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Correlation Coefficient Analysis for Grain Yield and Its Contributing Traits in Bread Wheat (*Triticum aestivum* L.)

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Abstract

Experimental plot was conducted to the study of correlation coefficient of 21 parents line × tester mating design in bread wheat (*Triticum aestivum* L.) under the area of Department Genetics and Plant Breeding, farm during the *rabi* season 2023-24 and 2024-25 was evaluated for correlation coefficient for 16 traits i.e., Day to 50% heading, Day to maturity, plant height, number of total tillers per plant, spike length, number of spikelets per spike, number of grains per spike, number of grains per plant, flag leaf area, harvest index, 1000 grain weight (g), biological yield per plant (g), gluten content, protein content, chlorophyll content, canopy temperature depression and grain yield per plant (g) in 181 treatments including 21 parents, their 80 F₁ and 80 F₂ generations. The findings revealed a strong positive genotypic correlation of grain yield per plant with biological yield, followed by spike length, number of total tillers, 1000-seed weight, chlorophyll content and gluten content in both the generations. While phenotypic correlations were generally lower than genotypic ones, they reinforced the importance of these traits in yield improvement. The results suggest that breeding programs focusing on these key traits can effectively enhance wheat yield potential.

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Bread wheat, grain yield, correlation, F₁ and F₂

Introduction

Wheat (*Triticum* spp.) is a self-pollinating annual cereal grain that is farmed throughout the tropics and subtropics of the world and is of significant importance to the global economy. One-fifth of the overall amount of calories and proteins that human beings require in their diets is supplied by wheat, which is consumed by roughly 40% of the world's population (Bhutto *et al.*, 2016). Wheat plants are grasses that are members of the Poaceae family, which is also known as the monocot

family. When it comes to the different species of wheat, there are sixteen in total, but these are further classified into three groups based on the commercial type of wheat (*Triticum aestivum* and *Triticum durum*) and the growing habits of the plant (winter habit wheat, spring wheat, and facultative wheat) (Iqbal *et al.*, 2022).

According to Vavilov (1951), the origin of wheat is attributed to the Mediterranean basin and Abyssinia for tetraploid species (2n = 28), Afghanistan for hexaploid species (2n = 42), and Asia for diploid species (2n = 14).

China, India, the United States, Russia, France, Pakistan, Germany, Ukraine, Turkey, Canada, and Australia are the world's leading producers of wheat. India is the world's second-largest producer of wheat, after China. According to Malav *et al.*, (2017), wheat grain is made up of 60–68% starch, 1.5–2.0% fat, 2.0–2.5% cellulose, 6–21% protein, and 1.8% minerals like zinc, iron, selenium, and magnesium, which include vitamins like thiamine and vitamin B

Currently, the world's leading wheat producers include China, India, the United States, Russia, France, and the European Union. In 2024–25, global wheat production is projected to reach approximately 800 million metric tons, while India's wheat production is estimated at around 115 million metric tons, maintaining its position as the world's second-largest wheat producer (FAO, 2024).

Climate change is making several problems worse and putting more strain on the world's wheat crop. Wheat yields are the most susceptible to various environmental stressors of any major crop (Dimitrov *et al.*, 2022). Wheat offers a wide variety of genetic variability, which is necessary for creating superior wheat cultivars. Breeders of wheat around the world are concentrated on increasing the production and adaptability of wheat to various environments. Selection and hybridization are frequently used to combine advantageous features and improve the genetic potential of wheat.

Wheat productivity continues to fall short of its genetic potential, contributing significantly to global food insecurity. This situation has been intensified by the reduction in cultivable land caused by expanding human populations, coupled with adverse climate change effects and modifications in cultivation practices, including the abandonment of traditional crop rotation systems. To address these challenges, it is essential to understand trait interrelationships in wheat improvement programs. Correlation analysis provides an effective approach for examining associations between various characteristics in genetically diverse germplasm, thereby supporting breeding objectives (Dhami *et al.*, 2018). By revealing the strength and direction of relationships between yield components and final grain production, correlation coefficients enable plant breeders to identify and select genotypes with favorable trait combinations. Consequently, this study aims to investigate how different agronomic and physiological traits interact and influence grain yield both directly and indirectly, with the ultimate goal of improving wheat productivity.

