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Diversity in Bread Wheat genotypes (*Triticum aestivum* L.) deciphered by Multivariate Biplot analysis

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ABSTRACT: Assessment of diversity by multivariate biplot analysis has been established as prerequisite in any breeding program. Twenty seven wheat genotypes were evaluated at research farm of CCSHAU to assess the relative contribution of morphological and nutritional traits to the total variation in yield. Large values had observed for days to maturity, plant height, tillers per meter along with small values for protein contents, spike length, biological yield per plant traits. Maximum range exhibited by plant height, spikelets per spike, and tillers per meter whereas biological yield per plant, protein contents, harvest index achieved minimum range. Iron and Zinc contents showed more variations as observed by points corresponding to values expressed in radar chart. One genotype expressed largest value of spikelets per spike that may be an outlier for this set of genoypes. Number grians per ear exhinited more of variatons in values followed by grian yield per plant for studied genotypes. Traits tillers per meter, germination percentage, days to heading, days to maturity denote nearly constant differences among the genotypes as observed by corresponding circles in Radar chart. Plant height and days to heading expressed more variations. Zinc contents had achieved positive correlation values with spike length & Fe while negative values of small magnitude with plant height, thousands kernel weight, harvest index. Iron content showed direct relationship with days to anthesis, days to heading, protein contents whereas indirect with thousands kernel weight and spike length values. Large positive values expressed by protein contents with days to an thesis, days to heading, days to maturity, thousands kernel weight a long with negative values for plant height &number of grains per ear. Broadly three clusters had been observed among genotypes as marked by different colors. Two groups consisted of P's and OP's separated by group consisted of HD3086, DPW621-50, WB-2 genotypes. Two dimensional clustering had seen grouping of grain yield per plot with harvest index and plant height while farther group consisted of days to anthesis, days to maturity, biological yield per plot & spikelets per spike.

Keywords: Diversity descriptive, correlation coefficient, Multivariate clustering, Biplot analysis.

INTRODUCTION

Wheat, an important staple food crop, is preferred over rice and maize as a source of protein in low and middle income nations (Lakra *et al*., 2020). Being the staple food crop of many countries with diverse climatic conditions, wheat varieties must have enough variability to tolerate to pests, pathogens and abiotic stresses (Ali *et al*., 2021). Assessment of diversity is prerequisite in any breeding program as magnitude of the variability of collection is an indispensable assist for rice improvement strategies. Multivariate analyses such as cluster and principal component analysis measures the amount of genetic diversity in respect of several characters and assesses the relative contribution of morphological traits to the total variation in yield. Regular studies of diversity being conducted by breeders to evaluate and utilize the diversity of breeding germplasm, also to determine the uniqueness and distinctiveness among genotypes to safe guard a breeders intellectual property rights (Fu, 2015). In addition, assessment of genetic distance is one of most suitable tools for selection of parents in a wheat crossing scheme for possible yield enhancement (Negisho *et al*., 2021). A number of suitable methods like principal component analysis, factor analysis and cluster analysis are presently available for the selection of parent, detection of genetic variability, centre of origin, study of interaction among the environments and tracking the course to crop evolution (Kumar *et al*., 2020). Multivariate biplot analysis has been recommended, most widely, in the analysis of crop genetic diversity. Several hierarchical clustering methods, including single linkage, complete linkage, simple average, median, unweighted paired group method using arithmetic averages (UPGMA) and Ward's of minimum variance have been used (Pixley *et al*., 2018). Each of these approaches has some distinctive features. However the grain yield influenced by spikelet per spike, number of effective tillers per plant, grain numbers per spike that is why statistical techniques correlation studies and principal component analysis provide reliable assessment of complex relationships among various traits (Laino *et al*., 2015; Ahmad *et al*., 2017; Devesh 2019). Diversity of bread wheat genotypes had been deciphered by multivariate hierarchical clustering by considering fifteen morphological traits simultaneously along with the biplot analysis utilizing two principal components.

