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Morphological diversity and genetic variability of wheat (*Triticum aestivum* L.) genotypes in the southern hills zone

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Abstract

The morphological diversity and genetic variability for 26 best-performing genotypes representing a spectrum of wheat varieties notified for different ecological zones of India were studied. The study aims to understand the relationship and contribution of quantitative characters and the genetic variation among the genotypes chosen. The field experiment was conducted in augmented randomized complete block design at ICAR-Indian Agricultural Research Institute (IARI), Regional Station, Wellington, The Nilgiris, Tamil Nadu, India. The correlation between flag leaf width (0.36), flag leaf area (0.38), and single plant yield (0.67) is positive and significant with the harvest index. Path coefficient analysis revealed the highest magnitude of direct positive effect on harvest index is through single plant yield (1.39), flag leaf area (1.03), and flag leaf width (0.77). The variability studies indicated that the traits flag leaf length, flag leaf width, flag leaf area, peduncle length, awn length, number of tillers per hill, single plant weight, single plant yield, and harvest index had high heritability and high genetic advance. The narrow difference between the values of GCV and PCV observed for all the characters under study suggested very low environmental influences upon them. The 26 genotypes were grouped into 7 clusters, each cluster represented a mix of genotypes notified for different ecological zones. This confirms the diversity among the genotypes irrespective of their notified ecological zones. The principal component analysis confirmed the correlations between the characters as obtained in correlation analysis highlighting the importance of flag leaf width, flag leaf area, and single plant yield. The above-mentioned three traits can be used as evaluating criteria for genotypes to be chosen in breeding programs in the southern hills zone.

Keywords: Notified wheat varieties, genetic parameters, correlation analysis, path analysis, genetic diversity, principal component analysis

Introduction

Wheat is the world's most significant cultivated crop as it is the primary staple food for the human diet across the globe. In the history of wheat genetic improvement, the emergence of dwarf and fertilizer-responsive cultivars has been a historic moment that has significantly increased the grain yield potential of the crop. Since then, the full realization of the increased potential has played a significant role in the development of wheat production processes and practices, increasing per-unit productivity to a level of grain production unseen in previous decades. In particular, scientists have sought to "breed a larger adaption into these cultivars and to put the developed material in widespread geographical distribution."

The effectiveness of breeding program is anticipated to increase as a result of developments in precision phenotyping and the integration of genetic and molecular methods in the breeding process (Mir *et al*., 2012; Kosová *et al*., 2014) [25, 19]. In this situation, indirect selection can be more effective than direct selection for increased yield since it focuses on the underlying physiological features that contribute to yield (Matthew *et al*., 2005) [24].

In India, a predetermined procedure and set of rules are used for the examination and release of crop cultivars for commercial production. A coordinated system of multilocation evaluation trials is typically used to evaluate the performance of new genotypes in terms of yield, agronomic, pathological, and quality characteristics. The outcomes of the multilocation trials are statistically analyzed, and test line performance is contrasted with check variety performance from the assessment trials. An index for assessing the performance of the test lines is considered to be the performance of the check cultivars. A long-standing, top-performing cultivar and a recently discovered/released variety are typically used as checks.

Agro-ecological areas are defined and confirmed through connections across sites in multi-environment wheat trials, which also offer useful information on the degree of genotype x environment interaction and the stability of genotypes. Candidates for release are evaluated by the All India Coordinated Crop Improvement Project on wheat across India's wheat-growing areas. Six agro-ecological zones were designated to demarcate wheat cultivating areas in India — the north-western plains zone (NWPZ), north-eastern plains zone (NEPZ), central zone (CZ), peninsular zone (PZ), northern hills zone (NHZ), and southern hills zone (SHZ). Saline and alkaline soil conditions of all the zones (S&AAS - AZ) can also be considered as a separate zone (Richard *et al.*, 2018) [33].

The objective of this study was to establish the morphological diversity, interrelationships, and direct and indirect effects of yield and yield attributing traits among the released wheat varieties and the selected checks representing all the wheat ecological zones using different statistical tools.

Materials and Methods

These studies were conducted at ICAR-Indian Agricultural Research Institute (IARI), Regional Station, Wellington, The Nilgiris, Tamil Nadu from November 2021 to March 2022. The experimental material consisted of selected 26 released wheat varieties (Table 1) that represent all the classified wheat growing zones. Best performing or the long-term adapted varieties were chosen as checks. The varieties were sown in an augmented randomized complete block design with 19 test and 7 check genotypes.

The field was divided into 7 blocks and the sowing was taken in 68 lines of each 1 m. Seeds were sown practicing hand dibbling maintaining bed to bed distance of 30 cm and line to line distance of 23 cm. All agronomic practices were kept uniform. At maturity five guarded plants from each replication were taken for recording the data on plant height (cm), flag leaf length (cm), flag leaf width (cm), flag leaf area (cm^2), peduncle length (cm), spike length (cm), number of spikelets per spike, awn length (cm), number of tillers per hill, single plant weight (g), single plant yield (g), and harvest index (%). The reason for choosing the harvest index as the targeted trait in this analysis is that the grain yield is proportional to the harvest index and their correlation is 1.00 (Donald and Hamblin, 1976) [10].

The mean adjusted values of the observations were illustrated as scatter plot (Fig.1). Flag leaf area was calculated using the formulae: LA = LL* LW * K where LA, LL, LW, and K are leaf area, leaf length, leaf maximum width, and a constant, respectively. The value of the constant (K) is 0.75 (Montgomery 1911). HI was calculated according to the following formula: Harvest index (%) = (Single plant yield / Single plant weight) × 100 (Amanullah and Inamullah, 2015) [1].

