

## Diversity of wheat (*Triticum aestivum*) genotypes deciphered by biplot analysis

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### ABSTRACT

Diversity of hundred and seventy six wheat genotypes had been studied as per fifteen relevant morphological traits in research farm of Haryana Agricultural University during cropping season 2016-17. Maximum range was observed for flag leaf area followed by number of grains per ear and plant height. The least deviation also expressed by flag leaf breadth trait. The phenotypic diversity were estimated by the Shannon-Weaver diversity index ( $H'$ ), by bifurcating set of genotypes in five classes, revealed maximum values for days to heading (cluster 2), number of tillers per plant (cluster 3), flag leaf length (cluster 2), flag leaf breadth (cluster 2), flag leaf area (cluster 4), plant height (cluster 5), ear length (cluster 2), ear weight (cluster 4), number of grains per ear (cluster 4), weight of grain per ear (cluster 2), number of spikelet per ear (cluster 2), thousand grains weight (cluster 4), Grain yield per plant (cluster 2), biological yield per plant (cluster 2) and Harvest Index (cluster 2). Simpson's index ( $1/D$ ) varied from 0.44 for biological yield to 0.54 for flag leaf breadth followed by ear weight. Association analysis among traits exhibited significant positive correlation of grain yield observed with number of tillers per plant, thousand grains weight and biological yield expressed high degree of linear association with grain yield per plant, number of tillers per plant, thousand grains weight, ear weight and weight of grains per ear. Harvest Index maintained positive and negative correlation with other traits though magnitudes were of small values. Biplot analysis had seen strong bondage of grain yield per plant with number of tillers per plant and biological yield per plant as well as of flag leaf length with thousand grains weight evident from group 1 as acute angles had exhibited by traits rays. Weight of grains per ear along with ear weight expressed strong relationship with number of spikelet per ear, number of grains per ear whereas similar behavior evident from plant height & flag leaf area as evident by acute angles among corresponding rays. Darwin software exploited to import the dissimilarity matrix for multivariate hierarchical clustering of genotypes. Two broad categories had seen which further partitioned into five and six sub groups as evident from respective nodes.

**Key words:** Shannon-Weaver and Simpson diversity indices, Multivariate Hierarchical clustering, Biplot analysis

### INTRODUCTION

Wheat (*Triticum aestivum*), world's widely grown cereal, provides 20% of the total protein, calories to human nutrition, and supplemented dietary intake of essential micronutrients, namely zinc, iron, manganese, magnesium etc. Mostly three species of wheat viz *Triticum aestivum*, *Triticum durum* and *Triticum dicoccum* out of reported seventeen have been cultivated at global level (Lakra *et al.*, 2020). More over bread wheat *Triticum aestivum* has been cultivated over more than 90% area of wheat cereal (Devesh *et al.*, 2019). The development of new bio fortified varieties required sustaining the demands of the growing population in a background of climate changes and pressure of abiotic and biotic stresses (Kumar *et al.*, 2020). The genetic diversity and its distribution facilitate selection of the diverse genetic resources to

facilitate crop improvement mechanism more efficiently (Ahmad *et al.*, 2017). A better utilization and judicious exploitation of available materials require detailed information on various traits, the level of association among traits and various diversity estimates (Ali *et al.*, 2021). Genetic variation in registered varieties is fundamental to the improvement of future breeding programs by providing a basis for selection of desirable parental combinations and promising performance of progenies (Mecha *et al.*, 2017). Analyses of genetic divergence and estimation of genetic distance between parents are useful for choosing parents in wheat hybridization programs (Phougat *et al.*, 2017) as the loss of diversity in domesticated crops due to the modernization of agriculture has been described as a greatest factor responsible for genetic erosion. Genetic erosion of cultivated diversity is reflected in a modernization

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bottleneck at diversity levels that occurred during the history of the crop (Laino *et al.*, 2015). Shannon-Weaver diversity index had been advocated for precise classification of diversity in wheat (Mengistu *et al.*, 2015). The present study had deciphered the diversity among wheat genotypes by diversity indexes, association analysis among important traits and biplot analysis to use in the breeding programme.