MATERIALS AND METHODS

A total of twenty seven bread wheat genotypes including popular check were evaluated under field trials laid out in a Randomized Block Design (RBD) with three replications in the research field area of Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during the Rabi season 2020-21. Recommended agronomic practices have been applied to ensure good harvest of wheat yield. Five randomly selected competitive plants for each genotype observed for important morphological and nutritional traits *viz* GY/Plot=grain yield per plot (q/ha), Ger.= germination (%), DH- Days to heading, DA- days to anthesis, DM=days to maturity, PH=plant height (cm), SL= Spike length (cm), PL=Peduncle length (cm), Spls= spikelets per spike, TM=Tiller per meter, GE=grains per ear, KW= 1000 kernel weight (g), BY/P= biological yield per plot, HI = Harvest index (%), PC= Protein content (%), Fe= Iron content (ppm), Zn= Zinc content (ppm). Reputed statistical software SAS version 9.3 along with JMP 9 was exploited for analysis and graphical presentations.

RESULTS AND DISCUSSION

A. Variability description among genotypes

Descriptive statistics of morphological and nutritional traits had been presented in Table 1. Large values had observed for days to maturity, plant height, tillers per meter along with small values for protein contents, spike length, biological yield per plot traits. Maximum range exhibited by plant height, spikelets per spike, tillers per meter whereas biological yield per plot, protein contents(ppm), harvest index achieved minimum range. Similar results were earlier recorded by Mengistu *et al*. (2015). Trait spike length expressed nearly normal variation as compared to spikelets per spike, nutritional component Zn expressed symmetrical nature as more or less equal number of observations would be below and above average values. Reasonable amount of variability had been observed among the studied genotypes as depicted by Fig. 1 and 2. Concentric circles in Radar chart depict values of 27 genotypes for the morphological and nutritional traits. Fe(ppm) and Zn(ppm) contents showed more variations as observed by points corresponding to values expressed in radar chart. One genotype expressed largest value of spikelets per spike that may be an outlier for this set of genoypes. Grains per ear exhinited more of variatons in values followed by grains yield per plot for studied genotypes. The radar diagram utilized by Porter & Niksiar (2018); Liano *et al*. (2015) to express the variability. Tillers per meter, Germination percentage, days to heading and days to maturity denote nearly constant differences among the genotypes as observed by corresponding circles in Radar chart. Plant height and days to heading expressed more variations in values achieved by genotypes during their field evaluation. Sufficient variability among genotypes provided ample scope for selection of promising genotypes by the concerned breeders (Phougat *et al*., 2017).

Parentage details of wheat genotypes.

Code	Genotypes	Pedigree details
G 1	P13649	HPYT 2015-16 (450)
G 2	P13828	T.DICOCCON CI9309.AE.SQUARROSA(409)//MUTUS/3/2*
G 3	P13829	HPYT 2016-17 413
G 4	P13832	CHIH95.2.6//WBLL1*2/KURUKU/3/WBLL1*2/KKTS/4/ND643/2*WBLL1/5/SAUAL/YANAC//SAUAL/6/WBLL1*2/BRAMBLING//VORB/FISCAL/3/BECARD
G 5	P13833	HPYT 16-17 (424)
G 6	P13834	HPYT 16-17 425
G 7	P13839	HPYT 16-17 428
G 8	P13849	ESWYT 2016-17 127
G 9	P13950	HPYT 2017-18 407
G 10	P13951	HPYT 2017-18 412
G 11	P13952	HPYT 2017-18 413
G 12	P13953	HPYT 2017-18 415
G 13	P13954	HPYT 2017-18 416
G 14	P13955	HPYT 2017-18 418
G 15	P13956	HPYT 2017-18 419
G 16	P13957	HPYT 2017-18 424
G 17	P13958	HPYT 2017-18 425
G 18	P13959	HPYT 2017-18 435
G 19	P13960	HPYT 2017-18 436
G 20	P13961	HPYT 2017-18 437
G 21	P13962	HPYT 2017-18 438
G 22	P13963	HPYT 2017-18 443
G 23	P13964	HPYT 2017-18 449
G 24	HPBW-1	T.DICOCCON CI9309/A.SQUARROSA(409)/3/MILAN/S87230//BAV92/4/2/2*MILAN/S87230//BAV92
G 25	WB-2	T.DICOCCON CI9309/A.SQUARROSA(409)/3/MILAN/S87230//BAV92/4/2/2*MILAN/S87230//BAV92
G 26	HD3086	DBW14/HD2733//HUW468
G 27	DPW-621-50	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES

Table 1: Descriptive measures of variability among traits.

Traits	GYP	Ger	DH	DA	DM	PH	SL	PL	Spls	TM	GE	KW	BYP	HI	PC	Fe	Zn
Mean	54.17	97.22	90.81	97.33	134.63	109.94	11.12	37.88	22.67	108.52	63.74	41.00	11.76	32.69	9.59	41.25	37.05
Standard Error	0.88	0.22	0.38	0.32	0.33	4.02	0.21	0.43	2.79	3.24	1.68	0.48	0.13	0.47	0.13	1.11	1.01
Median	54.51	98.00	90.00	97.00	135.00	105.50	11.10	37.50	20.00	104.00	61.00	41.00	11.80	32.60	9.40	40.85	35.85
Mode	49.68	98.00	89.00	98.00	135.00	106.50	10.50	36.80	20.00	102.00	60.00	43.30	11.80	33.40	8.70	45.15	36.27
Standard Deviation	4.55	1.15	1.98	1.64	1.71	20.88	1.09	2.24	14.50	16.84	8.72	2.50	0.65	2.46	0.70	5.78	5.24
Kurtosis	-0.23	1.23	2.22	1.25	-0.56	0.67	2.96	-0.78	26.64	0.83	-0.72	1.04	0.01	0.30	-0.91	1.14	9.37
Skewness	0.11	-1.44	1.27	0.88	-0.31	1.01	-0.19	0.15	5.15	1.05	0.09	-0.27	-0.21	0.73	0.34	0.68	2.57
Minimum	45.09	94.00	88.00	95.00	131.00	80.00	8.00	34.00	18.00	85.00	47.00	34.30	10.40	29.30	8.60	31.45	30.75
Maximum	62.79	98.00	97.00	102.00	137.00	164.00	14.00	42.00	95.00	153.00	81.00	46.20	12.90	38.80	11.00	57.25	58.00
Largest	62.79	98.00	97.00	102.00	137.00	164.00	14.00	42.00	95.00	153.00	81.00	46.20	12.90	38.80	11.00	57.25	58.00
Smallest	45.09	94.00	88.00	95.00	131.00	80.00	8.00	34.00	18.00	85.00	47.00	34.30	10.40	29.30	8.60	31.45	30.75
Confidence Level (95.0%)	1.80	0.46	0.78	0.65	0.68	8.26	0.43	0.88	5.74	6.66	3.45	0.99	0.26	0.97	0.28	2.29	2.07

GY/Plot=grain yield per plot (q/ha), Ger.= germination (%), DH- Days to heading, DA- days to anthesis, DM=days to maturity, PH=plant height (cm), SL= Spike length (cm), PL=Peduncle length (cm), Spls= spikelets per spike, TM=Tiller per meter, GE=grains per ear, KW= 1000 kernel weight (g), BY/P= biological yield per plot, HI = Harvest index (%), PC= Protein content (%), Fe= Iron content (ppm), Zn= Zinc content (ppm).