Correlation matrix (Pearson method), Variability parameters, and Principal component analysis were prepared using GRAPES: General Rshiny based Analysis Platform Empowered by Statistics Version 1.0.0 (Gopinath *et al.*, 2020) [13]. Path analysis (direct and indirect effects) was carried out using the TNAUSTAT- Statistical package developed Manivannan N (2014) [22]. Cluster analysis (Euclidian's distance measure and agglomerative ward's method) was made in STAR – Statistical Tool for Agricultural Research version 2.0.1 (http://bbi.irri.org). Graphical representations of the data were made using Microsoft Excel (2019).

Table 1: List of wheat genotypes used in the experiment

Genotypes	Genotype Name	Zone notified	Parentage
Genotype 1	HD 2932	CZ & PZ	KAUZ/STAR//HD 2643
Genotype 2	HI 1479 (SWARNA)	CZ	HD 2195/HD 2160/WH 283
Genotype 3	MP 1202	CZ	POCIS/3/KAUZ82. BOW//KAUZ
Check 1	HI 1544 (PURNA)	CZ	HINDI 62/BOBWHITE//CPAN 2099
Genotype 4	DBW 14	NEPZ	RAJ 3765/PBW 343
Genotype 5	HD 2733 (VSM)	NEPZ	ATTILA /3/TUI /CARC //CHEN / CHTO /4/ATTILA
Genotype 6	RAJ 4120	NEPZ	PBW 343/V 1
Check 2	DBW 110	NEPZ	KIRITAT/4/2*SERI *2/3/KAUZ*2/BOW //KAUZ
Genotype 7	HPW 155	NHZ	BT 2549/FATH
Genotype 8	HS 507 (PUSA SUKETI)	NHZ	KAUZ/MYNA/V UL/BUC/FLK/4/ MILAN
Genotype 9	VL 892	NHZ	WH 542/PBW 226
Check 3	VL 832	NHZ	PBW 65/CPAN 3031
Genotype 10	PBW 590	NWPZ	WH 594/RAJ38 14//W 485
Genotype 11	DBW 88	NWPZ	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES
Genotype 12	HD 3086	NWPZ	DBW 14/ HD 2733//HUW 468
Check 4	HD 2967	NWPZ & NEPZ	ALD/COC/USER/HD2160M/HD2278
Genotype 13	NIAW 1415	PZ	GW 9506/PRL// PRL
Genotype 14	PBW 596	PZ	PBW 343/ DHARWAR DRY//PBW 343
Genotype 15	RAJ 4037	PZ	DL 788-2/RAJ 3717
Check 5	MACS 6478	PZ	CS/TH SC//3 PVN/3/MIRLO/BUC/4/MILAN/5/TILHI
Genotype 16	KRL 210	S&AAS - AZ	PBW65/2*PASTOR
Genotype 17	KRL 213	S&AAS - AZ	CNDO/RI43/ENTE/M EXL-2/3/Ae. Squarrosa9TAUS0/4/WEAVER/5/28KAUZ
Check 6	KRL 19	S&AAS - AZ	PBW255/KRL 1-4
Genotype 18	HW 2044	SHZ	HD226*5/SUNST AR*6/C-80-1
Genotype 19	HD 3094 (COW(W)1)	SHZ	HD 2646/HW 2002A/CPAN 3057
Check 7	HW 5207 (COW3)	SHZ	MUTANT OF NP 200

CZ – Central zone, NEPZ – North-Eastern Plains zone, NHZ – Northern Hills Zone, NWPZ – North-Western Plains zone, PZ – Peninsular zone, S&AAS – AZ – Saline and alkaline soil conditions of all the zone

