

## Morphological Diversity and Traits Association in Bread Wheat (*Triticum aestivum* L.)

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**Abstract:** The objective of the present study was to evaluate hundred wheat varieties for morphological variability using principal component analysis at the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Cluster analysis and correlation coefficient was also performed. Plant height showed significant positive correlation with number of tillers and coleoptile length. Number of grains per spike had significant positive correlation with spike length. Out of eleven, four PCs exhibited more than 1 eigen value but the level of dissimilarity was low which indicates that the germplasm has narrow genetic base. The first four PCs were selected exhibiting 55.30% variation. 1000-grain weight was found with highest value of characters among the first three PCs. The PC1, PC2 PC3 and PC4 had 21.15%, 13.46%, 11.19% and 9.51% variability respectively, among the genotypes for the traits under study. By using K-Means Clustering, 6 clusters were identified. Among them most similar clusters were 4 and 6. These results suggested that plant height, number of tillers, number of grains per spike, spike length and root length were the most important characters in differentiating the genotypes.

**Key words:** Genetic diversity • Principal component analysis • Traits association • *Triticum aestivum* L.

### INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the world's most important food staples reckoned as man's most nutritious source of sustenance since its domestication in 15,000-10,000 BC. The world wide acclaim sticking with wheat as human food is gracefully projected by the Food and Agriculture Organization of the United Nation (FAO) symbol showing a wheat spike with the description "Let there be bread." Similarly, the International Maize and Wheat Improvement Centre (CIMMYT), the great international organizations, have chosen a wheat spike in its logo not only to embellish their insignia but also to implicitly give the all-too-obvious message of unrelenting struggle and undying hope that man must never part with while in search of a better life.

Wheat is also one of the most important cereal crops worldwide, in terms of production and utilization. It is a major source of energy, protein and dietary fiber in human nutrition. Agriculture is the mainstay of Pakistan's economy. Among the major field crops, wheat comes on

top, being a prime food cereal of Pakistan and occupies a position of primacy in matter of daily food consumption. It is the cheapest source of calories and proteins.

In developing countries, like Pakistan, cereals constitute a major bulk of an average diet and wheat contributes about 84% of the total cereal intake in Pakistan. Being a major staple food of over 140 million people of Pakistan, it is annually grown on approximately 8.5 million hectares with annual production of 23.29 million tons while per hectare average production is 2.7 tons [1]. To feed the ever increasing population of Pakistan, there is dire need of improving wheat yield potential on per unit area basis.

Due to extensive breeding for a limited number of economic traits, genetic diversity in wheat has been increasingly narrowed. Narrow genetic background has rendered improved varieties less tolerant to biotic and abiotic stresses. Early farmers grew genetically blended cultivars on a very large scale and thereby extended genotypes possessing broad genetic make up effective against various plant diseases. It has been established

that the use of genetically diverse varieties is an effective strategy in order to minimize genetic vulnerability [2]. Therefore, it is necessary to investigate genetic diversity in the currently used wheat germplasm in order to maintain a desirable level of genetic variation in future wheat breeding.

Genetic diversity of wheat genotypes can be evaluated using morphological and molecular markers [3]. Morphological characters like plant height, leaf area, and spike length, number of spikes per spike and 1000-grain weight contribute towards grain yield of wheat crop. Seedling characters are also used as an indicator for seedling vigor which is necessary for having a good crop stand. The influence of these yield components is highly variable in direction and magnitude. Environment also significantly influence grain yield, therefore, selection for yield on principal components having very strong association with yield is useful. The correlation coefficient analysis is useful in the identification of characters that are positively correlated with yield.

The objective of the present study is to characterize the wheat germplasm, in terms of diversity in morphological traits and association between each pair of these traits.

## MATERIALS AND METHODS

Hundred genotypes were selected from a large collection of wheat germplasm currently maintained at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. These samples comprised old and new varieties grown in different ecological regions of Pakistan, as well as some exotic lines. For the measurement of seedling characters, the varieties were sown in sand blocks in the experimental area of department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. After ten days of sowing coleoptile length, shoot length and root length of five seedlings of each variety were measured in centimeters (cm). Number of seminal roots was also counted of the same plants.

The same panel of genotypes was sown in field on 15<sup>th</sup> November 2007 using randomized complete block design with three replications. Each experimental unit comprised of one line of five meter length. Seed was dibbled to maintain row to row and plant to plant distance of 30 cm and 15 cm respectively. For data recording 10 plants from each experimental unit were selected randomly and tagged. Plant height of the main tiller of each guarded plant was measured in centimeters from the ground level

to tip of the spike excluding awns. Number of tillers was counted from each guarded plant at the time of harvesting. At maturity the spike length of the main tillers of tagged plants measured in centimeter (cm), from the base to the tip of the spike excluding awns. Flag leaf area was calculated using the formula, Flag leaf area (cm<sup>2</sup>) = Leaf length (cm) x Leaf width at middle (cm) x 0.74 (correction factor). Numbers of spikelets of the main spike were counted excluding basal sterile spikelets. The grains were counted from the spike of the main tiller, which was used for taking the number of spikelets per spike. Sample of 1000-grain from the selected plants of each line was taken at random and weighted in grams using electronic balance.