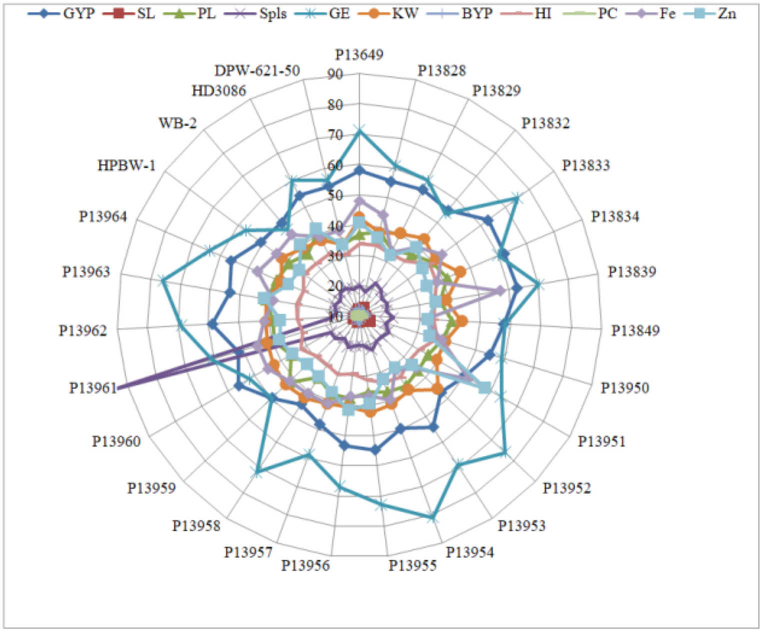

Fig. 1. Morphological and nutrional traitsfor the diversity among genotypes explanined by Radar chart.

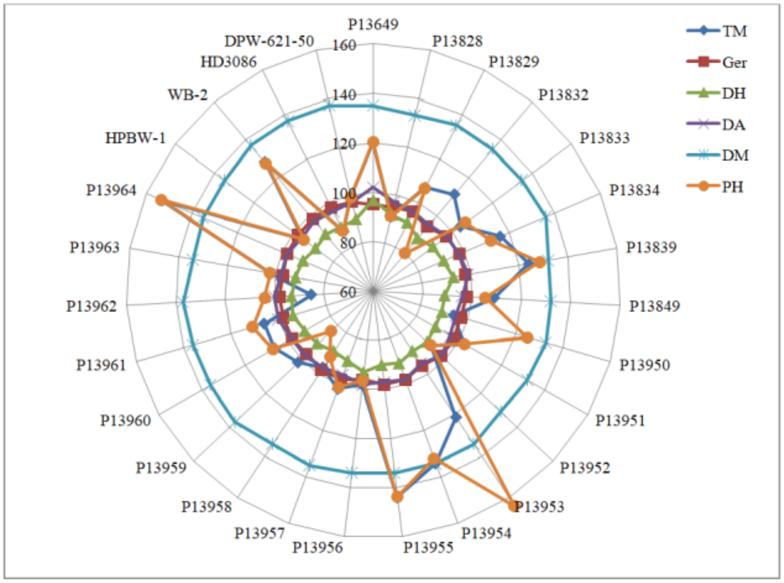

Fig. 2. Diversity among genotypes for morphological traits.

Table 2: Correlation coefficients to study association analysis.

