ESTIMATION OF VARIOUS CLASSIFACTORY ANALYSIS IN SOME HEXAPLOID WHEAT (*TRITICUM AESTIVUM* L.) GERMPLASM

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Abstract

Wheat (*Triticum aestivum* L.) germplasm of one hundred accessions were demonstrated for Cluster and Principal component analysis, the experimental plot was conducted during the growing season 2006 in augmented field design at research area of the Department of Plant Breeding and Genetics, Faculty of Agriculture, Gomal University, Dera Ismail Khan, KPK, Pakistan. Data were collected and analyzed for different polygenic traits. Eigenvalues > 1 were noted for three PCs out of ten, having 29.02%, 43.42% and 55.00% of the total variability with positive effects for most of the traits. While rest of the traits expressed moderate to low variability. Scatter diagram also depicted a wide range of genetic variability for various traits on the basis of altitude and latitude. According to cluster analysis all the accessions were divided into three main groups A, B and C, which were further divided in to thirteen sub-groups. Cluster 1 of group A, on the basis of mean analysis four accessions were found with 4% population, has less days to heading (84.5 ± 2.65). The Cluster 2nd accounts for 13% of the population with thirteen accessions. In group B, two accessions were found in cluster 5 with a contribution of 2% for two accessions PARC/NIAR 2450 (02), PARC/NIAR 2771 (03), having minimum days to maturity (132.5 ± 0.71). Cluster 7 contributes 3% of the population with three accessions, has a maximum number of tillers plant^{-1} (18.6 ± 1.65). Cluster 9 was noted for 1% of the population with one accession (PARC/JICA 3849 (01)), has less days to emergence (7) and greater plant height (149.8 cm). While in group C, clusters 12 consists four accessions with 4% contribution, having high 1000-grain weight (42.02 ± 2.88). Last cluster 13 of group C, contributed 2% to the population with two accessions PARC/MAFF 4275 (01), PARC/MAFF 4280 (01), having large spike length (20.8 ± 2.62 cm), greater number of spikelets spike^{-1}(29.3 ± 3.61), high grain yield plant^{-1} (3.96 ± 0.93 gm) and greater grain yield (kg ha^{-1}) (5001 ± 261).

Introduction

Wheat is the staple food for 35% of the world's population and is grown on 17% of the cultivated area in the world. A large proportion of man's essential nutrients is contained in the wheat grain i.e. carbohydrates (60 to 80%, mainly as starch); proteins (8 to 15% which contain adequate amounts of all essential amino acids except lysine, tryptophane and methionine); fats (1.5 to 2.0%); minerals (1.5 to 2.0%); and vitamins such as the B complex and vitamin E. It provides more calories and protein to human diet than any other crop. Hexaploid wheat was preadopted for domestication from about 7000 B.C. (Hillman, 1972). Wheat is known for a cool-season crop. The adaptation took place in the temperate regions from 30o to 60oN and 27° to 40°S latitudes, which receive annual rainfall of about 500-1200 mm (Rasheed *et al*., 2012).

Naturally it is proved, that the domestication of wheat should have taken place in the Fertile Crescent, since this is the center of its wild progenitor's geographical distribution (Zohary, 1970). Naturally distributed biological species were adapted to their changing environments through the conservation of high genetic variability in their natural populations, and this resulting variability is the promoting force behind the evolution of the species and speciation. A similar situation can be found in the widely distributed domesticated crops grown under cultivation. Diverse forms of landraces of crops adapted to local environment and agricultural practices have been developed during their long history of cultivation after domestication. The primitive forms of wheat are an important source of raw material and have significantly contributed for the improvement of wheat varieties because they exhibit enormous genetic variation (Simmonds, 1979).

The present study was done to analyze genetic variation and identify various wheat germplasms to improve yield by wheat breeding program.

Materials and Methods

One hundred accessions of wheat (*Triticum aestivum* L.) were obtained from the Institute of Agriculture Biotechnology & Genetic Resources (IABGR), NARC, Islamabad. All these accessions were sown in research area of the Department of Plant Breeding and Genetics, Faculty of Agriculture, Gomal University, Dera Ismail Khan, KPK, Pakistan for the season 2006, following the augmented field design. Each accession was dibbled by hand in a 2 meters row. 25cm distance was kept for plant to plant with a regular recommended cultural practices and fertilizer. Ten plants were selected randomly for data recording in the field and tagged accordingly, while grain yield plant^{-1}, 1000-grain weight and grain yield (Kg ha^{-1}) were taken in the laboratory.

