Genetic Diversity of Soybean Yield Based on Cluster and Principal Component Analyses

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Author's contribution

The sole author designed, analyzed and interpreted and prepared the manuscript.

Original Research Article

ABSTRACT

The objective of this study was to determine analysis of variance, descriptive statistics, cluster and principle components analysis to understand their genetic diversity for ten soybean genotypes on seed yield (ten/fed.) during 2014 and 2015 seasons. Results for analysis of variance indicated highly significant genotypes and years and significant genotypes x years interaction for seed yield. The soybean genotypes Giza 111, Giza 30 and Crawford for seed yield (ton/fed.) were produced the highest mean values. The 2014 season had greater than 2015 season for seed yield (ton/fed.) in most soybean genotypes. Standard deviation, standard error, coefficient of variation and range for seed yield (ton/fed.) has noticed considerable genetic diversity in the ten genotypes. The ten soybean genotypes based on seed yield were grouped into four clusters using cluster analysis. The first, second and third clusters comprised of two genotypes i.e., (Giza 32 and Crawford), (Giza 30 and Giza 111) and (Hybrid 129 and Hybrid 132), respectively. While, the fourth cluster consisted of four genotypes viz., Giza 21, Giza 22, Giza 35 and Clark. The second cluster had recorded highest mean seed yield, followed by the first, fourth and third clusters. The principle components analysis showed that PC1 and PC2 having eigen values highest than unity explained 82.55% of total variability among soybean genotypes attributable to seed yield and accounted with values 67.77% and 14.78%, respectively. PC1 and PC2 noticed positive association with all and most genotypes, respectively. Biplot obtained from the PC1 and PC2 almost confirmed the cluster analysis grouped. The biplot displayed positive and strong relationships between most studied genotypes. Based on

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the cluster and principle components analysis, the wide diversity among the studied genotypes were found, their direct use as parents in hybridization programs to maximize the use of genetic diversity and expression of heterosis and develop high yielding soybean varieties.

1. INTRODUCTION

The soybean [*Glycine max* (L.) Merrill] is a leguminous annual crop belonging to the family Fabaceae. It is the one of the most important vegetal food source in the world and grows in tropical, subtropical and temperate climates. Soybean is an important source of high quality, inexpensive protein and oil. Soybean has the highest protein content (40 to 42%) among food crops and is second only to ground nut in terms of oil content (18 to 22%) comprising 85% unsaturated fatty acids and is free from cholesterol, among food legumes, so it highly desirable in the human diet [1,2].

Multivariate analysis based on Mahalonobis's D2 statistics (MDS), principal component analysis (PCA) and principal coordinate analysis (PCoA) are mostly used to evaluate the magnitude of genetic diversity among the germplasm [3]. Several authors suggested first principal component (PC) scores as input variables for the clustering process [4]. Hierarchical cluster analysis has been suggested for classifying entries of germplasm collections based on degree of similarity and dissimilarity [5].

Principal component analysis explains the contribution of the most important traits that account for the total genetic variability. Principal component analysis (PCA) has various applications such as the study of genetic divergence between genotypes which permits the identification and selection of the most promising genotypes for cultivation and improvement, besides using in evaluating the relative importance of characters in the total variation available among genotypes [6]. PCA is also used in studies on adaptability and stability, in which genotypes with a potential for planting under specific growing conditions can be identified [7].

Cluster analysis, on the other hand, allows the classification of individuals into groups in order to maximize their homogeneity within a group and show heterogeneity among groups. The hierarchical method interconnects samples through their associations producing a dendrogram in which similar samples are grouped together [8]. For this reason cluster analysis has been used efficiently to select genotypes and is complementary to PCA [6].

Principal component and cluster analysis procedures were found to be efficient to assess genetic diversity for seed yield in soybean and were reported by many research workers [9-13].

The goal of this present study had to assess the amount of genetic diversity in a collection of soybean genotypes grown in Egypt using cluster analysis and principal components based on yield so that superior genotypes could be used as parents in breeding programs.

2. MATERIALS AND METHODS

2.1 Plant Material

The research work pertaining to study the genetic diversity of seed yield by using cluster and principal component analysis in ten genotypes of soybean was conducted at Research and Production Station, National Research Centre, Al Nubaria District, Al Behaira Governorate during the two seasons 2014 and 2015. The ten genotypes were as follows: Giza 21, Giza 22, Giza 30, Giza 32, Giza 35, Giza 111, Clark, Crawford, Hybrid 129 and Hybrid 132. Ten soybean genotypes were assessed using a randomized complete block design with four replications during the two seasons. Each plot was consisted of six rows of 3 m long and 0.50 m wide. Hills were spaced at 0.50 m and thinned at one plant per hill. All the recommended cultural practices of soybean production in the area were done as usually. All guarded plants were harvested to measure seed yield of each plot and then transformed to the unit of kg/fed.