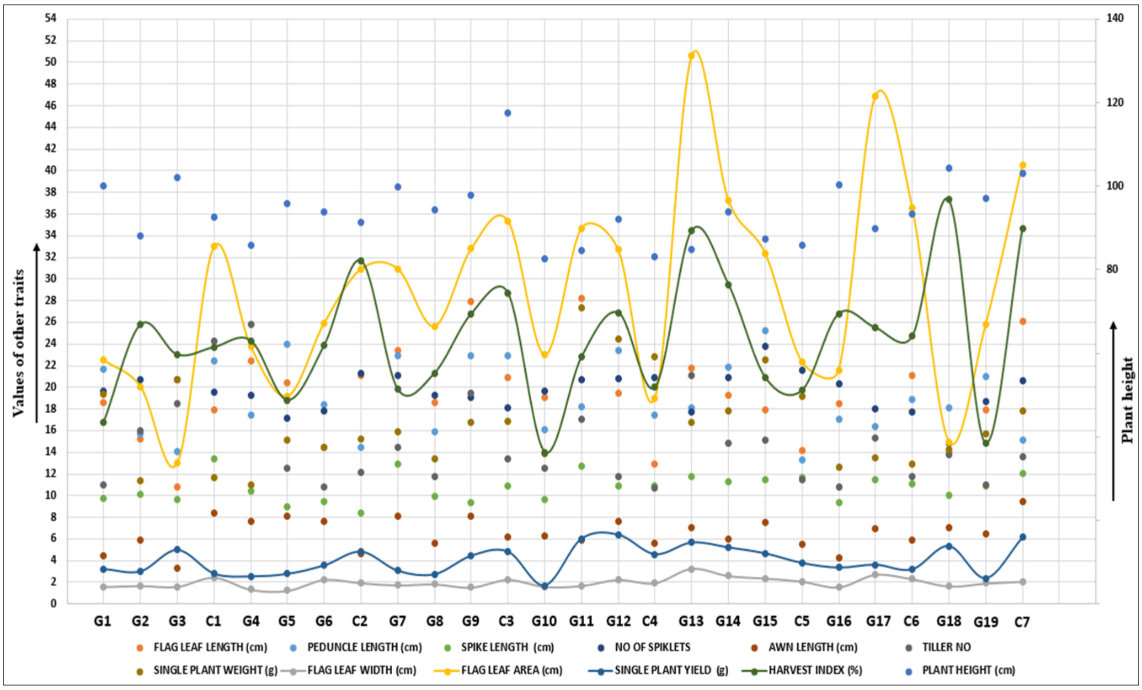


Fig 1: Scatter plot of adjusted mean values

Results and Discussion

Correlation analysis and correlogram

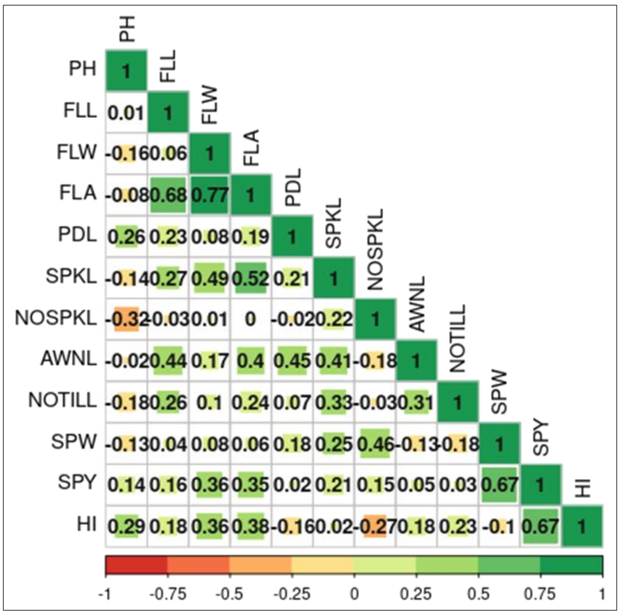
The majority of agronomic traits in agricultural crops are quantitative. One character, yield, emerges as a result of the interactions and activities of various component characters (Grafius, 1960) [14]. By examining its constituent characters, it is possible to better understand the genetic architecture of yield. This makes it possible for plant breeders to choose high-yield genotypes with specific characteristic combinations (Khan and Dar, 2010) [17]. To improve the process of crop development, correlation analysis is a powerful technique for determining the relationship between various attributes in genetically varied populations (Kandel *et al.*, 2018; Dhami *et al.*, 2018; Laxmi *et al.*, 2018) [16, 8, 20]. The correlations play a significant role in plant breeding because they show the level of reliance (correlation) between two or more variables.

The degree of reliance between the examined traits is shown via correlation analysis. Many wheat breeders use straightforward correlation coefficients to attempt to explain the relationships between grain yield and agronomic and morphological parameters.

In the current study, the correlation analysis showed that 3 of the traits were positively correlated and 8 of the traits were negatively correlated with the harvest index as indicated in the correlogram (Fig.2) which is created using the correlation values.

Single plant yield is significant (*P*<0.001) and positively correlated with harvest index (0.67^{***}). Flag leaf width (0.36^{*}) and flag leaf area (0.38^{*}) were highly significant (*P*<0.01) and are positively correlated with the harvest index. The adjusted mean value variations of the three positively significant correlated traits with harvest index were depicted in Fig.3. The harvest index showed a positive non-significant correlation with plant height (0.29), flag leaf length (0.18), spike length (0.02), awn length (0.18), and the number of tillers per hill (0.23).

Plant height, flag leaf length, and spike length showed a non-significant positive correlation with harvest index as reported by Renu *et al.* (2018) [31]. A positive correlation between plant height and grain yield was recorded by Reza *et al.* (2014) [32]. On the other hand, in some studies, negative correlations between grain yield and plant height were reported (Mondal *et al.*, 1997; Mohammad *et al.*, 2002) [27, 26]. Peduncle length (-0.16) and single plant weight (-0.1) showed a non-significant negative correlation with harvest index. The number of spikelets per spike (-0.27) showed a non-significant negative correlation with the harvest index which was against the findings of Renu *et al.* (2018) [31]. Ayer *et al.* (2017) [3] reported positive significant correlations between plant height, spike length, and single plant weight with harvest index. He also reported a non-significant positive correlation between peduncle length and spike length with harvest index.



	PH	FLL	FLW	FLA	PDL	SPKL	NOSPKL	AWNL	NOTILL	SPW	SPY	HI
PH	1											
FLL	0.01	1										
FLW	-0.16	0.06	1									
FLA	-0.08	0.68	0.77	1								
PDL	0.26	0.23	0.08	0.19	1							
SPKL	-0.14	0.27	0.49	0.52	0.21	1						
NOSPKL	-0.32	-0.03	0.01	0	-0.02	0.22	1					
AWNL	-0.02	0.44	0.17	0.4	0.45	0.41	-0.18	1				
NOTILL	-0.18	0.26	0.1	0.24	0.07	0.33	-0.03	0.31	1			
SPW	-0.13	0.04	0.08	0.06	0.18	0.25	0.46	-0.13	-0.18	1		
SPY	0.14	0.16	0.36	0.35	0.02	0.21	0.15	0.05	0.03	0.67	1	
HI	0.29	0.18	0.36	0.38	-0.16	0.02	-0.27	0.18	0.23	-0.1	0.67	1