	Ger	DH	DA	DM	PH	SL	PL	Spls	TM	GE	KW	BYP	HI	PC	Fe	Zn
GYP	-0.1988	0.3080	0.2086	0.0791	0.2279	-0.3012	0.2646	-0.1188	0.1714	0.0410	-0.0489	0.5390	0.6106	0.1915	0.1552	-0.1302
Ger		-0.1662	0.0812	0.0238	0.1661	-0.0768	0.1375	0.1332	0.0967	0.0708	0.0815	-0.0283	-0.1468	-0.0016	0.1547	0.0057
DH			0.9070	0.1377	0.1014	-0.0697	0.0659	0.3124	0.0917	0.2285	0.0394	0.3593	-0.1619	0.4011	0.3896	0.0425
DA				0.1824	0.0615	-0.1414	0.1069	0.3136	0.1285	0.3099	0.1737	0.2319	-0.2278	0.4996	0.4310	0.0338
DM					-0.1174	-0.0147	0.1936	0.1621	-0.0358	-0.4725	-0.1790	0.3330	-0.2477	0.3144	0.0005	-0.1067
PH						-0.0788	-0.0803	0.0084	0.7752	0.2785	-0.2171	0.2296	0.1917	-0.3321	0.0271	-0.1732
SL							-0.3052	0.0426	-0.0282	-0.1679	0.0575	-0.2838	-0.1854	-0.1569	-0.1976	0.3734
PL								0.1078	-0.1005	-0.0936	0.2276	0.2523	0.1852	0.2660	-0.0360	-0.0493
Spls									-0.0127	-0.0755	0.0861	0.2392	-0.2461	0.1677	0.1150	0.0222
TM										0.1523	-0.0264	0.2292	0.0480	-0.1563	0.1490	-0.0628
GE											0.1084	-0.2360	0.0914	-0.2237	-0.0373	0.0038
KW												-0.3611	0.1304	0.3282	-0.2380	-0.1724
BYP													-0.0537	0.1387	0.1561	-0.0762
HI														-0.1030	0.0056	-0.1510
PC															0.2245	0.0340
Fe																0.4363

B. Association analysis

Both type of correlation coefficient values depicted by studied traits as grain yield per plot exhibited a significant correlation coefficient values with days to heading, biological yield per plot, harvest index, peduncle length and negative with spike length, spikelets per spike, germination (%), Zn(ppm) etc (Table 2). Earlier Devesh *et al*. (2019) have recorded the similar pattern of significant positive correlation with grain yield. Germination percentage expressed only weak relationship with other traits. Days to heading exhibited tight positive relationship with days to anthesis, Protein content (ppm) & biological yield per plot. Large positive expressed by days to anthesis with Fe(ppm), PC(ppm), grains per ear, spikelets per spike and negative with harvest index. Negative values of high magnitude observed for days to maturity with grains per ear & Harvest index. Zn(ppm) had achieved positive correlation values with Spike length, Fe(ppm) while negative though of small magnitude with plant height, 1000 kernel weight, Harvest index. Iron content showed direct with days to anthesis, days to heading, PC (ppm) and indirect with 1000 kernel weight &Spike length values. Large positive values expressed by PC(ppm) with days to anthesis, days to heading, days to maturity, 1000 kernel weight along with negative values for plant height & grains per ear. Direct relationship of harvest index had been observed with grain yield per plot and indirect with days to anthesis, days to maturity, days to heading, Spikelets per spikes (Kumar *et al*., 2017). Plant height of genotypes expressed mostly negative values tillers per meter, germination percentage & biological yield per plot traits. Nearly indirect relationships observed for spike length trait. 1000 kernel weight, biological yield per plot, PC(ppm), harvest index showed direct association with Peduncle length as reported by Mecha *et al*. (2017). Days to heading and Plant height exhibit positive and significant correlation which is in accordance to the studies of Phougat *et al*. (2017).

C. Multivariate hierarchical clustering of genotypes

Using a univariate statistical analysis and standard deviations for each one of trait does not provide a complete insight into the complex analysis. Multivariate statistical methods are appropriate tools for the analysis of the complex structure. The hierarchical cluster analysis is a simple way of grouping the set of selected genotypes as per their similarities based on 15 morphological and nutritional variables. Multivariate techniques have been used to estimate the genetic divergence between accessions, like biometric models estimated by the Euclidean Distance and hierarchical grouping methods (Ali *et al*., 2021). Hierarchical clustering techniques have long been the most popular clustering method with Ward's method and average linkage probably being the best available (Awan *et al*., 2015). Multivariate clustering of genotypes based on studied traits had been carried out as per guidelines of popular Ward's method. Broadly three clusters had been observed as marked by different colors in clustering pattern as well as by clustering handle (Fig. 3a). Two groups consisted of P's and OP's separated by group consisted of HD3086, DPW621-50, WB-2 genotypes. Two dimensional clustering had been also carried out to group the genotypes as per variations observed in studied traits or traits may be grouped as by variability expressed by genotypes during field evaluation. GYP grouped with harvest index and plant height while further group consisted of days to anthesis, days to maturity, biological yield per plot & spikelets per spike traits (Fig. 3b).