2.2 Statistical Analysis and Procedures

A combined analysis of variance was performed to determine the effect of genotype (G), season (S) and G × S interaction on phenotypic data

from trials in two years was computed according to the method given by Gomez and Gomez [14]. Cluster analysis was performed using K-means clustering and tree diagrams based on eucladian distances was developed by Ward's method using the program Cluster 3.0 Software [15]. The principal component analysis method explained by [16] was followed in the extraction of the components. The percentage variability explained by each component was determined [16,17]. The data had subjected to descriptive statistics and principal component analysis as well as biplot graphical display were performed using the StatistiXL 1.11 software for the ten genotypes of seed yield (ton/fed.) in soybean.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance for soybean yield at ten genotypes is presented in Table 1. Analysis of variance of the genotypes, season and replication within season exhibited highly significant (P < 0.01), while the genotypes x season interaction had significant (P < 0.05) for soybean yield trait. The results indicated that, the genotypes effect was the predominant source of variation, followed by season and genotypes x season effects. The large genotypes mean square showed that the influence of genotypic effects on soybean yield trait are more important than the mean differences in environmental (season) effects and by far greater is important than genotypes x season interaction. The highly significant of genotype term suggested that genetic differences exist among genotypical response. This suggests that, genotypes need thorough and repeated testing before they can be recommended for particular environments or set of environments (years). Highly significant

mean sum square (MS) due to years indicated that growing environments had profound influence on the expression of different yield of the soybean genotypes. Significant MS due to genotypes x season interaction indicated that, the genotypes considerably interacted with the environmental conditions. In case the variance due to genotypes x season interaction is found significant the analysis may be further preceded for estimating the stability parameters [18]. Atnaf et al. [19] and Amira et al. [20] stated that, the combined analysis of variance over environments explained soybean grain yield were highly significantly affected by environments, genotypes and genotype x environment interaction. There was a significant variation (p<0.001) in the seed yield response among genotypes and season, but genotypes x season had insignificant [21].

3.2 Descriptive Statistics

Six basic statistics were calculated for soybean yield at each genotypes during the two seasons and presented in Table 2. Mean of soybean yield ranged from 1.27 to 1.63 ton/fed. The genotype Giza 111 gave the highest mean (1.63 ton/fed.), followed by the genotypes Giza 30 (1.59 ton/fed.) and Crawford (1.55 ton/fed.). However, the genotypes Hybrid 132 (1.27 ton/fed.), Hybrid 129 (1.28 ton/fed.) and Giza 21 (1.39 ton/fed.) have produced the lowest means for soybean yield.

Results regarding descriptive statistics for seed yield (ton/fed.) have showed considerable genetic diversity in the studied genotypes. Differences in genotype responses to genotypic and environments were observed in the standard deviation, C.V. % and range for the seed yield (ton/fed.) in soybean. This closer magnitude suggested that the greater role of variability is

Table 1. Analysis of variance for soybean yield (ton/fed.) at ten genotypes during the two seasons in Egypt

Source of variation	Degree of freedom	Sum square	Mean of sum square	Computed F
Season (S)	1	0.037	0.037	18.775**
Replication within season	6	0.215	0.036	18.196**
Genotypes (G)	9	1.021	0.113	57.611**
S x G	9	0.045	0.005	2.523*
Pooled error	54	0.106	0.002	

*= significant at P < 0.05 and ** = significant at P < 0.01*

**Table 2. Basic statistics for soybean yield of ten genotypes during the two seasons**

Parameters Genotypes	Means	Standard deviation	Standard error	CV%	Minimum	Maximum	Range
Giza 21	1.39	0.07	0.03	5.04	1.30	1.49	0.19
Giza 22	1.43	0.08	0.03	5.59	1.31	1.54	0.23
Giza 30	1.59	0.06	0.02	3.77	1.51	1.68	0.17
Giza 32	1.49	0.07	0.02	4.70	1.41	1.56	0.15
Giza 35	1.42	0.06	0.02	4.23	1.34	1.49	0.15
Giza 111	1.63	0.10	0.04	6.13	1.50	1.81	0.31
Clark	1.43	0.09	0.03	6.29	1.30	1.55	0.25
Crawford	1.55	0.09	0.03	5.81	1.43	1.68	0.25
Hybrid 129	1.28	0.05	0.02	3.91	1.21	1.34	0.13
Hybrid 132	1.27	0.07	0.03	5.51	1.11	1.34	0.23

