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Estimation of Genetic Diversity among Oat Genotypes through Agro-morphological Traits

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Abstract

During the present study diverse germplasm comprising 124 oat accessions including three checks was evaluated for various quantitative agro-morphological traits in the research field of PGRI, NARC, Islamabad during the year 2013-14. The principal objective of the research was to study the magnitude of genetic diversity and relationships between different genotypes and to identify promising genotypes of oat for the traits of economical importance. The seed material was collected from diverse ecologies of Pakistan and USA. Most of the traits showed considerable variations. Analysis of variance showed highest variance for number of spikelets spike^{-1} followed by plant height, seed yield plant^{-1}, days to 50% panicle initiation, days to maturity, leaf length, number of tillers plant^{-1}, spike length, grains spikelet^{-1}, 100 seed weight, leaves per tiller. Correlation analysis indicated that seed yield per plant was highly significantly and positively correlated with all the studied traits except days to 50% germination which showed non-significant relationship with seed yield per plant. PCA showed that 3 out of 13 PCs with eigen value of more than 1 accounted for 71.06% of the overall variations found among 124 genotypes of oat. Cluster analysis distributed 124 accessions of oat into five main clusters (I, II, III, IV & V) having 49, 1, 50, 21 and 3 genotypes. These outcomes can be successfully utilized for successful characterization and preservation of oat genetic resources.

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Introduction

Avena sativa L. (Poaceae) is annual cereal, widely grown as a fodder in temperate and subtropical countries (Iran Nejad, 1994, Assefa *et al.,* 2003). Oat is a cereal grain of the family Gramineae (Poaceae) with unknown center of origin, but likely in the Mediterranean basin or the Middle East (Murphy and Hoffman 1992). It belongs to grass family Poaceae (Gramineae) which is leading in importance in the order Poales (Bremer *et al.*, 2003). This family contributes to the world economy, food and industry through valuable crops i.e. wheat, rice and maize (Mabberley, 2008). It occurs at three ploidy levels, diploid, tetraploid, and hexaploid, with a base chromosome number of 7. Species numbers and names have varied depending on the classifier and the criteria used to delineate taxa (reviewed by Baum 1977). The primary cultivated oat (*A. sativa*) is a hexaploid of $2n= 6x = 42$ originating as an aggregation of three diploid genomes (AA, CC, DD). Oats are an important source of livestock feed worldwide, both as nutritious grain and as fodder crop. It is a very good source of protein, fiber and minerals. Among the cereals oat is highest protein grain crop. Although world oat production has declined gradually between 1930 and 1950, oats still remain an important grain crop for people in whole developing world and in developed economies for special uses. In many parts of the world oats are grown for use as grain and also as a forage and fodder crop. It can also be used as a straw for bedding, hay, haylage, silage and chaff. In most of the region, on average 25% of the area seeded to oat is cut for green feed. The major objectives in oat breeding are improved grain and forage yields.

It is one of the most important Rabi cereal fodder crop grown in winter throughout Pakistan both under irrigated and rain fed conditions. A well distributed rainfall of 400 mm and an optimum temperature range of 16-32°C during the four months duration is sufficient to meet its requirement as a fodder crop. Although 1/6th of the total crop area of Pakistan is under the cultivation of fodder crops annually, still the animals are generally underfed resulting in poor performance (Hussain *et al.,* 1993). The available fodder supply is 1/3 less than the actual needs of animals (Younas and Yaqoob, 2005). So a great deal of work is needed to be done in this regard here in Pakistan. The green yield of local oat landraces under rain fed conditions is about 20 t ha^{-1} (Bhatti, Hussein and Mohammad, 1992), which is insufficient to provide even maintenance for the number of livestock kept. In Baluchistan, wheat was a traditional fodder, but, with the introduction of improved oats, use of wheat fodder has fallen. Farmers harvest oats at 50 percent flowering, or later to maximize yield but at the expense of quality (Dost, 1997). It is an important fodder crop, mostly fed as green but surplus is converted into silage or hay to use during fodder deficit periods (Suttie and Reynolds, 2004). As compared to the other cereal crops, oat is broadly adapted to marginal environments with low fertility soils, cool-wet and low rainfall climates (Hoffman 1995; Buerstmayr *et al.,* 2007; Ren *et al.,* 2007). It is usually consumed as a whole-grain cereal and is distinct among the cereals due to its multifunctional feature and nutritional profile (Masood *et al.,* 2008). It is a cereal crop is used for human food and livestock feed worldwide (Peterson *et al.,* 2005; Achleitner *et al.,* 2008). In recent years, the demand in oat for human consumption has increased because of dietary benefits of whole grain and β-glucan (Achleitner *et al.,* 2008). The objectives of the current study were

