International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2025; 9(1): 858-863
www.biochemjournal.com
Received: 19-10-2024
Accepted: 24-11-2024

Sumit Kumar Singh
Department of Genetics and Plant Breeding, B.R.D. P.G. College, Deoria, Uttar Pradesh, India

Prata Narayan Singh
Head of The Department, Department of Genetics and Plant Breeding, B.R.D. P.G. College, Deoria, Uttar Pradesh, India

SC Gaur
Principal, Madan Mohan Malviya P.G. College, Bhatpar Rani, Deoria, Uttar Pradesh, India

HP Singh
Assistant Professor, Department of Genetics and Plant Breeding, B.R.D. P.G. College, Deoria, Uttar Pradesh, India

Syed Mohd Quatadah
Department of Genetics and Plant Breeding, B.R.D. P.G. College, Deoria, Uttar Pradesh, India

Kaushal Singh
Department of Genetics and Plant Breeding, B.R.D. P.G. College, Deoria, Uttar Pradesh, India

Corresponding Author:
Sumit Kumar Singh
Department of Genetics and Plant Breeding, B.R.D. P.G. College, Deoria, Uttar Pradesh, India

Genetic correlation and path coefficient studies in bread wheat (*Triticum aestivum* L.) under irrigated condition

Sumit Kumar Singh, Prata Narayan Singh, SC Gaur, HP Singh, Syed Mohd Quatadah and Kaushal Singh

DOI: https://doi.org/10.33545/26174693.2025.v9.i1k.3654

Abstract
Current research started with an objective to find out the genotypic and phenotypic relationships among yield-related characteristics in wheat (*Triticum aestivum* L.) by utilizing 55 wheat genotypes alongside one standard variety. Field trial was conducted at Research Farm of BRD PG College during rabi 2019-2020 Experimental material was evaluated in RBD design with 3 replications. The analysis of variance (ANOVA) indicated considerable genetic variability, suggesting a significant opportunity for the selection of superior genotypes. Path coefficient analysis revealed that traits such as days to 50% flowering, test weight, and grain hardiness exhibited substantial direct and indirect effects on grain yield. Important findings highlighted the positive genotypic impacts of grains per spike, spikelet per spike, and harvest index on yield, alongside notable environmental factors. These findings offer essential insights for wheat breeding programs, highlighting traits with high heritability and genetic progress for focused enhancement.

Keywords: Wheat genotypes, correlation, path coefficient analysis, heritability, grain yield

1. Introduction
Wheat (*Triticum aestivum* L.) is the primary food crop in many regions across the globe and also holds a significant position in Indian agriculture after rice. It is an essential cereal nutritionally important for food security, poverty reduction, and livelihoods (Chauhan *et al*., 2012) [7]. Widely grown as a staple food crop among cereals, it contributes approximately 30% to the country's food supply (Amanullah *et al*., 2019) [2]. Various components of grain yield frequently show differing degrees of association with grain yield and with each other. Determining variability among the traits and the relationship of specific characteristics with other traits that contribute to a crop's yield is crucial for formulating a successful breeding program (Araus *et al*., 2008) [3]. The selection of parents is critically important in a breeding program. To enable effective selection, it is necessary to gather information on the nature and extent of variation within a population, the associations of traits with yield, and among each other, along with the degree of environmental impact on the expression of these traits (Slafer, 2003) [9]. Consequently, it is vital for a breeder to assess variability using parameters such as phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance. Various components of grain yield frequently show differing degrees of association with grain yield and with each other. Studies on the association of characteristics provide a better understanding of yield components, aiding plant breeders in enhancing yield through indirect selection for highly heritable traits that are linked to yield. Correlation and path analysis can serve as crucial tools for revealing appropriate cause-and-effect relationships between yield and certain yield components (Tsegaye *et al*., 2012) [20]. Plant breeders have utilized path coefficient analysis in agriculture to assist in identifying traits that can be used as selection criteria to enhance crop yield (Dewey and Lu, 1959) [9].

2. Materials and Methods
The experimental materials for this study consisted of 55 wheat genotypes along with standard variety used as a check *viz.*, HD 2967 generated through crossing program 10 line

and 4 male testers in L X T mating design. The experiment was conducted during rabi 2020-21 at departmental Research Farm of BRD PG College, Deoria (Affiliated with DDU Gorakhpur University, Uttar Pradesh).

