Assessment of Genetic variability, correlation and path analysis in bread wheat (*Triticum aestivum* L.) genotypes for yield and its attributing traits

ABSTRACT

This study investigated the genetic variability and agronomic traits influencing wheat yield across multiple genotypes. Conducted during the 2021-2022 rabi season at the Research Farm of BRD PG College, Deoria, the experiment included 31 treatments and a standard check variety, HD-2967, arranged in a randomized block design (RBD) with three replications. Analysis of variance (ANOVA) revealed significant genetic variation among the genotypes for traits such as Days to 50% Flowering (DF), Days to Maturity (DM), Plant Height (PH), and Grain Yield per Plant (GYP). Genotypic correlation analysis showed significant positive associations between DF and DM, and negative correlations between DF, DM, and GYP, highlighting the complex trade-offs among traits. Traits like Test Weight (TW) and Biological Yield (BY) were positively correlated with GYP, indicating their potential as key selection criteria for breeding. Path coefficient analysis identified DF and Test Weight as having strong direct effects on GYP, while traits such as Plant Height and Number of Grains per Spike had negative impacts. These results provide valuable insights into the genetic and phenotypic relationships that can guide the development of superior wheat genotypes with improved yield potential.

Keywords: Wheat, Variability, Correlation, path analysis

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops globally, second only to rice, and serves as a major staple food for millions in South Asia. As a primary source of nutrition for over 40% of the global population, wheat is vital to food security (Peng *et al.*, 2011). In India, wheat is cultivated over an area of approximately 30.23 million hectares, yielding 93.50 million tonnes with a productivity of 3.09 tonnes per hectare during the 2015-2016 period (Anonymous, 2022). However, with India's rapidly growing population, the challenge of ensuring adequate food supply is becoming increasingly difficult. As expanding agricultural land is not a feasible solution, enhancing wheat productivity through the development of superior genotypes and better crop management practices is the only viable approach to meet the rising demand for food.Breeding methodologies must be designed to incorporate favorable changes through selection or hybridization of superior genotypes.

The selection of one trait in breeding often affects several associated traits, highlighting the importance of understanding the interrelationships among different yield components. Knowledge of these interrelationships is essential in breeding programs for selecting traits that are difficult to measure or have low heritability. A consistent association of yield components across various environments is crucial for optimizing breeding efficiency (Adunga and Labuschangne, 2003). Therefore, examining the magnitude and direction of correlations among yield traits is necessary to achieve higher yields. Furthermore, an understanding of these correlations is vital to predict the effects of selecting a specific trait in breeding programs (Falconer, 1989). While correlation studies provide valuable insights, they do not fully capture the complexity of direct and indirect effects. Path coefficient analysis, therefore, is an effective tool for partitioning these correlations into direct and indirect effects, particularly when multiple variables are involved. This study aims to analyze the relationships between key yield components, assess their interconnections, and evaluate their direct and indirect contributions to seed yield.

2. MATERIALS AND METHODS

The experimental materials for this study consisted of 32 wheat treatments*viz.*,PBW-502, DBW-14, PBW-343, SR 303, PBW 154, Kundan and CSW-18, DBW18, HD 3226, PBW 667 and HD-2967 The experiment was conducted during the 2019-2020 rabi season at the Research Farm of BRD PG College, Deoria (Affiliated with DDU Gorakhpur University, Uttar Pradesh).

3. STATISTICAL ANALYSIS

The analysis of variance (ANOVA) for the design of experiment was carried out following the procedure outlined by Panse and Sukhatme (1967). The genotypic variance was calculated using the formula suggested by Burton and Devane (1953). The coefficient of genotypic and phenotypic variation was calculated using Burton's (1952) formula, providing a measure of the extent of variation within the population. Heritability in broad sense (Hbs) was estimated according to the formula suggested by Burton and Devane (1953). The expected genetic advance for different characters under selection was estimated using the formula by Lush (1943) and Johnson *et al.* (1955). The genetic advance as a percentage of the mean was calculated using the formula given by Robinson and Comstock (1949). The association among different characters at both genotypic and phenotypic levels was determined using the method outlined by Searle *et al.* (1971). Direct and indirect effects were estimated using path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Data was processed in R using the Agricolae package (Version 1.3-5). Combining ability for each trait was calculated based on Hayes *et al.* (1955).

4. RESULTS AND DISCUSSION

4.1. Analysis of variance

The results of analysis of variance (ANOVA) indicated significant differences among the genotypes for most of the traits studied, suggesting a high degree of genetic variability. This variability is crucial for the selection and improvement of these traits in breeding programs. The significant differences among genotypes highlight the potential for selecting superior genotypes with desirable traits for further breeding (Begna *et al.*, 2022;Jagshoran*et al.*, 1995)(Table 1).

