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Research Article

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Genetic Profiling of Bread Wheat (*Triticum aestivum* L.): Analyzing Variation, Associations, Path Analysis, and Diversity to Revolutionize Crop Enhancement

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Abstract

This study involved examining 32 advanced wheat breeding lines sourced from BISA, Ludhiana and NBPGR, New Delhi. Executed at Lovely Professional University's Experimental farm for Plant Breeding and Genetics in Phagwara, Punjab, India, within the span of 2021-2022, this experiment utilized a meticulous randomized block layout replicated three times. The research focused on studying ten different characteristics. Genotypic variance significance was evident in all traits, reflecting genetic diversity. Phenotypic coefficient of variation (PCV) exceeded genotypic coefficient (GCV), likely due to genotype-environment interactions. Plant height and grain yield displayed moderate PCV and GCV, while days to flowering, days to maturity, spike length, 1000-seed weight, biological yield, and harvest index showed lower values. Effective tillers and grains per spike had higher PCV and GCV, indicating limited enhancement potential. Traits like effective tillers, plant height, grains per spike, and grain yield showed high heritability and genetic advance. Moderate genetic advance was noted in spike length, weight of a thousand seeds, overall biological productivity, and the index of harvesting efficiency. In contrast, flowering and maturity had low genetic advance. Eight of ten traits positively impacted yield of harvested grain, including time taken to reach maturity, height of plant, grain count per spike, seed weight per thousand, total biological output and harvest efficiency. Clustering analysis revealed the highest intra-cluster distance in cluster IV, followed by I and II. Clusters III and V lacked intra-cluster relations. Inter-cluster distances were highest between V and II, followed by other pairs. Plant height drove divergence, followed by grain yield, effective tillers and harvest index. This study suggests leveraging diverse genotypes for hybridization, supported by predictive statistical distances, for broad variations in wheat improvement strategies.

Keywords

Analysis of genetic variations, Common wheat, Clustering study, Correlation assessment, Path coefficient analysis

Introduction

Serving as a crucial staple on a global scale, wheat (*Triticum aestivum* L.) hailing from the Poaceae botanical family assumes paramount significance. Encompassing 17% of cultivated land, this grain plays a pivotal role in nourishing close to 50% of the global populace while constituting a substantial 20% proportion of overall caloric and protein intake in human sustenance. Within the gamut of wheat species, three distinct Triticum variants hold sway on a global scale: Bread wheat (*T. aestivum* L.), Macaroni wheat (*Triticum durum*), and *Triticum dicoccum*. The crop is self-pollinating and comes from Southwest Asia [1]. Hexa-

ploid wheat (*T. aestivum* L.) has a chromosome count of 42 (2n = 42), with genetic components AABBDD. In comparison, the Arabidopsis genome is 40 times larger than that of rice and about 6 times larger than corn's genome. Wheat is the most extensively grown cereal globally, covering 224.49 million hectares, yielding 792.40 million tons in the 2020-21 period. In India, wheat production reached 108.75 million tons, with an average national yield of 3424 kg/ha in the same period 2021. Although India already meets its wheat consumption needs, meeting the growing demands of the increasing population requires a substantial rise in wheat production. Consequently, enhancing wheat production stands out as a viable approach to fulfilling the nation's domestic requirements. Following the green revolution, the consistent growth in wheat yield has been linked to enhancements in both genetic factors and better farming techniques [2]. The primary objective of advancing genetics in any crop is to uncover insights into relationships, genetic diversity, and the mechanisms governing the inheritance of these genetic elements.

The coefficients of variation in genotype and phenotype offer valuable insights into the existing diversity within the material. Numerous research studies have identified genetic disparities among various wheat genotypes concerning traits associated with yield [3]. Heritability, coupled with substantial genetic advancement, proves to be a more advantageous tool for anticipating the forthcoming impact when choosing genotypes for yield-related traits, as suggested by Ibrahim et al. [4]. Studies involving correlations and path analysis enhance our comprehension of how distinct characteristics interrelate with grain yield. Correlations unveil the extent and orientation of connections between different traits contributing to yield. In the meantime, path coefficients, referred to as standardized partial regression coefficients, quantify how a predictor variable directly affects its corresponding response variable, considering both direct and indirect effects of predictors. Divergence analysis serves as a valuable technique for gauging the extent of biological population differentiation on a geographical scale. It also facilitates the exploration of the varying contributions of distinct elements to the overall differentiation within both intra-cluster and inter-cluster levels.