**Statistical Analysis:** The data collected from field experiment was analyzed through Principal Component Analysis (PCA) [4]. Cluster Analysis was done according to Ranjbar *et al.* [5] and Chaparzadeh *et al.* [6] using statistical software Minitab and Statistica. K-Means clustering was done for grouping of 100 genotypes. Principal Component Analysis on the basis of correlation was used for the determination of diversity in current germplasm.

## RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed highly significant genetic differences among the genotypes evaluated for all four seedling and field traits. Among the mean value of genotype for plant height genotype PUNJAB-85 had the highest mean value (102.13 cm) and genotype BACANORA had the lowest mean height (58.60 cm) was observed in Table (3). From means table it was found that genotype GENARO-81 had maximum number of tillers (17.57) and the genotype AS-2002 had minimum number of tillers (5.47).

Comparing the mean values maximum area of leaf was observed in genotype HD-2169 (39.23 cm<sup>2</sup>) and the minimum was observed in genotype PUNJAB-76 (28.60 cm<sup>2</sup>).

Means table showed that genotype PUNJAB-81 had the maximum number of spikelets per spike (22.23) followed by genotype PUNJAB-76 (21.83) and CHAKWAL-97 (21.77) and AUQAB-2000 had the minimum number of spikelets per spike (15.97). From the means table values genotype GALVEZ had the maximum number of grains per spike (67.58) while genotype AS-2002 had minimum number of grains per spike (50.02). Means value showed that genotype SHAFaq-06 had

Table 1: Mean squares of 11 traits of bread wheat (*Triticum aestivum* L.)

Sources of variation	df	Plant height	No. of tillers/plant	Leaf area	No. of spikelets/spike	No. of grains/spike	1000-grain weight	Spike length	Root length	Shoot length	No. of seminal roots	Coleoptile length
Genotypes	99	201.4**	12.29**	12.92**	5.59**	36.46**	18.16**	4.15**	5.60**	0.58**	0.3**	0.22**
Replications	2	139.3**	1.26 <sup>NS</sup>	0.27 <sup>NS</sup>	5.37**	174.67**	8.77**	5.18**	0.08 <sup>NS</sup>	0.03 <sup>NS</sup>	0.02 <sup>NS</sup>	0.005 <sup>NS</sup>
Error	198	15.2	0.748	0.87	0.27	5.28	0.68	0.7	0.02	0.02	0.007	0.009