4.2. Genotypic Correlation coefficient analysis

The genotypic correlation analysis provided critical insights into the relationships among agronomic traits and their impact on grain yield(Table 2). Days to 50% flowering (DF) exhibited a positive significant correlation with days to maturity (0.940), plant height (0.560), and harvest index (0.388), while showing a negative significant association with grain yield per plant (-0.984) and the number of grains per spike (-0.270). Similarly, days to maturity (DM) was positively correlated with DF (0.948) and harvest index (0.562), but negatively associated with grain yield (-0.988). Plant height (PH) showed significant positive correlations with test weight (0.314) but negative correlations with anthesis duration (-0.329) and the number of grains per spike (-0.149). Effective tillers per plant (ETP) correlated positively with biological yield (0.521) and harvest index (0.376), but negatively with grain yield (-0.016).Flag leaf area (FLA) was significantly associated with anthesis duration (0.341), test weight (0.302), and spike length (0.309), while the number of hairs on lodicules (HL) correlated positively with the number of grains per spike (0.414) and biological yield (0.418). Anthesis duration (AD) positively influenced the number of grains per spike (0.369) but was negatively associated with plant height

(-0.329). Grain yield per plant (GYP) exhibited significant positive correlations with biological yield (0.944), number of grains per plant (0.844), and test weight (0.327), while showing strong negative associations with DF (-0.984), DM (-0.988), PH (-0.992), and FLA (-0.981). Traits like test weight (TW) and spike length (SL) positively influenced grain yield and related traits but showed negative correlations with biological yield and harvest index. These findings provide a comprehensive dataset that highlights correlations to inform breeding strategies for enhanced grain yield and overall plant performance(Kumar *et al*., 2010).

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4.3. Phenotypic Correlation coefficient analysis

The phenotypic correlation analysis highlighted significant relationships among agronomic traits and their influence on grain yield(Table 3). Days to 50% flowering (DF) correlated positively with days to maturity (0.911), plant height (0.450), harvest index (0.323), and grain yield per plant (0.503), but negatively with the number of hairs on lodicules (-0.303) and grains per spike (-0.270). Days to maturity (DM) shared similar positive correlations with DF (0.911), plant height (0.380), and harvest index (0.397), while negatively correlating with traits like effective tillers per plant (-0.086) and biological yield per plant (-0.250). Plant height (PH) positively correlated with DF (0.450) and DM (0.380) but negatively with the number of grains per spike (-0.316). Effective tillers per plant (ETP) were associated with higher biological yield (0.297), while flag leaf area (FLA) positively impacted grain yield (0.382). The number of hairs on lodicules (HL) correlated with grain number (0.379) but inversely affected grain yield (-0.420). Anthesis duration (AD) positively influenced grain number (0.341). Grain yield per plant (GYP) showed significant positive correlations with DF (0.503), FLA (0.382), and spike length (0.223), while negatively correlating with HL (-0.420), grain number (-0.350), and biological yield (-0.446). These findings provide crucial insights into breeding programs for optimizing yield-related traits.(Nagireddy and Jyothula 2009).

4.4. Genotypic Path coefficient analysis

The path coefficient analysis provided insights into the direct and indirect effects of agronomic traits on grain yield per plant (GYP) (Table 4). Traits like days to 50% flowering (1.407) and test weight (2.492) exhibited strong positive direct effects, while traits such as plant height (-2.172) and number of grains per spike (-2.057) had significant negative direct impacts. Indirectly, traits like days to maturity, flag leaf area, and biological yield contributed positively through traits such as harvest index, test weight, and spike length. Conversely, traits like plant height and number of grains per spike showed complex indirect pathways, often counteracting their direct effects. Biological yield per plant (0.283) demonstrated a moderate positive direct impact with significant indirect contributions, underlining its importance. Harvest index (-1.299) and flag leaf area (-2.302) showed strong negative direct effects, despite some indirect positive contributions. The findings underscore the intricate relationships among traits, highlighting key selection criteria such as early flowering, test weight, and effective tillers for enhancing yield in breeding programs (Meles *et al*., 2017).

4.5. Phenotypic Path coefficient analysis

The phenotypic path coefficient analysis elucidated the direct and indirect effects of key agronomic traits on grain yield per plant (GYP), revealing complex interactions (Table 5). Traits like days to 50% flowering (1.116), flag leaf area (0.291), and harvest index (0.191) exhibited strong positive direct effects, underscoring their importance in yield improvement. In contrast, days to maturity (-0.952) and biological yield per plant (-0.260) had notable negative direct impacts, although they contributed positively via indirect pathways. Effective tillers per plant (-0.154) and test weight (-0.178) also showed negative direct impacts but played crucial roles in indirect yield enhancement through traits like spike length, flag leaf area, and harvest index. Conversely, traits such as the number of grains per spike (-0.112) and number of hairs on lodicules (-0.075) displayed negative direct effects but significant positive indirect contributions to yield components. The findings highlight the importance of integrating traits with strong direct and indirect effects, such as days to 50% flowering, flag leaf area, and harvest index, into breeding programs to optimize grain yield (Mecha *et al.*, 2017).