To determine genetic diversity in diverse oat germplasm on the basis of agro-morphological traits.

To identify promising oat genotypes for future breeding programmes.

Materials and methods

Research location

The present study was carried out in the research area of the Plant Genetic Resources Institute (PGRI), National Agriculture Research Centre (NARC), Islamabad during rabi season 2013-2014.

Experimental materials

The research materials comprised of 124 Oat genotypes (121 accessions and three checks) of diverse nature and these accessions were provided by the

Gene bank of Plant Genetic Resources Institute (PGRI). Out of these 124 accessions, 114 accessions belong to *Avena sativa* L. while remaining 10 accessions belong to *Avena fatua* L. The germplasm were evaluated for different qualitative and quantitative agro-morphological traits. The experiment was planted on 28th November, 2013 at Pakistan Genetic Resource Institute (PGRI) field in the augmented design. Row length was maintained at 3m, row to row distance was kept at 50cm having one accession per row.

Agronomic practices

All agronomic practices such as land preparation, weeding, irrigation etc were uniformly applied. Morphological data was recorded on five selected plants according to descriptors of International Board of Plant Genetic Resources (IBPGR) for oat.

Statistical analysis

Quantitative traits that were recorded during the present study includes days to 50% germination, days to 50% panicle initiation, plant height, leaf length, leaf width, number of tillers plant-1, number of leaves tiller-1, days to maturity, spike length, number of grains spikelet-1, number of spikelets spike-1, seed yield plant-1 and 100-seed weight.

.All the recorded data was averaged and the means of all the accessions were analyzed for simple statistics (mean, standard deviation, coefficient of variation and variance) among all the genotypes for different parameters. Simple correlation coefficient was calculated through the procedure of Steel and Torrie (1980) by means of plot mean values using software statistica 7.0. The agro-morphological traits recorded during the present study were also analyzed by arithmetical taxonomic techniques through multivariate analysis including cluster and principle component analysis followed by Sneath and Sokal, (1973). Means of all the traits were standardized through Z-scores to avoid the effects of scaling differences before the multivariate analysis. Euclidean distances coefficient were determined for the total pairs of genotypes. Resultant Euclidean distances coefficient matrices were used to assess the association among the oat genotypes through cluster analysis (NTSYS-pc, version 2.1). Furthermore, PCA (principal component analysis) was performed through the similar data matrix. The first three principle components were plotted to observe the differences between the studied accessions (Statistica, Version 7.0).

Results and discussions

For all 13 morphological parameters among various oat accessions notable intra and inter specific differences were observed through analysis of variance (Table 1).

Table 1. Basic statistics of morphological parameters of oat genotypes during the present study.

Traits	Mean	Minimum	Maximum	SD*	CV (%)**	Variance
DG 50%	20.3	14	29	3.3	16.4	11.1
DP 50%	123.9	113	147	8.6	6.9	73.3
PH	118.1	69.4	161.4	15.9	13.5	253.9
LL (cm)	34.4	24.9	45.9	4.7	13.7	22.3
LW (cm)	1.9	1	2.9	0.5	24.8	0.2
NTP	15.3	6	30	4.3	28.2	18.6
NLT	5.4	4.4	7.1	0.7	12.2	0.4
DTM	160.6	145	179	7.1	4.4	50.1
SL (cm)	29.9	20.9	41.3	4.3	14.2	18.1
NGS	2.4	1	3	0.8	32.1	0.6
NSS	59.6	25.8	118.6	21.2	35.6	449.9
SYP (g)	19.1	3.7	43.6	9.7	50.5	93.2
HSW (g)	2.7	1.3	4.6	0.7	25	0.4

*Standard deviation **Coefficient of Variation. Whereas DG 50% = Days to 50% Germination, DP 50= Days to 50% Panicle initiation,

PH= Plant Height, LL= Leaf Length, LW= Leaf Width, NTP== Number of tillers plant-1, NLT= Number of leaves tiller-1, DTM= Days to maturity, SL= Spike length, NGS= Number of grains spikelet-1, NSS= Number of spikelets spike-1, SYP= Seed yield plant-1, HSW= 100-Seed Weight.

