight, commonly known as test weight ranged from 38.45 to 42.55 g with 39.93 g as mean value. About 33.33% of the genotypes showed high test weight above the grand mean. The mean BYPP ranged from 61.25 to 69.69 g/p with a grand mean of 64.70 g/p. About thirteen of the genotypes showed biological yield above the grand mean. The mean Harvest Index performed from 35.66 to 44.78% with a grand mean of 39.31%. The GY, a major trait in wheat, it ranged from 22.31 (PBW 677) to 28.29 g/p (PBW 677 × MP3382). About seventeen of the genotypes showed higher grain yield then the grand mean 25.40 g/p. Furthermore, Sajjad *et al.* (2011) noted considerable variation in GY, TW, and the NGPS. Our findings also align with the conclusions drawn by Mecha *et al.* (2016) and Poudel *et al.* (2021).

Overall, comparing mean data of parent's vs hybrids, it is clear that all the developed genotypes through crossing were outperforming the parents for all the traits related to growth, yield and were early to flower and mature as well. These segregants and traits selection can be further confirmed through genetic analysis and inter relation in between traits.

Table 3: Mean performance of parents and hybrids for the traits studied during rabi season 2022-23

Sr. No.	Parents and Hybrids	Days to 50% flowering (DFPF)	Days to maturity (DM)	Plant height (cm) (PH)	Number of tillers per plant (NTPP)	Spike length (cm) (SL)	No of grains per spike (NGPS)	1000 seed weight (TGW)	Biological yield per plant (g) (BYPP)	Harvest Index (HI)	Grain yield per plant (g) (GYPP)
1	RUJ 4037	83.00	127.00	96.02	5.27	15.59	48.00	38.53	61.86	38.13	23.57
2	DBW107	83.33	127.33	96.04	5.30	15.47	49.33	39.00	61.89	39.44	24.35
3	WH703	83.67	128.67	92.53	5.33	14.84	50.00	39.33	63.11	36.59	23.06
4	PBW 677	83.67	128.00	96.17	5.30	16.31	48.33	38.67	61.85	36.10	22.31
5	DBW 110	84.33	128.00	95.35	5.00	16.43	49.67	38.45	61.25	36.76	22.41
6	DBW 93	84.67	126.33	93.44	5.17	16.31	49.00	38.46	64.39	35.72	22.99
1	PBW343	83.00	126.00	92.02	5.63	16.23	49.67	39.07	63.04	39.23	24.71
2	MP3336	84.67	125.33	95.97	6.20	15.89	51.67	39.05	62.43	38.27	23.90
3	MP3382	84.67	126.00	96.00	5.97	16.23	49.67	38.74	62.25	38.67	24.06
1	RUJ 4037 × PBW343	80.67	121.33	100.00	5.90	16.48	49.00	38.95	64.87	40.86	26.49
2	RUJ 4037 × MP3336	82.00	122.33	101.91	6.27	16.86	48.00	41.37	67.99	38.27	26.02
3	RUJ 4037 × MP3382	81.00	125.00	100.41	6.27	17.09	50.00	41.17	63.55	40.15	25.48
4	DBW107 × PBW343	82.33	122.00	101.77	6.27	15.65	47.33	41.39	65.70	40.34	26.47
5	DBW107 × MP3336	80.33	122.00	100.21	7.47	16.96	58.00	39.35	67.79	35.66	24.17
6	DBW107 × MP3382	82.00	124.67	101.44	6.10	16.21	47.67	39.51	64.43	40.61	26.11
7	WH703 × PBW343	81.33	121.00	100.47	6.60	17.77	51.67	39.55	65.42	38.72	25.31
8	WH703 × MP3336	82.00	123.00	100.34	5.53	16.33	50.00	41.85	66.20	39.37	26.05
9	WH703 × MP3382	82.00	124.00	100.18	5.07	17.69	47.33	39.41	65.98	39.34	25.88
10	PBW 677 × PBW343	81.00	124.33	100.49	6.73	16.45	48.00	39.67	67.48	37.69	25.42
11	PBW 677 × MP3336	80.00	120.00	96.71	8.03	19.58	56.67	42.06	64.23	43.79	28.12
12	PBW 677 × MP3382	78.33	119.67	99.78	7.73	19.25	55.33	41.95	63.18	44.78	28.29
13	DBW 110 × PBW343	82.33	124.00	101.54	6.93	16.63	49.67	39.50	68.07	37.56	25.56
14	DBW 110 × MP3336	79.67	118.67	100.60	7.67	19.98	55.67	41.02	65.51	42.43	27.74
15	DBW 110 × MP3382	79.00	120.67	98.03	8.37	20.02	55.00	40.77	63.86	42.61	27.22
16	DBW 93 × PBW343	82.33	124.67	100.55	6.83	17.66	48.67	39.25	69.69	36.55	25.48
17	DBW 93 × MP3336	80.00	121.00	97.35	8.43	19.83	58.00	42.55	64.71	43.13	27.91
18	DBW 93 × MP3382	82.00	124.33	100.92	7.30	19.17	53.67	39.39	66.05	40.46	26.72
	Mean	**81.98**	**123.90**	**98.38**	**6.40**	**17.14**	**50.93**	**39.93**	**64.70**	**39.31**	**25.40**
	Min	78.33	118.67	92.02	5.00	14.84	47.33	38.45	61.25	35.66	22.31
	Max	84.67	128.67	101.91	8.43	20.02	58.00	42.55	69.69	44.78	28.29
	SE(d) ±	1.14	1.17	1.12	0.50	0.47	1.62	0.80	2.01	1.58	0.75
	C.D. at 5%	2.28	2.35	2.25	1.00	0.95	3.25	1.61	4.05	3.17	1.52
	C.V. (%)	1.70	1.16	1.39	9.51	3.38	3.89	2.46	3.81	4.91	3.64