## MATERIALS AND METHODS

The study material comprised of hundred and seventy six wheat genotypes collected from advanced generation of wheat breeding lines having wide variation for various agromorphological traits. The experiment was conducted at Research Farm, CCS Haryana Agricultural University during 2016-2017 crop seasons. The recommended agronomic practices were followed to harvest good yield. The genotypes were evaluated for 15 traits namely; DH: Days to heading, NTP: No of tillers per plant, FLL: Flag Leaf length(cm), FLB: Flag Leaf breadth(cm), EW: Ear weight(g), FLA: Flag leaf area((cm<sup>2</sup>), PH: Plant height(cm), EL: Ear length(cm), NGE: Number of grains per ear, GWE: Weight of grain per ear(g), NSE: Number of spikelet per ear, GW: Thousand grain weight, GY: Grain yield per plant(g), BY: Biological yield per plant(gm), HI: Harvest Index(%). Phenotypic diversity among the wheat selections accessions based on the 15 quantitative traits carried out by Shannon-Weaver diversity index (H) and Simpson's index. The genotypes were classified into five groups based on their means and standard deviations of each trait (Shakhatreh *et al.*, 2010). The five groups are: (1) Mean + 2 standard deviations. (2) Mean + 1 standard deviation. (3) Mean +1 standard deviation. (4) Mean - 1 standard deviation. (5) Mean - 2 standard deviations. The correlation coefficients among these traits were considered to measure the association among various traits and their significance. The Shannon-Weaver diversity index (H') has been widely used in studies of phenotypic diversity (Sarkar *et al.*, 2010). This index was defined as

$$H = - \sum_{i=1}^5 p_i \ln(p_i)$$

where n is the number of phenotypic classes for a character, ln was the natural logarithm and p<sub>i</sub> was the proportion of the total number of entries in the i-th class. H was estimated for each character.

Simpson's index was computed as,

$$\frac{1}{D} = 1 / \sum_{i=1}^5 \frac{n_i(n_i - 1)}{N(N - 1)}$$

where n<sub>i</sub> was the frequency of genotypes belonging to i-th group and N was the total number of observations.

## RESULTS AND DISCUSSION

### Variability in traits

Basic descriptive statistics expressed good level of variability among the collection for 15 morphological traits (Table 1). A maximum range value was observed for flag leaf area followed by number of grains per ear and plant height. The least deviation was expressed by flag leaf breadth trait. Maximum variance was achieved by flag leaf area, plant height and biological yield per plant. Lowest values of standard error had been seen for flag leaf breadth, weight of grain per ear & ear weight. The high CV for weight of grain per ear, number of tillers per plant, ear weight, flag leaf area traits and for days to heading along with plant height the coefficient of variation were comparatively less. The values deciphered diversity in the materials, wide range of values was observed for flag leaf area (19.2-50.7cm<sup>2</sup>), biological yield (24-47 g/plant), and grain yield (30.8-48.2 g/plant), days to heading (85.7-102), number of tillers (5.2-13.3) and harvest index (33.9-44.6%). The phenotypic variation on various morphological traits has also been reported by number of researchers (Bhandari *et al.*, 2017; Devesh *et al.*, 2019).

### Diversity analysis

Diversity indexes of Shannon-Weaver (H) and Simpson's (1/D) were given in Table 2. The maximum values diversity index (H) was exhibited for days to heading (in cluster 2), number of tillers per plant (in cluster 3), flag leaf