3. Statistical Analysis

The variance analysis (ANOVA) for the experimental design was performed according to the method outlined by Panse and Sukhatme (1967) [22]. The calculation of $\sigma 2g$ was done using the equation proposed by Burton and Devane (1953) [6]. The GCV and PCV were determined using Burton's (1952) equation, which offers a measure of variation within the population. Heritability in the broad sense (Hbs) was estimated based on the equation suggested by Burton and Devane (1953) [6]. The predicted genetic advance for various traits under selection was calculated using the formula by Lush (1943) [13] and Johnson *et al*. (1955) [11]. The genetic advance expressed as a percentage of the mean was determined by applying the formula provided by Robinson and Comstock (1949) [15]. The relationships among different traits at both genotypic and phenotypic levels were assessed using the approach described by Searle *et al*. (1971) [16]. Direct and indirect impacts were evaluated through path coefficient analysis as recommended by Wright (1921) [21] and further explained by Dewey and Lu (1959) [9].

4. Result and Discussion

4.1 Analysis of variance

Analysis of variance (ANOVA) indicating significant variability among genotypes for most of the characters under study, exhibiting a substantial genotypic variation is present among the genotypes which could be used in further statistical analysis. This variability is essential for the selection and enhancement of these traits in breeding programs. The notable differences among genotypes emphasize the opportunity for choosing superior genotypes with favourable traits for additional breeding (Begna *et al*., 2022) [5]. (Table 1).

4.2 Genetic parameters

The genetic variability estimates of eighteen characters exhibits higher PCV value compared to GCV for all traits, indicating significant environmental influence (Table 2). High variability was recorded in number of effective tillers per plant (PCV = 59.46%, GCV = 18.52%) and grain hardness (PCV = 40.11%, GCV = 39.90%). Grain yield/ spike, Spike length (cm), Grains per spike, and Spikelet per spike exhibit significant variability. High heritability (>75%) was recorded for traits like grain hardness (98.90%), spike length (87.90%), and gluten content (87.10%), while moderate heritability (50% to 75%) was noted for traits including grain yield/spike, spikelet/ spike, and 50% flowering. GAM (%) was very high for grain hardness (81.74) and high for traits like spike length (30.57%) and grain yield per spike (25.88%). These findings suggest that traits having highest heritability value coupled GA, such as grain hardness and spike length, are particularly promising for selection in wheat genetic improvement programs (Singh *et al*., 2020) [18].