Materials and Methods

Basic material consisting of 21 (16 lines and 5 testers) morphological diverse genotypes *viz.*, DBW-187, DBW-316, DBW-222, DBW-173, DBW-308, PBW-826, PBW-835, HD-3388, HD-3386, HD-2967, HD-3086, HD-3293, K-1616, K-17111, K-9107, K0307, HI-1653, HI-1654, HI-1612, K-1006 and PBW-833 were obtained from the germplasm maintained at Section of *Rabi* Cereals of the university in order to develop material to be evaluated for the study.

The experimental material consisted of 181 treatments (21 parents + 80 F₁S + 60 F₂S) was sown in a Randomized Block Design with three replications at Student Instruction Farm, C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.) during *Rabi*, 2024-25. Each parent and F₁S were planted in single row while each F₂S was planted in two rows of 3-meter length plots with inter and intra-row spacing of 22.5 cm and 10 cm, respectively. Recommended cultural practices and fertilizer dose were applied to raise good crop.

Data recorded for 16 characters *viz.*, Day to 50% heading, Day to maturity, plant height, Number of productive tillers per plant, spike length, Number of spikelets per spike, number of grains per spike, Number of grains per plant, flag leaf area, Harvest index, 1000 grain weight (g), Biological yield per plant (g), gluten content, protein content, chlorophyll content, canopy temperature depression and grain yield per plant.

Estimation of Correlation coefficients

The estimates of phenotypic and genotypic correlation were worked out as given under Dewey and Lu (1959):

Genotypic correlation:

$$R_{xy}(g) = \text{Cov. } xy(g) / [V_x(g) \cdot V_y(g)]^{0.5}$$

Where,

Cov.xy (g) = genotypic covariance between character X and Y was obtained as follows:

$$\text{Cov. } xy(g) = [\text{Cov. } Xy(p) - \text{Cov. } Xy(e)]/r$$

V_x (g) and V_y (g) = Genotypic variance for the characters x and y respectively

r = number of replications.

Phenotypic correlation:

$$r_{xy}(p) = \text{Cov. } Xy(p) / [V_x(p) \cdot V_y(p)]^{0.5}$$

Where,

$Cov.Xy(p)$ = Phenotypic correlation between the character x and y and this was obtained as follows:

$Cov.xy(p) = Cov.xy(g) + Cov.xy(e)$

$Vx(p)$ and $Vy(p)$ = Phenotypic variance for the characters x and y, respectively.

$xy(e)$ = the error variance obtained from the ANOVA of x and y characters.

Test of significance of correlation coefficients:

The significance of phenotypic coefficient was tested against r'' values from r'' Table of Fisher and Yates (1938) for (n-2) degree of freedom where n'' is number of treatments.

Results and Discussion

Correlation study was carried out between all the sixteen characters at genotypic and phenotypic levels. The phenotypic and genotypic correlation coefficient of F_1 and F_2 computed among the sixteen characters under study has been presented in Table 1, 2 and Table 3, 4 respectively.

Genotypic Correlation in F_1 Generation:

Grain yield per plant recorded a significant positive correlation with number of total tillers per plant (0.346), spike length (0.522), number of spikelets per spike (0.193), number of grain per spike (0.529), chlorophyll content (0.393), flag leaf area (0.126), 1000-seed weight (0.133), biological yield per plant (0.574) and gluten content (0.370). Positive but non-significant relationships were observed with harvest index (0.043). In contrast, negative significant protein content (-0.247) and days to 50% heading (-0.263), whereas canopy temperature depression (-0.019), days to maturity (-0.110) and plant height (-0.090) expressed negative and non-significant correlations with grain yield per plant.

Among all traits showing positive significant relationships, biological yield per plant exhibited the highest association with grain yield. These findings suggest that this trait plays a crucial role in determining grain yield, which is consistent with earlier studies (Kumar *et al.*, 2017; Abdurezake *et al.*, 2024). The strong dependence of grain yield on biological yield indicates that genetic improvement in total biomass production is a prerequisite for achieving higher grain yields in modern wheat cultivars (Foulkes *et al.*, 2011).

