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Assessing genetic diversity of exotic lines of soybean based on D² and principal component analysis

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Abstract

The existing soybean genotypes are having narrow genetic base, the incorporation of new sources of genes is indispensable when searching for alleles that contribute to a greater diversity of varieties. The objective of the present study is to determine cluster and Principal Component Analysis to understand the genetic diversity of 50 exotic lines of soybean (including two checks, JS 20-98 and JS 20-34) on seed yield during the 2019 *Kharif* season. Fifty soybean genotypes were grouped into five clusters. The maximum percentage of contribution towards genetic divergence was shown by the number of seeds per plant and the minimum contribution was shown by the number of primary branches per plant. Cluster I showed a maximum intra-cluster D² value of 231.14 while a maximum inter-cluster distance was observed between cluster IV and cluster V. The principal components analysis showed that PC1, PC2, PC3, PC4 and PC5 had Eigen values higher than unity and explained 83.49% of the total variability among soybean genotypes attributable to seed yield. Based on the cluster and principal components analysis, wide diversity among AGS 48, EC 396055, EC 389153, EC 114572, JS 20-34(C) and EC 23001B lines were found, their direct use as parents in hybridization programs to maximize the use of genetic diversity and to expression of heterosis and develop high yielding soybean varieties.

Keywords: Soybean, principal component analysis, D², diversity, cluster analysis

Introduction

Soybean [*Glycine max* (L.) Merrill] is one of the leading oilseed crops grown for its edible oil and protein in India as well as the world over. At present, soybean ranks first in the world and third in India among the major oilseed crops (Anonymous, 2012) [1] after groundnut and rapeseed-mustard. Soybean seeds are packed with 40% protein (glycine, tryptophan, and lysine) (Quayam *et al.*, 1985) [2], 20% oil, low in fat with no cholesterol, essential heart-friendly omega-3 fatty acids, vitamins A, B, D, 25-30% carbohydrates and 5% ash. In 2019–20, in India, soybean production reached 13.63 mt from an area of 11.34 mha with a productivity of 1200 kg/ha (Directors Report, IISR, 2020) [3] and 6.73 mt production from an area of 5.516 mha with a productivity of 1285 kg/ha in Madhya Pradesh (Directors Report, IISR, 2020) [3]. The country achieved a maximum production of 14.67 mt of soybean during *Kharif* 2012. However, there has been very modest development over the years, and there is a need to extend the genetic foundation for setting new yield records. Nevertheless, it's time-consuming to work with a huge data collection containing a large number of variables. To explore the patterns of variation among germplasm collections, multivariate analysis such as Principal Component Analysis (PCA) and cluster analysis is the most preferred technique for estimating genetic variability. Principal Component Analysis (PCA) allows us to see the correlations between significant agronomic parameters visually, assess varieties based on numerous attributes, discover potential breeding sources, and suggest possible selection techniques. Genetic diversity is essential for plant survival in nature and for agricultural enhancement. Due to higher diversity in segregating generations, which may be exploited for improvement, genetic divergence amongst parents plays a critical role in cultivar development (Nimbalkar *et al.*, 2017) [4]. The Mahalanobis D² statistic is a useful tool for calculating genetic divergence between genotypes and relating clustering patterns to geographic origin. The genetic distance had a significant influence on the efficient selection of parents for the hybridization programme. Mating of diverse parents aids in the isolation of better yielding recombinant progenies. The purpose of this study was to assess genetic diversity among superior genotypes and their potential for use in soybean breeding strategies.

Materials and Methods

During the *Kharif* season of 2019, the experiment was conducted at the Seed Breeding Farm, Department of Plant Breeding and Genetics, JNKVV, Jabalpur. The experimental materials consisted of 50 genotypes including two national checks. The experiment was set up in a randomized complete block design (RCBD) with three replications, with a plot size of 1.2m x 3.0m and row to row and plant to plant distances of 40 cm and 7cm, respectively. To determine the genetic divergence across populations, Mahalanobis generalized distance D^2 (1936) [5] was used to examine the data obtained on various features. Tocher's approach, as described by Rao (1952) [6], was used to group the populations into several clusters. Ward's approach was used to create tree diagrams based on Euclidian distances, and cluster analysis was conducted using clustering. The components were extracted using the Principal Component Analysis approach by using the Statistix 11.11 programme. The data was treated with descriptive statistics and principal component analysis.