\*\* indicates highly significance at p<0.01

<sup>NS</sup> indicates non significant

Table 2: Mean values of the morphological traits

S. No.	Genotypes	Pl. height	No. of tillers	Leaf area	S lets perspike	Grains 1000 perspike	Spike length	Root length	Shoot length	Semi-nal Roots	Coleo-ptile length	
1	AS-2002=WD-97603	73.40	5.47	31.77	17.57	50.02	50.73	11.12	10.26	6.57	4.97	3.87
2	AUQAB-2000	95.43	6.17	34.86	15.97	56.90	50.67	14.49	12.14	7.23	4.70	4.17
3	BAYA-S	89.00	8.70	33.16	16.23	60.55	45.33	12.56	12.18	6.26	5.00	4.16
4	BAUS=BAGULA	83.63	7.43	34.21	17.16	59.51	47.87	13.20	12.65	6.39	4.47	4.01
5	BACANORA T88=BCN	58.60	7.20	35.88	19.20	63.20	48.67	13.69	15.51	7.11	4.80	4.02
6	BHAKKAR-2000	82.33	9.53	31.73	20.67	55.05	51.33	12.74	15.13	7.12	5.00	4.16
7	BLUE SILVER=SONALIKA	72.00	8.53	35.69	17.50	52.65	49.00	13.78	15.52	6.29	5.00	4.13
8	BT2549/FATH	86.93	9.07	33.77	18.09	61.84	50.00	13.92	15.60	7.10	4.80	4.00
9	BULBUL	65.80	7.33	31.17	20.55	60.07	51.67	14.47	13.79	7.20	5.00	4.29
10	BYRSA-87=SUNBIRD	87.40	8.57	31.13	19.22	62.40	45.67	13.94	12.40	7.90	4.73	4.30
11	BAVIACORAM-92=V-97097	66.07	7.53	34.15	17.70	60.33	48.33	14.41	14.14	6.16	5.00	4.35
12	CHENAB-70	86.60	8.97	31.05	20.90	57.94	48.00	12.42	13.68	7.18	4.87	4.11
13	CHENAB-79	77.53	9.00	32.57	20.53	65.02	51.40	14.65	14.23	6.94	5.13	4.30
14	CHAKWAL-86	79.20	10.00	32.42	19.86	59.27	50.03	13.47	12.00	7.13	4.40	4.13
15	CHAKWAL-97	79.40	8.47	30.53	21.77	61.34	46.93	13.01	13.60	6.57	4.80	4.29
16	CHAM-4	77.13	7.83	32.67	18.33	54.89	51.17	10.86	12.94	6.66	5.00	3.95
17	CHAM-6=NESSER	78.67	7.73	32.68	19.77	61.77	49.13	11.25	10.42	7.43	4.57	4.28
18	CHILERO=CHILS	88.80	6.67	36.08	18.90	62.88	47.73	12.17	11.88	7.60	4.37	4.20
19	CROW"SS"	78.53	7.10	33.09	17.41	61.78	49.45	14.22	12.29	6.80	4.80	4.20
20	CHENAB-2000	86.17	7.40	31.52	18.47	55.39	52.00	11.51	11.50	7.52	4.80	4.51
21	ERA	92.00	7.63	31.17	20.97	60.24	46.30	11.48	13.12	6.78	5.23	3.93
22	FAISALABAD-83	74.20	9.07	33.37	18.33	55.57	47.00	12.87	13.68	7.49	5.00	4.13
23	FAISALABAD-85	91.60	9.33	34.22	18.10	54.28	48.67	11.60	13.23	6.78	4.40	4.29
24	FALKE=V-91183	85.17	9.00	35.40	19.53	62.73	50.73	13.10	14.33	6.56	4.60	3.92
25	FLORKWA-2	71.90	6.60	31.04	20.33	58.58	50.27	12.10	14.40	6.68	4.10	3.90
26	FAREED-6	87.60	7.30	32.19	18.53	64.38	51.33	8.22	14.20	6.54	4.60	4.16
27	FRONTANA	83.77	9.57	32.91	18.83	59.41	48.30	13.06	14.58	7.19	4.40	3.84
28	GA-2002	86.00	9.93	32.67	15.93	64.93	51.67	13.41	13.23	6.28	5.07	4.09
29	GALVEZ=JUNCO	85.87	8.87	34.52	20.60	67.58	51.73	13.06	13.59	6.90	4.60	4.11
30	GENARO-81	99.13	17.57	32.56	19.53	59.04	51.20	11.31	12.74	6.76	4.40	3.93
31	HD-2009	86.13	9.10	30.04	19.40	60.51	48.00	13.17	14.15	6.48	5.00	3.79
32	HD-2169	73.10	10.57	39.23	17.70	58.43	46.20	12.36	15.54	6.98	5.00	4.15
33	HD-2169/BOWS	92.40	8.90	32.23	17.57	62.67	48.63	11.02	11.41	7.52	4.43	4.21
34	HD-2179	77.92	8.03	33.24	17.00	59.48	51.40	12.34	13.98	6.82	5.00	3.92
35	HD-2204	71.80	8.13	34.67	20.60	59.62	46.77	12.61	15.00	6.67	4.40	4.24
36	HD-2236	70.63	10.80	34.64	20.07	59.13	50.77	12.40	13.38	7.18	4.80	4.21
37	HD-2285	87.37	10.60	31.03	18.33	63.14	48.33	13.31	12.63	6.72	4.83	4.02
38	HD-2329	86.73	9.87	30.28	18.67	62.57	48.57	12.57	12.44	7.12	5.00	4.08
39	HP-1744	77.40	8.07	35.97	19.77	57.23	52.33	12.05	13.00	6.06	5.00	3.98
40	HP-1761	84.93	8.40	32.99	19.73	56.54	45.23	10.58	12.42	7.39	4.83	3.81
41	HARTOG=HTG.(PAVON)	75.07	9.47	33.07	22.00	64.16	51.40	12.13	11.67	6.34	5.27	4.09
42	IMURIS-79=IMU	82.80	8.00	33.70	20.27	63.57	52.10	12.60	12.73	6.76	4.73	3.96
43	INQILAB-91	80.77	8.40	35.83	19.95	57.74	48.67	13.71	12.48	6.18	5.00	4.15
44	IQBAL-2000	81.73	7.00	35.37	18.33	59.73	48.40	12.34	12.20	6.24	4.90	4.29
45	KANCHAN	85.60	8.67	36.23	17.85	59.70	52.10	13.07	13.30	7.38	5.00	3.95