Among these genotypes considerable variations were observed for parameters of days to 50% germination, days to 50% panicle initiation, plant height, leaf length, leaf width, number of tillers per plant, number of leaves per tiller, days to maturity, spike length, number of grains per spikelet, number of spikelets per spike, 100 seed weight and seed yield per plant.

Table 2. Correlation coefficients among 13 quantitative traits in diverse germplasm of oat.

Traits	DTG 50%	DPI 50%	PH	LL	LW	NTP	NLT	DM	SL	NGS	NSSP	SYP
DPI 50%	0.42**											
PH	-0.08	-0.13										
LL	0.13	0.56**	0.21*									
LW	0.20	0.72**	0.03	0.80**								
NTP	-0.07	0.11	0.35**	0.39**	0.42**							
NLT	-0.04	0.47**	0.37**	0.52**	0.58**	0.42**						
DM	0.39**	0.82**	-0.10	0.50**	0.68**	0.18*	0.44**					
SL	0.20*	0.54**	0.45**	0.54**	0.61**	0.33**	0.60**	0.57**				
NGS	0.14	0.27**	0.07	0.52**	0.58**	0.43**	0.27**	0.31**	0.37**			
NSSP	0.35**	0.71**	0.23*	0.58**	0.74**	0.26**	0.56**	0.64**	0.83**	0.40**		
SYP	0.00	0.26**	0.35**	0.59**	0.61**	0.70**	0.44**	0.33**	0.51**	0.54**	0.42**	
HSW	-0.08	0.09	0.02	0.30	0.27**	0.18*	0.02	0.15	0.17	0.38**	0.09	0.45**

Where, ** = highly significant, * = significant.

For all these morphological parameters the common statistical data i.e. coefficient of variation, range, variance and mean was noted during the year 2013-14 (Table 1). During this study through analysis of variance, highest variance was found for number of spikelets per spike followed by plant height, seed yield per plant, days to 50% panicle initiation, days to maturity, leaf length, number of tillers per plant, spike length, days to 50% germination respectively. The variance for the above traits was 449.9, 253.9, 93.2, 73.3, 50.1, 22.3, 18.6, 18.1 and 11.1. Relatively low level of variability was seen in number of grains per spikelet, 100 seed weight, number of leaves per tiller, and leaf width respectively.

Table 3. Principal Component Analysis Based on Agro-Morphological Traits.

	PC1	PC2	PC3
Eigen values	5.85	2.01	1.38
Cummulative Eigen values	5.85	7.86	9.24
% Total Variance	45.01	15.45	10.60
Commulative %	45.01	60.46	71.06
Traits	Eigen Vectors		
Days to 50% Germination	0.273	-0.591	-0.015
Days To 50% Panicle Initiation	0.743	-0.553	-0.020
Plant Height	0.269	0.562	0.606
Leaf Length	0.811	0.080	-0.124
Leaf Width	0.903	-0.098	-0.166
No. of tillers /plant	0.536	0.568	-0.011
No.of leaves/tiller	0.698	0.136	0.403
Days to Maturity	0.739	-0.469	-0.064
Spike length	0.812	0.006	0.342
No. of grains/ spiklet	0.616	0.215	-0.431
No. of Spikelets/Spike	0.841	-0.244	0.234
Yield/Plant	0.718	0.499	-0.183
100-Seed weight	0.314	0.322	-0.640

The mean values of the oat genotypes for days to 50% germination, days to 50% panicle initiation and days to maturity were 20.3, 123.9 and 160.6 with a range of 14 to 29, 113 to 147 and 145 to 179 days respectively. These characters can be further evaluated to find out both about early and late maturity. The oat accession 16041 took minimum days tomaturity i.e. 145 days while another genotype 22346 took maximum days to maturity (179 days). Both early and delayed maturity are vital for breeding programs trying for variation of plant germplasm to a variety of ecological areas on photoperiod and thermo-sensitivity (Suddihiyam *et al.,* 1992; Rehman *et al.,* 2009).