Variability components, heritability and genetic advance

In every breeding program, genetic variation is an essential prerequisite. The genetic variability observed results from the combined effects of relevant genes and environmental factors. Estimating variance components such as Heritability (h^2), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), and Genetic advance in percent over mean (GAM) aids breeders in crop improvement by leveraging selection on existing variation (Katral *et al.*, 2022) (Table 4).

Table 4: Estimates of genetic variability, heritability (bs), coefficient of variation and genetic advance for quantitative traits in wheat

Characters	Mean	Range		Variance		Heritability (%)	Genetic advance		Coefficient of variation	
		Min.	Max.	var (g)	var (p)		GA	GA% mean	GCV (%)	PCV (%)
DFPF	81.98	78.33	84.67	2.41	4.34	55.46	2.38	2.90	1.89	2.54
DM	123.90	118.67	128.67	7.09	9.14	77.61	4.83	3.90	2.15	2.44
PH (cm)	98.38	92.02	101.91	8.10	9.98	81.18	5.28	5.37	2.89	3.21
NTPP	6.40	5.00	8.43	0.98	1.35	72.60	1.74	27.17	15.48	18.17
SL (cm)	17.14	14.84	20.02	2.18	2.52	86.68	2.83	16.53	8.62	9.26

NGPS	50.93	47.33	58.00	9.96	13.88	71.75	5.51	10.81	6.20	7.32
TGW (g)	39.93	38.45	42.55	1.29	2.25	57.24	1.77	4.43	2.84	3.76
BYPP (g)	64.70	61.25	69.69	2.96	9.02	32.81	2.03	3.14	2.66	4.64
HI	39.31	35.66	44.78	4.93	8.65	56.97	3.45	8.78	5.65	7.48
GYPP (g)	25.40	22.31	28.29	2.67	3.52	75.79	2.93	11.54	6.43	7.39

The PCV ranged from 2.44% (DM) to 18.17% (NPTPP) and GCV varied from 1.89% (DFPH) to 15.48% (NPTPP) (Table 4). The PCV values exceeded the GCV values for all the traits studied, indicating the impact of environmental factors on the expression of these traits. In 1986, Deshmukh and colleagues categorized PCV and PCV into low (0-10%), moderate (10-20%), and high (20% and above) values. According to this classification, the only trait exhibiting moderate PCV and GCV value was the NTPP. Similarly, Chaudhary *et al.* (2022) demonstrated moderate PCV for this trait. This suggests that selection could be effective for this characteristic, and its phenotypic expression would serve as a reliable indicator of genotypic potential. In contrast, all other traits had low PCV and GCV, indicating limited scope for selection due to their susceptibility to environmental influence. Earlier Tarkeshwar *et al.* (2019) and Kumar *et al.* (2020) noted low PCV and GCV for DFPF, DM and PH in bread wheat genotypes. Further, Khairnar *et al.* (2018) elaborated moderate to high PCV and GCV for DFPF, NTPP, TGW, GPS and GWPS.