Other traits, including number of grains per spike, chlorophyll content, number of total tillers per plant, gluten content, and spike length, also exhibited significant positive correlations with grain yield, indicating their important roles in yield determination (Azad *et al.*, 2024; Khan *et al.*, 2013; Kumar *et al.*, 2014; Zhang *et al.*, 2023).

Phenotypic Correlation in F_1 Generation.

Grain yield per plant recorded a significant positive correlation with number of total tillers per plant (0.258), spike length (0.333), number of spikelets per spike (0.357), number of grains per spike (0.381), flag leaf area (0.222), chlorophyll content (0.378) 1000-seed weight (0.135), biological yield per plant (0.482), and gluten content (0.324). Positive but non-significant relationships were observed with harvest index (0.038), days to maturity (0.022), and canopy temperature depression (0.106). In contrast, significant negative correlations were observed with protein content (-0.336), and days to 50% heading (-0.296), whereas plant height (-0.001) expressed a negative but non-significant correlation with grain yield per plant.

Biological yield per plant showed the highest positive association with grain yield at both genotypic and phenotypic levels, followed by traits such as spike length, gluten content, number of grains per spike, chlorophyll content, number of total tillers per plant and 1000-seed weight. However, the phenotypic correlation coefficients were generally lower than the genotypic ones, indicating that environmental factors might mask the full genetic potential of these traits. Traits showing significant negative correlations with grain yield per plant included days to 50% heading and protein content. Similar results were reported in previous studies, where days to heading showed a negative relationship with yield (Avinashe *et al.*, 2011), grain protein content consistently exhibited an inverse relationship with grain yield (Zhang *et al.*, 2020; Khan *et al.*, 2019),

Genotypic Correlation in F_2 Generation

Grain yield per plant recorded a significant positive correlation with number of total tillers per plant (0.346), spike length (0.522), number of spikelets per spike (0.193), number of grain per spike (0.529), chlorophyll content (0.393), flag leaf area (0.126), 1000-seed weight (0.133), biological yield per plant (0.574) and gluten content (0.370). Positive but non-significant relationships were observed with harvest index (0.043).

Table.1 Estimates of Genotypic correlation coefficients computed between 16 characters of wheat in F1 Generation.

Cha	D50	DM	PH (cm)	NTTP	SL (cm)	NSS	NGS	FLA (cm ²)	1000sw	Biop	HI (%)	PRC (%)	GC (%)	CHL	CTD	GYP (g)
D50	1	0.633**	0.140*	-0.212**	-0.125*	-0.075	-0.007	-0.298**	-0.331**	-0.183**	0.077	0.432**	-0.514**	0.530**	-0.03	-0.263**
DM			-0.005	0.128*	0.046	-0.184**	0.059	0.019	0.117*	-0.073	-0.026	0.013	-0.192**	0.084	-0.096	-0.11
PH (cm)				-0.007	-0.115*	-0.109	0.016	-0.292**	-0.161**	0.044	-0.046	0.260**	-0.144*	0.186**	0.041	-0.09
NTTP					0.268**	0.253**	0.291**	0.257**	0.244**	0.291**	-0.058	-0.327**	0.221**	-0.263**	-0.017	0.346**
SL (cm)						0.066	0.532**	-0.088	0.074	-0.009	0.331**	-0.003	-0.096	0.069	-0.328**	0.522**
NSS							-0.034	0.356**	0.205**	0.066	0.045	-0.032	0.102	-0.142*	-0.025	0.193**
NGS								0.056	0.200**	0.137*	0.171**	-0.195**	0.133*	-0.057	-0.068	0.529**
FLA (cm ²)									0.316**	0.171**	-0.117*	-0.412**	0.506**	-0.540**	-0.028	0.126*
1000sw										0.088	-0.032	-0.487**	0.065	-0.095	0.076	0.133*
Biop											-0.779**	-0.067	0.342**	-0.395**	0.095	0.574**
HI (%)												-0.097	-0.181**	0.207**	-0.083	0.043
PRC (%)													-0.446**	0.414**	-0.171**	-0.247**
GC (%)														-0.816**	0.062	0.370**
CHL															-0.073	0.393**
CTD																-0.019
GYP (g)																1

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

Table.2 Estimates of phenotypic correlation coefficients computed between 16 characters of wheat in F1 Generation.