due to the genotypes and environment conditions. The descriptive statistics depend on the diversity of the environments in the experiments. If environments are quite diverse then these measures may not be very meaningful. However, if the range of environments could not be very restricted, then these support broad base inference [22]. Khan et al. [23] mentioned the results of quantitative traits indicated that there were wide variations (high degree of divergence) in 115 soybean genotypes.

The Fig. 1 showed that, the 2014 season had higher than the 2015 season of all studied genotypes for seed yield (ton/fed.) except Giza 21, Hybrid 129 and Hybrid 132 genotypes. The genotypes Giza 111, Giza 30 and Crawford were recorded the maximum mean values (1.67, 1.62 and 1.62 ton/fed., respectively) during the 2014 season. In normality the genotype Giza 111 is standard of seed yields for soybean in Egypt, which ranged from 1.5 to 1.7 ton/fed. Comparison of genotypes, the values of mean performances detected that, the Giza 111 had higher than the other genotypes for seed yield.

The differences in soybean yield for all studied genotypes are due to favorable and unfavorable environmental conditions. Since the interaction of genotype and environment had been signified, the application of compound variance analysis and attendances mean comparison based on calculated error was not sufficient.
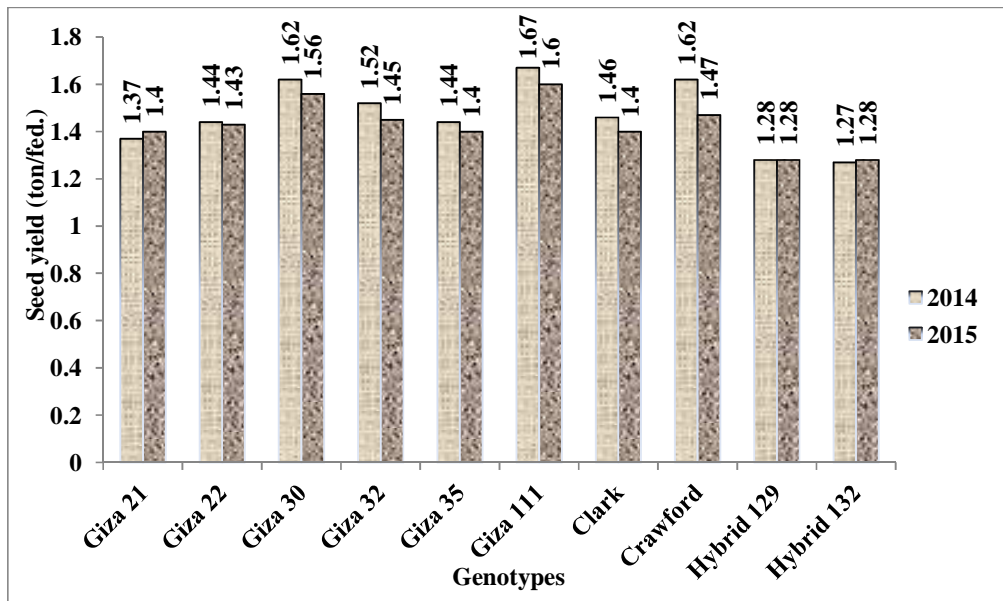
Fig. 1. Estimated mean of soybean grain yield during 2014 and 2015 seasons

3.3 Cluster Analysis

Cluster analysis was used as a tool to classify ten genotypes for soybean yield during 2014 and 2015 seasons. The cluster analysis technique differentiate the high yielding and low yielding environments into groups and sub-groups based on genotypic mean yield performance over environments. Cluster analysis based on seed yield (ton/fed) resulted into two main groups (A and B) and four cluster classes from genotypes under this study in soybean (Fig. 2). Group A was comprised of four genotypes and contain two clusters (clusters 1 and 2). However, six genotypes in group B had further sub-divided into 2 clusters (clusters 3 and 4). The first, second and third clusters comprised of two genotypes i.e., (Giza 32 and Crawford), (Giza 30 and Giza 111) and (Hybrid 129 and Hybrid 132), respectively. However, the fourth cluster consisted of four genotypes viz., Giza 21, Giza 22, Giza 35 and Clark. The distribution of genotypes in the study indicated that the geographical origin has bearing on clustering pattern. Zafar Iqbal, et al. [24], Sarkaut [25] and Khan et al. [23] reported that, the result of cluster analysis for seed yield showed genotypes soybean were divided into five, four and six groups, respectively. The results of cluster analysis suggested that there is variation among the genotypes for soybean yield [9]. Ghiday and Sentayehu [11] and Mahbub et al. [13] mentioned that, the cluster analysis grouped the 49 and 28 soybean genotypes into five different clusters, respectively. This indicates the presence of moderate diversity among the tested genotypes.