Table 4 presents the heritability in broad sense, genetic advance (GA), and genetic advance in percent over mean (GAM) for the traits under investigation. According to Robinson et al. (1949), heritability was categorized into three groups: high (>60%), moderate (30-60%), and low (<30%). High h2 (bs) estimates were recorded for DM (77.61), PH (81.18), NTPP (72.60), SL (86.68), NGPS (71.75), and GYPP (75.79%). Conversely, other traits exhibited moderate levels of heritability. The notable heritability observed in these traits indicates that genetic factors primarily drive the variation, with less influence from environmental factors. This suggests potential for improvement through selective breeding. Similarly, Kumar *et al.* (2020) reported high broad-sense heritability estimates for DM and GYPP. Additionally, Kumar *et al.* (2022) noted high heritability estimates for traits such as DFPF, SLPP, and GYPP. Emmadishetty and Gurjar (2023) observed very high heritability estimates coupled with substantial genetic advances for traits including NTPP, NTPP, BYPP, HI, and GYPP.

Evaluating genetic advance assists in discerning the nature of gene action contributing to the expression of diverse polygenic traits. A high genetic advance value signifies the presence of additive, while a low value implies the influence of non-additive gene action on trait expression (Singh and Narayanan, 1993). Falconer and Mackay (1996) categorized GAM into three levels: low (0-10%), moderate (10-20%), and high (20% and above). All the characters under study expressed low GA. High heritability coupled with high GAM was noted for the NTPP, while SL and the NGPS exhibited high heritability with moderate GAM. Similarly, the results of Degewione *et al.* (2013) and Mecha *et al.* (2016) closely align with our findings.

Association analysis for precise selection

The correlation coefficient was calculated for all traits at phenotypic level (PL) and genotypic level (GL) both and presented in Table 5. This coefficient quantifies the extent and direction of correlation between pairs of traits, aiding in the selection process for yield enhancement (Verma *et al.,* 2019). It was noted that correlation values at GL were higher than PL, indicating association between trait is strongly due to genotypes.

The correlation analysis for dependant trait grain yield per plant GYPP revealed a positive association with its all the growth and yield contributing component traits at both the levels (Table 5). The positive correlation among desirable traits aids breeders in selection. The GYPP showed significant and positive correlations with the HI (GL=0.921, PL=0.809) followed by 1000 seed weight (GL=0.963, PL=0.566), SL (cm) (GL=0.823, PL=0.645), NTPP (GL=0.803, PL=0.683), PH (cm) (GL=0.613, PL=0.492), NGPS (GL=0.557, PL=0.392) at 1% level of significance. Traits BYPP and NGPS were also had positive and significant correlation with GYPP followed by the other traits. While, it showed negatively significant association with phenological traits DFPH (GL=-0.941, PL=-0.697) and DM (GL=-0.942, PL=-0.759) at 1% significant level. Ojha *et al.* (2018) and Nasri *et al.* (2014) also confirm that PH, SL, and TGW are important parameters for yield determination. Das (2014) noted significant positive association of GY with SL, NGPS, 1000 grain weight and HI. Mecha *et al.* (2016) noted that the GY had a positive correlation with the SL and the TGW.

DFPF possessed significantly negative correlation with all the traits except for DM (GL=0.963, PL=0.709) It had the significant positive correlation. Similarly, DM also had highly significant and negative association with all the traits, indicating favourable effects to early maturity and vice versa. PH had positive and significant relation with all the traits except for NGPS, where it had non-significant correlation. Amongst all other growth and yield contributing traits there was positive and strong association, while NGPS had non-significant association with BYPP (GL=0.123, PL= -0.057). This indicates at inter dependence of these traits to contribute to the GYPP. Avinashe *et al.* (2015) observed a significant positive correlation between GYPP and HI, BYPP, SL, and TW. Dragov and Dechev (2016) found a positive association between PH and TW in durum wheat. A positive association between TW and GWPS was recorded by Stoyanov and Dunchev (2022).

Estimates of direct and indirect effects on yield

Path coefficient involves partial regression analysis, which decomposes the correlation coefficient into direct and indirect effects on characters (Falconer and Mackay, 1996). In general, traits with a positive direct impact and demonstrating a notable correlation coefficient with grain yield are regarded as factors that positively influence grain yield. These traits should be given special consideration during the selection process (Ojha *et al.*, 2018). Path coefficient analysis was performed utilizing phenotypic and genotypic correlations to determine the direct and indirect influences of various traits on GYPP (refer to Tables 6).