Table 1: Description of traits variability

Measure	DH	NTP	FLL	FLB	FLA	PH	EL	EW	NGE	GWE	NSE	GW	GY	BY	HI
Mean	95.14	8.72	22.41	1.87	32.43	103.40	11.02	2.57	48.50	1.77	20.04	41.40	13.85	35.40	39.16
Standard Error	0.26	0.13	0.18	0.01	0.45	0.37	0.11	0.04	0.36	0.03	0.12	0.22	0.15	0.36	0.15
Median	95.84	8.78	22.43	1.87	31.53	104.10	11.23	2.56	47.68	1.79	19.89	41.73	13.74	35.94	39.19
Mode	97.33	7.40	21.37	1.83	27.97	106.13	11.23	2.36	47.33	1.46	20.00	43.94	11.43	30.28	40.50
Standard Deviation	3.47	1.71	2.39	0.18	6.02	4.94	1.49	0.48	4.79	0.35	1.58	2.93	1.96	4.83	2.01
Variance	12.02	2.91	5.69	0.03	36.25	24.41	2.21	0.23	22.96	0.12	2.51	8.58	3.85	23.32	4.04
Kurtosis	-0.25	-0.19	0.14	0.87	0.39	-0.26	-1.07	0.74	0.59	0.48	-0.03	0.52	-0.49	-0.71	-0.31
Skewness	-0.48	0.33	0.20	0.29	0.64	-0.39	-0.12	0.26	0.67	0.28	0.07	-0.56	0.11	-0.04	-0.13
Range	16.33	8.10	12.02	1.10	31.49	24.40	5.88	2.98	25.34	2.07	9.55	17.59	10.25	22.88	10.61
Minimum	85.67	5.23	17.07	1.32	19.16	89.33	8.15	1.42	38.33	1.04	14.89	30.83	8.87	24.10	33.95
Maximum	102.00	13.33	29.09	2.42	50.65	113.73	14.03	4.40	63.67	3.11	24.44	48.42	19.12	46.98	44.56
CV	3.65	19.61	10.66	9.63	18.56	4.78	13.52	18.68	9.88	19.77	7.88	7.08	14.15	13.64	5.13

DH- Days to heading, FLA: Flag leaf area (cm<sup>2</sup>), NSE: No. of spikelet per ear, NTP-No of tillers per plant, PH: Plant height (cm), GW: Thousand grain weight, FLL: Flag Leaf length (cm), EL: Ear length (cm), GY: Grain yield per plant (gm), FLB: Flag Leaf breadth (cm), NGE: No. of grains per ear, BY: Biological Yield per plant (gm), EW: Ear weight (gm), GWE: Weight of grain per ear (gm), HI: Harvest Index (%)

length (in cluster 2), flag leaf breadth (in cluster 2), flag leaf area (in cluster 4), plant height (in cluster 5), ear length (in cluster 2), ear weight (in cluster 4), number of grains per ear (in cluster 4), weight of grain per ear (in cluster 2), number of spikelet per ear (in cluster 2), thousand grain weight (in cluster 4), grain yield per plant (in cluster 2), biological yield per plant (in cluster 2) and harvest Index (in cluster 2). Simpson's index (1/D) varied from 0.44 for biological yield to 0.54

for flag leaf breadth followed by ear weight. Among clusters, higher values for flag leaf breadth, ear weight, number of grains per ear, thousand grain weight were observed in cluster two whereas least values of ear length, number of grains per ear, grain yield per plant, biological yield per plant were in cluster 1 whereas for days to heading, plant height, thousand grain weight were observed in cluster 5.

Table 2: Diversity analysis by Shannon-Weaver's (H) and Simpson's indexes for morphological traits among clusters and overall