Analysis of data: The Principal Component Analysis (PCA), Cluster Analysis (CA) and Scatter diagram was computed by using the computer software "STATISTICA" and "SPSS" following the numerical taxonomic techniques and methods of Sneath & Sokal (1973).

Results and Discussion

Principal component analysis (PCA) based on phenotypic traits: Principal component analysis (PCA) is a technique to analyze data for reducing the variability of a large numbers of interacted variables and maintaining as such of the variation as possible. It also indicates an unrelated set of variables and gave additional useful information of the parameters to explore the groups. These factors are structured to retain the first few among all of the original variables.

It was obvious from the analysis that three PCs out of ten were selected having >1 eigenvalue and contributed 55.00% variation among one hundred wheat germplasms for all parameters (Table 1). It was noted that principal component first contributed 29.02%, Principal component second 43.42%, and Principal component third 55.00% of the total genetic variability for all the genotypes. The principal component 1st had 29.02 % of the total variation in all morphological parameters (Table 1). It demonstrated positively contribution for days to maturity only. While negative contribution were noted for days to emergence, days to heading, plant height, number of tillers plant-1, spike length, number of grains spike-1, grain yield plant-1, 1000-grain weight and grain yield (kg ha-1). The principal component 2nd was found for 43.42% variation and depicted mainly the patterns of divergence with a positive contribution for days to emergence,

number of tillers plant-1, spike length, number of grains spike-1 and grain yield plant-1. While, the said PC was observed for negative association in days to heading, days to maturity, plant height, 1000-grain weight and grain yield (kg ha-1). The last principal component 3rd was accounted for 55% of the total variation with a positive contribution for days to maturity, number of tillers plant-1, spike length, number of grains spike-1, grain yield plant-1 and Grain yield (kg ha-1). While, negative contribution was found in days to emergence, days to heading, plant height and 1000-grain weight.

Principal component (PC) first and principal component (PC) second contributed 43.42% of the total genetic variability, which revealed that parameters contributed maximum variations was the PC 2nd. The combined contribution of principal component second and principal component third revealed that most of the parameters have positive effects.

Further more, all the wheat accessions were plotted in the scattered diagrams to observe the relationship amongst all the germplasms, which were presented in (Figs. 1 & 2) accordingly. In the scatter diagram it was cleared that the Principal component first and principal component second contributed cumulative variance of 43.42%, which demonstrates that germplasms from each area has their own divergence and was grouped separately. The independent grouping of all the accessions was due to genetic variation for different traits.

Table 1. Principal component analysis of wheat accessions.