Table 4. Promising accessions of oat identified during the present study based on agro-morphological traits.

Trait	Range	Accession
NTP^{-1}	≥23	22341, 22390, 22410, 000801, 000807, 000820
NGS^{-1}	≥ 250	22368, 22410, 000821, 000824, 000825, 000831,000837, 000794
NSS^{-1}	≥ 100	22346, 22377, 22378, 000794, 000819, 000831
HSW	≥ 3.6	22325, 22326, 22329, 22377, 22385, 22390, 22412, 22413, 000792, 000804, 000810, 000818
SYP^{-1}	≥ 34	22326, 22347, 22348, 22413, 000801, 000804, 000808, 000818,000820, 000827
SL	≥ 36	22338, 22346, 22347, 22377, 22378, 22389, 22410, 22412,000819,000821
DM	≤ 151	16031, 16032, 16041, 16042, 16043, 16045, 16060,16069, 16071,16082

Correlation coefficients analysis

The assessment of the extent to which the variables differ together or a measure of a quantity of relationship is called correlation. (Steel and Torrie, 1980). Simple correlation coefficient was carried out among the mean values of 13 quantitative traits of oat accessions (Table2). Correlation analysis revealed that seed yield plant^{-1} had a highly significant and positive correlation with plant height, number of tillers per plant, number of leaves per tiller, days to maturity, spike length, number of grains per spikelet and number of spikelets spike^{-1}. So selecting genotypes with greater number of tillers per plant, number of spikelets per spike and number of grains per spikelet can indirectly enhance the seed yield in oat crop.

These results were in close correspondence with Rabiei *et al.,* (2011) who suggested that selecting for early maturity effected on days to flowering, Ahmad *et al.,* (2013) who reported that number of spikelets per plant, number of leaves per plant, plant height and 1000 seed weight should be given emphasis for future seed yield improvement programs. Similarly, Dinesh Tulsiram Surje and Dilip Kumar De (2014), Krishna *et al.,* (2014) also reported similar results to our findings, Souza and Sorrels (1991) reported that days to maturity is highly significantly and positively correlated with grain yield and 100-seed weight, this shows that breeding for maturity will enhance the seed yield in oat crop. Hence seed yield in oat can be improved by selecting genotypes with greater number of tillers per plant, spikelets per spike and grains per spikelet as suggested by the current study.

Cluster Analysis Based on Agro-Morphological Parameters

On basis of agronomic and morphologic characters the unweighted pair group method using, arithmetic averages (UPGMA) is most commonly used (Mohammadi & Prasanna, 2003).

Through cluster analysis based on agro-morphological parameters, a total of 124 genotypes of oat were divided into five main clusters during the present study (Fig. 1). The five main clusters were further divided into sub groups. In cluster-I 40 genotypes of oat were found and this cluster was further divided into two groups (Group I-1) containing 38 genotypes and group I-2 having 2 genotypes, respectively.