Traits	Shannon Weaver's diversity index (H)						Simpson's index (1/D)					
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Overall	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Overall
DH	0.1283	0.2825	0.2714	0.2825	0.0000	0.9647	0.0014	0.0211	0.4406	0.0211	0.0000	0.4842
NTP	0.1012	0.2537	0.2540	0.2537	0.1283	0.9908	0.0006	0.0136	0.4793	0.0136	0.0014	0.5086
FLL	0.1012	0.2599	0.2540	0.2537	0.1152	0.9840	0.0006	0.0150	0.4793	0.0136	0.0010	0.5095
FLB	0.1012	0.2471	0.2316	0.2099	0.1405	0.9303	0.0006	0.0123	0.5278	0.0068	0.0018	0.5494
FLA	0.0694	0.2537	0.2845	0.3059	0.1405	1.0539	0.0002	0.0136	0.4109	0.0302	0.0018	0.4568
PH	0.0860	0.2825	0.2714	0.2925	0.0294	0.9618	0.0004	0.0211	0.4406	0.0245	0.0000	0.4867
EL	0.0000	0.3279	0.2967	0.2925	0.0509	0.9679	0.0000	0.0432	0.3822	0.0245	0.0001	0.4501
EW	0.0860	0.2403	0.2355	0.2599	0.0860	0.9077	0.0004	0.0111	0.5195	0.0150	0.0004	0.5464
NGE	0.0294	0.2471	0.2393	0.2537	0.1405	0.9099	0.0000	0.0123	0.5114	0.0136	0.0018	0.5392
GWE	0.0509	0.2772	0.2540	0.2599	0.1012	0.9432	0.0001	0.0195	0.4793	0.0150	0.0006	0.5145
NSE	0.0509	0.2717	0.2467	0.2599	0.0860	0.9152	0.0001	0.0179	0.4952	0.0150	0.0004	0.5286
GW	0.1152	0.2471	0.2430	0.2659	0.0509	0.9221	0.0010	0.0123	0.5032	0.0164	0.0001	0.5331
GY	0.0294	0.3059	0.2845	0.2925	0.0694	0.9816	0.0000	0.0302	0.4109	0.0245	0.0002	0.4658
BY	0.0294	0.3246	0.2967	0.2925	0.0509	0.9941	0.0000	0.0409	0.3822	0.0245	0.0001	0.4477
HI	0.1012	0.2876	0.2813	0.2876	0.0694	1.0270	0.0006	0.0228	0.4182	0.0228	0.0002	0.4647

### Association analysis

To understand the nature of relationships among traits correlation coefficients were calculated and tabulated (Table 3). Significant positive correlation of grain yield was observed with number of tillers per plant, thousands grain

weight and biological yield expressed high degree of linear association with grain yield per plant, number of tillers per plant, thousands grain weight, ear weight and weight of grain per ear. Harvest index maintained positive and negative correlation with other traits though magnitudes were of small values. Thousands grain weight

Table 3: Correlation analysis among observed traits

	NTP	FLL	FLB	FLA	PH	EL	EW	NGE	GWE	NSE	GW	GY	BY	HI
DH	-0.059	-0.088	0.132	0.053	-0.122	0.117	-0.029	-0.028	-0.080	0.120	-0.047	0.089	0.076	0.047
NTP		0.373	0.027	0.184	0.205	0.142	0.168	0.147	0.124	0.133	0.258	0.783	0.742	0.171
FLL			0.187	0.717	0.244	0.162	0.191	0.187	0.198	0.074	0.069	0.261	0.277	-0.019
FLB				0.614	-0.150	0.104	0.179	0.086	0.150	0.119	0.141	0.018	0.020	0.000
FLA					0.015	0.138	0.256	0.268	0.296	0.211	0.149	0.203	0.218	-0.023
PH						0.104	0.354	0.160	0.316	0.150	0.131	0.191	0.229	-0.097
EL							0.098	-0.041	0.064	0.257	0.134	0.111	0.090	0.050
EW								0.571	0.877	0.546	0.303	0.274	0.352	-0.181
NGE									0.588	0.437	-0.025	0.202	0.268	-0.147
GWE										0.499	0.323	0.262	0.338	-0.177
NSE											0.173	0.190	0.242	-0.114
GW												0.339	0.359	-0.019
GY													0.927	0.277
BY														-0.099

had shown direct correlation with most of traits except of days to heading and number of grains per ear. Number of spikelet per ear had expressed positive correlation values with most of the traits. Ear length, flag leaf area and flag leaf breadth also expressed positive correlation values. This indicates that selection of genotypes with high biomass will identify the genotype with high grain yield. The correlation studies among various traits were reported by number of workers (Ahmad *et al.*, 2017; Lakra *et al.*, 2020).