Materials and Methods

Experimental material

A set of thirty-two advanced breeding lines (Table 1) sourced from the Borlaug Institute for South Asia (BISA) and the National Bureau of Plant Genetic Resources (NBPGR) was utilized. The study occurred at Lovely Professional University's Research Farm in Phagwara, Punjab, India, during the 2021-22 academic years. This location sits at 31° 19' 32 N latitude and 75° 34' 45 E longitude, with an elevation of 243 meters above sea level. The area experiences a humid subtropical climate with cold winters and hot summers spanning from April to June, while winters range from November to February. Summer temperatures vary from around 48 °C (118 °F) highs to 25 °C (77 °F) lows, and winter temperatures range between 19 °C (66 °F) highs and -7 °C (19 °F) lows. The climate is primarily dry, except for a short southwest monsoon period in July and August, with an average annual rainfall of 70 cm.

Table 1: Thirty-two advanced wheat breeding lines used for the study.

S. No.	Lines	Source
1	CWY 620	BISA
2	VB 2565	NBPGR
3	SAW310	BISA
4	IC 78737	NBPGR
5	IC 532889	NBPGR
6	ESW 107	BISA
7	SAW 324	BISA
8	SAW 333	BISA
9	SAW 316	BISA
10	ESW 140	BISA
11	K9644	NBPGR
12	ESW 139	BISA
13	EC 66520	NBPGR
14	SAW 303	BISA
15	GS 9007	NBPGR
16	CWY 637	BISA
17	ESW 143	BISA
18	CWY 623	BISA
19	GS 8049	NBPGR
20	Faisalabad 2008	NBPGR
21	ESW 138	BISA
22	HTW 48	BISA
23	GS 6003	NBPGR
24	SAW 309	BISA
25	ESW 111	BISA
26	EC 532116	NBPGR
27	ESW 110	BISA
28	HTW 43	BISA
29	GS 6031	NBPGR
30	CWY 612	BISA
31	EC 55681	NBPGR
32	GS 6012	NBPGR

Note: BISA: Borlaug Institute for South Asia. NBPGR: National Bureau of Plant Genetic Resources

Experimental design

The materials used for the experiment were grown in randomized block design with three replications. To plant the seeds, furrows on lines were used. These lines were grown in four row plots of 2-meter length. The material was planted row to row 30 cm and plant to plant 10 cm on November 12, 2022. The experiment was carried out in strict accordance with all recommended procedures and guidelines, ensuring comprehensive adherence to the prescribed package of practices.

Data observations

Data from five plants per plot were taken into consideration and statistical analysis was carried out using the meaning of the data points. Over the course of the growth season, the subsequent 10 characteristics were monitored: Days to 50% flowering, days to maturity, number of effective tillers, plant height (cm), spike length (cm), number of grains per spike, 1000-seed weight, biological yield (g), harvest index (%), and grain yield per plant (g) were recorded.

Data analysis

The analysis of variance and covariance was carried out by using the method as described by Panse and Sukhatme [5]. Phenotypic and genotypic coefficients of variation were calculated as percentages using Burton's formula [6]. Broad-sense heritability, also in percentages, was estimated following Hanson et al. method [7]. Genetic advance refers to improvement in mean genotypic value over the parent population. Expected genetic advance was computed as per Johnson et al. approach [8]. Correlation coefficients between traits were determined using variance and covariance components, following AI-Jibouri et al. formula [9]. The direct and indirect contributions of traits to total correlation coefficients with grain yield were assessed via path coefficient analysis, based on Dewey and Lu [10]. D^2 analysis, based on Mahalanobis [11], evaluated genetic divergence among entries, clustered using Torcher's method by Praveen [12]. Intra and inter cluster distances were calculated per Prasad's formula [13].

Table 2: Analysis of variance for seed yield and its components in bread wheat.