D. Biplot analysis

Results of the principal component analysis (PC) indicated that the first two components were important in explaining the variation among the 27 genotypes evaluated under field trials and cumulatively accounted for 33.6 % of the total variation for studied traits (Table 3). The first principal component (PC) accounted for 18.9% of the total variation. It illustrated the variations in days to anthesis, days to heading, PC(ppm), biological yield per plot, Fe(ppm), spikelets per spike, days to maturity.

Principal component two contributed 14.6% to the total variation. Traits including plant height, peduncle length, tillers per meter, harvest index, PC(ppm), Germination percentage were to contribute more to second PC. Out of the 15 traits evaluated, 09 were found to contribute most to the first two principal components (Table 3) and were therefore considered most discriminate to summarize phenotypic variation among the accessions through hierarchical cluster analysis.

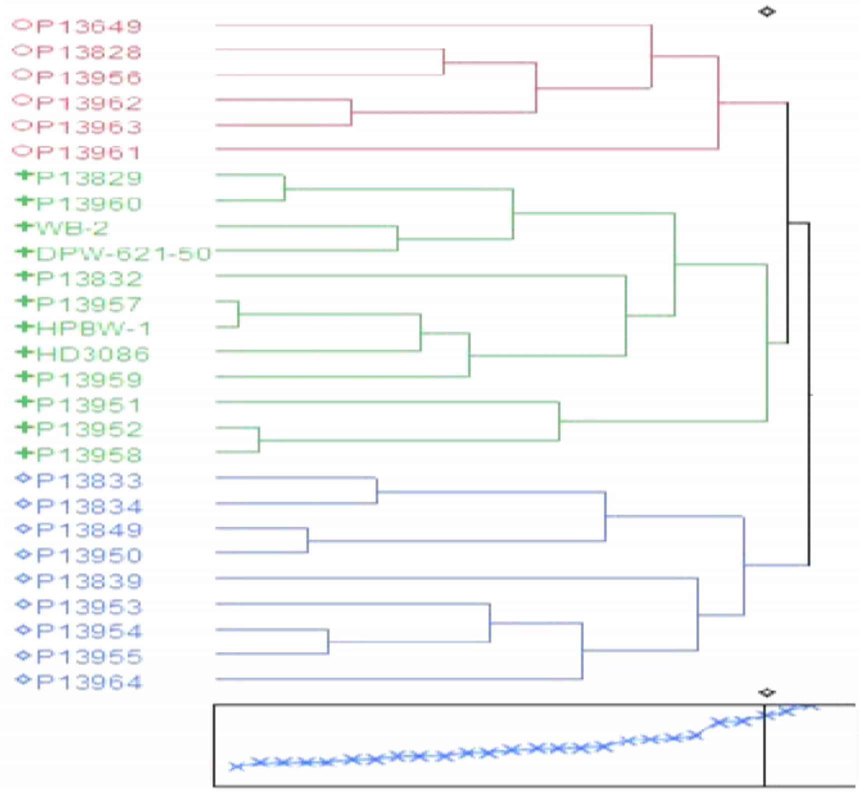

Fig. 3a. Number of clusters among genotypes as per multivariate analysis.