At the genotypic and phenotypic levels, HI demonstrated the highest positive direct impact (GL=0.9215, PL=0.9999) on GY, followed by BYPP with a coefficient of (GL=0.4570, PL=0.6258). NTPP (0.0076, 0.0017) also had positive but negligible direct effect on dependent trait at both the levels respectively. The residual effects values were also low, indicating no important excluded for the studied materials. Dutamo *et al.* (2015) reported similar direct effects on GYPP, while Mecha *et al.* (2016) found that biomass yield had a positive direct influence on GYPP. The negative direct effects noted at both SL and GL by NGPS and 1000-grain weight on GYPP, despite their positive significant associations at both levels, imply that the associations are likely driven by indirect effects. Similarly, Kotal *et al.* (2010) observed a negative direct impact of TW on GY in bread wheat genotypes. At both PL and GL, traits such as PH, NTPP, SL, and TGW demonstrated positive indirect effects on GYPP through BYPP and HI, as shown in Tables 6 and 8, respectively. Kumari *et al.* (2017) reported that HI had the highest direct positive impact on GYPP, followed by BYPP, NTPP, SW, and NGPS. Similar results were observed by Kumar *et al.* (2020), Tarkeshwar *et al.* (2020), and Singh *et al.* (2021) in their respective studies.

Conclusion

The analysis of variance of the present study indicated a substantial level of variability among the genotypes for the studied traits. High heritability, along with moderate genetic advance, was found for number of tillers per plant, numbers of grains per spike, spike length and harvest index indicating additive gene action in its expression. Most of the traits exhibited low to moderate levels of GCV and PCV. Grain yield per plant showed a positive correlation with most of the growth and yield contributing traits, except for days to 50% flowering and days to maturity which had negative, significant and ideally desired correlation with grain yield per plant. Consequently, selecting parents and genotypes/hybrids produced based on these traits will lead to accurate selection for generation advancement and yield enhancement.

Table 5: Genotypic correlation coefficient among ten metric traits of wheat

Characters	Level	Days to 50% heading	Days to maturity	Plant height (cm)	Numbers of tillers per plant	Spike length (cm)	No. of grains per spike	1000 seed weight	Biological yield per plant	Harvest Index	Grain yield per plant (g)
Days to 50% flowering (DFPF)	GL	1.000	0.963**	-0.622**	-0.946**	-0.868**	-0.719**	-0.915**	-0.447**	-0.876**	-0.941**
	PL	1.000	0.709**	-0.393**	-0.585**	-0.604**	-0.504**	-0.439**	-0.252*	-0.536**	-0.697**
Days to maturity (DM)	GL		1.000	-0.638**	-0.839**	-0.790**	-0.671**	-0.827**	-0.549**	-0.822**	-0.942**
	PL		1.000	-0.486**	-0.678**	-0.662**	-0.509**	-0.567**	-0.335**	-0.549**	-0.759**
Plant height (cm) (PH)	GL			1.000	0.435**	0.329**	-0.002	0.439**	0.903**	0.287**	0.613**
	PL			1.000	0.300**	0.256*	0.037	0.340**	0.512**	0.178	0.492**
Numbers of tillers per plant (NTPP)	GL				1.000	0.918**	0.928**	0.722**	0.503**	0.686**	0.803**
	PL				1.000	0.681**	0.636**	0.507**	0.232*	0.535**	0.683**
Spike length (cm) (SL)	GL					1.000	0.798**	0.657**	0.302**	0.800**	0.823**
	PL					1.000	0.662**	0.470**	0.133	0.557**	0.645**
No of grains per spike	GL						1.000	0.567**	0.123	0.578**	0.557**

(NGPS)	PL						1.000	0.389**	-0.057	0.426**	0.392**
1000 seed weight (TGW)	GL							1.000	0.417**	0.901**	0.963**
	PL							1.000	0.093	0.506**	0.566**
Biological yield per plant (BYPP)	GL								1.000	0.106	0.485**
	PL								1.000	-0.324**	0.293**
Harvest Index (HI)	GL									1.000	0.921**
	PL									1.000	0.809**

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

Table 6: Phenotypic and genotypic direct and indirect effects of component traits on yield per plant (g)