Cha	D50	DM	PH (cm)	NTTP	SL (cm)	NSS	NGS	FLA (cm ²)	1000sw	Biop	HI (%)	PRC (%)	GC (%)	CHL	CTD	GYP (g)
D50	1	0.290**	0.075	-0.169**	-0.004	-0.132*	-0.011	-0.171**	-0.231**	-0.122*	0.041	0.342**	-0.408**	0.419**	-0.01	-0.197**
DM			-0.003	0.108	-0.059	-0.059	0.034	-0.009	0.155**	-0.076	-0.005	-0.08	-0.150**	0.071	-0.074	-0.072
PH (cm)				-0.071	-0.087	-0.063	-0.023	-0.127*	-0.230**	0.011	0.096	0.160**	-0.073	0.111	0.019	-0.016
NTTP					0.156**	0.209**	0.266**	0.200**	0.218**	0.243**	-0.066	-0.284**	0.202**	-0.238**	-0.038	0.290**
SL (cm)						-0.085	0.381**	-0.061	0.009	0.031	0.197**	0.017	-0.091	0.059	-0.190**	0.341**
NSS							-0.05	0.249**	0.118*	0.042	0.077	-0.054	0.091	-0.123*	-0.028	0.191**
NGS								0	0.171**	0.127*	0.141*	-0.151**	0.106	-0.05	-0.081	0.453**
FLA (cm ²)									0.087	0.148**	-0.121*	-0.362**	0.455**	-0.469**	-0.024	0.158**
1000sw										-0.01	-0.018	-0.378**	0.038	-0.059	0.066	0.118*
Biop											-0.740**	-0.03	0.309**	-0.374**	0.103	0.465**
HI (%)												-0.104	-0.151**	0.180**	-0.084	0.07
PRC (%)													-0.435**	0.378**	-0.141*	-0.236**
GC (%)														-0.800**	0.061	0.333**
CHL															-0.089	0.347**
CTD																-0.038
GYP (g)																1

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

Table.3 Estimates of phenotypic correlation coefficients computed between 16 characters of wheat in F₂ Generation.

Cha	D50	DM	PH (cm)	NTTP	SL (cm)	NSS	NGS	FLA (cm ²)	1000sw	Biop	HI (%)	PRC (%)	GC (%)	CHL	CTD	GYP (g)
D50	1	0.163**	0.267**	-0.368**	-0.295**	0.127*	-0.115*	-0.382**	-0.591**	-0.231**	0.088	0.348**	-0.428**	0.450**	-0.229**	-0.314**
DM			0.217**	0.074	0.016	0.087	0.061	0.054	0.099	0	-0.018	0.104	-0.157**	0.024	-0.045	0.014
PH (cm)				-0.147*	-0.128*	0.02	-0.03	0.019	-0.127*	0.033	-0.014	-0.028	-0.047	0.092	-0.194**	-0.018
NTTP					0.201**	0.001	0.085	0.198**	0.304**	0.317**	-0.206**	-0.193**	0.171**	-0.280**	0.059	0.254**
SL (cm)						0.384**	0.481**	-0.151**	0.125*	0.05	0.219**	0.104	-0.096	0.069	0.048	0.493**
NSS							0.340**	0.023	-0.092	0.228**	0.073	-0.091	-0.038	-0.047	-0.084	0.446**
NGS								-0.120*	0.126*	0.091	0.152**	0.095	-0.073	0.079	0.019	0.446**
FLA (cm ²)									0.339**	0.257**	-0.178**	-0.378**	0.566**	-0.572**	0.117*	0.168**
1000sw										0.130*	-0.057	-0.229**	0.161**	-0.208**	0.011	0.222**
Biop											-0.765**	-0.407**	0.352**	-0.376**	0.046	0.575**
HI (%)												0.188**	-0.171**	0.161**	-0.004	0.079
PRC (%)													-0.618**	0.673**	0.06	-0.372**
GC (%)														-0.813**	0.026	0.346**
CHL															-0.087	0.400**
CTD																0.118*
GYP (g)																1

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

Table.4 Estimates of phenotypic correlation coefficients computed between 16 characters of wheat in F₂ Generation.