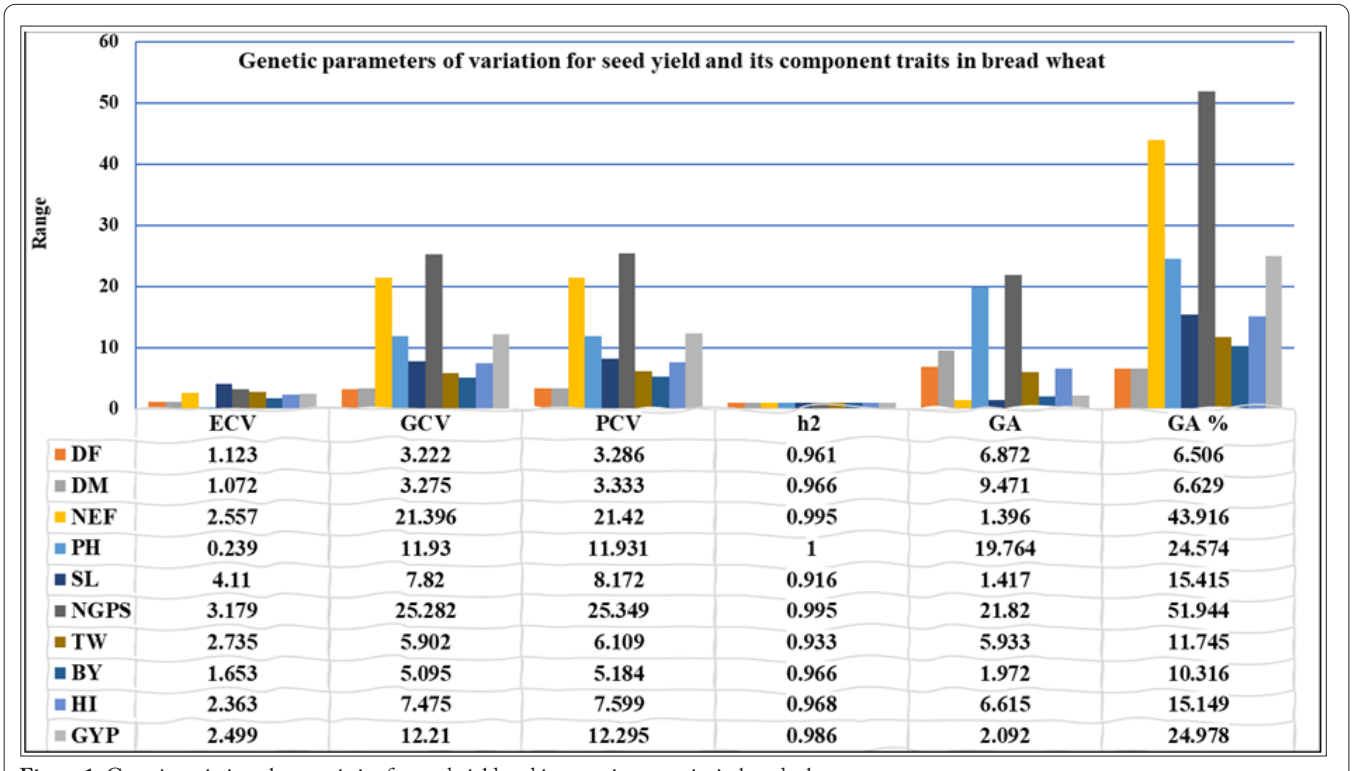
S. No.	Trait	Replication (df = 2)	Treatment (df = 31)	Error (df = 62)	CV (%)
1	Days to fifty per cent flowering	2.37	36.14**	1.4	1.12
2	Days to maturity	4.66	68.01**	2.34	1.07
3	Number of effective tillers	0	1.39**	0	2.55
4	Plant height	0.05	276.22**	0.03	0.23
5	Spike length	0.05	1.69**	0.14	4.11
6	Number of grains per spike	7.44*	340.14**	1.78	3.17
7	1000-seed weight	1.82	28.57**	1.9	2.73
8	Biological yield	0.05	2.94**	0.09	1.65
9	Harvest index	0.42	33.02**	1.06	2.36
10	Grain yield per plant	0	3.17**	0.04	2.49

Experimental Results

The analysis of variances indicated a significant mean sum of squares attributed to genotypes for all characters, highlighting substantial genetic variability within the studied material. The lack of significant variation for replication underscores minimal environmental error contribution (Table 2).