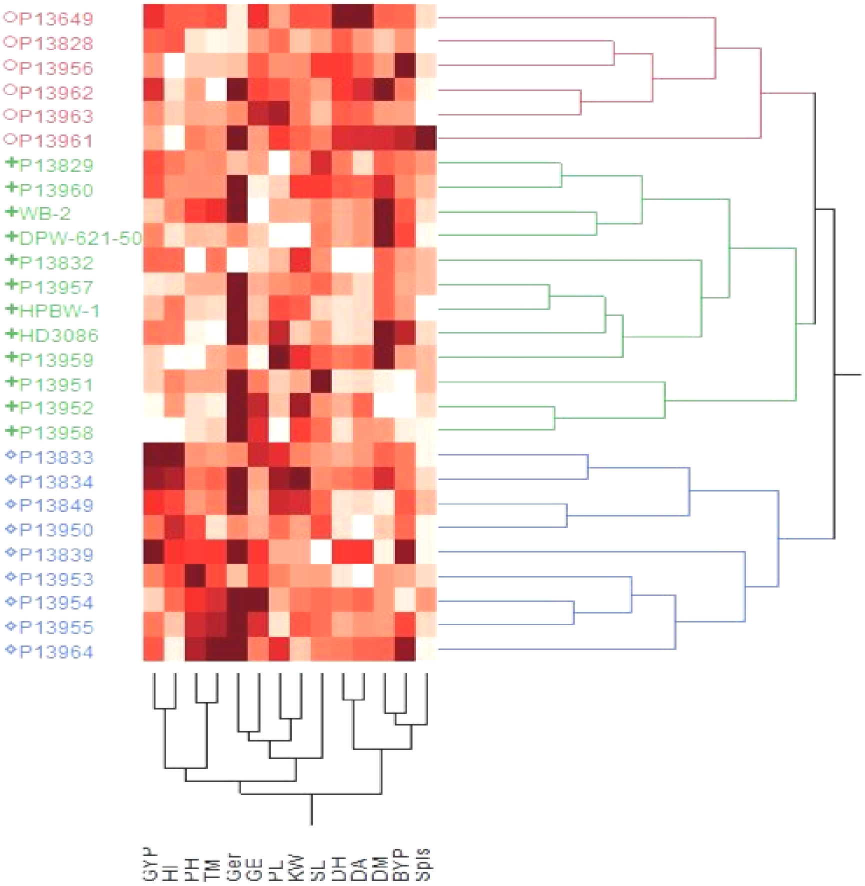

Fig. 3b. Hierarchical Clustering of genotypes based on traits as per Ward's method.

Table 3: Loadings of traits as per first two principal components.

Traits	PC1	PC2
GY/P	0.2966	-0.3141
Ger %	0.0188	0.0092
DH	0.4562	0.0620
DA	0.4587	0.1045
DM	0.1997	0.2255
PH	0.0940	-0.4965
SL	-0.2056	0.1960
PL	0.1885	0.0286
Spls	0.2111	0.1943
TM	0.1254	-0.3932
GE	0.0196	-0.2568
KW	-0.0072	0.1226
BY/P	0.3546	-0.1253
HI %	-0.0234	-0.3624
PC(ppm)	0.3168	0.3069
Fe(ppm)	0.2814	0.0279
Zn(ppm)	-0.0086	0.1857
% contribution	18.9	14.6