4.3. Character association

4.3.1 Correlation coefficient analysis

Analysis of genotypic and phenotypic correlations for various traits of wheat reveals key insights for plant breeding programs (Table 3 & 4). DFF indicated positive and significant genotypic correlations for GYP (0.960**), HI (0.918**), TW (0.903**), GYS (0.870**), SL (cm) (0.844**), GYS (0.742**), SP (0.691**), PHT (cm) (0.690**), ETP (0.592**), GP (0.554**), and PC (0.481**). Phenotypically, it also showed significant positive correlations with GYP (0.752**), SL (cm) (0.657**), and HI (%) (0.643**). Both correlations indicated significant negative relationships with GH (-0.498** genotypically, -0.415** phenotypically) and SM (-0.311* genotypically, -0.239 phenotypically). DTM showed negative correlation with ETP (-0.382**) and GP (-0.329**), consistent with phenotypic data (Fufa *et al*., 2024) [10]. PHT (cm) demonstrated significant positive genotypic correlations with ETP (0.845**), GP (0.738**), and HI (%) (0.668**), while phenotypically, it correlated positively with GYP (0.451**), HI (%) (0.411**), and SL (%) (0.318*). Both correlations highlighted significant negative relationships with GH (-0.569** genotypically, -0.366** phenotypically). The ETP exhibited significant positive genotypic correlations with SM (0.951**), GH (0.470**), and FLA (0.378**), and phenotypically, it showed non-significant positive correlations with SM (0.243) and GH (0.141). FLA demonstrated significant positive genotypic correlations with GP (0.909**), HI (%) (0.852**), SL (0.653**), and GP (0.584**), which were also associated phenotypically with GYS (0.573**), HI (%) (0.572**), and SL (0.425**). SL exhibited significant positive genotypic correlations with GYP (0.999**), TW (0.950**), GYP (0.945**), GYS (0.870**), and SP (0.857**), mirrored phenotypically by correlations with GYP (0.757**), and GYS (0.720**). SP demonstrated significant positive genotypic correlations with TW (0.903**), GYP (0.896**), and GYS (0.841**), also found phenotypically with TW (0.707**), GYS (0.690**), and GYP (0.634**).GP exhibited significant positive genotypic correlations with HI (0.921**), TW (0.850**), GYP (0.846**), GC (0.785**), and GYP (0.766**), consistent with phenotypic data showing positive correlations with GYS (0.644**), HI (%) (0.660**), and GC (0.632**). GYS showed significant positive genotypic correlations with TW (0.976**), GYP (0.995**), and HI (%) (0.681**), as well as phenotypically with GYP (0.735**), TW (0.619**), and HI (%) (0.497**). BYP (g) exhibited significant positive genotypic correlations with test weight (0.888**) and protein content (0.052**), and phenotypically with test weight (0.394**) and grain yield per plant (0.277*). Harvest index exhibited significant positive genotypic correlations with grain yield per plant (0.813**), gluten content (0.516**), and test weight (0.448**), similarly seen phenotypically with grain yield per plant (0.801**) and gluten content (0.392**). 1000 grain weight exhibited significant positive genotypic correlations with grain yield per plant (0.901**) and gluten content (0.354*), and phenotypically with grain yield per plant (0.485**) and gluten content (0.207). Current finding is in close agreement with the study of Sewore *et al.*, (2024) [17] and Li *et al*., (2023) [12].

4.3.2 Path coefficient analysis

Genotypic and phenotypic path coefficient estimates provide comprehensive insights into the direct as well as indirect contribution of various traits on grain yield/ plant (Table 5 & 6). For DFF, the genotypic analysis exhibits direct effect of 0.284 and positive indirect effects through SL (0.240), grain yield / spike (0.247), TW (0.256), HI (0.261), and GP

(0.211), with negative indirect effects through GH (-0.140) and SM (-0.088). Phenotypically, the direct effect was 0.043, with positive indirect effects through plant height (0.020), HI (0.037), TW (0.022), PC (0.020), and GC (0.026). DM had a positive direct effect on GYP genotypically (0.084) and phenotypically (0.053). Genotypically, it exerted positive indirect effects through TW (0.080), BYP (0.053), and GYS (0.033). Phenotypically, positive indirect effects were through days to DFF (0.018), PH (0.023), PL (0.015), SL (0.012), SP (0.045), GYP (0.033), BYP (0.053), and TW (0.080) (Baye *et al.*, 2020) [4].

Effective tillers per plant showed a negative direct effect on grain yield per plant in both genotypic (-0.027) and phenotypic (-0.027) analyses. Genotypically, it had positive indirect effects through TW (0.040) and BYP (0.004). Phenotypically, positive indirect effects through BYP (0.004), HI (0.005), TW (0.040), PC (0.011), DT (0.010), PL (0.007), and SP (0.012). Exhibited a negative direct effect on GYP genotypically (-0.290) and phenotypically (-0.214). Genotypically, it had positive indirect effects through seed moisture (0.117) and GH (0.116) with positive indirect effects through ETP (0.122), SM (0.117), and GH (0.116).GP had a negative direct effect on yield per plant genotypically (-0.320) and a positive effect phenotypically (0.093). Genotypically, it had positive indirect effects through SM (0.133) and GH (0.137), with negative indirect effects through FLA (-0.291) and SL (-0.278). Phenotypically, positive indirect effects were through DFF (0.237), PH (0.090), ETP (0.093), FLA (0.291), SL (0.278), SP (0.119), GYP (0.271), HI (0.295), TW (0.272), PC (0.152), and GC (0.251), with negative indirect effects through days to maturity (-0.105), BYP.