Evaluation of variability: genotypic and phenotypic

In the context of variation analysis, the PCV consistently outperformed the GCV across all examined traits, indicating a stronger influence of environmental factors on trait variation than genetic factors (Figure 1). Among the traits, number of grains per spike displayed the highest PCV, suggesting substantial phenotypic diversity in this characteristic. This was mirrored by the highest GCV observed in the same trait, indicating significant genetic variability that could be harnessed through selective breeding. On the other hand, traits like days to maturity, days to 50% flowering, and biological yield exhibited low PCV and GCV values, indicating a relatively stable expression influenced by both genetic and environmental stability. Environmental coefficient of variation further revealed that spike length was most responsive to environmental fluctuations, followed by number of grains per spike and number of effective tillers. These findings provide valuable insights for future research and practical applications in crop improvement and management.



	ECV	GCV	PCV	h2	GA	GA %
DF	1.123	3.222	3.286	0.961	6.872	6.506
DM	1.072	3.275	3.333	0.966	9.471	6.629
NEF	2.557	21.396	21.42	0.995	1.396	43.916
PH	0.239	11.93	11.931	1	19.764	24.574
SL	4.11	7.82	8.172	0.916	1.417	15.415
NGPS	3.179	25.282	25.349	0.995	21.82	51.944
TW	2.735	5.902	6.109	0.933	5.933	11.745
BY	1.653	5.095	5.184	0.966	1.972	10.316
HI	2.363	7.475	7.599	0.968	6.615	15.149
GYP	2.499	12.21	12.295	0.986	2.092	24.978

Figure 1: Genetic variation characteristics for seed yield and its constituent traits in bread wheat.

Heritability

Heritability estimates for broad sense were determined for all traits as shown in figure 1, ranging from 91.6% to 100%. Notably, plant height exhibited the highest heritability at 100%, followed closely by number of grains per spike and number of effective tillers at 99.5%. Other traits also displayed significant heritability, ranging from 91.6% to 98.6%, emphasizing the strong genetic influence across the spectrum of characteristics. These findings underline the potential for targeted breeding strategies in enhancing various traits for improved crop outcomes.

Genetic advance

The genetic advance as a percentage of mean was assessed for various traits at a 5% selection intensity. Traits with the highest genetic advances above 20% included quantity of grains per individual spike (51.94%), count of productive tillers per plant (43.91%), plant height (24.57%) and grain yield per plant (24.97%). Traits like spike length, harvest index, 1000-seed weight and biological yield showed moderate genetic advances ranging from 10% to 15.41%. Characteristics time to maturity and time to reach fifty percent flowering had relatively lower genetic advances below 10%. The study identifies traits with substantial potential for improvement through breeding, guiding effective selection strategies for enhancing crop characteristics.

Correlation coefficient analysis

The correlation analysis (Figure 2) reveals connections between morpho-agronomic traits. Days to 50% flowering and days to maturity are highly associated, with the former also relating to one thousand seed weight. Number of effective tillers per plant correlates with plant height, while plant height links to number of effective tillers per plant, spike length, and biological yield. Spike length strongly associates with plant height and biological yield, and notably with harvest index and grain yield per plant. number of grains per spike correlates with biological yield, harvest index, and grain yield per plant. One thousand seed weight relates to days to 50% flowering. Biological yield is highly associated with spike length, harvest index, and grain yield per plant, and moderately with plant height and number of grains per spike. Harvest index significantly correlates with biological yield, and moderately with spike length and number of grains per spike. Lastly, grain yield per plant significantly associates with biological yield and moderately with spike length and number of grains per spike. These associations provide insights into breeding and management strategies.