Cha	D50	DM	PH (cm)	NTTP	SL (cm)	NSS	NGS	FLA (cm ²)	1000sw	Biop	HI (%)	PRC (%)	GC (%)	CHL	CTD	GYP (g)
D50	1	-0.015	0.183**	-0.291**	-0.142*	0.065	-0.104	-0.270**	-0.373**	-0.124*	0.053	0.274**	-0.325**	0.336**	-0.128*	-0.296**
DM			0.185**	0.063	-0.049	0.046	0.043	0.036	0.074	-0.012	0.016	0.015	-0.116*	0.021	-0.044	0.022
PH (cm)				-0.186**	-0.073	0	-0.036	0.06	-0.173**	0.025	0.054	-0.036	-0.032	0.07	-0.121*	-0.001
NTTP					0.105	-0.006	0.082	0.158**	0.277**	0.257**	-0.191**	-0.167**	0.152**	-0.248**	0.022	0.258**
SL (cm)						0.176**	0.381**	-0.111	0.06	0.05	0.142*	0.08	-0.084	0.062	0.05	0.333**
NSS							0.249**	0.002	-0.1	0.199**	0.083	-0.074	-0.028	-0.038	-0.077	0.357**
NGS								-0.141*	0.099	0.087	0.131*	0.1	-0.079	0.077	0.011	0.381**
FLA (cm ²)									0.125*	0.215**	-0.171**	-0.331**	0.506**	-0.507**	0.105	0.220**
1000sw										0.035	-0.043	-0.183**	0.123*	-0.162**	-0.03	0.163**
Biop											-0.731**	-0.356**	0.328**	-0.355**	0.055	0.471**
HI (%)												0.159**	-0.155**	0.141*	0.006	0.082
PRC (%)													-0.597**	0.633**	0.048	-0.336**
GC (%)														-0.799**	0.033	0.324**
CHL															-0.101	0.378**
CTD																0.106
GYP (g)																1

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

In contrast, negative significant protein content (-0.247) and days to 50% heading (-0.263), whereas, days to maturity (-0.110) and plant height (-0.090) expressed negative and non-significant correlations with grain yield per plant.

Phenotypic Correlation in F₂ Generation

Grain yield per plant recorded a significant positive correlation with number of total tillers per plant (0.258), spike length (0.333), number of spikelets per spike

(0.357), number of grain per spike (0.381), chlorophyll content (0.378), flag leaf area (0.222), 1000-seed weight (0.135), biological yield per plant (0.482) and gluten content (0.324). Positive but non-significant relationships were observed with harvest index (0.038), canopy temperature depression (0.106) and days to maturity (0.022). In contrast, negative non-significant correlation with days to 50% heading (-0.296) and protein content (-0.336), whereas plant height (-0.001) expressed negative and non-significant correlations with grain yield per plant.

In the F₂ generation, biological yield per plant exhibited the highest positive genotypic and phenotypic correlation, followed by traits such as number of total tillers per plant, spike length, number of spikelets per spike, flag leaf area, chlorophyll content, 1000-seed weight, and gluten content. Similar trends have also been reported in earlier studies.

In conclusion, the comparative analysis across F₁ and F₂ generations reveals that biological yield per plant consistently proved to be the most reliable indicator of grain yield in both generations, with stable positive contributions from spike length, number of total tillers, 1000-seed weight, chlorophyll content and gluten content. The remarkable consistency in the performance of these key morphological and physiological traits across generations provides strong evidence for their utility as dependable selection criteria in practical wheat breeding programs. Nevertheless, the observation that phenotypic correlations remained consistently lower than genotypic correlations serve as an important reminder of how environmental factors can obscure the true genetic worth of these traits, thereby reinforcing the need for comprehensive multi-generational evaluations to ensure more accurate trait assessment and enable better-informed breeding decisions.

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