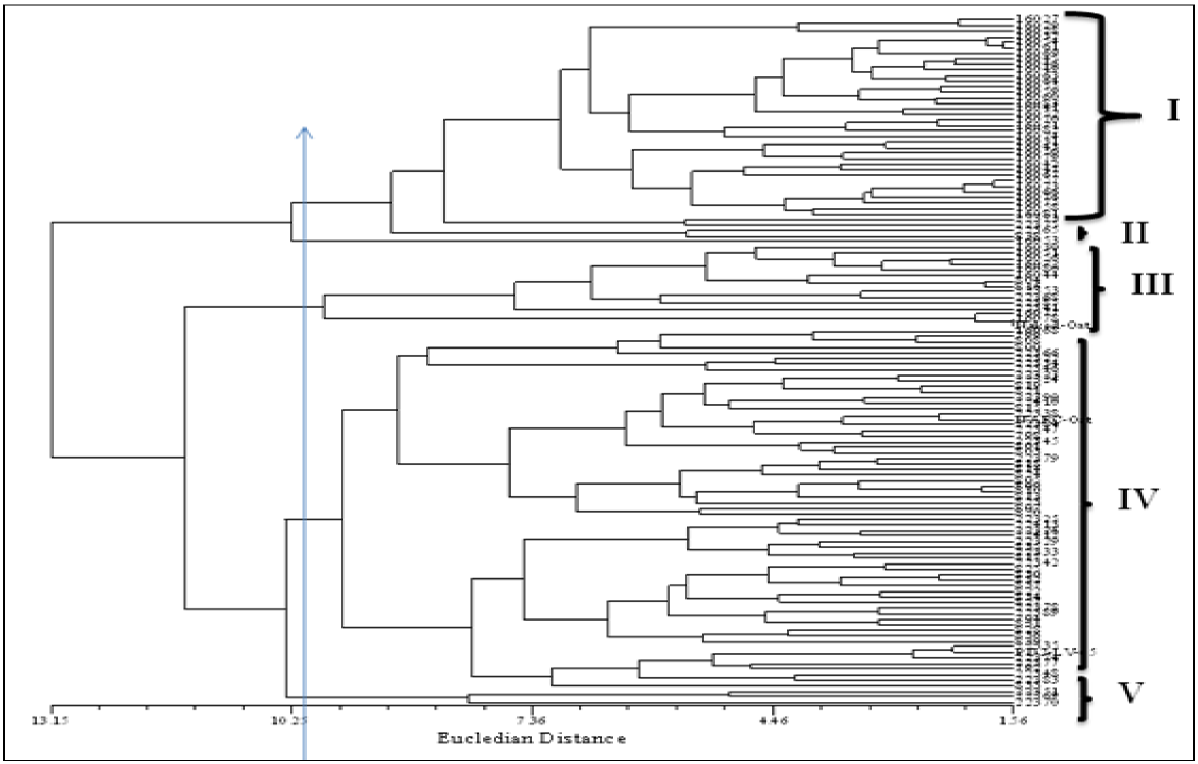

Fig. 1. Dendrogram showing the genetic relationships between oat genotypes based on agro-morphological traits.

In cluster II only one accession was found followed by group III having a total of 15 genotypes which were further subdivided into two groups i.e. group (III-1) consisting of 12 genotypes and group (III-2) having 3 genotypes including a check cultivar i.e.

Naked oat. Cluster IV was the largest among all the clusters comprising a total of 65 genotypes which were further splitted into two groups. Group IV-1 was the largest with a total of 33 genotypes including a check variety i.e. NARC-Oat while group IV-2 was the one with 32 oat accessions including a check cultivar named as PD2-LV-65. Cluster V is the one which included a total of three genotypes i.e. 22351, 22369 and 22370. Cluster I comprised of 40 genotypes which were taller in height, less number of tillers/plant, early maturing, below average seed yield/plant, average.

Cluster II consist of only one genotype which is tall in height, lowest in number of tillers per plant, early maturing, lesser grains per spikelet, lowest seed yield per plant. Similarly cluster III included 15 genotypes which were shortest in plant height, maximum number of tillers per plant, medium days to maturity, above average seed yield per plant. Cluster IV was the largest and the genotypes that made this cluster were tallest in plant height, medium number of tillers per plant, maximum days to maturity, high yielding. Cluster 5 included three genotypes and all of them were medium to taller plant height, maximum number of tillers per plant, late in maturing, largest spike, average seed yield per plant.

The results of cluster analysis indicated that there is considerable variation between the accessions for the studied agro-morphological traits and it also indicated that the studied accessions were distinctly divided into its particular groups. Grouping of oat accessions into different clusters was not associated with the geographic distribution instead accessions were mainly grouped due to their agro-morphological difference.