Path coefficient analysis

Path coefficient analysis (Table 3) was employed to identify both direct and indirect influences on correlations. Among the ten characters studied, six demonstrated positive and direct effects on grain yield per plant, including days to maturity, plant height, number of grains per plant, 1000-seed weight, biological yield and harvest index. Conversely, three characters - days to 50% flowering, number of effective tillers per plant, and spike length had negative and direct effects on grain yield per plant. Notably, days to 50% flowering exerted positive indirect effects on grain yield per plant through harvest index, biological yield, days to maturity, 1000-seed weight, number of grains per spike, and number of effective tillers per plant,

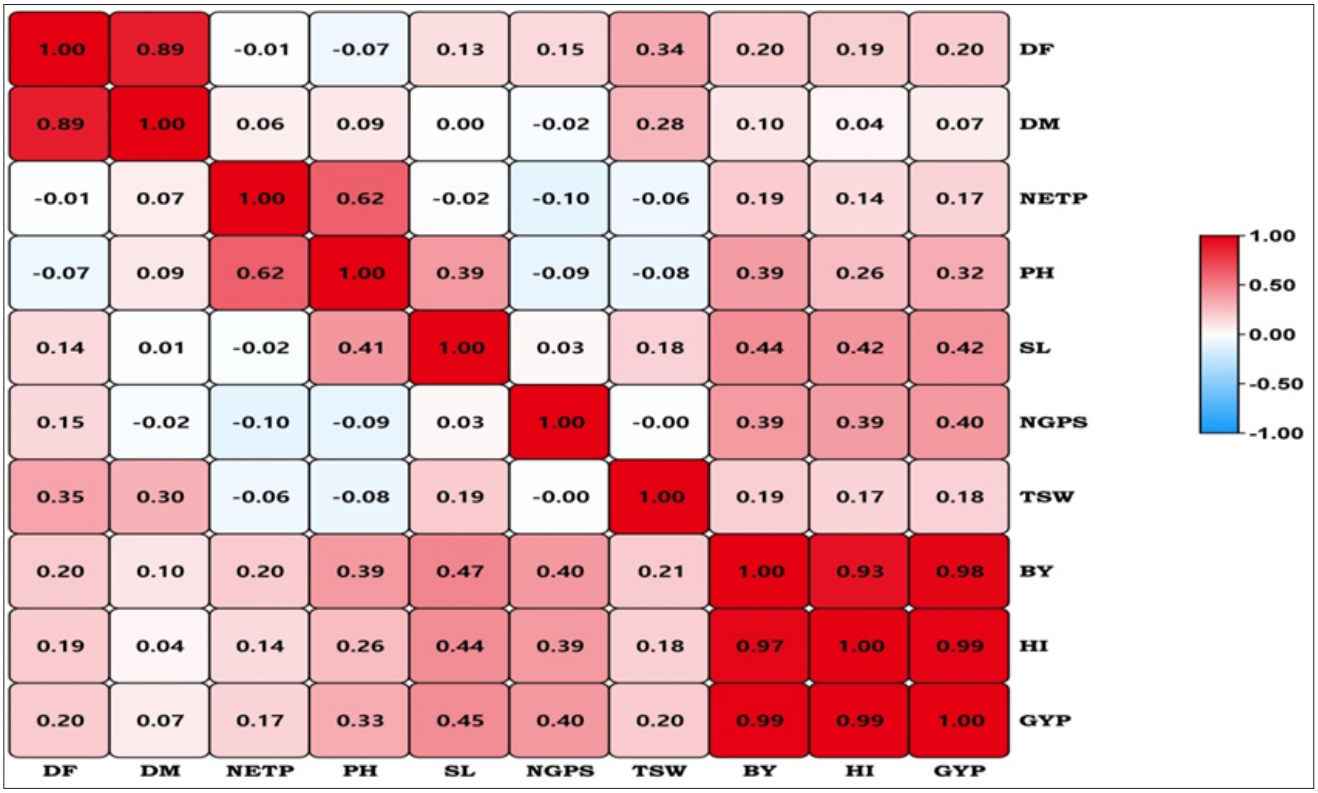


Figure 2: Genotypic and phenotypic correlation coefficient among characters in bread wheat.

Table 3: Phenotypic path coefficient analysis (direct effects on seed yield given in bold) of wheat.