Trait	PC1	PC2	PC3
Eigenvalue	2.90	1.44	1.16
Cumulative eigenvalue	2.90	4.34	5.50
Proportion of variance %	29.02	14.40	11.58
Cumulative variance	29.02	43.42	55.00
	Eigenvectors		
Days to emergence (DE)	-0.050	0.419	-0.445
Days to heading (DH)	-0.133	-0.473	-0.178
Days to maturity (DM)	0.015	-0.527	0.355
Plant height (PH)	-0.211	-0.207	-0.431
Tillers per plant (Tillers)	-0.389	0.018	0.043
Spike length (SL)	-0.164	0.485	0.146
Seeds per spike (S/S)	-0.481	0.081	0.169
Grain Yield per plant (GY/P)	-0.474	0.045	0.277
1000-Seed weight (1000-SW)	-0.227	-0.182	-0.573
Grain yield (kg/ha)	-0.499	-0.057	0.038
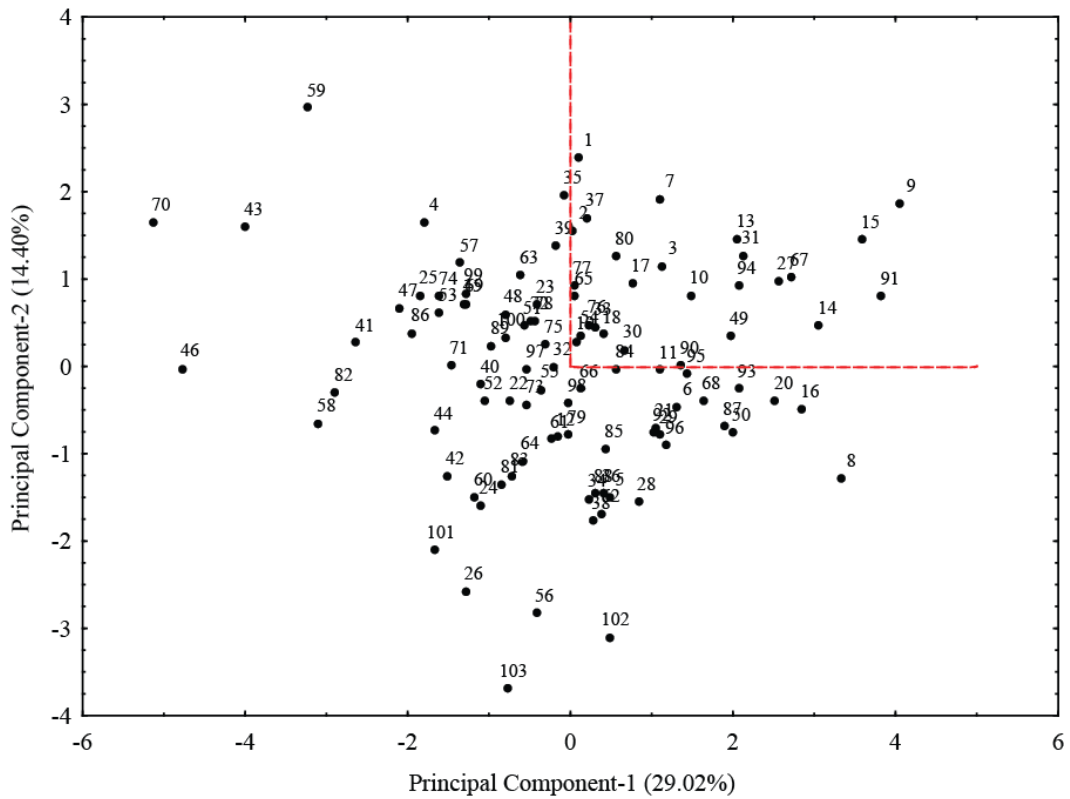
PCA 1-2 (2006)
Fig. 1. Scatter diagram based on average regional genetic diversity (1-2) PCs in wheat accession.
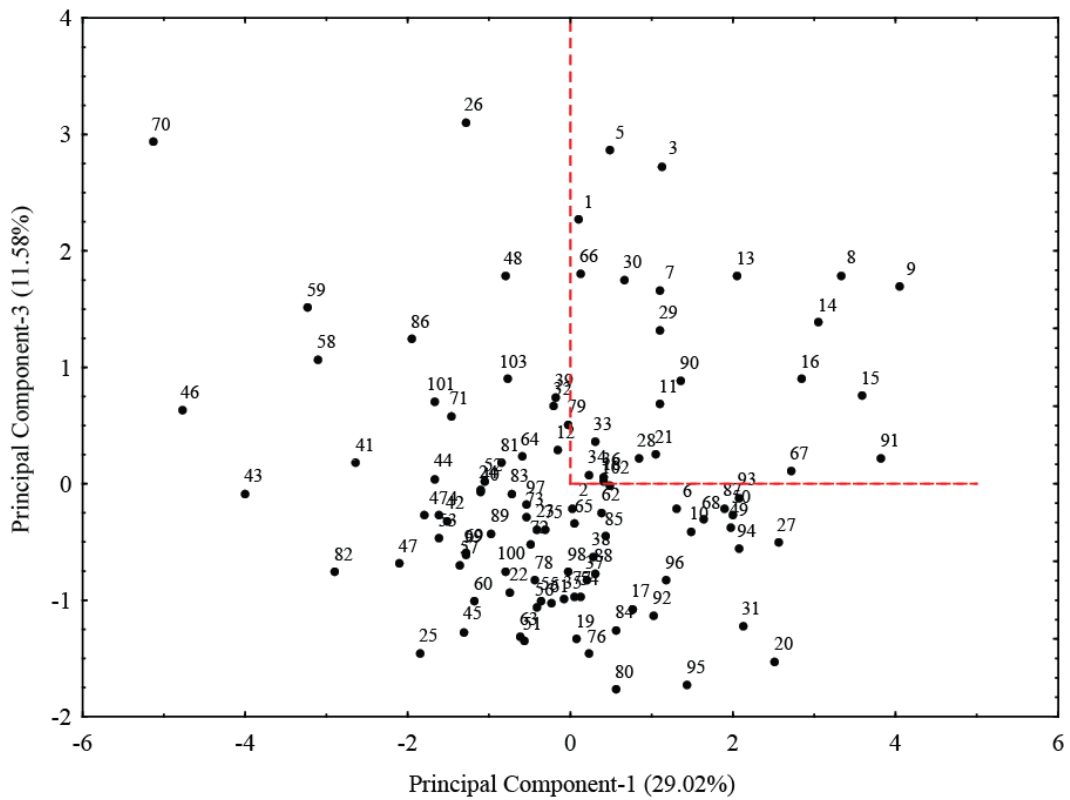
PCA 1-3 (2006)
Fig. 2. Scatter diagram based on average regional genetic diversity (1-3) PCs in wheat accession.