Characters	**Level**	**Days to 50% heading**	**Days to maturity**	**Plant height (cm)**	**Numbers of tillers per plant**	**Spike length (cm)**	**No of grains per ear**	**1000 seed weight**	**Biological yield**	**Harvest Index**	**Yield per plant (g)**
Days to 50% flowering (DFPF)	GL	**-0.0662**	-0.0081	0.0485	-0.0072	0.0312	0.0233	0.0496	-0.2045	-0.8074	-0.941**
	PL	**-0.0014**	0.0025	0.0034	-0.0010	-0.0027	0.0032	0.0008	-0.1579	-0.5442	-0.697**
Days to maturity (DM)	GL	-0.0638	**-0.0084**	0.0498	-0.0064	0.0284	0.0218	0.0448	-0.2511	-0.7570	-0.942**
	PL	-0.0010	**0.0035**	0.0042	-0.0011	-0.0029	0.0033	0.0010	-0.2096	-0.5567	-0.759**
Plant height (cm) (PH)	GL	0.0412	0.0054	**-0.0780**	0.0033	-0.0118	0.0001	-0.0238	0.4126	0.2643	0.613**
	PL	0.0006	-0.0017	**-0.0086**	0.0005	0.0011	-0.0002	-0.0006	0.3204	0.1808	0.492**
Numbers of tillers per plant (NTPP)	GL	0.0626	0.0070	-0.0340	**0.0076**	-0.0330	-0.0301	-0.0391	0.2298	0.6321	0.803**
	PL	0.0008	-0.0024	-0.0026	**0.0017**	0.0030	-0.0041	-0.0009	0.1451	0.5426	0.683**
Spike length (cm) (SL)	GL	0.0574	0.0066	-0.0256	0.0070	**-0.0360**	-0.0259	-0.0356	0.1381	0.7373	0.823**
	PL	0.0009	-0.0023	-0.0022	0.0011	**0.0044**	-0.0042	-0.0008	0.0833	0.5653	0.645**
No of grains per spike (NGPS)	GL	0.0476	0.0056	0.0002	0.0070	-0.0287	**-0.0324**	-0.0307	0.0562	0.5327	0.557**
	PL	0.0007	-0.0018	-0.0003	0.0011	0.0029	**-0.0064**	-0.0007	-0.0356	0.4322	0.392**
1000 seed weight (TGW)	GL	0.0606	0.0069	-0.0343	0.0055	-0.0236	-0.0184	**-0.0542**	0.1904	0.8299	0.963**
	PL	0.0006	-0.0020	-0.0029	0.0009	0.0021	-0.0025	**-0.0018**	0.0583	0.5131	0.566**
Biological yield per plant (BYPP)	GL	0.0296	0.0046	-0.0704	0.0038	-0.0109	-0.0040	-0.0226	**0.4570**	0.0975	0.485**
	PL	0.0004	-0.0012	-0.0044	0.0004	0.0006	0.0004	-0.0002	**0.6258**	-0.3290	0.293**
Harvest Index (HI)	GL	0.0580	0.0069	-0.0224	0.0052	-0.0288	-0.0187	-0.0488	0.0484	**0.9215**	0.921**
	PL	0.0008	-0.0019	-0.0015	0.0009	0.0025	-0.0027	-0.0009	-0.2028	**0.9999**	0.809**

Residuals effect at GL = 0.00106 *, ** significant at 5% and 1% level, respectively Residual effect at PL= 0.00115

References

Avinashe, H.A., Shukla, R.S., Dubey, N. and Jaiwar, S. 2015. Correlation and path analysis for yield and yield contributing characters in bread wheat *Triticum aestivum* L. 2015. *Electronic Journal of Plant Breeding*, **6**(2), 555-559.

Bekele, H., Verkuiji, W. and Mawangi, T. 2000. Adaptation of improved heat technologies in Addaba and Doddola Worede's of the Bale highlands of Ethiopia. CIMMYT/EARO, Addis Ababa, Ethiopia.

CAS Secretariat (CGIAR Advisory Services Shared Secretariat) 2020. CGIAR Research Program 2020 reviews, WHEAT, Rome, CAS Secretariat Evaluation Function.

Chaudhary, R.P., Singh, V., Bahadur, V., Tarkeshwar and Kumar, M. 2022. Genetic Variability, Heritability, and genetic advance for yield and its components in wheat (*Triticum aestivum* L.). *International Journal of Agriculture Sciences*, **14**(4), 11256-11258.