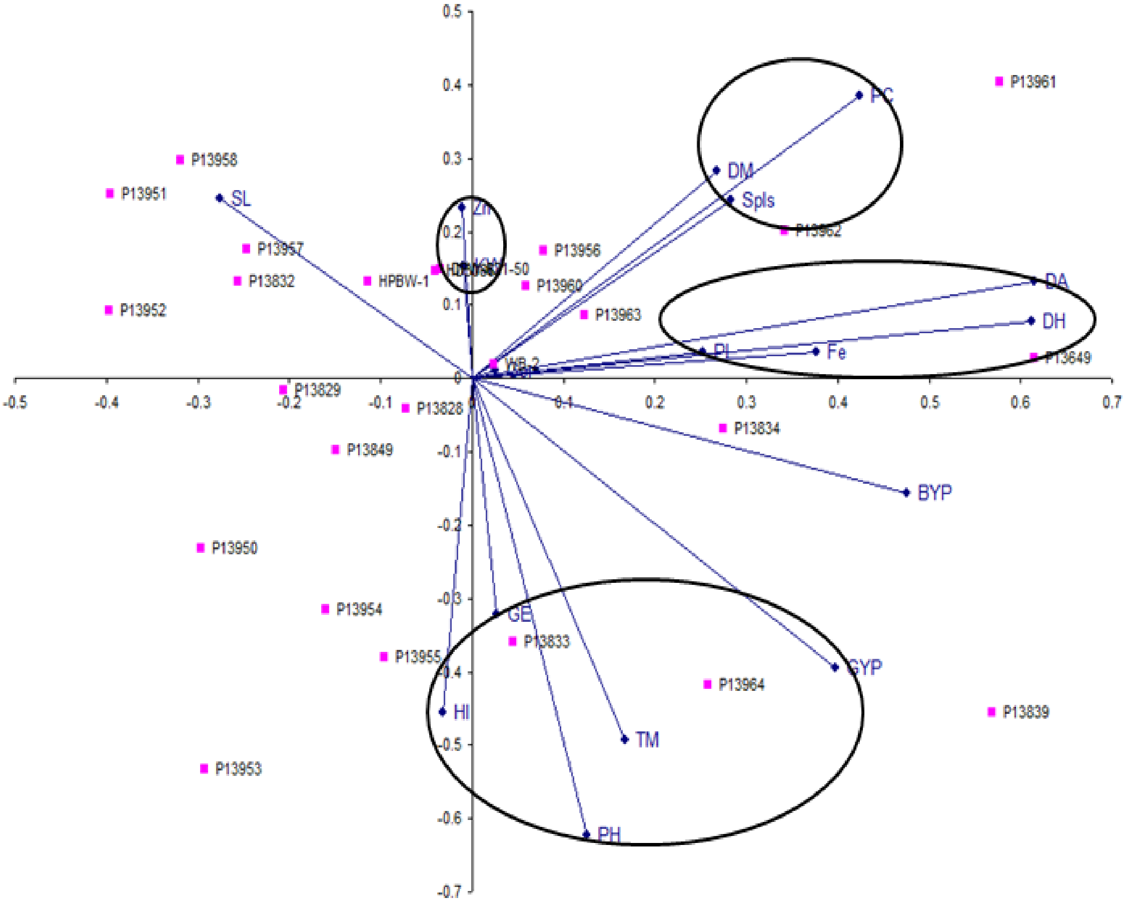

Fig. 4. Biplot analysis of morphological and nutritional traits of wheat genotypes.

The biplot analysis is an appropriate method to analyse interaction between genotypes and traits and narrowing down the number of traits to the ones contributing a major portion to the variability Devesh *et al*. (2019). The first two components explained 33.6% of the total variation in genotypes (Fig. 4). The high positive correlation has been observed between days to maturity, PC(ppm), spikelets per spiketraits and also of days to anthesis, days to heading, Fe(ppm) seen in figure. Zn(ppm), harvest index and 1000 kernel weight expressed tight association. The difference between the biplot origin and genotype position in the biplot is the vector length of the genotype and it is a measure of the distinctiveness of the genotype from other genotypes as reviewed by Joshi and Okuno (2010). In the biplot vectors of traits showing acute angles are positively correlated whereas those showing obtuse or straight angles are negatively correlated and those with right angles have no correlation. The genotypes having long length of the vector have higher or extreme values for one or more characters. Selection among such genotypes may be performed either for further trials or for their use as parents in breeding programs.

CONCLUSIONS

Grain yield and nutritive values had a positive correlation with number of tillers per plant, flag leaf area, plant height, ear length, grain weight per ear and thousand grain weight. Simultaneous selection diverse genotypes possessing morphological and nutritional traits will improve the grain quality and yield of wheat to sustain the nutritional security of Indian population.

Conflict of interests. None.

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