The results of the Principal component analysis were at par with the cluster analysis. This made the possibility for selection of wheat genotypes that satisfy specific sets of characteristics as identifying by Rouamba *et al.,* (1996) and Brown (1991), who declared that multivariate analysis could be used to deal with germplasm conservation. Generally PCs with eigen value larger than 1.0 are retained, but Jolliffe (1986) suggested that retaining PCs with eigen value as low as 0.75 could also prove beneficial if the input matrix is of correlation type.

Most of the quantitative traits contributed negative genetic variance for both PC1 and PC2, therefore these traits need further investigation that may gives an indication of presence of genetic variation for its potential use in crop improvement. The results of the present study showed a wide range of genetic diversity. This provides an opportunity to select specific traits for a particular region to develop site-specific high yielding wheat varieties for sustainable crop production. The present investigation further suggests that in future the wheat collecting missions should concentrate their efforts on sampling as many geographical and ecologically distinct areas as possible, which was already suggested by the findings of Gerard Branlard *et al.,* (2003), Khan *et al.,* (2007 a), Khan *et al.,* (2002), Levy *et al.,* (1988), Magdalena *et al.,* (2002) and Mohibullah *et al.,* (2012), who reported the collecting expeditions to the area, where the germplasm is under threat along with the areas where existing genetic diversity has not yet been gathered.

Cluster analysis: Cluster analysis based on ten qualitative and quantitative traits depicts three main groups among one hundred wheat germplasms. The dendrogram based on Euclidean distance coefficients suggested the existence of three main groups are A, B and C, which were further sub-divided into 13 clusters respectively (Fig. 3).

The grouping based on various traits along with mean and standard deviations is presented in (Tables 2 and 3). First A group consists of 5 clusters, in which the Cluster 1 contains four accessions with 4% population having less days to emergence (7.5 ± 2.65), short days to heading (84.5 ± 2.65), short days to maturity (145.3 ± 13.40), minimum plant height (47.2 ± 12.34), highest spike Length (15 ± 0.85) and maximum grain yield (kg ha^{-1}) (4352 ± 189.6). The Cluster 2nd accounts for 13% of the population with thirteen accessions consists of small spike length (12.3 ± 1.63), small no. of spikelets spike^{-1} (15.8 ± 2.93), less grain yield plant^{-1} (1.9 ± 0.15), low 1000-seed weight (27.1 ± 7.54) and minimum grain yield (kg ha^{-1}) (3368 ± 439). The Cluster 3rd depicts 4% of the population and comprised of four accessions, which consists of maximum days to heading (106 ± 1.41), maximum days to maturity (152 ± 7.35), small no. of tillers plant^{-1} (6.5 ± 1.56) and greater 1000-seed weight (38.7 ± 0.94). 4th cluster has a huge contribution in group A i.e., 37% of the population and consists of thirty seven accessions with maximum days to emergence (12.5 ± 0.36), maximum plant height (111.6 ± 25.18), greater number of tillers plant^{-1} (9.96 ± 1.36), greater number of spikelets spike^{-1}(19.2 ± 1.79) and maximum grain yield plant^{-1} (2.4 ± 0.41).