Fig 2: Correlogram of different morphological traits of 26 genotypes during 2021 – 2022

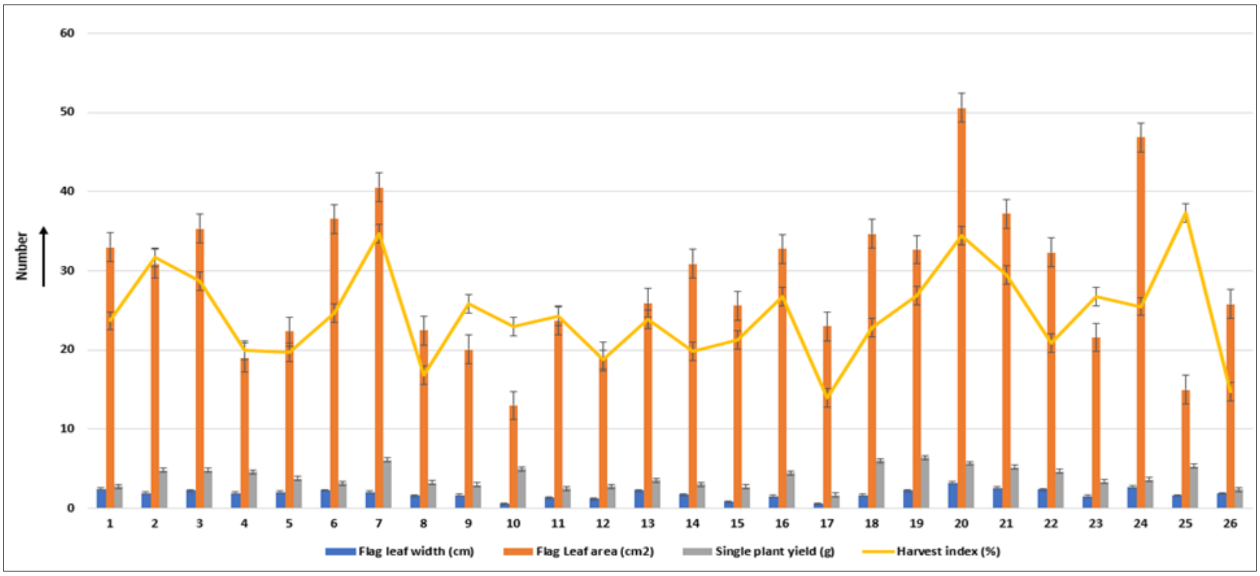


Fig 3: Mean values variation of positively significant morphological traits with Harvest index (%)

Path Coefficient Analysis

The relative contribution of each independent variable to the prediction of changes in the dependent variable is measured using path analysis. A path coefficient, which assesses the direct impact of one feature on another and enables the division of the correlation coefficient into direct and indirect effects, is a standardized partial regression coefficient (Dewey and Lu, 1959; Divya *et al.*, 2017) [7, 9]. Path coefficients demonstrate a direct interaction between independent and dependent variables (Lidansky, 1988) [21]. Plant breeders have employed path coefficient analysis in agriculture to help them find features that can be used as selection criteria to increase crop output (Ghimire *et al*., 2019; Bhujel *et al*., 2018; Bishnu *et al*., 2018) [12, 4, 5].

Table 2 lists the direct and indirect effects examined in this investigation. The highest positive direct effect on harvest index was exerted by single plant yield (1.3921), followed by flag leaf area (1.0354).

The positive direct effect on harvest index was also exhibited by flag leaf width (0.7699), flag leaf length (0.5366), peduncle length (0.0319), spike length (0.0186), number of spikelets per spike (0.0161), and number of tillers per hill (0.0019).

The plant height, awn length, and single plant weight exhibited a direct negative effect on harvest index with the values of -0.02, -0.06, and -1.06 respectively. Aycicek and Yildirim (2006) [2] also pointed out that plant height had a negative direct effect on grain yield. Ayer *et al.* (2017) [3] reported the positive direct effect of flag leaf area and single plant yield along with the negative direct effect of plant height, spike length, and peduncle length on harvest index. High positive direct effects of flag leaf length and peduncle length on grain yield were reported by Okuyama *et al.* (2005) [28].

Table 2: Direct and indirect effects of other component traits on harvest index at genotypic level during 2021 – 2022

Traits	PH	FLL	FLW	FLA	PDL	SPKL	NOSPKL	AWNL	NOTILL	SPW	SPY	HI
PH	-0.0222	0.0055	-0.0721	0.0409	0.0082	-0.0025	-0.0051	0.0012	-0.0004	0.1354	0.2012	0.2900
FLL	-0.0002	0.5366	0.1478	-0.6700	0.0072	0.0050	-0.0005	-0.0273	0.0005	-0.0375	0.2231	0.1848
FLW	0.0021	0.1030	0.7699	-0.8994	0.0083	0.0096	-0.0003	-0.0198	0.0002	-0.0935	0.5502	0.4303*
FLA	0.0009	0.3472	0.6688	1.0354	0.0096	0.0098	-0.0002	-0.0282	0.0004	-0.0816	0.5459	0.4371*
PDL	-0.0057	0.1215	0.1993	-0.3129	0.0319	0.0038	-0.0004	-0.0276	0.0001	-0.1946	0.0250	-0.1594
SPKL	0.0030	0.1450	0.3966	-0.5463	0.0066	0.0186	0.0036	-0.0251	0.0006	-0.2671	0.2886	0.0242
NOSPKL	0.0071	-0.0155	-0.0146	0.0154	-0.0007	0.0042	0.0161	0.0109	0.0000	-0.4938	0.2054	-0.2657
AWNL	0.0004	0.2384	0.2477	-0.4755	0.0143	0.0076	-0.0028	-0.0615	0.0006	0.1333	0.0743	0.1767
NOTILL	0.0041	0.1412	0.0727	-0.2167	0.0022	0.0062	-0.0004	-0.0189	0.0019	0.1923	0.0435	0.2281
SPW	0.0028	0.0189	0.0678	-0.0795	0.0058	0.0047	0.0075	0.0077	-0.0003	-1.0626	0.9275	-0.0997
SPY	-0.0032	0.0860	0.3043	-0.4060	0.0006	0.0039	0.0024	-0.0033	0.0001	-0.7080	1.3921	0.6688***