Test weight had a negative direct effect on GYP in both genotypic (-0.219) and phenotypic (-0.219) analyses, with genotypically positive indirect effects through DFF (0.256), PH (0.229), DM (0.080), PL (0.062), SL (0.410), SP (0.410), GP (0.410), grain yield and GC (0.368), and negative indirect effects through SM (-0.410), GH (-0.410), ETP (-0.410), FLA (-0.410), BYP (-0.410), HI (-0.410), PC (-0.410), and DM (-0.410). Phenotypically, the indirect effects were similar. Grain hardiness had a direct effect on seed yield per plant genotypically (0.015) and phenotypically (0.015), with positive indirect effects genotypically through DFF (0.284), PC (0.368), PH (0.015), DM (0.010), PL (0.062), SL (0.410), SP (0.410), GYP (0.410), and TW (0.410), and negative indirect effects through BYP (-0.410), SM (-0.410), ETP (-0.410), FLA (-0.410), and HI (-0.410). Phenotypically, the indirect effects were similar (Pandey *et al.*, 2021) [14].

Table 1: Analysis of variance for experimental design

Traits	Replications (df=2)	Treatments (df=54)	Error (df=108)
Days to 50% flowering (DFF)	8.90	67.23**	19.06
Plant height (PH)	64.97	59.87**	33.37
Days to maturity (DM)	17.46	71.89**	14.76
Effective tillers per plant (ETP)	90.67	54.12**	48.88
Flag leaf area (FLA)	9.61	16.98**	7.32
Peduncle length (PL)	28.93	33.26**	5.22
Spike length (SL)	37.3	15.16**	1.84
Spikelet per spike (SP)	16.53	29.33**	9.04
Grain Per Spike (GP)	42.41	56.35**	15.89
Grain yield/spike (GYS)	1.56	0.78**	0.22
Biological yield/plant (BYP)	7.17	24.87**	9.06
Harvest index (HI)	48	87.45**	31.04
Test Weight (TW)	6.05	15.05**	10.52
Seed Moisture (SM)	0.06	2.32**	0.85
Grain Hardiness (GH)	57.65	136.69**	13.28
Protein content (PC)	4.67	3.77**	1.18
Glutein (GC)	1.30	2.26**	0.29
Grain yield/plant (GYP)	5.62	9.64**	3.18

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively

Table 2: Estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense h^2(bs) and genetic advance in per cent of mean (GAM %)

S.N.	Characters	GCV (%)	PCV (%)	Heritability in broad sense (%)	GAM (%)
1	Days to 50% flowering	5.04	5.96	71.70	8.80
2	Plant height	2.95	4.44	44.30	4.05
3	Days to maturity	3.90	4.38	79.50	7.16
4	Effective tillers per plant	18.52	59.46	69.70	11.88
5	Flag leaf area	3.68	4.88	56.90	5.72
6	Peduncle length	6.39	6.96	84.30	12.08
7	Spike length	15.83	16.89	87.90	30.57
8	Spikelet per spike	11.61	13.96	69.20	19.90
9	Grains per spike	12.06	14.23	71.80	21.05
10	Grain yield/spike	14.88	17.63	71.30	25.88
11	Biological yield/plant	7.18	9.00	63.60	11.79
12	Harvest index (%)	10.16	12.66	64.50	16.82
13	Test Weight	2.79	5.08	60.10	3.15
14	Seed Moisture %	6.56	8.24	63.40	10.76
15	Grain Hardiness	39.90	40.11	98.90	81.74
16	Protein content	7.37	8.89	68.70	12.58
17	Glutein content	9.28	9.94	87.10	17.85
18	Grain yield/Plant	60.83	13.23	67.10	18.28