Table 2: Continued

46	KARWAN-2	83.27	8.13	31.22	19.10	64.98	50.79	11.43	14.65	7.36	4.40	4.10
47	KASYON/BOWS	84.53	8.53	30.86	20.15	59.44	53.27	10.25	12.52	7.09	4.97	4.18
48	KAUZ-S	92.33	10.27	31.55	20.33	62.46	51.07	9.73	15.00	7.30	4.80	4.27
49	KENTANA	90.23	9.00	30.58	21.20	63.42	45.67	13.54	12.28	6.79	4.80	4.25
50	KOHINOOR-83	78.73	9.30	28.82	17.20	55.50	53.00	10.46	10.82	7.00	4.80	4.07
51	KOHISTAN-97	77.82	8.93	32.72	17.93	61.19	49.60	11.41	12.52	6.34	4.40	4.07
52	KOHSAR-95	88.20	9.43	32.75	19.20	59.69	50.77	12.34	13.11	6.84	4.93	4.29
53	KUFRA-1	91.50	9.27	31.85	19.71	62.50	51.33	13.19	10.44	7.15	4.00	4.07
54	LU-26	85.23	9.53	32.30	19.40	54.12	55.53	12.31	10.80	7.21	4.40	4.00
55	LYP-73	89.00	9.37	35.10	19.40	56.73	55.00	12.36	9.71	6.68	5.00	4.29
56	MANGO	85.53	10.00	34.26	22.07	62.25	51.00	10.40	11.26	7.12	4.60	4.17
57	MANTHAR	86.67	9.53	33.00	19.53	54.31	51.60	10.78	11.28	6.94	4.60	4.15
58	MEXIPAK-65	81.93	8.47	34.20	19.80	55.24	50.57	11.64	13.22	6.20	4.40	4.16
59	METAL TAIL	93.73	9.47	32.82	20.30	57.71	51.10	13.52	11.14	7.82	4.40	4.15
60	MH-97=ATTILA	87.20	12.03	35.07	20.87	56.16	48.40	11.24	12.77	6.61	4.80	4.25
61	MILAN	94.27	8.87	30.26	19.27	55.98	51.13	10.76	10.42	6.89	4.40	4.45
62	MILAN/HD-832	87.13	9.07	36.29	18.52	64.16	53.33	14.31	10.78	6.36	5.17	4.26
63	MONCHOS	91.07	12.00	34.02	19.47	62.54	52.10	11.82	11.18	7.47	4.87	4.59
64	MONS/CROWS	94.27	9.50	31.83	20.13	57.28	48.50	11.28	11.26	6.46	5.17	4.57
65	MYNAS	77.53	9.33	32.20	20.87	59.74	50.07	12.47	11.39	6.65	5.00	4.04
66	NACOZARI-76	90.67	12.00	35.16	19.60	54.68	51.47	12.03	13.24	7.03	4.47	4.07
67	NAEEM-82	87.47	10.23	32.67	18.47	63.79	49.00	12.74	12.94	6.26	4.40	4.74
68	NL-623	95.93	9.83	35.21	20.40	61.37	47.83	13.05	12.32	7.16	4.80	4.52
69	OASIS	93.53	9.90	35.88	21.03	62.67	49.00	12.08	10.58	6.85	4.70	4.14
70	PAK-81	93.93	12.10	33.43	19.20	53.57	51.08	11.35	11.53	6.71	5.13	4.72
71	PARI-73	96.93	10.53	33.83	21.12	57.84	46.33	13.58	11.30	7.00	4.30	4.08
72	PARWAZ-94	88.87	11.27	35.04	20.30	62.70	51.43	12.63	14.04	6.62	4.80	4.22
73	PASBAN-90	100.53	11.50	32.37	20.73	57.84	51.10	11.86	11.24	7.12	4.43	4.82
74	PASINA-90	98.27	12.00	33.10	19.15	65.47	51.77	12.64	10.90	7.74	5.00	4.73
75	PAVON-76	93.53	14.00	32.57	20.20	58.40	50.20	11.69	11.70	7.92	5.00	4.00
76	PBW-343=ATTILA	92.20	11.10	34.33	19.77	55.09	52.30	11.98	12.89	6.30	4.20	4.60
77	PUNJAB-76	98.50	16.43	28.60	21.83	63.42	50.33	13.28	10.81	6.62	4.40	4.94
78	PUNJAB-81	97.73	15.80	37.33	22.23	61.19	52.10	13.49	12.20	7.30	4.20	4.24
79	PUNJAB-85	102.13	11.60	30.50	21.23	63.98	52.97	11.66	12.10	6.53	4.27	3.86
80	PUNJAB-96	88.20	9.00	33.55	21.53	63.98	47.93	14.46	14.42	6.30	4.80	4.76
81	SA-42	94.47	10.47	31.86	18.93	58.21	52.63	12.09	11.50	7.30	5.00	4.37
82	SA-75	93.03	11.27	31.00	18.39	54.86	50.57	11.71	14.11	6.68	5.17	4.59
83	SATLUJ-86	85.93	10.00	32.97	19.53	58.21	49.47	12.08	13.50	6.37	4.13	4.92
84	SEHER-6	99.87	9.27	30.17	20.13	58.21	54.67	12.64	11.64	6.36	4.80	4.58
85	SHAFaq-6	93.53	11.67	32.13	19.00	59.63	58.77	12.95	13.28	6.48	4.20	4.78
86	SHAHKAR-95	90.10	12.40	28.93	18.37	62.31	52.03	12.75	12.04	6.18	4.00	4.63
87	SH-2002	74.17	11.20	35.13	19.27	55.24	53.03	13.85	14.11	7.52	4.40	4.27
88	SHALIMAR-88	82.90	12.07	34.74	21.00	58.58	48.83	13.40	11.63	6.22	4.47	4.20
89	SINDH-81	81.83	8.43	34.83	19.17	56.16	50.40	10.71	13.10	7.46	4.80	4.24
90	TRAP#1	76.37	10.87	36.67	20.70	65.08	52.10	12.47	12.84	6.80	5.00	4.40
91	UFAQ	92.83	9.17	35.40	20.33	56.73	45.27	13.14	13.96	7.14	4.80	4.78
92	WATAN/2*ERA	84.30	10.00	37.90	20.67	59.51	52.07	9.73	14.00	6.69	4.00	4.51
93	WL-711	86.07	12.00	32.50	20.07	57.47	47.33	13.35	14.27	7.20	4.97	4.40
94	V-87094(WATAN)	86.23	12.00	32.77	19.20	55.24	54.33	11.50	13.38	6.66	5.00	4.71
95	YECORA-70	86.74	13.00	34.50	20.33	58.02	48.33	12.45	11.48	6.58	4.40	4.71
96	ZA-77	76.83	10.13	36.19	20.80	63.16	46.33	11.76	14.64	7.20	4.60	4.53
97	ZAMINDAR-80	82.00	10.93	36.21	18.43	53.19	54.67	12.11	12.76	6.58	4.00	4.59
98	ZARDANA-89	86.77	9.53	32.69	21.93	61.19	49.33	12.83	13.35	7.22	4.67	4.79
99	ACC.8528	83.27	12.18	33.33	18.19	56.16	47.84	11.03	13.48	6.59	4.80	4.22
100	ACHYUTA	85.53	10.33	37.37	20.63	59.70	48.77	12.13	12.90	6.94	4.60	4.48