### Biplot analysis

The principal components analysis (PCA) was performed with the standardized values for 15 morphological traits. The first two PCs accounted for 42.4% (PC1 = 28.3% and PC2 = 14.1%) of the total variation in the original variables (Table 4). The relationships among morphological traits showed in a biplot of PC1 and PC2 (Fig 1). Traits number of tillers per plant, grain yield per plant, biological yield per plant, flag leaf length encircled separately in quadrant whereas flag leaf area, number of spikelet per ear, ear weight, weight of grain per ear, plant height grouped altogether in different quadrant. Harvest Index had maintained distance from both groups and occupied place in other quadrant. Degree of strong bondage of grain yield per plant with number of tillers per plant and biological yield per plant as well as of flag leaf length with thousand grain weight

evident from group 1 as acute angles had exhibited by these traits rays (Kumar *et al.*, 2020). Weight of grain per ear along with ear weight expressed strong relationship with number of spikelet per ear, number of grains per ear whereas similar behavior evident from plant height & flag leaf area as evident by acute angles among corresponding rays (Devesh *et al.*, 2019). More over right angle observed between harvest index and flag leaf length. Trait harvest index also exhibited obtuse angles with ear weight, weight of grain per ear, number of spikelet per ear, and number of grains per ear expressed weak relationship.

Table 4: Loadings of traits as per first two principal components

Traits	PCA1	PCA2
DH	0.0041	0.0395
NTP	0.3000	0.4404
FLL	0.2488	0.0733
FLB	0.1286	-0.1275
FLA	0.2604	-0.0771
PH	0.1932	-0.0362
EL	0.1134	0.0449
EW	0.3647	-0.3229
NGE	0.2782	-0.2944
GWE	0.3575	-0.3330
NSE	0.2720	-0.2567
GW	0.2177	0.0929
GY	0.3424	0.4338
BY	0.3680	0.3246
HI	-0.0366	0.3218
% variation	28.31	14.12