Traits	DF	DM	NETP	PH	SL	NGPS	TSW	BY	HI	GYP
DF	**-0.0219**	-0.0194	0.0003	0.0015	-0.0028	-0.0033	-0.0073	-0.0043	-0.0041	0.1955
DM	0.0218	**0.0246**	0.0016	0.0023	0	-0.0006	0.007	0.0024	0.001	0.0723
NETP	0.0001	-0.0004	**-0.0055**	-0.0034	0.0001	0.0006	0.0003	-0.0011	-0.0008	0.1687
PH	-0.0008	0.0011	0.0074	**0.0119**	0.0047	-0.0011	-0.001	0.0046	0.0031	0.3228
SL	-0.0021	0	0.0003	-0.0065	**-0.0166**	-0.0005	-0.0029	-0.0073	-0.0069	0.4212
NGPS	0.0007	-0.0001	-0.0005	-0.0005	0.0001	**0.0048**	0	0.0019	0.0019	0.3971
TSW	0.0014	0.0012	-0.0003	-0.0003	0.0008	0	**0.0043**	0.0008	0.0007	0.1795
BY	0.0846	0.0423	0.083	0.165	0.188	0.1681	0.0803	**0.4272**	0.3975	0.9768
HI	0.1117	0.023	0.0824	0.1528	0.2469	0.2291	0.0988	0.5525	**0.5939**	0.9862

Note: Days to 50% flowering, DM = Days to maturity, NETP = Number of effective tillers per plant, PH = Plant height, SL = Spike length, NGPS = Number of grains per spike, TSW = 1000 seed weight, BY = Biological yield/plant, HI = Harvest index, GYP = Grain yield/plant.

while also showing negative indirect effects through spike length, days to 50% flowering, and plant height (Figure 3). This analysis unraveled complex relationships and offers insights for optimizing crop improvement strategies.

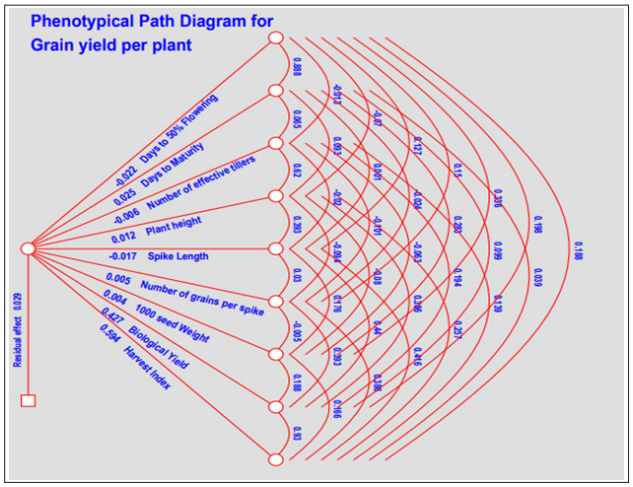


Figure 3: Phenotypic pathway diagram for plant grain yield.

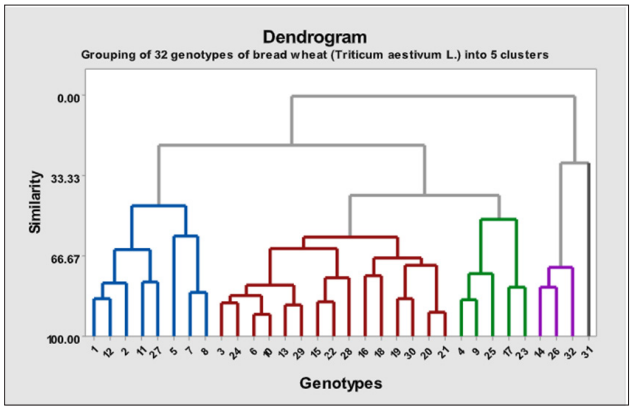


Figure 4: Categorization of 32 bread wheat genotypes (*T. aestivum* L.) into 5 distinct clusters.