maximum 1000-grain weight (58.77gm) followed by genotype LU 26 (55.53gm) and genotype HP-1761 had minimum 1000-grain weight (45.23gm) (Table 3). Among means genotype CHENAB-79 had maximum (14.65cm) followed by genotypes AUQAB-2000 (14.49cm) and genotype FAREED-06 had minimum (8.22 cm) spike length. From the means table values genotype BT2549 had the maximum root length (15.60 cm) followed by genotype HD-2169 (15.54 cm) and genotype LYP-73 had the minimum values (9.71 cm). Among the means genotype PAVON-76 had maximum shoot length (7.92 cm) followed by genotype BYRSA-87 (7.90 cm) and genotype HP-1744 had minimum shoot length (6.06 cm). From the means table, data showed that genotype HARTOG had maximum (5.27) while genotypes ZAMINDAR-80, KUFRA-1, WATAN-92 and SHAHKAR-95 had minimum (4.00) number of seminal roots. Means values showed that genotype PUNJAB-76 had maximum (4.94 cm) closely followed by genotype SATLUJ-86 with a value of 4.92 cm while genotype HD-2009 had minimum (3.79 cm) coleoptile length (Table 2).

Bharadwaj *et al.* [7] reported that the significant differences among the rice genotypes indicated the necessity to group them into clusters to identify the divergent groups.

**Correlation Coefficient Analysis:** Correlation measures the interdependence between a pair of characters. Knowledge of correlation is required to obtain the expected response of other characters when selection is applied to the character of interest in a breeding program. Correlation of morphological traits was calculated by studying the data of germplasm lines of wheat (Table 3).

Plant height showed significant positive correlation with number of tillers and coleoptile length. Narwal *et al.* [8] also reported direct effect of plant height and number of tillers and Richards *et al.* [9] and Liatukas *et al.* [10] about the direct effect of plant height and coleoptile length. While plant height had significant negative correlation with leaf area, root length and seminal roots. Plant height showed positive correlation with some yield contributing traits like spikelets per spike, number of grains per spike and 1000-grain weight.

Number of tillers per plant had significant positive correlation with spikelets per spike and coleoptile length. It verifies the work of Bhutta *et al.* [11] about the positive significant correlation between number of tillers and spikelets per spike. While significant negative correlation with number of seminal roots. Number of tillers per plant had positive correlation for number of grains per spike, shoot length and 1000-grain weight.

Leaf area had significant positive correlation with root length only. While negative correlation with spikelets per spike, number of grains per spike, 1000-grain weight, shoot length and seminal roots. It showed positive correlation with spike length.

Number of spikelets per spike had positive correlation only with number of grains per spike. The results are in accordance with the finding of Kashif and Khaliq [12]. Number of spikelets per spike had negative correlation with some yield contributing traits like 1000-grain weight, spike length, root length and seminal roots. While number of grains per spike had significant positive correlation with spike length. It is supported by the work of Khaliq *et al.* [13] and Okuyama *et al.* [14]. Number of grains per spike had negative correlation with 1000-grain weight. 1000-grain weight had significant negative correlation with root length. It showed negative correlation for spike length, shoot length and seminal roots.