*, *** Correlation is significant at p=0.05 and p= 0.001 levels (two tailed), respectively; Residue = 0.1048;

PH – Plant height (cm), FLL – Flag leaf length (cm), FLW – Flag leaf width (cm), FLA – Flag leaf area (cm^2), PDL – Peduncle length (cm), SPKL – Spike length (cm), NOSPKL – Number of spikelets per spike, AWNL – Awn length (cm), NOTILL – Number of tillers per hill, SPW – Single plant weight (g), SPY – Single plant yield (g), HI – Harvest index (%)

Variability parameters

High heritability coupled with high genetic advance were estimates recorded for flag leaf length, flag leaf width, flag leaf area, peduncle length, awn length, number of tillers per hill, single plant weight, single plant yield, and harvest index (Table 3). Improvement from direct selection was anticipated because these characteristics were governed by additive gene activity. For yield and its components, Khan (1990) [18] showed significant heritability together with considerable genetic advance, highlighting the significance of additive genetic variation. High heritability estimates show that genotypic variance accounted for a significant fraction of the total variance and that these characteristics vary among the population (Singh *et al*., 2017) [34]. Heritability in broad sense (hBS) assessments and genetic advance values were taken into consideration by wheat breeders since hBS alone is not a reliable predictor of the amount of exploitable genetic diversity (Masood and Chaudary 1987) [23].

For all the traits, there was no difference or very little difference between the phenotypic and genotypic coefficients of variation. This suggests that they are primarily due to genetic effects. These results partially concur with Imtiaz Uddin and Shamsuddin's conclusions (1999) [15]. Fig. 4 illustrates the data of GCV, PCV, hBS, and GAM.

Table 3. Variability parameters among 26 wheat genotypes during 2021 – 2022

Trait	Phenotypic Variance	Genotypic Variance	GCV	GCV category	PCV	PCV category	hBS	hBS category	GA	GAM	GAM category
PH	44.763	44.585	7.11	Low	7.124	Low	99.6	High	13.75	14.64	Medium
FLL	19.279	19.279	22.48	High	22.48	High	100	High	9.058	46.39	High
FLW	0.074	0.074	14.63	Medium	14.63	Medium	100	High	0.56	30.19	High
FLA	41.484	37.118	22.35	High	23.63	High	89.48	High	11.89	43.62	High
PDL	9.936	9.936	16.62	Medium	16.62	Medium	100	High	6.503	34.29	High
SPKL	1.071	1.071	9.664	Low	9.664	Low	100	High	2.135	19.94	Medium
NOSPKL	3.011	1.97	7.157	Low	8.85	Low	65.4	High	2.341	11.94	Medium
AWNL	1.504	1.494	18.72	Medium	18.78	Medium	99.32	High	2.513	38.48	High
NOTILL	15.724	14.93	26.36	High	27.05	High	94.95	High	7.767	52.99	High
SPW	18.789	18.789	26	High	26	High	100	High	8.942	53.63	High
SPY	1.58	1.58	31.14	High	31.14	High	100	High	2.593	64.25	High
HI	0.003	0.003	23.21	High	23.44	High	98.06	High	0.116	47.41	High