Genetic divergence analysis

Based on Mahalanobis [11], in D^2 analysis all the thirty-two (32) genotypes were grouped into five (5) clusters (Figure 4). Cluster II was the largest with 15 genotypes, followed by clusters I, III, IV and V with 8, 5, 3 and 1 genotype respectively. Genotypes within clusters showed closer relationships than those across different clusters. Distinct differences in means for all attributes were observed among different clusters (Table 4). Cluster I, comprising 8 genotypes, showed the highest mean for days to maturity (143.65) and the lowest for number of effective tillers per plant (3.14). Cluster II, with 15 genotypes, displayed the highest mean for days to maturity (140.28) and the lowest for number of effective tillers per plant (2.7). Cluster III, involving 5 genotypes, had the highest mean for days to maturity (150.33) and the lowest for number of effective tillers per plant (3.85). Cluster IV, with 3 genotypes, exhibited the highest mean for days to maturity (139.78) and the lowest for number of effective tillers per plant (3.83). Lastly, Cluster V, consisting of 1 genotype, displayed the highest mean for days to maturity (143.67) and the lowest for number of effective tillers per plant (4.27). These cluster-specific differences offer insights into the variations and traits present among the examined genotypes.

The contribution of ten traits to total genetic diversity (Figure 5) showed that plant height per plant was the primary factor, accounting for 80.0% divergence, followed by grain yield per plant (7.1%), number of grains per spike (6.4%), number of effective tillers per plant (5.6%), while days to fifty per cent flowering, spike length, and biological yield had negligible contributions (0.00%). This analysis highlights the predominant role of certain traits in shaping genetic diversity within the examined genotypes.

Discussion

The examination of variance revealed a notably substantial average sum of squares attributed to genotypes for all characteristics, at both 1% and 5% levels of significance. These points to enduring genetic diversity. This is in line with findings from previous studies by Sharma et al. [14], Anwar et al. [15] and Sindhu et al. [16].

Phenotypic and genotypic coefficient of variation

The presence of significant variability in genotypes offers potential for crop improvement. PCV and GCV were com-

Table 4: Cluster averages of yield and quality characteristics in bread wheat varieties (*Triticum aestivum* L.).

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to fifty per cent flowering	106	105	111.67	102.56	104.67
Days to maturity	143.65	140.28	150.33	139.78	143.67
Number of effective tillers	3.14	2.7	3.85	3.83	4.27
Plant height	79.74	68.47	89.33	96.44	109.57
Spike length	9.14	8.92	9.29	9.68	10.22
Number of grains per spike	41.45	46.98	41.8	31.24	56.4
1000-seed weight	50.46	50.61	53.33	49.56	51.33
Biological yield	19.19	18.46	18.86	19.44	20.57
Harvest index	43.95	42.25	42.17	44.14	46.24
Grain yield per plant	8.47	7.8	7.95	8.6	9.51

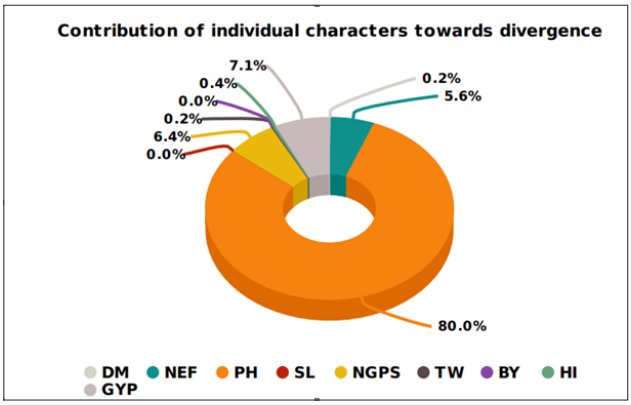


Figure 5: Contribution of individual characters towards divergence.

puted for 10 traits across 32 genotypes. GCV, representing heritable genetic variation, is suitable for comparing different traits' variability. In this study, PCV exceeded GCV for all traits (Figure 1), suggesting both genetic and environmental influences on observed variation. Highest PCV and GCV values indicate quantitative inheritance influenced by environment, while lower values suggest less environmental impact. GCV and PCV were classified into low (below 10%), medium (10-20%), and high (above 20%) categories for conclusions. number of grains per spike, number of effective tillers, grain yield per plant, plant height, spike length, harvest index, and thousand seed weight had the highest GCV and PCV, indicating potential for improvement. Days to maturity, days to 50% flowering, and biological yield exhibited low GCV, implying limited scope for enhancement.