PC1=28.31; PC2=14.12; TOTAL = 42.43%

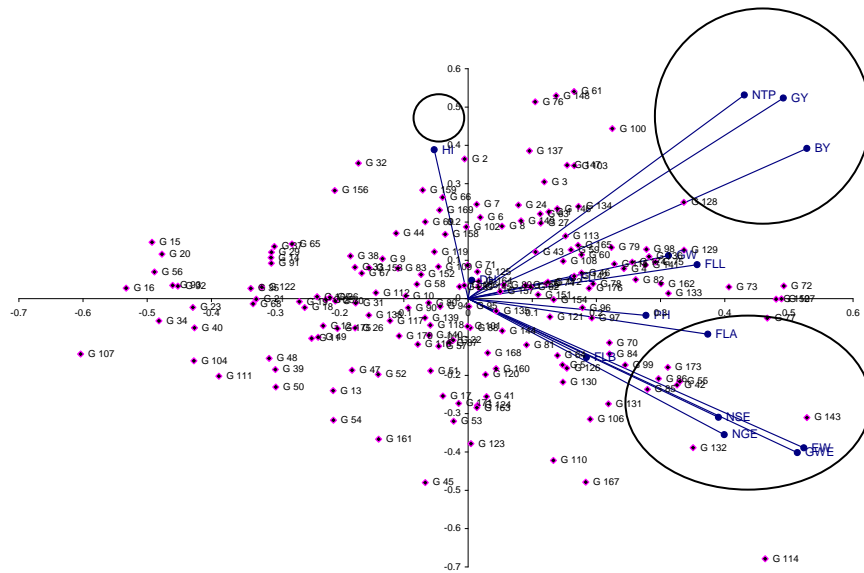


Fig 1: Biplot analysis of genotypes and traits for classification

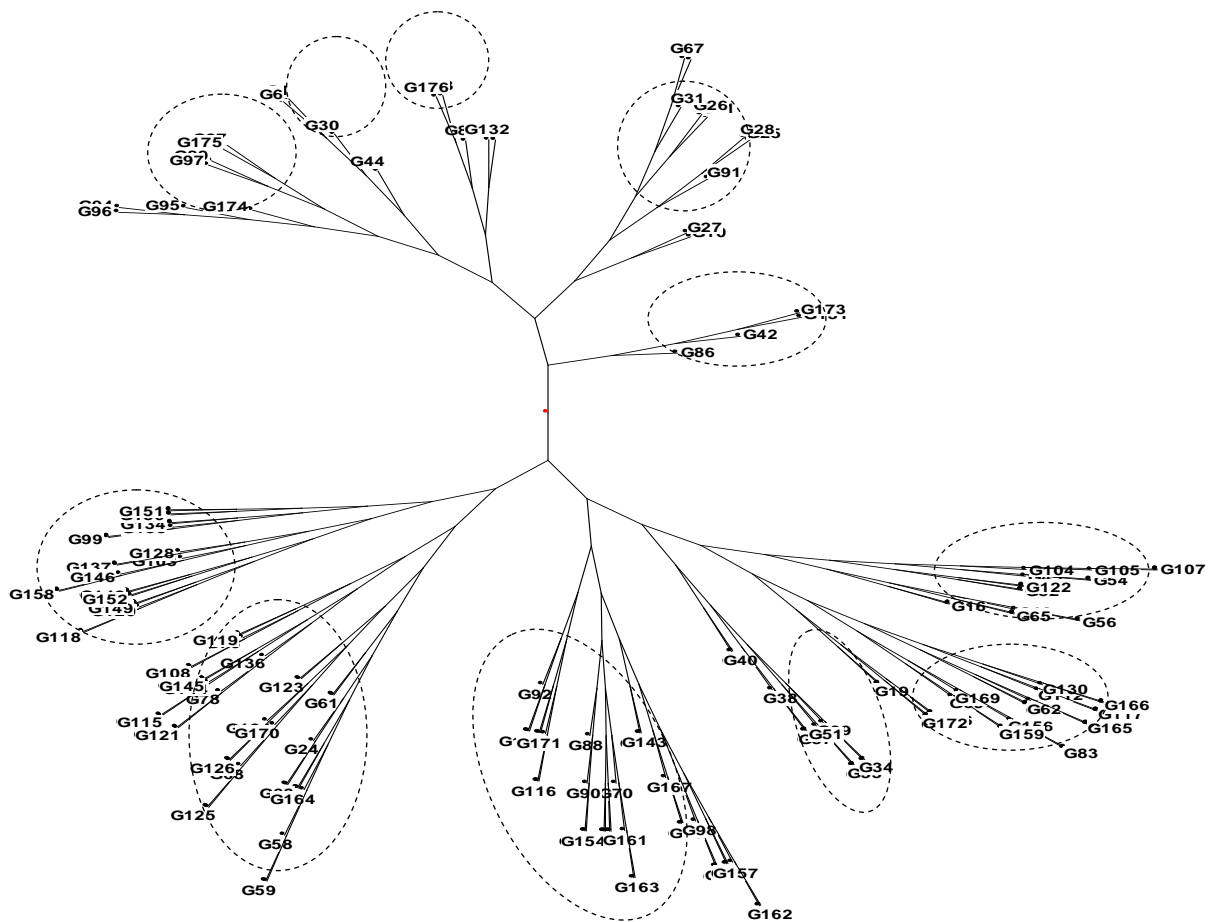


Fig 2: Multivariate hierarchical clustering of genotypes based on dissimilarity matrix of traits by Darwin software

## Hierarchical Clustering

Multivariate hierarchical clustering approach had been considered for the further classification of 176 wheat genotypes. Software NTSYS-PC version 2.1 had been employed to standardize the data values as traits were measured by different units (Fig 2). The standardized values of traits were converted to dissimilarity matrix among genotypes. Darwin software exploited to import the dissimilarity matrix and generating clusters of genotypes as per 15 morphological traits simultaneously. Two broad groups had seen in figure which further partitioned into five and six sub groups as classification evident from the respective nodes of clusters (Ali *et al.*, 2021).

Sufficient variability exists in the material for most of the traits in the present study. The identification of suitable genotypes for different traits will help in the development of better yielding genotypes in changing scenario of biotic and abiotic stress. Multivariate hierarchical analysis clearly helped in differentiating genotypes into major groups by considering various traits simultaneously. Based on distance between genotypes of different clusters, contrasting parents were identified and may be used in the hybridization programme to generate wider variability for selection in the breeding programme. Designing a crossing programme by identifying genotypes of interest from different clusters will make the breeding process more directional and effective.

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