**Principal Component Analysis:** The average data was analyzed by using principal component analysis. The data matrix of 11x100 was prepared for the analysis. Out of eleven, four principal components (PCs) exhibited more than one eigen value and showed about 55.29% of variability so these four were given due importance for further explanation (Table 3). The PC1 had 21.15%, PC2 showed 13.45%, PC3 exhibited 11.18% and PC4 showed 9.50% variability among the genotypes for the traits under study. Eigen value and variance associated with each Principal Component, decreased gradually and stopped at 0.36 and 3.23% respectively.

The first PC was more related to plant height, number of tillers, spikelets per spike, 1000-grain weight and coleoptile length as it was cleared from the values of Table 5 for PC1. Poor in leaf area, spike length, root length and number of seminal roots but positive effect of yield contributing traits like number of tillers, spikelets per spike and 1000-grain weight so it must be considered. In the second PC only 1000-grain weight was given due importance and genotypes were low in mostly yield contributing traits like number of tillers, spikelets per spike, grains per spike and spike length.

The third principal component exhibited positive effects for root length, leaf area, 1000-grain weight and coleoptile length. It showed maximum variation for these characters but poor in plant height, spikelets per spike, number of grains per spike and spike length.

Table 3: Correlation matrix among the morphological characters.

	Plant height roots	No. of Seminal tillers	Leaf area	Spikelets/spike wt.	Grains/spike	1000 grain	Spike length	Root length	Shoot length	
No. of tillers	0.473**									
Leaf area	-0.221*	0.000								
Spikelts/spike	0.157	0.313**	-0.006							
Grains/spike	0.066	0.008	-0.045	0.209*						
1000GrainWt.	0.132	0.188	-0.075	-0.040	-0.098					
Spike Length	-0.148	-0.038	0.118	-0.020	0.227*	-0.145				
Root Length	-0.425**	-0.129	0.207*	-0.058	0.072	-0.227*	0.149			
Shoot Length	0.120	0.034	-0.028	0.090	0.032	-0.063	-0.046	-0.085		
Seminal Roots	-0.204*	-0.213*	-0.032	-0.132	-0.003	-0.146	0.093	0.078	-0.003	
ColeoptileLength	0.308**	0.345**	0.001	0.195	-0.006	0.116	0.033	-0.107	-0.076	-0.150

Table 4: Eigenvalues and %total variance for first 4 PCs

	Eigenvalue	% Total Variance	Cumulative Eigenvalue	Cumulative%
PC1	2.32	21.15	2.32	21.15
PC2	1.48	13.45	3.80	34.60
PC3	1.23	11.18	5.03	45.79
PC4	1.04	9.50	6.08	55.29

The fourth principal component was more related to shoot length, leaf area and spikelets per spike. Genotypes were poor for plant height, number of grains per spike, 1000-grain weight and spike length. It had negative impact towards the yield.

From first four PCs it was cleared that among all the 11 variables, 1000-grain weight had high weight age value and spike length had lowest value. Mostly, yield contributing traits were poor in these PCs except PC first. From this study it is cleared that a good hybridization breeding program can be initiated by the selection of genotypes from the PC1 and PC2.

On the basis of first two Principal Components, varieties were given scores Table 3. According to first PC, PUNJAB-76 had highest score (3.07), PASBAN-90 and PUNJAB-81 had 2.12 and 2.00 scores respectively. BACANORA had lowest score i.e - 2.57. According to PC2, AS-2002 had highest score (3.37), KOHINOOR-83 and CHAM-4 had 2.95 and 1.87 respectively. PUNJAB-96 had lowest score (-2.51). Evaluation of germplasm on the basis of morphological characters was done by many scientists. Ranjbar *et al.* [5], Escobar-Hernandez *et al.* [15], Sapra and Lal [16] used Principal Component method for grouping of germplasm. From these scores given to genotypes on the basis of first and second PC, breeders can select genotypes with highest score having desirable characters for further breeding programmed.

Table 5: Principal components (PCs) for eleven characters in 100 germplasm lines of wheat (1-4)

Variables	Eigen vectors			
	PC1	PC2	PC3	PC4
Plant height	0.513	0.019	-0.184	-0.073
No. of tillers/plant	0.459	-0.223	0.177	0.073
Leaf area	-0.167	-0.258	0.482	0.407
No. of spikelets/spike	0.266	-0.432	-0.120	0.230
No. of grains/spike	0.010	-0.490	-0.370	-0.273
1000-grain weight	0.254	0.308	0.283	-0.195
Spike length	-0.169	-0.457	-0.007	-0.394
Root length	-0.358	-0.313	0.249	0.154
Shoot length	0.077	-0.016	-0.490	0.608
No. of seminal roots	-0.276	0.067	-0.282	-0.266
Coleoptile length	0.351	-0.224	0.300	-0.196

**Scree Plot:** Scree plot explained the percentage variance associated with each principal component obtained by drawing a graph between eigenvalues and Principal component numbers. PC1 showed 21.15% variability with eigenvalue 2.32 in germplasm which then reduced gradually. Elbow type line is obtained which after 4<sup>th</sup> PC tended to straight. After that little variance observed in each PC and it ended at 3.23% at 11<sup>th</sup> PC with eigen value 0.35. From graph it was cleared that maximum variation was present in first PC. So selection of genotypes from this PC will be useful.