Table 3: Estimation of genotypic correlation for 18 traits in wheat

Traits	DFF	PH	DM	TPP	FLA	PL	SL	SP	GP	GYS	BYP	HI	TW	SM	GH	PC	GC	GYP
DFF	1.000	0.348*	0.267	0.040	0.420**	0.224	0.657**	0.505**	0.573**	0.608**	0.102	0.643**	0.384**	-0.239	-0.415**	0.350**	0.440**	0.752**
PH		1.000	0.173	-0.004	0.162	-0.055	0.318*	0.175	0.159	0.279*	0.079	0.411**	0.138	-0.142	-0.366**	0.135	0.097	0.451**
DM			1.000	-0.113	-0.159	0.162	0.107	0.426**	-0.219	0.304*	0.491**	0.005	0.415**	-0.018	-0.014	-0.066	-0.217	0.301*
TPP				1.000	0.105	-0.047	0.025	-0.157	0.049	-0.075	-0.044	0.037	-0.161	0.243	0.141	0.029	0.140	0.017
FLA					1.000	-0.028	0.425**	0.114	0.573**	0.282*	-0.423**	0.572**	-0.020	0.009	-0.191	0.236	0.394**	0.345*
PL						1.000	-0.008	0.031	0.030	0.032	0.127	0.045	0.056	-0.100	0.031	0.100	0.008	0.125
SL							1.000	0.669**	0.720**	0.757**	0.175	0.629**	0.551**	-0.279*	-0.410**	0.374**	0.523**	0.774**
SP								1.000	0.435**	0.690**	0.529**	0.272	0.707**	-0.218	-0.333*	0.249	0.272	0.634**
GP									1.000	0.644**	-0.173	0.660**	0.327*	-0.256	-0.361	0.348	0.632**	0.594**
GYS										1.000	0.329*	0.497**	0.619**	-0.232	-0.327*	0.276	0.409**	0.735**
BYP											1.000	-0.343*	0.394**	-0.151	-0.158	0.010	-0.138	0.277*
HI												1.000	0.224	-0.196	-0.237	0.184	0.392**	0.801**
TW													1.000	-0.173	-0.205	0.102	0.207	0.485**
SM														1.000	0.396**	-0.106	-0.067	-0.322*
GH															1.000	-0.150	-0.149	-0.362**
PC																1.000	0.727**	0.230
GC																	1.000	0.348*
GYP																		1.000

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively

Table 4: Estimation of phenotypic correlation for 18 traits in wheat

Traits	DFF	PH	DM	ETP	FLA	PL	SL	SP	GP	GYS	BYP	HI	TW	SM	GH	PC	GC	GYP
DFF	1.000	0.348*	0.267	0.040	0.420**	0.224	0.657**	0.505**	0.573**	0.608**	0.102	0.643**	0.384**	-0.239	-0.415**	0.350**	0.440**	0.752**
PH		1.000	0.173	-0.004	0.162	-0.055	0.318*	0.175	0.159	0.279*	0.079	0.411**	0.138	-0.142	-0.366**	0.135	0.097	0.451**
DT			1.000	-0.113	-0.159	0.162	0.107	0.426**	-0.219	0.304*	0.491**	0.005	0.415**	-0.018	-0.014	-0.066	-0.217	0.301*
ETP				1.000	0.105	-0.047	0.025	-0.157	0.049	-0.075	-0.044	0.037	-0.161	0.243	0.141	0.029	0.140	0.017
FLA					1.000	-0.028	0.425**	0.114	0.573**	0.282*	-0.423**	0.572**	-0.020	0.009	-0.191	0.236	0.394**	0.345*
PL						1.000	-0.008	0.031	0.030	0.032	0.127	0.045	0.056	-0.100	0.031	0.100	0.008	0.125
SL							1.000	0.669**	0.720**	0.757**	0.175	0.629**	0.551**	-0.279*	-0.410**	0.374**	0.523**	0.774**
SP								1.000	0.435**	0.690**	0.529**	0.272	0.707**	-0.218	-0.333*	0.249	0.272	0.634**
GP									1.000	0.644**	-0.173	0.660**	0.327*	-0.256	-0.361	0.348	0.632**	0.594**
GYS										1.000	0.329*	0.497**	0.619**	-0.232	-0.327*	0.276	0.409**	0.735**
BYP											1.000	-0.343*	0.394**	-0.151	-0.158	0.010	-0.138	0.277*
HI												1.000	0.224	-0.196	-0.237	0.184	0.392**	0.801**
TW													1.000	-0.173	-0.205	0.102	0.207	0.485**
SM														1.000	0.396**	-0.106	-0.067	-0.322*
GH															1.000	-0.150	-0.149	-0.362**
PC																1.000	0.727**	0.230
GC																	1.000	0.348*
GYP																		1.000

*, ** indicate significance at the 0.05 and 0.01 probability levels, respectively