Conclusion

The analysis of variance (ANOVA) demonstrated significant genetic variability among the wheat genotypes for various agronomic traits, highlighting the potential for selection and improvement through breeding programs. Genotypic correlation analysis revealed that traits such as Days to 50% Flowering (DF), Days to Maturity (DM), and Plant Height (PH) exhibited strong correlations with each other and with grain yield, underlining the intricate relationships between phenological, morphological, and yield-related traits. Specifically, DF showed a negative correlation with grain yield per plant, while traits like Biological Yield and Number of Grains per Spike positively influenced yield potential. Path coefficient analysis indicated that DF and Test Weight had strong positive direct effects on grain yield, while traits like Plant Height and Number of Grains per Spike exerted negative direct impacts. Furthermore, indirect effects mediated through traits like Harvest Index and Biological Yield further emphasized the complexity of trait interactions. These findings suggest that breeding programs targeting early flowering, optimized plant architecture, and improved test weight could effectively enhance grain yield in wheat. Identifying key traits, such as DF, Harvest Index, and Biological Yield, will help streamline breeding strategies for better yield performance, offering valuable insights for future wheat improvement.

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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Table: 1: Analysis of variance for yield and its contributing characters

SOV	df	DF	DM	PH	ETP	FLA	HL	AD	GPS	TW	SL	BYPP	HI	GYPP
Replication	2	1.30	90.30**	11.24	2.77**	9.81	5.57	11.06	1.02	4.25*	0.02	33.69**	5.40	349.06
Treatments	30	131.50 **	33.46**	48.27**	1.68**	17.15**	24.83**	293.25**	14.72**	3.16**	0.84**	8.86*	29.07	19.35**
Error	60	146.17	7.13950	20.68	0.50	4.00	2.30	29.84	1.65	0.91	0.08	4.60	8.35	23.08

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

Table 2: Estimates of at genotypic correlation coefficient for component characters with grain yield

Traits	DF	DM	PH	ETP	FLA	HOL	AD	GPS	TW	SL	BYP	HI	GYP
DF	1.000	0.940**	0.560**	-0.090	0.170	-0.320*	0.040	-0.270*	-0.006	-0.025	-0.492	0.388**	-0.984**
DM		1.000	0.514**	-0.236	-0.038	-0.173	0.122	-0.198	-0.012	-0.113	-0.401	0.562**	-0.988**
PH			1.000	-0.102	0.221	-0.280*	-0.329*	-0.451**	0.314*	0.013	-0.670**	-0.179	-0.992**
ETP				1.000	0.266	0.119	0.254	-0.211	-0.152	0.114	0.521**	0.376**	-0.016
FLA					1.000	0.063	0.341*	-0.031	0.302*	0.329*	0.237	-0.023	-0.981**
HOL						1.000	0.269	0.414**	-0.048	-0.125	0.418**	-0.206	0.958**
AD							1.000	0.369**	0.104	-0.045	0.219	-0.089	0.367**
GPS								1.000	0.376**	0.338*	0.216	-0.345*	0.844**
TW									1.000	0.443**	-0.197	-0.080	0.327*
SL										1.000	-0.416**	-0.190	-0.280*
BYP											1.000	-0.447**	0.944**
HI												1.000	-0.467**
GYP													1.000

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

Table 3: Estimates of at phenotypic correlation coefficient for component characters with grain yield

Traits	DF	DM	PH	ETP	FLA	NHL	AD	GPS	TW	SL	BYP	HI	GYP
DF	1.000	0.911**	0.450**	-0.057	0.158	-0.303*	0.055	-0.246	-0.002	-0.041	-0.333*	0.323*	0.503**
DM		1.000	0.380**	-0.086	0.007	-0.146	0.120	-0.149	-0.018	-0.123	-0.250	0.397**	0.245
PH			1.000	-0.145	0.128	-0.221	-0.245	-0.316*	0.253	-0.024	-0.156	0.061	0.257
ETP				1.000	0.232	0.101	0.182	-0.178	-0.130	0.100	0.297*	0.134	-0.065
FLA					1.000	0.060	0.251	-0.043	0.183	0.268	0.163	-0.077	0.382**
HOL						1.000	0.227	0.379**	-0.002	-0.095	0.264	-0.163	-0.420**
AD							1.000	0.341*	0.076	-0.025	0.143	-0.016	-0.083
GPS								1.000	0.336*	0.309*	0.122	-0.268	-0.350*
TW									1.000	0.324*	-0.167	-0.083	-0.051
SL										1.000	-0.267	-0.141	0.223
BYP											1.000	-0.101	-0.446**
HI												1.000	0.195
GYP													1.000

