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Clustering analysis of soybean germplasm (*Glycine max* L. Merrill)

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Abstract
The present investigation was carried out to determine the genetic diversity of 273 soybean germplasm. Cluster analysis was performed for quantitative traits in soybean. Based on cluster analysis, the genotypes were grouped into 7 clusters of which cluster IV is the largest clusters consisting of sixty-seven genotypes while cluster VI was the smallest with five genotypes. The maximum intra-cluster distance was obtained for cluster VI (5.415) consisting of 67 genotypes. The highest inter cluster distance values were observed between cluster VI and III (8.096). The minimum intra-cluster distance (2.491) was shown by cluster II. The intra cluster distance varied from 2.49 to 5.41. The highest inter cluster distance values were observed between cluster VI and III. The lowest inter-cluster D^2 value was found between cluster IV and III (2.471). The inter cluster distance varied from 2.471 to 8.096. All the intercluster distances were larger than the intra-cluster distance indicating the presence of wider diversity among genotypes of distance groups. These studied which will allow breeders further improvement in the varieties for quantitative traits through hybridization.

Keywords: Diversity, soybean germplasm, cluster analysis, quantitative

Introduction

Soybean (*Glycine max* L. Merrill) is a premier oilseed crop of the India as well as the world with high nutritive value, providing 40 per cent protein and 20 per cent edible oil besides minerals and vitamins. It belongs to the family Leguminosae and is a self-pollinated crop having chromosome number 2n=40. Soybean could be regarded as an ideal food for the people of poor and some developing countries as it contains high quality of protein and reasonable quantity of oil as a source of energy.

Multivariate analysis acts as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels. The present study aimed to select suitable highly diverse genotypes as parents for improvement programs through heterotic breeding. More diverse the parents, the higher are the chances of obtaining more amounts of heterotic expression so that breeders are always focus and search diverse parent for hybridization program.

Cluster analysis and Principal Component Analysis (PCA) are the tools available for summarizing and describing the inherent genetic variation in crop genotypes. This technique helps in identification of traits that help in distinguishing selected genotypes based on similarities in one or more traits and classify the genotypes into separate groups (Ariyo, 1987 and Nair *et al.*, 1998) [2, 5].

Materials and Methods

The experimental material of the present study was content 273 germplasm lines of soybean including three checks obtained from AICRP on soybean, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishvavidyalaya, Raipur, Chhattisgarh, India during *kharif* 2015 and rabi 2015-16 and *kharif* 2016 were grown in an augmented design and divided into six blocks. In augmented design, each entry was grown in single row of 2 m length, spaced at 30 cm between rows and 20 cm between plants.

All the recommended package of practices was adopted to raise the normal crop. The crop was sown in the field on 27th June; 2015.

The observations were recorded on thirteen quantitative traits namely, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, pod bearing length

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(cm), number of pod bearing node, number of pods per plant, number of seeds per pod, number of seed per plant, 100-seed weight (g) Seed yield per plant (g), protein content (on moisture free basis) and oil content. Agglomerative Hierarchical Clustering (AHC) was done by using Pearson Correlation Coefficient and Unweight Pair Group Method with Arithmetic Mean (UPGMA) as Agglomeration method by XLSTAT 2014 version 5.03.

Result and Discussions
Cluster analysis is commonly used to study genetic diversity and for forming core subset for grouping accessions with similar characteristics into one homogenous category. The important objective of any plant researcher is to identify an optimum number of plant traits which are sufficient to explain the maximum variability in the crop growth from sowing to harvest.

Cluster analysis among 273 genotypes of soybean was studied and their clustering pattern on the basis of quantitative characters has been presented in Table 1.

The 273 genotypes of soybean for seed yield and their components were grouped into 7 clusters. The highest number of genotypes appeared in cluster IV, which included 67 genotypes namely JS-335, Bragg, JS-80-21, Indira soya-9, Birsa soya 1, PK-10-24, MACS-58, SL-599, JS-15-14, JS-79-263, JS-80-54, SL-328, PB-1, EC-389179, EC-391167, TS-99-76, PS-564, Shilajeet, PK-317, PS-1024, PK-515, Himso-15-63, KB-165, TS-128-5, NRC-56, TS-148, SL-518, NRC-57, MACS-756, DS-98-14, PK-13-14, JS(SH)96-31, MACS-7 DS-228, MACS-693, MACS-694, PK-12-25, JS(SH)94-21, PK-327, EC-391181, SL-517, B-5-97-12, Himso-15-21, MAUS-144, PS-1476, MAUS-145, MAUS-71, RAUS-5, MAUS-61-2, RSC-10-01, RSC-10-17, NRC-2012-E-2-10-1-1, NRC-2012-E-2-6-4-1, NRC-2006-A-23, NRC-2007-A-3-1, NRC-2006-A-7, NRC-2006-I-1, Cat-1368, EC-107416, GP-393, HIMSO-175, JS-20-47, JS-20-47, NRC-2014-M-2-1-3, NRC-2014-K-3-9-1-3-2, NRC-2014-Q-1-9-1-2 and NRC-2014-M-2-1-5.