Results and Discussion

Cluster Analysis

The analysis of variance showed highly significant differences among the population for all the 11 characters studied. The trait number of seeds per plant (32.73%) contributed most towards genetic divergence followed by days to maturity (27.84%), days to flower initiation (11.92%), biological yield (11.76%), pods per plant (10.04%), 100 seed weight (4.49%) whereas magnitude of genetic divergence was less than one percent for plant height (0.9%), seed yield per plant (0.24%), primary branches per plant (0.08%) as described in table 1. Neelima *et al.* (2017) [7] showed similar findings for 100 seed weight, seeds per plant, days to flower initiation, and days to maturity. Mishra (2016) [8] for seed per plant and Mishra (2015) [9] for 100 seed weight, Joshi (2018) [10] for days to maturity, plant height, pods per plant, and biological yield per plant.

Based on D^2 values, 50 genotypes were grouped into 5

clusters using Tocher's method. Marconato (2016) [11] categorized 93 genotypes into 8 clusters, Mahesh (2017) [12] grouped 40 genotypes into 6 clusters and Yadav (2017) [13] grouped 29 clusters into 7 clusters all in accord with the current study. Cluster I is only polygenotypic with 46 genotypes. The remaining four clusters have only one genotype each. Cluster I showed a maximum intra-cluster D^2 value (231.14), while other clusters were mono-genotypic with no intra-cluster divergence. The highest inter-cluster divergence was observed between genotypes of clusters IV and V (2170.93) whereas least inter-cluster divergence was observed between genotypes of clusters II and III (84.50). Neelima (2017) [7], Bellaloui *et al.* (2017) [14], and Joshi *et al.* (2018) [10] all found similar findings.

Principal Components Analysis (PCA)

Out of eleven, only five principal components (PCs) exhibited more than 1.00 Eigenvalue and showed about 83.49% variability among the traits studied. Hence these five principal components were given due importance for further explanation. The PC1 had the highest variability (31.88%). Scree plot had laid out between eigenvalue and principal component showed total variation be 31.889 (PC1) followed by 15.74% (PC2), 14.24% (PC3), 11.95% (PC4) and 9.66 (PC5). The total variation of five PCs was recorded to be 83.49%. Semi curve line obtained after the fifth PC with little variation observed in each PC indicated that maximum variation was found in PC1; therefore, the selection of lines for characters under PC1 may be desirable, given in table 3. El-Hashash (2016) [15] showed similar findings for seed yield per plant, pods per plant, the quantity of seed per plant and harvest index. Concerning pods per plant and seed yield per plant, consider Manav *et al.* (2017) [16]. Plant height, primary branches per plant, nodes per plant, pods per plant, pods per plant, number of seeds per plant, biological yield per plant, and seed yield per plant have all been reported by Dubey *et al.* (2018) [17], Uikay *et al.* (2021) [18] for pod traits, Verma *et al.* (2021) [19] for seed yield/plant.

Table 1: Percent contribution of characters towards divergence in 50 genotypes of soybean

S. No	Characters	Times Ranked 1 st	% Contribution of traits towards divergence
1	Number of seed per plant	401	32.73%
2	Days to maturity	341	27.84%
3	Days to flower initiation	146	11.92%
4	Biological yield	144	11.76%
5	Pods per plant	123	10.04%
6	100 seed weight	55	4.49%
7	Plant height	11	0.9%
8	Seed yield per plant	03	0.24%
9	Primary branches per plant	01	0.08%
10	Number of nodes per plant	00	00
11	Harvest Index	00	00