Abbreviations as mentioned below table. 2

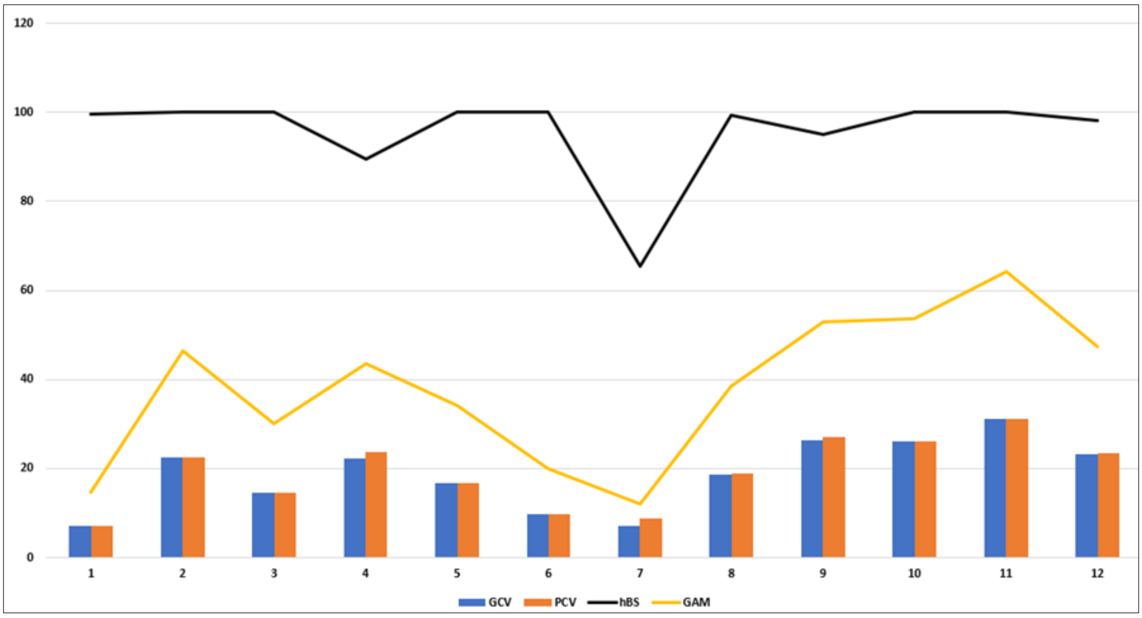


Fig 4: Variation of Genetic coefficient of variation, phenotypic coefficient of variation, Heritability in broad sense, Genetic advance per mean

Cluster analysis

Researchers often employ univariate statistics, which are generated from the mean values and standard deviations of each researched variable; however, this approach does not give general information about the analyzed data (Forina and Lanteri, 1984) [11]. Multivariate statistical methods are capable of inspecting and evaluating a matrix of complex values.

The use of hierarchical cluster analysis (HCA) is known as a simple way of categorizing the researched data based on their similarities. The HCA contains mathematical applications for each data set in terms of the multidimensional space defined by the variables specified (Bruns and Faigle, 1995) [6]. This method is related to a matrix of proximity between the samples, which generates a similarity diagram known as a dendrogram. Hierarchical clusters are generated by a large number of mathematically grouped samples in multidimensional space. Methods for grouping are based on a specific algorithm that uses information from the proximity matrix to generate a similarity dendrogram (Forina and Lanteri, 1984) [11]. By comparing the closest two data that displayed comparable values for the researched attributes, a similarity dendrogram statement is made between the data. Therefore, the higher similarity between the investigated qualities and the computations indicates a greater relationship between them.

The 26 wheat genotypes were grouped into 7 clusters (Table 4). Based on their adjusted mean values. This confirms the presence of wide genetic diversity among the notified wheat genotypes. The formed 7 clusters included a variety of genotypes from various zones depicted as a dendrogram (Fig.5).

Overall, this analysis showed that there is no relationship between the morphological traits and the ecological zones released for cultivation, revealing high levels of genetic diversity among the genotypes.

Table 4: Distribution of 26 wheat genotypes into different clusters

Genotype Number	Genotype Name	Zone notified	Cluster
G 1	HD 2932	CZ & PZ	I (4 Genotypes)
G 5	HD 2733 (VSM)	NEPZ	
G 6	RAJ 4120	NEPZ	
G 19	HD 3094 COW(W)1	SHZ	
G 2	HI 1479 (SWARNA)	CZ	II (5 Genotypes)
C 2	DBW 110	NEPZ	
G 8	HS 507 (PUSA SUKETI)	NHZ	
G 10	PBW 590	NWPZ	
G 16	KRL 210	S&AAS - AZ	
G 3	MP 1202	CZ	III (3 Genotypes)
C 4	HI 1544 (PURNA)	CZ	
C 5	HD 2967	NWPZ & NEPZ	
C 1	MACS 6478	PZ	IV (4 Genotypes)
G 4	DBW 14	NEPZ	
G 7	HPW 155	NHZ	
G 9	VL 892	NHZ	
C 3	VL 832	NHZ	V (3 Genotypes)
G 18	HW 2044	SHZ	
C 7	HW 5207 (COW3)	SHZ	
G 11	DBW 88	NWPZ	VI (4 Genotypes)
G 12	HD 3086	NWPZ	
G 14	PBW 596	PZ	
G 15	NIAW 1415	PZ	
G 13	RAJ 4037	PZ	VII (3 Genotypes)
G 17	KRL 213	S&AAS - AZ	
C 6	KRL 19	S&AAS - AZ	