Mean of genotypes (Table 3) revealed that, the second cluster had recorded highest mean soybean yield, which could be marked for the selection of seed yield potential genotypes through further evaluation, followed by the first, fourth and third clusters. So, it is apparent that through cluster analysis it is possible to differentiate high, medium and low yielding years and/ or genotypes. Classifying the results of the cluster analysis identified majority genotypes suitable for sown and which confirm the results of the compared means yield. The results of cluster analysis suggested that there is genetic diversity among the genotypes for yield. Hybridization among these genotypes provided more possibility to having more genetic diversity and could be used in breeding programs to achieve maximum heterosis and yield improvement in soybean.
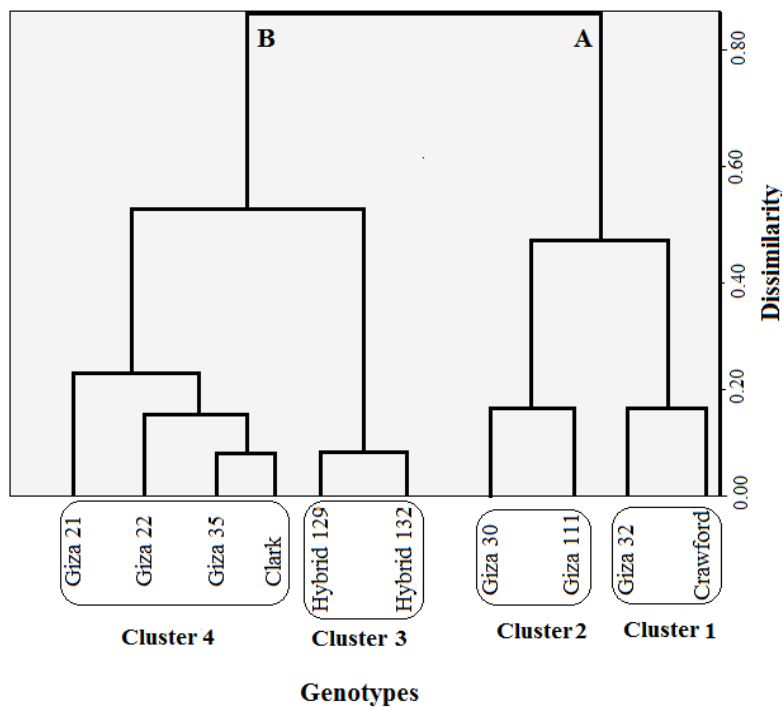

Fig. 2. Tree diagram for ten genotypes of soybean yield using hierarchical cluster analysis (Ward's method)

Table 3. Genotypes mean of soybean yield for each cluster formed by Ward´s clustering analyses

Clusters	No. of genotypes	Genotypes	Seed yield (ton/fed)
1	2	Giza 32 and Crawford	1.52
2	2	Giza 30 and Giza 111	1.61
3	2	Hybrid 129 and Hybrid 132	1.28
4	4	Giza 21, Giza 22, Giza 35 and Clark	1.42

3.4 Principle Components Analysis (PCA)

Important components analysis is used to limit the number of primary variables, to describe the total variation of a population and to explain the traits contribution to total variation [26]. In Table 4, eigenvalues, the percent of variance and cumulative variance from principal components analysis (PCA) for ten soybean genotypes at seed yield carried by them are given.

The eigenvalues are often used to determine how many factors to retain. The sum of the eigenvalues is usually equal to the number of variables. Eigen values can be considered in an index that affects the intensity of the principal components. If the characteristic value is lower than one, it explains that the explanatory power of principal components is lower than the average explanatory power of the original variables. Generally, if eigen value is higher than one, it can be used as an inclusion criterion. In this study, the first two main PCAs extracted had eigen value more than one (Eigen value >1). However, the other PCAs were recorded eigenvalues less than one (Eigen value < 1). The eigenvalues for PC1 and PC2 were 6.78 and 1.48, respectively. In the PCA three eigen values by Zafar Iqbal et al. [24], Aondover et al. [10] and

Khan et al. [23] and four eigen values by Vianna et al. [6] were greater than one eigenvalues for seed yield among the soybean genotypes.