Group B includes 6 clusters from 5 to 11, in which the cluster 5 also contains two accessions with a contribution of 2%, having maximum days to emergence (16.5 ± 0.36), greater days to heading (108.5 ± 0.71), maximum days to maturity (132.5 ± 0.71) and less plant height (48.1 ± 1.67). The cluster 6 of group B depicts 9% contribution and consists of nine accessions. Cluster 7 contributes 3% of the population and includes three accessions having two useful traits i.e., maximum number of tillers plant^{-1} (18.6 ± 1.65) and maximum spike length (14 ± 0.59).The accessions of this cluster can be used to enhance biomass production. Cluster 8 has the huge contribution i.e., 16%, which consists of sixteen accessions, with maximum 1000-grain weight (40.6 ± 2.27), days to emergence, days to heading, days to maturity, number of tillers plant^{-1}, plant height (cm), spike length (cm), number of spikelets spike^{-1}, grain yield plant^{-1} (gm) and yield (kg ha^{-1}). Cluster 9 accounts for 1% of the population with one accession (PARC/JICA 3849 (01)), having less days to emergence (7), greater plant height (149.8), less number of spikelets spike^{-1} (23.7), high grain yield plant^{-1} (3.3) and high grain yield (kg ha^{-1}) (4801). This accession is suitable for high elevation areas of Pakistan, where wheat crop duration is relatively long. Cluster 10 represents 3% of the population and comprised three accessions having lowest days to heading (87.3 ± 4.93). Cluster 11, which was the last cluster of B group contains two accessions with 2% contribution having minimum days to emergence (15 ± 1.41), greater days to maturity (190 ± 0.85), less number of tillers plant^{-1} (7.3 ± 0.28), short spike length (10.5 ± 0.92), less no. of spikelets spike^{-1} (15.95 ± 0.92), low grain yield plant^{-1} (1.99+0.06), less 1000-grain weight (19.5) and with lowest grain yield (kg ha^{-1}) (3058+56.6).