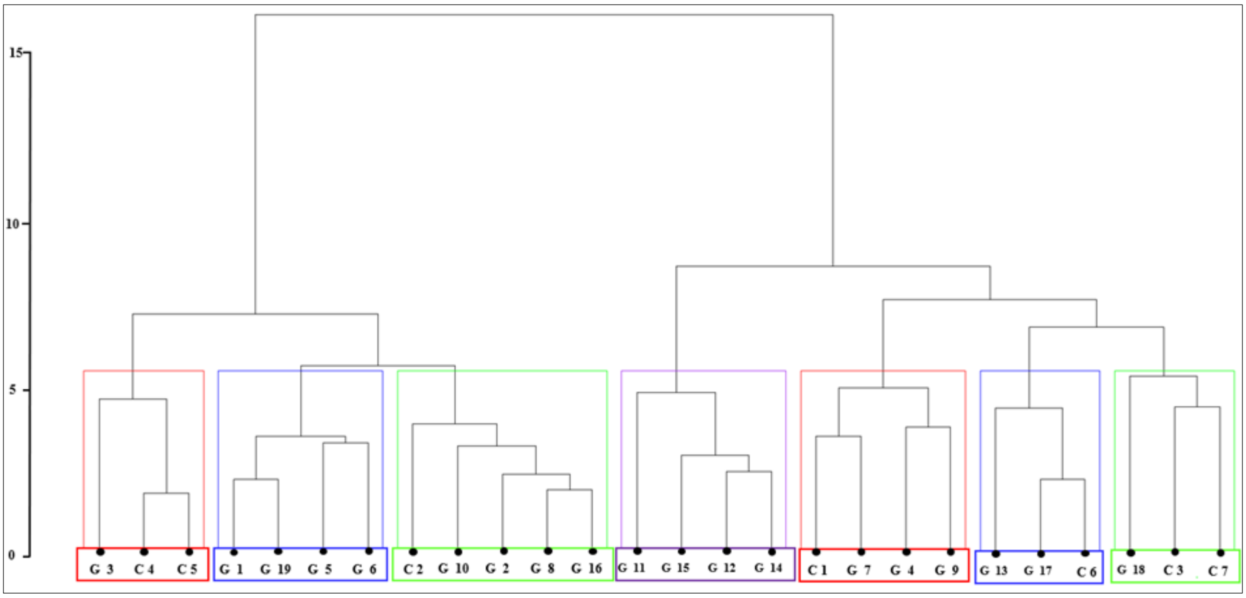


Fig 5: Dendrogram developed based on morphological traits using agglomerative clustering method

Principal Component Analysis

The multivariate analysis Principal Component Analysis (PCA) decreases the dimensionality of the data while maintaining covariance. PCA determines the eigenvalues and eigenvectors of the covariance matrix of the investigated characters when used with genotype data. The information is condensed into a handful of principal components (PCs), each of which describes a smaller percentage of the genetic variance. The samples and their distances from one another can then be seen in a colorful scatter plot by projecting individual genotypes onto the area covered by the PC axes. Sample overlap is viewed as a reflection of shared ancestry in this depiction (Patterson, Price, and Reich 2006; Price *et al.*, 2006) [29, 30]. The distances between clusters are said to mirror the genetic and geographic distances between them, which is PCA's most alluring trait for population geneticists.

After PCA, the number of retained principal components can be calculated using eigenvalues. An eigenvalue > 1 indicates that PCs account for more variance than accounted by one of the original variables in standardized data. This is commonly used as a cut-off point for which PCs are retained.

Eigenvalues greater than 1 are noted for PC 1 (3.368), PC 2 (2.011), PC 3 (1.757), and PC 4 (1.409) and showed maximum variability (71.21%) among the traits studied (Table 5). PC 2 and PC 3 showed maximum variances for yield traits while other components showed maximum variances for yield attributing traits. The variances contributed by each character to the principal components were mentioned in the Table 6.

The squared cosine (cos^2) values are depicted as a color complex indicator in Fig. 6 and 7, estimate the quality of the representation. A high cos^2 suggests that the variable on the primary component is well represented. In this instance, the variable is situated rather close to the correlation circle's edge. A low cos^2 indicates that the variable is not perfectly represented by the PCs. In this case, the variable is close to the center of the circle. The closer a variable is to the circle of correlations, the better its representation on the factor map (and the more important it is to interpret these components). In the current study, the traits plant height and peduncle have cos^2 values lesser than 0.2, so further interpretation of these characters can be neglected.

From the morphological traits PCA (Fig. 6), it can be understood that the traits like flag leaf area, flag leaf width, spike length, awn length, and single grain yield have high cos^2 values and made less angle of deviation (acute angle) conveys considerable positive correlation with harvest index. Similarly, the number of spikelets per spike and single plant weight had high cos^2 values and made a higher angle of deviation (obtuse angle) conveying a considerable negative correlation with the harvest index.

Analyzing the genotypes PCA (Fig. 7) G 13 (NIAW 1415) had a very high value for the first principal component and we can expect this genotype to show an overall high value for the traits under study. In PC1, G 3 (MP 1202) showed less value and we expect this genotype to have an overall low value for each of those traits under study. G 11 (DBW 88) had a very high value for the second principal component, while G 10 (PBW 590) displays less value interpreting that they show an overall high and low value respectively for the characters under study.

Table 5: Eigen Values and variance percentages of principal components

Principle component	Eigenvalue	Percentage of variance	Cumulative percentage of variance
PC1	3.368	28.07	28.07
PC2	2.011	16.755	44.825
PC3	1.757	14.644	59.469
PC4	1.409	11.744	71.213
PC5	0.97	8.082	79.295
PC6	0.825	6.876	86.172
PC7	0.597	4.976	91.148
PC8	0.486	4.046	95.194
PC9	0.442	3.687	98.881
PC10	0.13	1.085	99.966
PC11	0.003	0.022	99.988
PC12	0.001	0.012	100

Table 6: Loading of the traits onto principal components

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
PH	0.039	6.243	16.533	22.881	0.713	1.108	35.962	2.379
FLL	11.386	2.788	1.975	1.875	11.08	44.745	1.77	0.005
FLW	14.173	0.808	0.626	8.293	34.184	1.299	0	5.64
FLA	23.555	0.217	0.058	1.569	4.768	12.623	1.675	2.87
PDL	3.035	0.931	4.928	40.568	2.867	4.657	0.612	26.376
SPKL	13.75	1.715	7.521	0.085	1.928	10.059	9.264	32.338
NOSPKL	0.05	27.872	5.901	0.009	3.059	0.157	16.372	0.217
AWNL	10.089	8.74	5.807	4.174	0.687	1.778	21.676	16.63
NOTILL	4.955	3.823	4.145	6.717	30.129	21.746	4.09	13.536
SPW	1.678	34.322	0.373	9.727	1.76	0.012	4.824	0
SPY	9.641	10.298	21.482	1.109	4.818	0.748	3.489	0.006
HI	7.649	2.243	30.652	2.992	4.006	1.067	0.266	0.004