Table 5: Genotypic path with seed yield per plant

Traits	DFF	PH	DM	ETP	FLA	PL	SL	SP	GP	GYS	BYP	HI	TW	SM	GH	PC	GC	GYP
DFF	0.284	0.168	0.062	0.057	0.196	0.085	0.240	0.196	0.211	0.247	0.043	0.261	0.256	-0.088	-0.140	0.137	0.157	0.752**
PH	-0.201	-0.340	-0.093	-0.288	-0.101	0.032	-0.179	-0.097	-0.095	-0.142	-0.053	-0.227	-0.171	0.093	0.194	-0.078	-0.035	0.451**
DT	0.018	0.023	0.084	-0.032	-0.019	0.015	0.012	0.045	-0.028	0.033	0.053	0.000	0.080	-0.006	-0.002	-0.008	-0.024	0.301*
ETP	-0.006	-0.023	0.010	-0.027	-0.010	0.007	0.000	0.012	-0.008	-0.001	0.004	0.005	0.040	-0.029	-0.013	0.011	-0.004	0.017
FLA	0.025	0.011	-0.008	0.014	0.036	-0.003	0.024	0.006	0.033	0.015	-0.025	0.031	-0.002	0.001	-0.010	0.013	0.021	0.345*
PL	-0.045	0.014	-0.026	0.037	0.012	-0.151	0.001	-0.003	0.001	-0.004	-0.029	-0.003	-0.021	0.026	-0.005	-0.015	0.000	0.125
SL	0.326	0.203	0.056	0.004	0.252	-0.001	0.386	0.331	0.336	0.365	0.097	0.315	0.405	-0.153	-0.169	0.189	0.233	0.774**
SP	-0.200	-0.083	-0.155	0.122	-0.049	-0.006	-0.248	-0.290	-0.108	-0.244	-0.214	-0.123	-0.522	0.117	0.116	-0.105	-0.102	0.634**
GP	-0.237	-0.090	0.105	-0.093	-0.291	0.003	-0.278	-0.119	-0.320	-0.271	0.093	-0.295	-0.272	0.133	0.137	-0.152	-0.251	0.594**
GYS	0.014	0.007	0.006	0.000	0.007	0.001	0.015	0.014	0.014	0.016	0.008	0.011	0.022	-0.007	-0.006	0.006	0.008	0.735**
BYP	0.140	0.145	0.587	-0.120	-0.636	0.181	0.233	0.685	-0.270	0.431	0.928	-0.325	0.824	-0.176	-0.185	0.049	-0.147	0.277*
HI	0.075	0.782	-0.005	-0.212	0.997	0.023	0.956	0.495	0.078	0.798	-0.410	0.171	0.524	-0.411	-0.337	0.268	0.604	0.801**
TW	-0.223	-0.124	-0.233	0.358	0.016	-0.035	-0.259	-0.445	-0.210	-0.340	-0.219	-0.111	-0.247	0.073	0.092	-0.041	-0.087	0.485**
SM	0.017	0.015	0.004	-0.056	-0.002	0.009	0.021	0.022	0.022	0.022	0.010	0.019	0.016	-0.053	-0.027	0.007	0.003	-0.322*
GH	0.038	0.044	0.002	-0.037	0.020	-0.003	0.034	0.031	0.033	0.030	0.015	0.022	0.029	-0.038	-0.077	0.015	0.012	-0.362**
PC	-0.064	-0.031	0.012	0.051	-0.049	-0.013	-0.065	-0.048	-0.063	-0.050	-0.007	-0.031	-0.022	0.018	0.025	-0.133	-0.105	0.230
GC	0.099	0.019	-0.052	0.024	0.105	0.000	0.108	0.063	0.141	0.090	-0.029	0.092	0.063	-0.012	-0.029	0.142	0.179	0.348*