Group C being a last, includes two clusters i.e., 12 and 13. In which cluster 12 consists four accessions with contribution of 4%, having less days to emergence (11.3 ± 3.4), short days to heading (101.5 ± 5.26), short days to maturity (147.5 ± 10.61), small plant height (97.4 ± 4.53), less no. of tillers plant^{-1} (12.4 ± 0.28), short spike length (14.5 ± 0.65), less number of spikelets spike^{-1} (28.2 ± 2.39), low grain yield plant^{-1} (3.1 ± 0.3), low 1000,seed weight (30.95 ± 5.02) and less grain yield (kg ha^{-1}) (4952 ± 151.5). Last cluster 13, contributed 2% to the population with two accessions, having high days to emergence (11.5 ± 0.71), greater days to heading (103 ± 4.24), high days to maturity (154.5 ± 3.7), greater plant height (118.4 ± 2.4), high number of tillers plant^{-1} (13.4 ± 4.69), large spike length (20.8 ± 2.62), greater number of spikelets spike^{-1}(29.3 ± 3.61), high grain yield plant^{-1} (3.96 ± 0.93), high 1000-seed weight (42.02 ± 2.88) and greater grain yield (kg ha^{-1}) (5001 ± 261) These traits indicated that some of the accessions could be used to enhance photosynthetic activities, biomass production and grain yield in plants, which could be used for crop improvement. Several potentially important desirable traits had been identified and those could be exploited for specific trait improvement and assemblage of core collections from a bulk genetic stock by Ranade & Farooki (2002), Routray *et al.,* (2007), Samuel *et al.,* (2002), Sandhu & Gill (2002), Shehata (2004), Shuaib *et al.,* (2007), Singh (2006), Sultana *et al.,* (2007), Mohibullah *et al.,* (2011) and Vierling *et al.,* (1994).
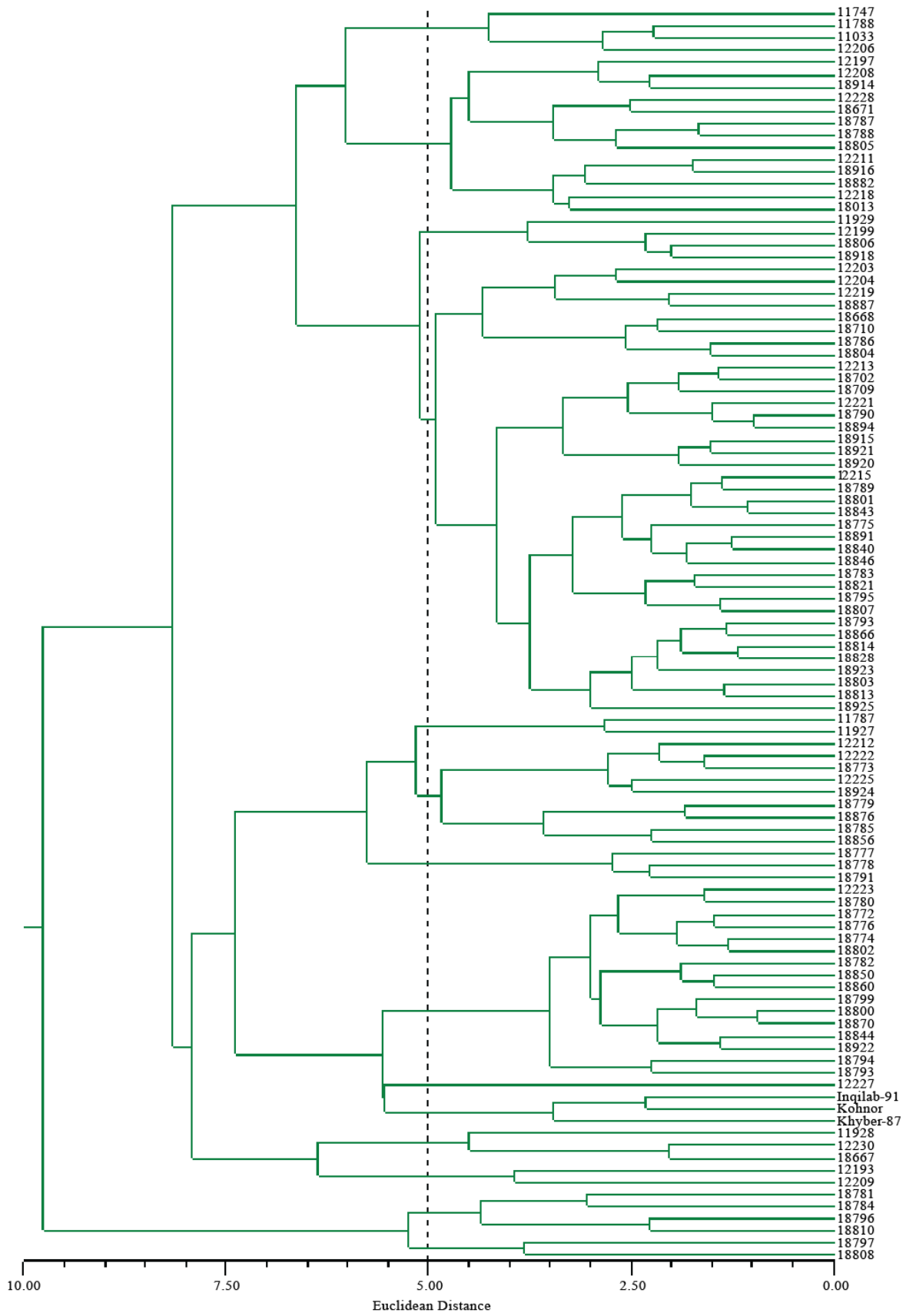
Fig. 3. Linkage distance for cluster-2006.

Table 2. Grouping based on various clusters for one hundred wheat germplasms.