Table 6: Comparison profile of the six clusters of wheat germplasm classified by K- means clustering

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
No. of accessions	11	21	26	14	3	25
Plant height	74.04	95.89	78.58	88.15	63.48	85.38
No. of tillers/plant	8.68	11.34	8.74	9.37	7.35	9.98
Leaf area	33.90	32.85	33.59	32.65	33.73	33.90
No. of spikelets/spike	18.78	19.94	19.79	19.31	19.15	19.50
No. of grains/spike	56.07	58.82	61.64	62.78	61.19	56.82
1000-grain weight	50.02	50.92	49.78	49.60	49.55	50.45
Spike length	12.22	12.40	12.70	12.46	14.18	11.89
Root length	13.51	11.89	12.64	12.94	14.47	12.82
Shoot length	6.82	6.96	6.72	6.87	6.82	6.87
No. of seminal roots	4.76	4.64	4.82	4.71	4.93	4.62
Coleoptile length	4.08	4.43	4.18	4.23	4.22	4.26

Table 7: Pair wise Euclidean distances (D<sup>2</sup>) between six clusters of 100 accessions of wheat.

Cluster No.1	1	2	3	4	5	6
1	0.0					
2	45.29	0.0				
3	4.89	28.81	0.0			
4	22.46	7.52	8.60	0.0		
5	13.14	98.63	21.46	56.51	0.0	
6	12.02	10.81	6.58	4.19	46.78	0.0

**Scatter Plot:** A Principal component scatter plot of the wheat varieties depicted that the accession those are close together are perceived as being similar when rated on the 11 variables. Genotypes which are further apart were different from each other with respect to distance between them. Graph showed that mostly genotypes were not diverse from each other as they are congested to same area. While genotypes 1, 5, 7, 50, 77, 78 and 80 (AS-2002, BACANORA T88, BLUE SILVER, KOHINOOR-83, PUNJAB-76, PUNJAB-81 and PUNJAB-96) were present at distance from other varieties with respect to PC1 and PC2 so more diverse.

**Biplot:** A Principal component biplot showed that variables are super imposed on the plot as vectors. Distance of each variable with respect to PC1 and PC2 showed the contribution of this variable in the variation of germplasm. It showed that as a whole 1000-grain weight, plant height, shoot length and number of seminal roots contributed towards the variability in the germplasm. While in PC1 only most of the yield contributing traits were responsible for the variability which was good for further use of this germplasm in breeding programs. While in case of PC2 only 1000-grain weight was responsible for variation of germplasm.

**Cluster Analysis:** The entries in this study were grouped into six clusters based on average linkage, each cluster contained accessions that were highly similar. Cluster 1 consisted of 11 accessions, cluster 2 of 21, cluster 3 of 26, clusters 4 of 14, cluster 5 of 3 and cluster 6 of 25 accessions Table 6. Mean value for each cluster (Table 6) revealed that accessions in cluster 1 had moderate in most of the characters but lower in spikelets per spike, no. of grains per spike and coleoptile length.

Accessions grouped in cluster 2 had highest plant height, no. of tillers, spikelets per spike, 1000-grain weight, shoot length and coleoptile length but lowest in root length. Genotypes in cluster 3 were moderate for all the characters studied except shoot length which had lowest mean. Cluster 4 had highest mean for no. of grains per spike only and lowest for leaf area.

Cluster 5 contained accessions that contained lowest means for plant height, no. of tillers and 1000-grain weight. It showed highest values for the spike length, root length and no. of seminal roots. Cluster 6 contained accessions with highest leaf area mean and lowest for spike length and no. of seminal roots. Current results are in accordance with the findings of Ranjbar *et al.* [5], Naghavi and Jhansouz [17].

According to Euclidean distances (D<sup>2</sup>) among clusters (Table 7), the six clusters were statistically different from each other. The most similar clusters were on the one hand, cluster 4 and 6 (4.19 units) and on the other hand, cluster 1 and 3 (4.89 units). The largest intercluster distance (98.63 units) was between cluster 2 and 5. This result showed that plant height, no. of tillers, no. of grains per spike, spike length and root length are the most important characters in differentiating the genotypes. Cluster 4 and 5 with intercluster distance