R Square = 0.992 Residual Effect = 0.088

*, ** significant at 5% and 1 % level of significance

Table 6: Phenotypic path with seed yield per plant

Traits	DFF	PH	DM	ETP	FLA	PL	SL	SP	GP	GYS	BYP	HI	TW	SM	GH	PC	GC	GYP
DFF	0.057	0.020	0.015	0.002	0.024	0.013	0.037	0.029	0.033	0.035	0.006	0.037	0.022	-0.014	-0.024	0.020	0.026	0.752**
PH	-0.006	-0.016	-0.003	0.000	-0.003	0.001	-0.005	-0.003	-0.003	-0.005	-0.001	-0.007	-0.002	0.002	0.006	-0.002	-0.002	0.451**
DT	-0.006	-0.004	-0.021	0.002	0.003	-0.003	-0.002	-0.009	0.005	-0.006	-0.010	0.000	-0.009	0.000	0.000	0.001	0.005	0.301*
ETP	0.001	0.000	-0.002	0.017	0.002	-0.001	0.000	-0.003	0.001	-0.001	-0.001	0.001	-0.003	0.004	0.002	0.001	0.002	0.017
FLA	0.010	0.004	-0.004	0.003	0.024	-0.001	0.010	0.003	0.014	0.007	-0.010	0.014	-0.001	0.000	-0.005	0.006	0.010	0.345*
PL	-0.001	0.000	-0.001	0.000	0.000	-0.005	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.001	0.000	-0.001	0.000	0.125
SL	-0.004	-0.002	-0.001	0.000	-0.002	0.000	-0.005	-0.004	-0.004	-0.004	-0.001	-0.003	-0.003	0.002	0.002	-0.002	-0.003	0.774**
SP	0.020	0.007	0.017	-0.006	0.005	0.001	0.027	0.040	0.017	0.028	0.021	0.011	0.028	-0.009	-0.013	0.010	0.011	0.634**
GP	-0.010	-0.003	0.004	-0.001	-0.010	-0.001	-0.012	-0.007	-0.017	-0.011	0.003	-0.011	-0.006	0.004	0.006	-0.006	-0.011	0.594**
GYS	0.018	0.008	0.009	-0.002	0.008	0.001	0.022	0.020	0.019	0.029	0.009	0.014	0.018	-0.007	-0.009	0.008	0.012	0.735**
BYP	0.060	0.046	0.285	-0.025	-0.246	0.074	0.102	0.307	-0.100	0.191	0.581	-0.199	0.229	-0.088	-0.092	0.006	-0.080	0.277*
HI	0.603	0.385	0.005	0.034	0.537	0.042	0.590	0.255	0.620	0.466	-0.322	0.938	0.210	-0.184	-0.223	0.173	0.368	0.801**
TW	-0.003	-0.001	-0.003	0.001	0.000	0.000	-0.004	-0.005	-0.002	-0.004	-0.003	-0.002	-0.007	0.001	0.001	-0.001	-0.001	0.485**
SM	0.008	0.005	0.001	-0.009	0.000	0.004	0.010	0.008	0.009	0.008	0.005	0.007	0.006	-0.035	-0.014	0.004	0.002	-0.322*
GH	-0.001	0.000	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.000	0.000	-0.362**
PC	0.005	0.002	-0.001	0.000	0.003	0.001	0.005	0.003	0.005	0.004	0.000	0.003	0.001	-0.001	-0.002	0.013	0.010	0.230
GC	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.348*

R Square = 0.934 Residual Effect = 0.073

*, ** significant at 5% and 1 % level of significance

Conclusion

Analysis of variance for almost all the traits under study varies significantly, revealed substantial genetic variability among the genotypes for most of the traits studied. Highest GCV (%) has been recorded for grain yield per plant (GYP) followed by grain hardiness (GH), Effective tillers per plant (ETP) and Spike length (SL). It indicates genotypes playing vital role in variation. Similarly highest PCV has been recorded by effective tillers per plant (TPP) followed by grain hardiness (GH), indicating these traits are much influence by environmental factor while traits like DFF, PH, Dm, Pl, BYP, TW, SM and GC recorded lowest PCV value indicating these traits are very less influenced by environmental factor and could be give preference in trait selection during breeding program. Estimates of genotypic and phenotypic correlation indicating the relationship of different traits on grain yield. Most of the major yield attributing traits viz., DFF, PH, DM, SL, SP and GPS have positive and significant correlation with grain yield per plant (GYP) indication that through manipulation on these traits seed yield could be enhanced. Estimates of genotypic path exhibits that grain yield per plant (GYP) is indirectly associated with ETP, FLA, SL, SP, GP, GYS, HI and TW. It indicates through selection and enhancement of these traits would provide fruitful result in enhancing the grain yield.