Groups	Cluster	Frequency	% Age	Germplasms
Group A	Cluster 1	4	4	PARC/NIAR 2303 (05), PARC/NIAR 2450 (02), PARC/NIAR 2828 (03), PARC/JICA 3830 (06)
	Cluster 2	13	13	PARC/JICA 3823 (03), PARC/JICA 3831 (01), PARC/MAFF 4353 (04), PARC/JICA 3850 (01), PARC/PGRI 4082 (01), PARC/MAFF 4268 (03), PARC/MAFF 4269 (01), PARC/MAFF 4279 (03), PARC/JICA 3832 (01), PARC/MAFF 4354 (02), PARC/MAFF 4308 (01), PARC/JICA 3839 (01), PARC/MAFF 4353 (03)
	Cluster 3	4	4	PARC/NIAR 2809 (01), PARC/JICA 3826 (03), PARC/MAFF 4279 (04), PARC/MAFF 4355 (02)
	Cluster 4	37	37	PARC/JICA 3830 (03), PARC/JICA 3830 (04), PARC/JICA 3839 (02), PARC/MAFF 4310 (01), PARC/MAFF 4272 (01), PARC/PGRI 4131 (01), PARC/MAFF 4268 (02), PARC/MAFF 4279 (02), PARC/JICA 3835 (05), PARC/MAFF 4270 (02), PARC/PGRI 4124 (01), PARC/JICA 3840 (02), PARC/MAFF 4269 (03), PARC/MAFF 4311 (01), PARC/MAFF 4354 (01), PARC/MAFF 4356 (02), PARC/MAFF 4356 (01), PARC/JICA 3838 (01), PARC/MAFF 4269 (02), PARC/MAFF 4278 (01), PARC/MAFF 4294 (01), PARC/MAFF 4265 (01), PARC/MAFF 4288 (04), PARC/MAFF 4292 (01), PARC/MAFF 4296 (01), PARC/MAFF 4267 (01), PARC/MAFF 4285 (01), PARC/MAFF 4274 (01), PARC/MAFF 4279 (05), PARC/MAFF 4270 (03), PARC/MAFF 4303 (01), PARC/MAFF 4282 (02), PARC/MAFF 4287 (03), PARC/MAFF 4358 (01), PARC/MAFF 4279 (01), PARC/MAFF 4282 (01), PARC/MAFF 4359 (01)
Group B	Cluster 5	2	2	PARC/NIAR 2450 (02), PARC/NIAR 2771 (03)
	Cluster 6	9	9	PARC/JICA 3834 (03), PARC/JICA 3841 (01), PARC/MAFF 4264 (02), PARC/JICA 3845 (01), PARC/MAFF 4358 (03), PARC/MAFF 4266 (02), PARC/MAFF 4306 (02), PARC/MAFF 4268 (01), PARC/MAFF 4300 (03)
	Cluster 7	3	3	PARC/MAFF 4265 (03), PARC/MAFF 4266 (01), PARC/MAFF 4270 (01)
	Cluster 8	16	16	PARC/JICA 3841 (02), PARC/MAFF 4266 (04), PARC/MAFF 4264 (01), PARC/MAFF 4265 (02), PARC/MAFF 4264 (03), PARC/MAFF 4278 (02), PARC/MAFF 4266 (06), PARC/MAFF 4297 (05), PARC/MAFF 4301 (04), PARC/MAFF 4277 (01), PARC/MAFF 4277 (02), PARC/MAFF 4304 (02), PARC/MAFF 4295 (04), PARC/MAFF 4357 (01), PARC/MAFF 4273 (01), PARC/MAFF 4276 (01)
	Cluster 9	1	1	PARC/JICA 3849 (01)
	Cluster 10	3	3	PARC/NIAR 2803 (04), PARC/JICA 3852 (02), PARC/MAFF 4231 (01)
	Cluster 11	2	2	PARC/JICA 3816 (01), PARC/JICA 3831 (02)
Group C	Cluster 12	4	4	PARC/MAFF 4266 (05), PARC/MAFF 4267 (02), PARC/MAFF 4274 (02), PARC/MAFF 4280 (03)
	Cluster 13	2	2	PARC/MAFF 4275 (01), PARC/MAFF 4280 (01)

Table 3. Mean and standard deviation of each cluster in wheat germplasms.