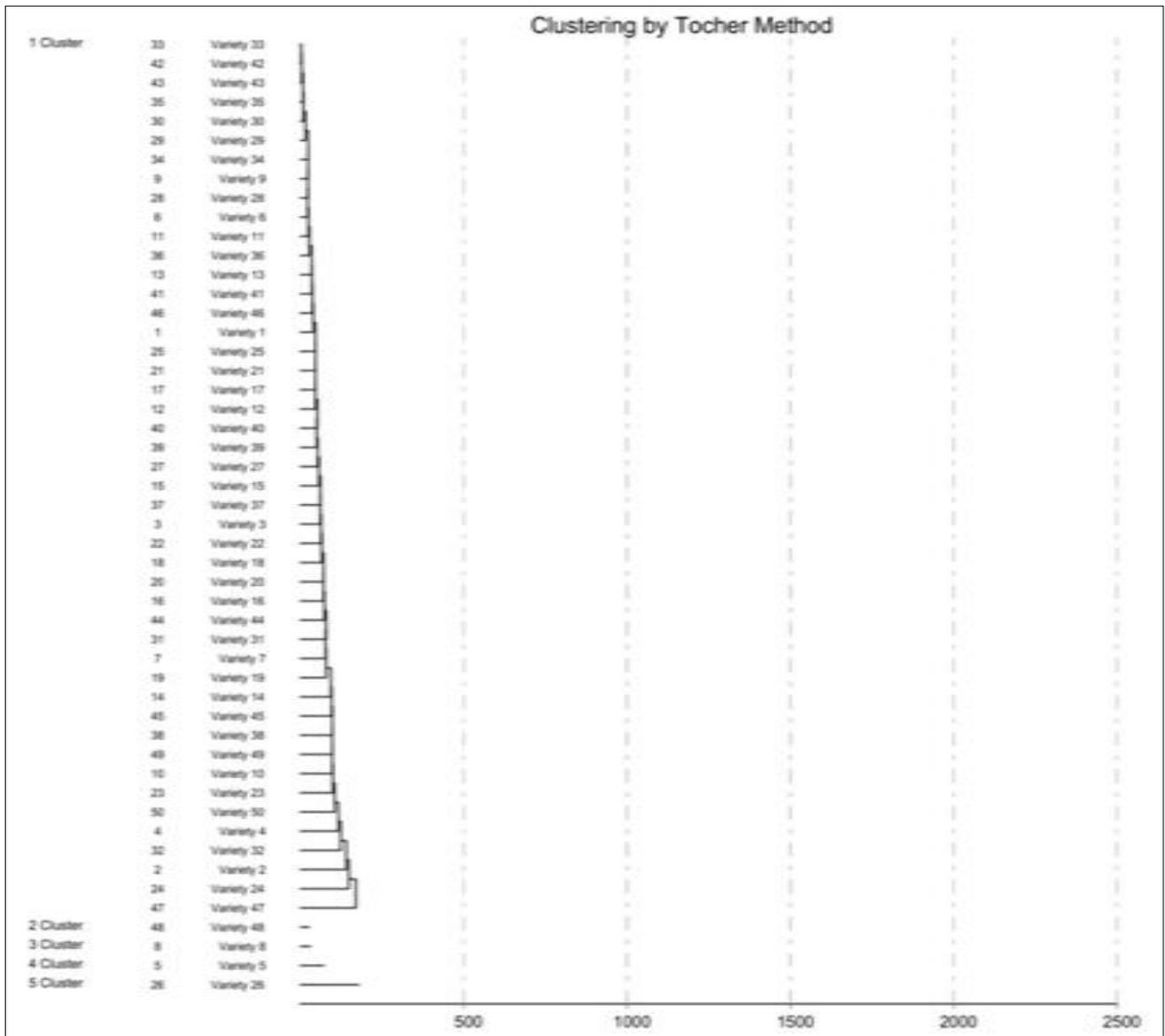


Fig 1: Clustering by tocher's method

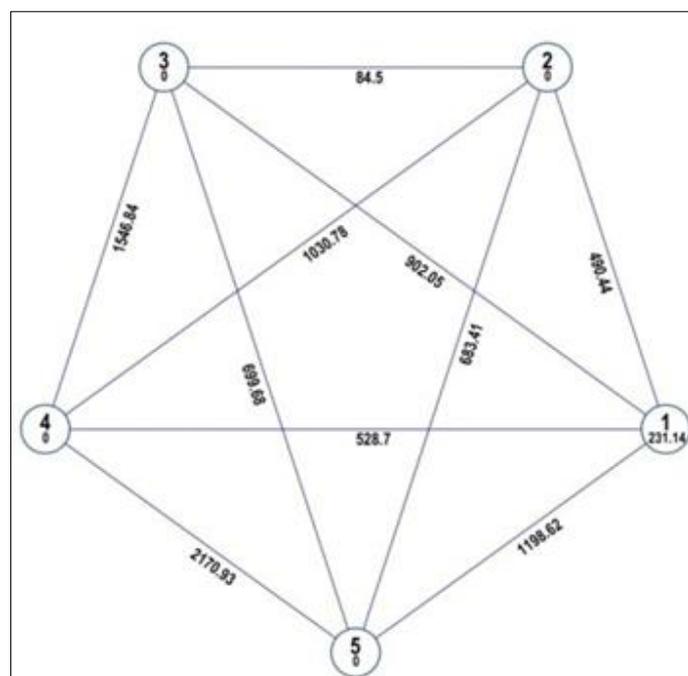


Fig 2: Mahalanobis euclidean distance

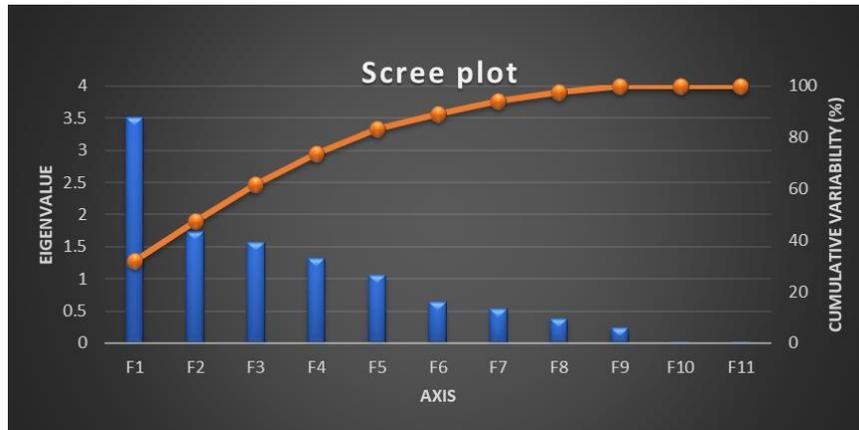


Fig 3: Scree plot

Table 2: Principal components for eleven yield contributing traits of soybean genotypes

Traits	Principal Components				
	PC1	PC2	PC3	PC4	PC5
Days to flower initiation	0.339	-0.591	0.498	-0.228	-0.086
Days to maturity	0.430	-0.293	0.286	-0.496	0.287
Plant height	0.396	0.150	0.039	-0.501	0.587
No. of primary branches/plant	-0.054	0.534	0.185	0.370	0.543
No. of nodes/plant	0.230	-0.124	0.774	0.198	-0.277
No. of pods/plant	0.596	-0.498	-0.345	0.248	0.260
No. of seeds/plant	0.861	-0.191	-0.323	0.249	-0.057
100 seed weight	0.422	0.719	0.373	-0.187	-0.166
Biological yield/plant	0.601	0.296	-0.391	-0.411	-0.331
Harvest index	0.707	0.056	0.270	0.506	0.132
Seed yield/plant	0.927	0.286	-0.113	0.075	-0.176

Table 3: Interpretation of rotated component matrix for the traits having values >0.5 in each PCs

Characters	PC 1	PC 2	PC 3	PC 4	PC 5
	Number of pods per plant	Number of primary branches per plant	No. of nodes/plant	Harvest Index	Plant height
Number of seeds per plant	100 seed weight			Number of primary branches per plant	
Biological yield per plant					
Harvest Index					
Seed yield per plant					

Conclusion

The considerable genetic variability among the tested genotypes for seed yield was exhibited using cluster analysis and principal components analysis. These findings suggest that there is a good chance of increasing soybean production through extensive hybridization by crossing genotypes in the distant clusters. Based on the present data, 50 genotypes may be classified into five clusters. AGS 48, EC 396055, EC 389153, EC 114572, JS 20-34(C), and EC 23001B were identified as putative genotypes based on principal component analysis, with number of pods per plant, number of seeds per plant, seed yield per plant, biological yield per plant, plant height at maturity, number of primary branches per plant, harvest index, and 100 seed weight identified as important traits. In the future, these lines and attributes may be used in soybean breeding programs to create superior genotypes by hybridization or direct selection.

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