Acknowledgments

I extend my heartfelt thanks to my advisor, Dr. Pratap Narayan Singh, for their kind support, perceptive feedback, and essential guidance during entire research project. Furthermore, I appreciate the BRD PG College, Deoria administration, for offering the necessary facilities needed for carrying out field research as well as laboratory facilities.

Conflict of Interest Declaration

The authors declare no conflicts of interest.

Ethical issues

None.

References

1. Agricolae: Statistical Procedures for Agricultural Research. Available from: https://cran.r-project.org/web/packages/agricolae/index.html [Accessed November 3, 2023].
2. Amanullah KS, Imran KH, Arif M, Altawaha AR, Parmar B. Organic matter management in cereals based system: symbiosis for improving crop productivity and soil health. Sustainable Agriculture Reviews. 2019;29:67-92.
3. Araus JL, Slafer GA, Royo C, Serret MD. Breeding for yield potential and stress adaptation in cereals. Critical Reviews in Plant Science. 2008;27(6):377-412.
4. Baye A, Berihun B, Bantayehu M, Derebe B. Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. Cogent Food & Agriculture. 2020;6(1):1752603.
5. Begna T, Gichile H, Yali W. Genetic diversity and its impact in enhancement of crop plants. Global Journal of Agricultural Research. 2022;10(2):13-25.
6. Burton GW, DeVane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45(10):478-481.
7. Chauhan BS, Mahajan G, Sardana V, Timsina J, Jat ML. Productivity and sustainability of the rice-wheat cropping system in the Indo-Gangetic Plains of the Indian subcontinent: problems, opportunities, and strategies. Advances in Agronomy. 2012;117:315-369.
8. de Mendiburu F. *Agricolae tutorial* (Version 1.3-5). Universidad Nacional Agraria: La Molina, Peru; 2021.
9. Dewey DR, Lu K. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agronomy Journal. 1959;51(9):515-518.
10. Fufa M, Gedebo A, Leta T, Lule D. Genetic variation, genetic advance, heritability and correlation analysis of phenotypic traits in tetraploid wheat (*Triticum turgidum* spp.) landraces and some improved cultivars of Ethiopia. Plant Genetic Resources. 2024;22(1):45-58.

11. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47(7):314-318.
12. Li Y, Tao F, Hao Y, Tong J, Xiao Y, He Z, *et al* Variations in phenological, physiological, plant architectural and yield-related traits, their associations with grain yield and genetic basis. Annals of Botany. 2023;131(3):503-519.
13. Lush JL. Animal Breeding Plans. 3rd ed. Iowa State College Press; 1943.
14. Pandey R, Maharjan B, Acharya S, KC B, Pandit R, Regmi R, *et al*. Correlation and path coefficient analysis of yield in wheat: A review. Russian Journal of Agricultural and Socio-Economic Sciences. 2021;5(113):121-127.
15. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agronomy Journal. 1949;41(8):353-359.
16. Searle SR, Casella G, McCulloch CE. Linear Models. Wiley; 1971.
17. Sewore BM, Abe A. Genetic variability and trait associations in bread wheat (*Triticum aestivum* L.) genotypes under drought-stressed and well-watered conditions. CABI Agriculture and Bioscience. 2024;5:64.
18. Singh V, Sharma A, Gupta R, Kumar P. Analysis of phenotypic and genotypic variability in wheat. International Journal of Current Microbiology and Applied Sciences. 2020;9(9):123-134.
19. Slafer GA. Genetic basis of yield as viewed from a crop physiologist's perspective. Annals of Applied Biology. 2003;142(2):117-128.
20. Tsegaye D, Dessalegn T, Dessalegn Y, Share G. Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum* Desf). Agricultural Research and Reviews. 2012;1(4):107-112.
21. Wright S. Correlation and causation. Journal of Agricultural Research. 1921;20(7):557-585.
22. Panse VG, Shukhatme PV. Statistical Methods for Agricultural Workers (2nd Ed). ICAR, Publications, New Delhi; 1967.