Chaurasia, M.K., Tarkeshwar, Adhikari, S., Chand, G., Kumar, K., Nageshwar and Gaur, S.C. 2023. Genetic association and multivariate analysis for precise selection of elite genotypes among indigenous genotypes of bread wheat. *Agricultural Mechanization in Asia(AMA),***54** (7), 14661-14683.

Das, B. 2014. Genetic diversity, variability and correlation studies of spike characters in bread wheat under boron deficient soil condition. *Electronic Journal of Plant Breeding*, **5**(1), 77-81.

Degewione, A., Dejene, T., and Sharif, M. 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum*) genotypes.*International Research Journal of Agricultural Sciences,***1**(2), 19- 29.

Desheva, G. 2016. Correlation and path coefficient analysis of quantitative characters in winter bread wheat varieties. *Trakia J. Sci.*, **1**, 24-29.

Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**(9), 515-518.

Dragov, R. and Dechev, D. 2016. Genetic distance by important economic traits between bulgarian and foreign cultivars of durum wheat. *Science & Technologies*, **6**(6), 41-47.

Dudley, I.W. and Mall, R. F. 1969. Interpretation and use of estimates of h^2 and genetic advance in plant breeding. *Crop Sci.*, **9**, 257-262.

Dutamo, D., Alamerew, S., Eticha, F., and Assefa, E. 2015. Path coefficient and correlation studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) germplasm. *World Applied Sciences Journal*, **33**(11), 1732-1739.

Emmadishetty, C.S. and Gurjar, D. 2023. Studies of genetic variability, heritability and genetic advance for yield component traits in bread wheat *Triticum aestivum* L. *Electronic Journal of Plant Breeding*, **13**(4), 1214-1219.

Falconer, D.S. and Mackay, T.F.C. 1996. Introduction to quantitative genetics. Ed. 4. Longman.

Hanson, C., Robinson, H. and Comstock, R. 1956. Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal*, **48**(6), 268-272.

Hanson, W.D. 1963. Heritability. Statistical genetics and plant breeding. Humphrey Press, 125-140.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Genotypic and phenotypic correlation in Soybean and their implication in selection. *Agron. J.*, **47**, 477-483.

Katral, A., Biradar, H., Harijan, Y., Aruna, Y.R., Hadimani, J. and Hittalmani, S. 2022. Genetic analysis and traits association study in marker-assisted multi-drought-traits pyramided genotypes under reproductive-stage moisture stress in rice (*Oryza sativa* L.). *Euphytica*, **218**(3), 21.

Khairnar, S.S., Bagwan, J.H., Yashavantha Kumar, K.J., Baviskar, V.S., Honrao, B.K., Surve, V.D., Khade, V.M., Chavan, A.M. and Bankar, B.N. 2018. Studies on genetic variability parameters and character association in bread wheat *Triticum aestivum* L. under timely and late sown environments of irrigated condition. *Electronic Journal of Plant Breeding*, **9**(1), 190-198.

Kotal, B.D., Arpita, D., and Choudhury, B.K. 2010. Genetic variability and association of characters in wheat (*Triticum aestivum* L.). *Asian journal of crop science*, **2**(3), 155-160.

Kumar, A., Gaur, S.C., Tarkeshwar, Singh, R., Prasad, H., Yadav, M. and Kumar, K. 2022. Studies on genetic variability, heritability and genetic advance for grain yield and yield attributing traits in bread wheat (*Triticum aestivum* L. em. Thell). *Frontiers in Crop Improvement*, **10**(1), 29-31.

Kumari, M., Kumar, M., Singh, V., Kumar, S.V. and Rathi, M. 2017. Trait association and morphological diversity in wheat *Triticum aestivum* L. genotypes. *Electronic Journal of Plant Breeding*, **8**(2), 534-540.

LACC/IGW2018. 4th Latin American Cereals Conference. Book of Abstracts. CDMX, Mexico, International Maize and Wheat Improvement Center (CIMMYT).

Majumder, D.A.N., Shamsuddin, A.K.M., Kabir, M.A. and Hassan, L. 2008. Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. *Journal of Bangladesh Agricultural University*, **6** (2), 227–234.