Hereditary traits and genetic improvement

The consideration of hereditary traits and genetic improvement together is more informative for effective trait improvement and selection. High or moderate heritability coupled with high or moderate genetic advance signifies additive gene effects and effective selection potential, whereas low genetic advance in such cases indicates non-additive gene effects and limited selection effectiveness. Traits with high heritability included plant height, number of grains per spike, no of effective tillers, grain yield per plant, harvest index, biological yield, days to maturity, days to fifty per cent flowering, 1000- seed weight and spike length. Traits with significant heritability and substantial genetic progress, such as number of grains per spike, no of effective tillers, plant height, and grain yield per plant, exhibited additive gene action. Length of spike, Harvest index, 1000-seed weight, and biological yield showed moderate genetic advance, while days to maturity and days to fifty per cent flowering displayed low genetic advance. Similar outcomes were reported by Sharma et al. [14], Anwar et al. [15] and Sindhu et al. [16].

Correlation coefficient analysis

The grain yield's genetic makeup depends on the interactions of yield-contributing components. Correlation studies, crucial for understanding relationships between traits, revealed positive associations between grain yield and spike length, number of grains per spike, biological yield, and harvest index. These traits should be prioritized in selection criteria for wheat yield enhancement. Genotypic correlations were generally stronger than phenotypic ones.

Analysis of path coefficients

Examination of path coefficient quantifies the direct and indirect impacts of independent traits on a dependent one by using standard partial regression coefficients, which are dimensionless and interpretable. This analysis assumes a comprehensive depiction of causal factors affecting the outcome, like grain yield per plant. Within the range of 10 traits, six displayed direct positive effects on grain yield per plant, encompassing maturity duration, plant stature, grains per spike, weight of 1000 seeds, biological yield and harvest index. Conversely, three attributes demonstrated negative direct impacts: time to attain 50% flowering, productive tiller count and spike length. Due to their distinct direct and indirect impacts, these traits require special consideration in selection strategies. A similar outcome was reported by Anwar et al. [15].

Genetic divergence

Genetic divergence stemming from genetic factors forms the basis for hereditary improvement, driving plant breeders to explore diverse crops for improvement programs. Accurate information about genetic divergence is crucial for effective breeding programs, with genetically distinct parents leading to more favorable heterotic effects. The D^2 statistic, pioneered by Mahalanobis [11], quantifies genetic variability in multivariate analysis. This study conducted a genetic divergence analysis among 32 wheat genotypes to identify suitable lines for hybridization programs. Results suggest using genotypes from different clusters to achieve desired variation through predictive statistical distances. A similar outcome was reported by Sindhu et al. [16]. Considering both genetic diversity and performance, parents from clusters V, II and I can be selected. The rationale behind such clustering is that genotypes within the same cluster are less diverse from each other, emphasizing the importance of selecting parents from diverse clusters to achieve desired heterosis. Thus, while genetic diversity guides parent selection, performance and cluster means should also be considered in crop improvement programs.

Conclusion

The study emphasizes the significance of genetic factors in enhancing wheat yield, exploring key genetic parameters such as variation coefficients, heritability and genetic advance. These insights offer a path for selective breeding to improve specific wheat traits. Additionally, the research delves into correlations and path coefficient analysis of various yield-related traits, shedding light on the intricate relationships between these characteristics and their direct and indirect impacts on grain yield. The variance analysis revealed highly significant variances for all the traits studied, indicating greater variability in the existing material. The PCV was higher than the GCV for all the characters. PCV, GCV is highly observed for number of effective tillers per plant and number of grains per spike which suggests greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. Lastly, the study uncovers genetic divergence among different wheat genotypes, highlighting the need to select diverse parents for hybridization programs to achieve desired genetic diversity and heterotic effects. Overall, this research enhances our comprehension of the genetic factors influencing wheat production and provides valuable insights for future wheat breeding and management approaches aimed at meeting the growing global demand for this essential crop.

Acknowledgements

None.

Conflict of Interest

None.

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