The results obtained through cluster analysis of oat genotypes are in agreement with the findings of Tang *et al.*, (2014), Iannucci *et al.,* (2011), Sohbat Bahraminejad *et al., (2012),* Boczkowska (2014), Souza and Sorrells (1991).

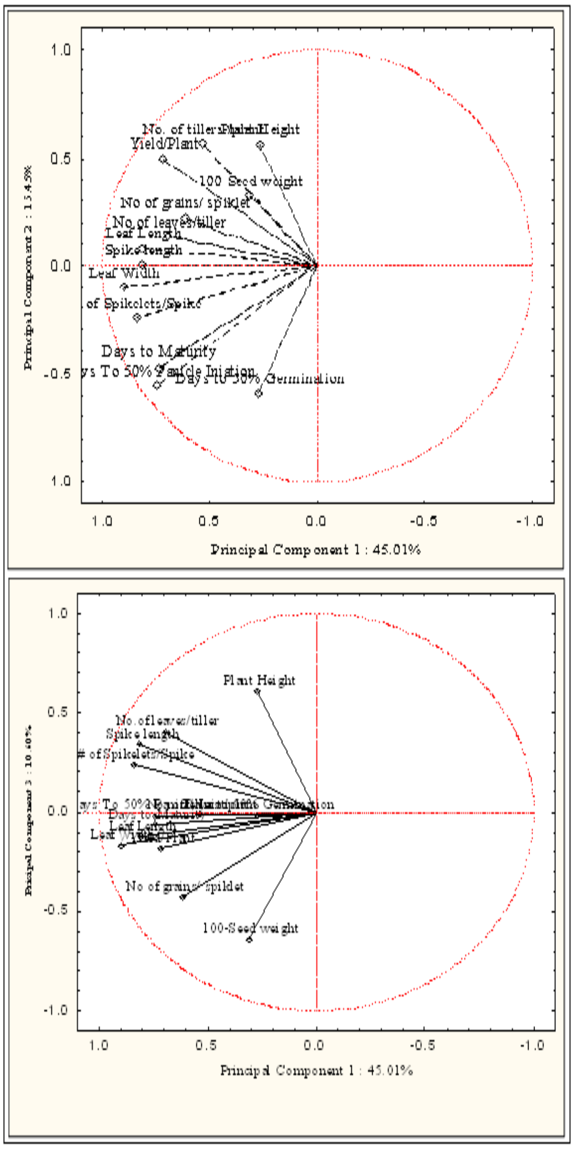

Fig. 2. Scatter plots showing the contribution of 13 quantitative traits to the total variation in the first three principal components in 124 accessions of oat.

All of these scientists suggested that the distribution of oat genotypes into different groups is not due to their differences in origin but these differences are due to differences in morphological parameters. Substantial level of genetic diversity was documented for different agro-morphological traits during the

Principal component analysis

Principal, component analysis based on 13 agro-morphological, traits during year 2013-2014, showed that 3 of the 13 principal components with an eigen value above than 1.0 accounted for 71.06% of the total variation among 124 accessions of oat. PC I which is most important explained 45.01%, PC II contributed 15.45% and PC III contributed 10.60% of total morphological variability (Table 3, Fig 2.). PCA revealed that plant height, leaf length, leaf width, number of tillers plant-1, number of leaves tiller, days to maturity, spike length, number of grains per spikelet, number of spikelets per spike and seed yield per plant were among the most important descriptors which accounted for more than half of the all phenotypic variation in the evaluated oat germplasm. Further, study of all these traits will help us in recommending best oat germplasm in future breeding programme. In the present study it was noticed that these grouping were not because of the collection and origination of genotypes from the same origin because there were found some genotypes which originated from same sites but were grouped in different clusters. Further study of all these traits will help us recommending better genotypes of oat in future breeding programmes. Similar results were also recorded by Iannucci *et al.,* (2011) followed Zaheri *et al.,* (2012), Souza and Sorrells (1991) and Tang *et al.,* (2014). All of these scientists and plant breeders found that the division of genotypes into different groups through PCA was just due to their agro morphological differences but not due to collection and origination sites of these genotypes

Conclusion

Through agro-morphological techniques valuable diversity was found among the genotypes for the traits of leaf length, days to maturity, leaf width, plant height, spike length, spikelets spike^{-1}, tillers plant^{-1} and seed yield plant^{-1} and most of the traits studied during the present study were found to be highly significant which shows that there is a great potential in these studied genotypes for the said traits, which can be used in future breeding programmes for selecting the promising genotypes.