Mecha, B., Alamerew, S., Assefa, A., Assefa, E. and Dutamo, D. 2016. Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes. *Global Journal of Science Frontier Research, D Agriculture and Veterinary,***16**(7), 1-17.

Nageshwar, Singh, S.V., Yadav, V.K., Kumar, J., Kumar, K., Tiwari, U., Gaur, S.C., Tarkeshwar, Kumar, S. and Tiwari, A. 2023. Study of heritability and genetic advance for the selection of improved genotype based on quantitative and quality characters in bread wheat (*Triticum aestivum* L.). *Agricultural Mechanization in Asia (AMA),***54**(8), 15077-15085.

Nasri, R., Kashani, A., Paknejad, F., Vazan, S. and Barary, M. 2014. Correlation, path analysis a stepwise regression in yield and yield component in wheat (*Triticum aestivum* L.) under the temperate climate of Ilam province, Iran. I*ndian Journal of Fundamental and Applied Life Sciences,***4**(4), 188-198.

Ojha, R., Sarkar, A., Aryal, A., K.C., R., Tiwari, S., Poudel, M. and Shrestha, J. 2018. Correlation and path coefficient analysis of wheat (*Triticum aestivum* L.) genotypes. *Farming and Management*, **3**(2), 136-141.

Panse, V.G. and Shukhatme, P.V. 1967. Statistical methods for agricultural workers, 2nd Ed., ICAR, New Delhi, 381.

Poudel, M.R., Poudel, P.B., Puri, R.R., and Paudel, H.K. 2021. Variability, correlation and path coefficient analysis for agro-morphological traits in wheat genotypes (*Triticum aestivum* L.) under normal and heat stress conditions. *International Journal of Applied Sciences and Biotechnology,***9**(1), 65-74.

Robinson, H.F., Comstock, R.E. and Harvey, P.H. 1949. Estimates of heritability and the degree of dominance in corn. *Agron. J.*, **41**(8), 353-359.

Sajjad, M., Khan S.H. and Khan, A.S. 2011. Exploitation of germplasm for grain yield improvement in spring wheat (*Triticum aestivum*). *Int. J. Agric. Biol.*, **13**, 695-700.

Schober, P., Boer, C., and Schwarte, L.A.2018. Correlation coefficients, appropriate use and interpretation. *Anesthesia & analgesia*, **126**(5), 1763-1768.

Searle, S.R. 1961. Phenotypic, genotypic and environment correlation. *Biometrics*, **17**, 474-775.

Singh, P., and Narayanan, S.S. 1993. Biometrical techniques in plant breeding. 1st ed. Kalayani Publishers, New Delhi, India.

Singh, S., Singh, S., Tarkeshwar, Mourya, S. and Singh, V. 2021. Correlation and path analysis of quantitative traits in different wheat (*Triticum aestivum* L. Em. Thell) genotypes under reclaimed salt affected soil. *The Pharma Innovation Journal*, **10**(5), 1637-1639.

Stoyanov, G. and Dunchev, D. 2020. Influence of the leaf fertilization on the productivity of two common wheat varieties. *Agricultural University - Plovdiv, Scientific Works*, **LXII**(1), 169-175.

Tarkeshwar, Gaur, S.C., Singh, S.P., Sahu, R.K., Kumar, K., Yadav, M. and Yadav, G. 2019. Genetic divergence analysis on some bread wheat (*Triticum aestivum* L. Em. Thell) genotypes. *Frontiers in Crop Improvement*, **7**(2), 103-105.

Tarkeshwar, Kumar, K., Yadav, M., Gaur, S.C., Chaudhary, R.P. and Mishra, G. 2020. Studies on correlation and path coefficient for yield and its component traits in bread wheat (*Triticum aestivum* L. em. Thell). *Int. J. Curr. Microbiol. App. Sci.*, **11**(Special),688-696.

Tubiello, F.N., Rosenzweig, C.R., Goldberg, A., Jagtap, S. and Jones, J.W. 2008. U.S. National Assessment Technical Report, Effect of Climate Change on U.S. Crop Production Part I, Wheat, Potato, Corn and Citrus.

USDA-FAS 2022. World Agricultural Production. United States Department of Agriculture, Foreign Agricultural Service.

Verma, S.P., Pathak, V.N. and Verma, O.P. 2019. Interrelationship between yield and its contributing traits in wheat (*Triticum aestivum* L). *International Journal of Current Microbiology and Applied Sciences*, **8**(2), 3209-3215.