The PC1 and PC2 contributed 67.77% and 14.78% of the total variability observed among ten genotypes of seed yield in soybean, respectively. So these two PCs were given due importance for further explanation. The accumulated variance contribution ratios of the PC1 and PC2 of symmetric variation were 82.55% of the variability among studied genotypes evaluated for seed yield in soybean. This result indicates that the yield variation of the soybean seed is mostly explained by PC1 and PC2 of symmetric variation. On the other hand, the remaining components contributed only 17.45% towards the total diversity for these soybean genotypes. The eigen values from PCA contributed 69.77% [24,10], 71.60% [6] and 71.11% [23] of the total variation for seed yield among the 139, 17, 11 and 115 genotypes of soybean, respectively. Kargar et al. [12] stated that, the three components explained 74.79% of traits variation with varimax rotation method under stress condition. Also they added that, the contribution of first, second and third components were 32.57%, 27.20 and 15.02

Table 4. Eigen values, the percent of variance and cumulative variance, eigenvectors obtained from PCA among ten soybean genotypes for seed yield during the two seasons

Value	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen value	6.78	1.48	0.86	0.50	0.22	0.12	0.04
% of variance	67.77	14.78	8.64	5.04	2.21	1.20	0.36
Cumulative %	67.77	82.55	91.19	96.23	98.44	99.64	100.00
Giza 21	0.25	-0.52	-0.30	0.30	-0.31	0.42	-0.05
Giza 22	0.33	-0.37	-0.11	-0.27	0.01	0.15	-0.15
Giza 30	0.31	0.24	-0.52	0.05	0.01	-0.49	-0.13
Giza 32	**0.36**	0.16	-0.07	0.22	-0.41	-0.34	0.36
Giza 35	0.34	0.13	-0.24	0.11	0.78	0.19	0.01
Giza 111	**0.35**	-0.14	-0.09	-0.54	-0.08	-0.08	0.05
Clark	**0.35**	0.14	0.35	0.00	0.06	0.26	0.68
Crawford	0.21	**0.65**	0.02	-0.19	-0.32	0.48	-0.39
Hybrid 129	0.32	-0.01	0.38	0.61	0.02	-0.06	-0.37
Hybrid 132	0.31	-0.18	0.54	-0.27	0.08	-0.32	-0.28

respectively. The results of the principal component analysis revealed that five principal components (PC1 to PC5) accounted nearly for 79.06% of the total variation [11]. Mahbub et al. [13] mentioned that, the principle component analysis yielded four of the eigen values above unity accounted for 91.55% of the total variation. The first three principles accounted for 83.23% of the total variation.

In Table 4, the eigenvectors that represent the obtained eigenvalues indicated that force and direction of the effect of the particular genotypes on PC1 and PC2. The PC1 and PC2 have positive association with all studied genotypes except Giza 21, Giza 22, Giza 111, Hybrid 129 and Hybrid 132 in PC2. Hence, the major contributing genotypes for the genetic diversity in PC1 were Giza 32, Giza 111 and Crawford genotypes and Crawford genotypes in PC2. These results indicating that, the PC1 and PC2 reflected the yield potential of each genotype from these genotypes through some yield component aspects. Therefore, separation of these genotypes can be performed through a diagram, which forms one of the vectors of this component. Zafar Iqbal et al. [24] noticed that quantitative traits contributed positively to first three principal components and hence these could be given considerable importance for the genetic material under investigation. The first two principle components were positive and negative eigenvector values for seed yield in soybean genotypes [23].

3.5 Biplot

The first two PCs were plotted to observe the relationship between ten genotypes i.e., Giza 21 (1), Giza 22 (2), Giza 30 (3), Giza 32 (4), Giza 35 (5), Giza 111 (6), Clark (7), Crawford (8), Hybrid 129 (9) and Hybrid 132 (10) of soybean yield are shown in (Fig. 3A). PCA reflects the importance of the largest contributor to the total variation at each axis of differentiation [27]. PCA biplot (Fig. 3A) based on the PC1 and PC2 showed genetically different ten genotypes by the pattern on scattering. The dispersion of genotypes in biplot indicated the presence of fair amount of genetic diversity. The genotypes closer to each other had little or no differences with respect to seed yield. Biplot obtained from the PC1 and PC2 almost confirmed the cluster analysis grouped. Genotypes far from the origin exhibited more variability for seed yield and could be

utilized as diverse parents in broadening the genetic base of soybean through hybridization. Vianna et al. [6] mentioned that from the PCA biplot, most of the genotypes identified by the PCA were grouped in the same cluster, indicating a similarity between them. Therefore, based on the homogeneity existing in the groups, it was possible to make a second selection focusing on seed yield.