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

Table 4: Estimates of at genotypic path coefficient for component characters with seed yield

Traits	**DF**	**DM**	**PH**	**ETP**	**FLA**	**HOL**	**AD**	**GPS**	**TW**	**SL**	**BYP**	**HI**	**GYP**
DF	**1.407**	1.333	0.795	-0.137	0.242	-0.453	0.058	-0.389	-0.008	-0.036	-0.693	0.546	-0.984**
DM	-0.559	**-0.590**	-0.303	0.139	0.023	0.102	-0.072	0.117	0.007	0.067	0.236	-0.332	-0.988**
PH	-1.227	-1.117	**-2.172**	0.222	-0.480	0.608	0.714	0.979	-0.681	-0.029	1.455	0.388	-0.992**
ETP	-0.039	-0.094	-0.041	**0.398**	0.106	0.047	0.101	-0.084	-0.061	0.045	0.207	0.150	-0.016
FLA	-0.396	0.088	-0.509	-0.612	**-2.302**	-0.144	-0.786	0.070	-0.696	-0.757	-0.545	0.052	-0.981**
HOL	-0.490	-0.264	-0.426	0.182	0.095	**1.522**	0.409	0.630	-0.072	-0.191	0.636	-0.313	0.958**
AD	0.011	0.033	-0.089	0.068	0.092	0.072	**0.270**	0.100	0.028	-0.012	0.059	-0.024	0.367**
GPS	0.569	0.407	0.927	0.433	0.063	-0.852	-0.760	**-2.057**	-0.773	-0.696	-0.445	0.709	0.844**
TW	-0.014	-0.030	0.781	-0.379	0.753	-0.118	0.259	0.936	**2.492**	1.104	-0.491	-0.200	0.327*
SL	-0.003	-0.011	0.001	0.011	0.032	-0.012	-0.004	0.033	0.043	**0.096**	-0.040	-0.018	-0.280*
BYP	-0.140	-0.114	-0.190	0.148	0.067	0.118	0.062	0.061	-0.056	-0.118	**0.283**	-0.127	0.944**
HI	-0.504	-0.730	0.232	-0.489	0.029	0.267	0.116	0.448	0.104	0.246	0.581	**-1.299**	-0.467**

R SQUARE = 0.966 RESIDUAL EFFECT = 0.367

Table 5: Estimates of at phenotypic path coefficient for component characters with seed yield

Traits	**DF**	**DM**	**PH**	**ETP**	**FLA**	**HOL**	**AD**	**GPS**	**TW**	**SL**	**BYP**	**HI**	**GYP**
DF	**1.116**	1.017	0.502	-0.064	0.176	-0.338	0.061	-0.275	-0.002	-0.046	-0.371	0.361	0.503**
DM	-0.868	**-0.952**	-0.361	0.082	-0.006	0.139	-0.114	0.142	0.018	0.117	0.238	-0.378	0.245
PH	0.005	0.004	**0.010**	-0.002	0.001	-0.002	-0.003	-0.003	0.003	0.000	-0.002	0.001	0.257
ETP	0.009	0.013	0.022	**-0.154**	-0.036	-0.016	-0.028	0.027	0.020	-0.015	-0.046	-0.021	-0.065
FLA	0.046	0.002	0.037	0.068	**0.291**	0.017	0.073	-0.013	0.053	0.078	0.048	-0.023	0.382**
HOL	0.023	0.011	0.017	-0.008	-0.005	**-0.075**	-0.017	-0.028	0.000	0.007	-0.020	0.012	-0.420**
AD	0.002	0.005	-0.010	0.007	0.010	0.009	**0.039**	0.013	0.003	-0.001	0.006	-0.001	-0.083
GPS	0.028	0.017	0.035	0.020	0.005	-0.042	-0.038	**-0.112**	-0.038	-0.035	-0.014	0.030	-0.350*
TW	0.000	0.003	-0.045	0.023	-0.033	0.000	-0.014	-0.060	**-0.178**	-0.058	0.030	0.015	-0.051
SL	-0.005	-0.016	-0.003	0.013	0.036	-0.013	-0.003	0.041	0.043	**0.133**	-0.035	-0.019	0.223
BYP	0.087	0.065	0.041	-0.077	-0.043	-0.069	-0.037	-0.032	0.044	0.070	**-0.260**	0.026	-0.446**
HI	0.062	0.076	0.012	0.026	-0.015	-0.031	-0.003	-0.051	-0.016	-0.027	-0.019	**0.191**	0.195

R SQUARE = 0.712 RESIDUAL EFFECT = 0.365