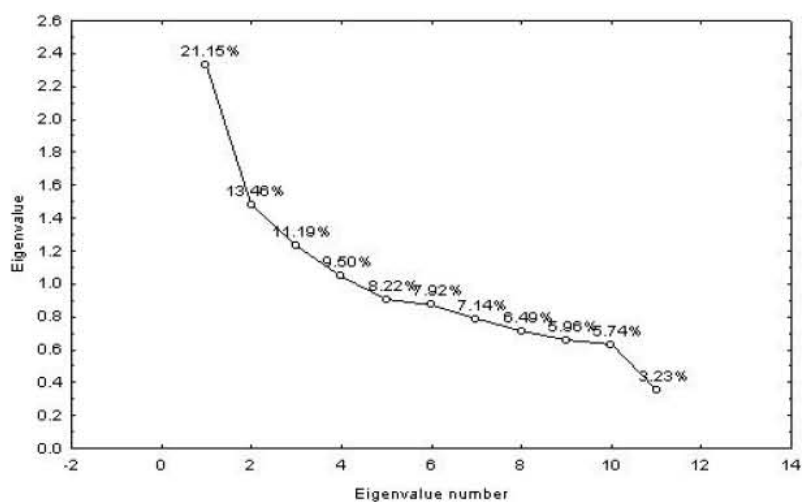


Fig. 1: Scree plot of principal component analysis between eigen values and number of principal component

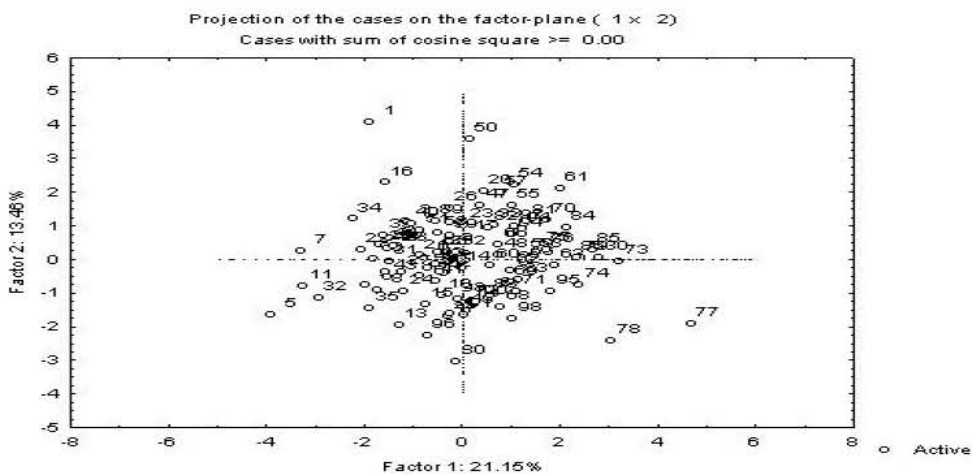


Fig. 2: Two dimensional ordination of 100 germplasm lines of wheat on principal component axis 1 and 2

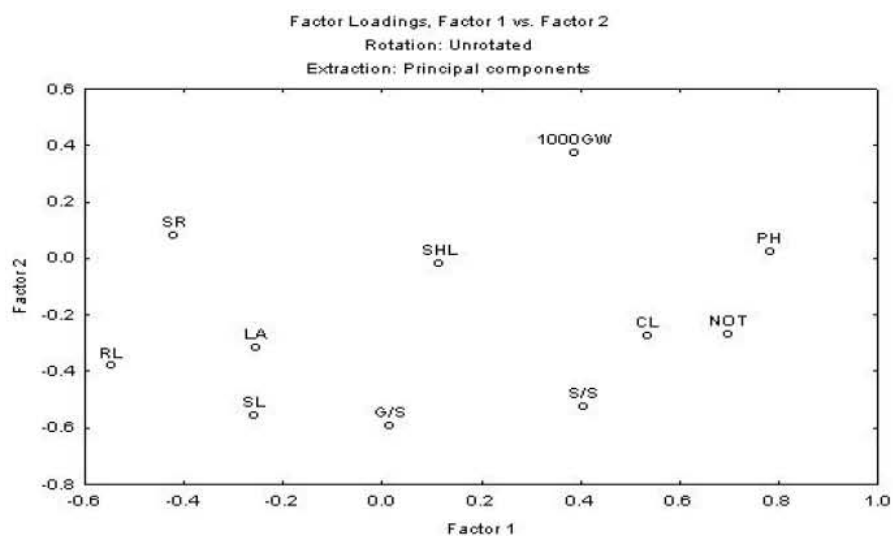


Fig. 3: Principal components biplot of 100 wheat germplasm lines



(56.51 units) showed that dissimilarity was due plant height, no. of tillers, no. of grains per spike, spike length, root length and no. of seminal roots. This analysis abled me to define groups of genotypes that were significantly different from each other for characters of interest. Similar results related to germplasm grouping were reported by Ayana and Bekele [18] and Grenier *et al.*, [19]. By observing mean values of all the 6 clusters, it was cleared that for high yield, selection of genotypes from cluster 3 and cluster 4 will be useful. They had comparatively highest mean values for most of the yield contributing traits.

### CONCLUSION

Principal component analysis and correlation coefficients analysis in germplasm collections facilitate reliable classification of genotypes, identification of subsets of core genotypes and correlated morphological characters with possible utility for specific breeding purposes.

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