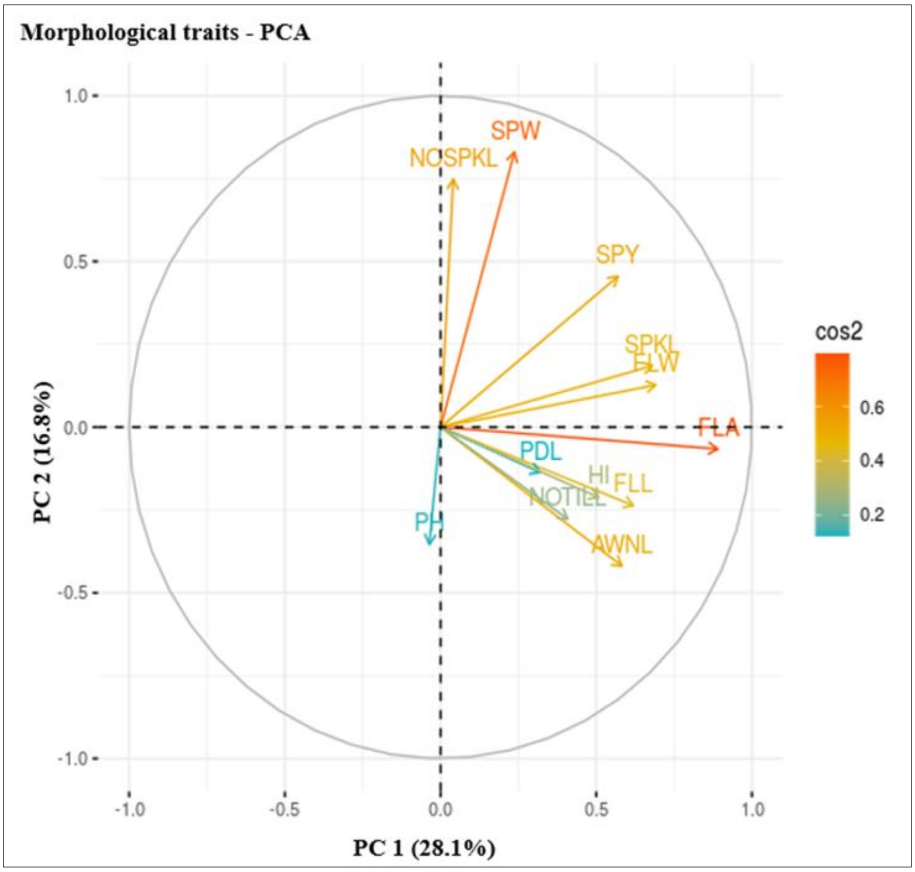


Fig 6: Principal components of morphological traits

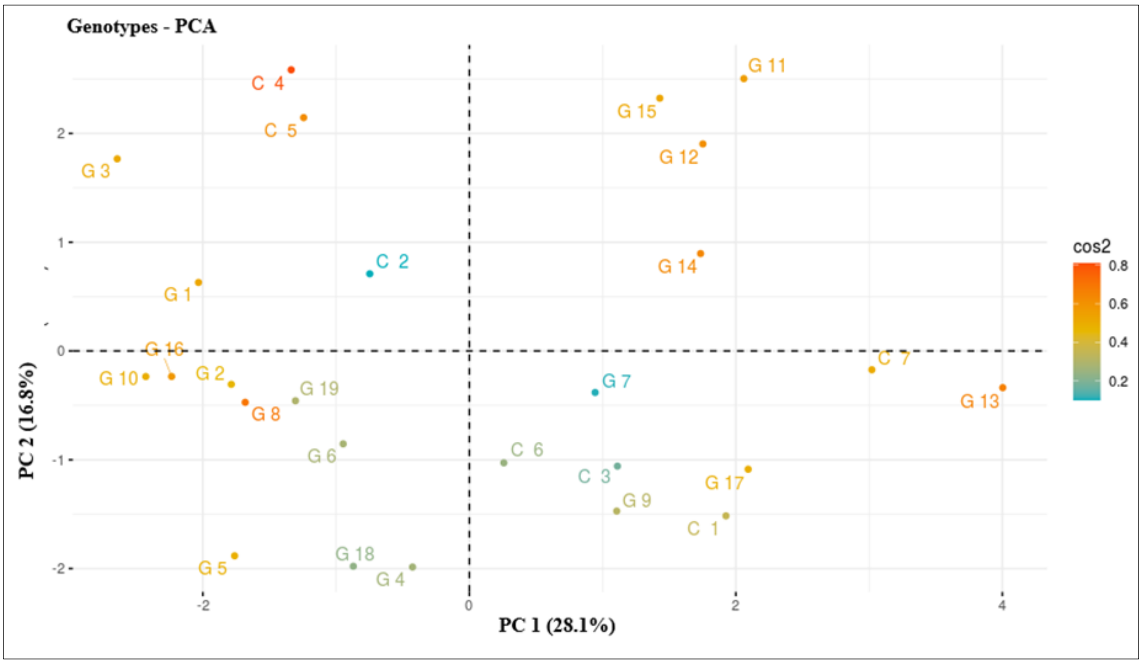


Fig 7: Principal components of morphological traits and genotypes

Conclusion

The present study showed the existence of wide ranges of variations for the traits studied among notified wheat varieties. The varieties NIAW 1415 and MP 1202 were found to be best performing. Flag leaf width, flag leaf area, and single plant yield were found to have direct effects and positively correlated with the harvest index. These characters could be considered as the main components for selection criteria in breeding program in the Southern hills zone.

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