Traits	Group A				Group B							Group C	
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12	Cluster 13
Days to emergence	7.5 ± 2.65	10.5 ± 2.18	13.3 ± 1.71	12.5 ± 0.36	16.5 ± 0.5	13.8 ± 0.47	12.7 ± 0.88	8.3 ± 0.33	7 ± 0.00	11 ± 3.46	15 ± 1.41	11.3 ± 3.4	11.5 ± 0.71
Days to heading	84.5 ± 2.65	99.5 ± 5.72	106 ± 1.41	102.5 ± 4.09	108.5 ± 0.71	95.7 ± 7.00	102.7 ± 4.51	104.3 ± 3.4	106 ± 0.00	87.3 ± 4.93	97.5 ± 12.02	101.5 ± 5.26	103 ± 4.24
Days to maturity	145.3 ± 13.40	146.5 ± 6.51	152 ± 7.35	149.9 ± 4.90	132.5 ± 0.71	144.4 ± 3.32	145 ± 5.29	154 ± 4.26	188 ± 0.00	171.5 ± 24.7	190 ± 0.58	154.5 ± 3.7	147.5 ± 10.61
Plant height	47.2 ± 12.34	108.5 ± 36.4	56.1 ± 23.7	111.6 ± 25.18	48.1 ± 11.67	140.96 ± 24.65	110.9 ± 22.1	134.4 ± 26.6	149.8 ± 0.00	98.3 ± 48	49.95 ± 3.61	118.4 ± 24	97.4 ± 4.53
No. of tillers plant^{-1}	9.2 ± 2.48	7.7 ± 1.19	6.5 ± 1.56	9.96 ± 1.36	12.9 ± 4.81	11.5 ± 2.71	18.6 ± 1.65	18.6 ± 1.37	8.2 ± 0.00	10.7 ± 4.31	7.3 ± 0.28	13.4 ± 4.69	12.4 ± 0.28
Spike length	15 ± 0.85	12.3 ± 1.63	13.2 ± 2.43	12.97 ± 1.52	11.9 ± 1.41	11.6 ± 1.52	14.0 ± 0.59	11.4 ± 1.5	11.9 ± 0.00	12.7 ± 1.82	10.5 ± 0.92	14.5 ± 0.65	20.8 ± 2.26
No. of spikelets spike^{-1}	17.6 ± 2.07	15.8 ± 2.93	16.1 ± 0.75	19.2 ± 1.79	21.1 ± 0.71	21.6 ± 3.7	17.9 ± 1.84	17.8 ± 1.56	23.7 ± 0.00	16.5 ± 1.23	15.95 ± 0.92	28.2 ± 2.39	29.3 ± 3.61
Grain yield plant^{-1}	2.4 ± 0.40	1.9 ± 0.15	2.1 ± 0.42	2.4 ± 0.41	2.9 ± 0.11	3.0 ± 0.30	2.1 ± 0.7	2.5 ± 0.24	3.3 ± 0.00	2.3 ± 0.15	1.99 ± 0.06	3.1 ± 0.35	3.96 ± 0.93
1000-Seed weight	28.6 ± 2.88	27.1 ± 7.54	38.7 ± 0.94	37.9 ± 6.6	31.9 ± 4.24	35.99 ± 8.03	32.7 ± 8.28	40.9 ± 2.27	21.0 ± 0.00	36.3 ± 5.25	19.5 ± 0.00	42.02 ± 2.88	30.95 ± 5.02
Grain yield (kg/ha)	4352 ± 189.6	3368 ± 439	4034 ± 321	4317.4 ± 261.9	4407 ± 171	4575.1 ± 292.5	4191 ± 105.1	4388.8 ± 210.1	4801 ± 0.00	4152 ± 142.4	3058 ± 56.6	4952 ± 151.5	5001 ± 261

Conclusion

The overall contribution of PC 1st, PC 2nd and PC 3rd represents high genetic variation for all the traits with positive effects. According to scattered diagram genetic variability was also proved for all the traits. The cluster analysis showed relative differences and were placed separately on the basis of genetic variation for all the parameters. The germplasm PARC/NIAR 2450 (02), PARC/NIAR 2771 (03), PARC/MAFF 4275 (01) and PARC/MAFF 4280 (01), exhibited maximum positive contribution for minimum days to maturity, maximum spike length, maximum number of spikelets spike-1 and maximum grain yield (kg ha-1). These parameters depicted that the said germplasms may be used for in future breeding strategies in the related agro-climatic conditions, which is possible for farmers to double, triple or even quadruple their wheat yield.

Acknowledgements

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