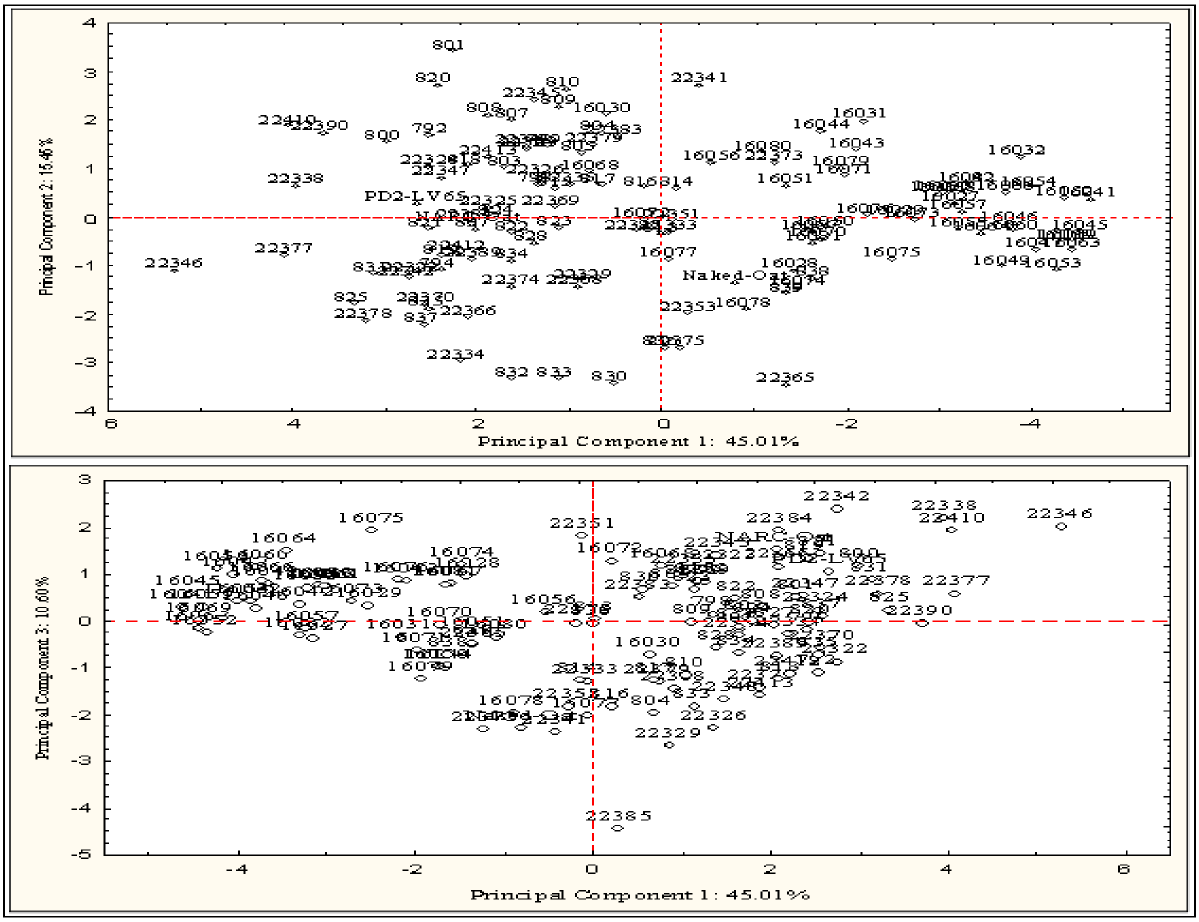

Fig. 3. Scatter plots showing the genetic relationships among 124 accessions of oat as revealed by first three principal components.

The present research study will be useful to provide morphological based genetic diversity knowledge of oat to various researchers, academia and genetic resources managers dealing with the crop.

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