The PC1 and PC2 contributing 82.55% of the total variance 67.77% of the variability comes from the X-axis and 14.78% of additional original variability from the Y-axis. The two first PCs were plotted to observe relationships between the ten genotypes and each principle component of soybean yield by redrawing the contour with estimated coefficients for the corresponding principal component. The correlation coefficients among the genotypes indicate that the plot currently shows the relationship among the genotypes that had relatively large loading on both PCA1 and PCA2 axes. The most prominent relations shown in (Fig. 3A), and a strong positive association were found for Giza 22 with Giza 21, Giza 111 and 132; for Giza 35 with Giza 30, Giza 32, Giza 111 and Clark; for Clark with Giza 32, Giza 111, Hybrid 129 and Hybrid 132; for Giza 30 with Giza 32, Giza 111 and Hybrid 129; for Hybrid 132 with Giza 111 and Hybrid 129 and for Giza 32 with Giza 111 genotypes. These results suggest that it is possible to discriminate between these genotypes based on seed yield in soybean. The discriminatory power of the genotypes in each principal component is measured by the correlation between each genotype and a principal component. Principal component analysis is a technique that is useful for the description of the relations that occur between genotypes for seed yield in soybean. The obtained non correlated variables may be used for further analysis, where the assumption of no co-linearity of variables is required.

3.6 Scree Plot

The Scree plot (Fig. 3B) of the PCA for ten genotypes on seed yield in soybean during the two seasons demonstrated that the first two eigenvalues correspond to the whole percentage of the variance in the dataset. Also, notice that there is break in the plot that separates the meaningful components from the trivial components. Most researchers would agree that components 1 and 2 are probably meaningful.

(A)   **(B)**
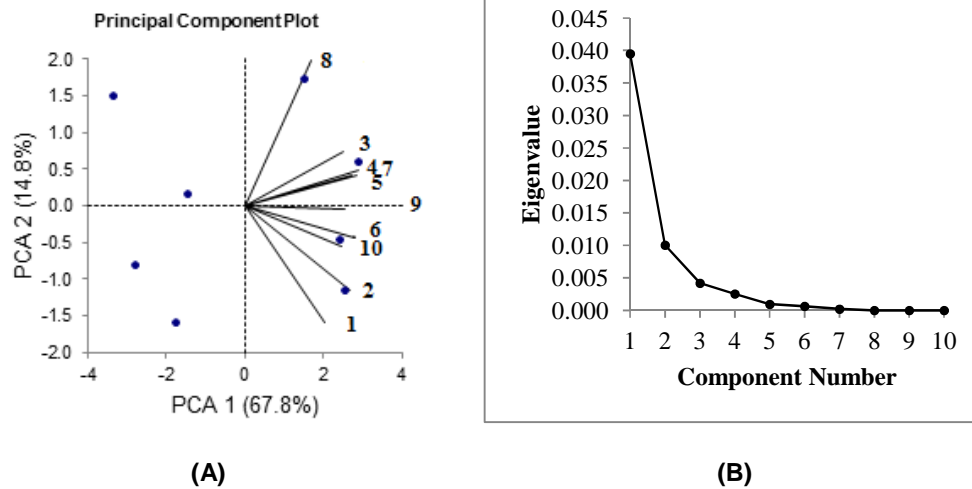
Fig. 3. (A) Plot of PC1 and PC2 showing the contribution and relationship of 10 genotypes for seed yield during 2014 and 2015 seasons, and (B) scree plot of PCA between eigen values and number of component number

4. CONCLUSIONS

The analysis of variance, descriptive statistics, cluster analysis and principle components analysis detected that the wide genetic diversity among the studied genotypes for seed yield. Biplot obtained from two first components confirmed the cluster analysis grouped. These results indicate the presence of excellent opportunity to bring about improvement soybean yield through wide hybridization by crossing genotypes in farthest clusters.

COMPETING INTERESTS

Author has declared that no competing interests exist.

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