The second group which had highest number of genotypes appeared in cluster III, which included 59 genotypes are NRC-2, MAUS-47, PS-10-92, PK-416, NRC-2012-F-1-18-1, NRC-2012-M-127-3, NRC-2012-M-127-2-4, NRC-2012-12-1-9, NRC-2011-C-5-5, NRC-2011-B-1-8-1-43, NRC-2011-1-14-10, NRC-2011-F-1-15, NRC-2011-G-3-13, NRC-2011-E-2-1-9-1, NRC-2008-G-1-12, NRC-2008-B-3-17, NRC-2008-D-5-3, NRC-2008-F-1, NRC-2008-B-1-9-1, NRC-2008-G-1-8-2, NRC-2008-B-2-6-2, NRC-2007-A-2-3, NRC-2008-G-2-6, NRC-2008-J-8-1-1, NRC-2009-2, NRC-2009-3, NRC-2009-5, NRC-2009-8, NRC-2009-10, NRC-2009-11, NRC-2009-12, NRC-2009-13, NRC-2009-14, NRC-2006-F-2-2, NRC-2006-M-6, NRC-2007-B-1-19, NRC-2007-B-2-4, NRC-2007-4-1-36, NRC-95-02-03, VS-2157, VS-495, VS-2002-9,

VS-2004-9, VS-2004-18, VS-2004-13, VS-2173, VLS-47, VS-2005-22, NRC-95-03-01, AMS-148, Cat-2502, EC-100027, EC-125738, EC-232019, EC-389148, EC-389148, EC-685256, GP-448 and JS-20-81.

Cluster VII included 39 genotypes namely RSC-10-04, RSC-10-05, RSC-10-30, NRC-2008-B-3-21-1, NRC-2008-B-2-2-2, NRC-2009-1, NRC-2009-4, NRC-2007-C-1-5, NRC-2007-12-7-2, NRC-2007-1-3, NRC-95-05-03, NRC-2006-4-1-2, NRC-2006-4-13, NRC-2006-J-7, VLS-2, VS-2005-28, VS-2005-37, NRC-95-03-03, NRC-95-03-02, NRC-96-05-03, NRC-95-08-01, AMS-60-2-34, AMS-MB-5-18, Cat-2722, Cat-3299, EC-15966, EC-34078, EC-685250, EC-685255, JS-20-42, JS-20-78, NRC-2014-G-1-2-1-5, NRC-2014-N-3-10-4-4-1, NRC-2014-K-1-7-2-3-2, NRC-2014-P-8-2-3-1-1, NRC-2014-R-1-5-1-3-3, NRC-2014-N-2-7-3-1-1, JS-20-71 and JS-20-79.

Cluster II included 38 genotypes namely NRC-20, PK-472, JS-93-05, NRC-2012-G-J-14-1, NRC-2012-E-2-5-1-2, NRC-2012-C-4-13-2, NRC-2012-A-3-2-1-1, NRC-2012-F-1-18-3, NRC-2011-E-4-11-1-1, NRC-2009-15, AMS-39-2-1, EC-685243, JS-20-72, JSM-227, MAUS-703, PI-283327, PRAB-1, Delhi-3, Delhi-4, Delhi-6, Delhi-7, Delhi-7, Delhi-9, Delhi-10, Delhi-13, Delhi-14, Delhi-14, Delhi-15, Delhi-16, Delhi-18, Delhi-19, Delhi-23, Delhi-24, Delhi-25, Delhi-26, NRC-95-10-03, JS-20-30, JS-20-74 and JS-20-87.

Cluster V included 33 genotypes namely PK-10-29, JS-92-14, PK-12-41, JS-95-60, JS-98-21, MMS-36, EC-34117, B-458, JS-90-41, JS-18-13, JS-82-180, RSC-10-02, RSC-10-16, RSC-10-18, RSC-10-29, RSC-10-46, NRC-2012-B-1-8-1-4-1-1, NRC-2012-G-3-16-2, NRC-2012-F-25-4, NRC-2012-M-127-1, NRC-2012-4-1-2-2-5, NRC-2012-J-2-2-1, NRC-2012-I-1-6, NRC-2011-A-3-7, NRC-2011-A-3-10, NRC-2011-C-N-11, NRC-2011-F-1-23, NRC-2011-A-3-22, NRC-2011-A-3-6, NRC-2009-6, NRC-2006-C-7, NRC-2007-L-1-5 and NRC-2007-J-3.

Cluster I included 32 genotypes namely RSC-10-15, JSM-117-4, NRC-2008-F-6, NRC-2009-9, VS-2004-14, VS-2005-19, VS-2005-21, NRC-95-06-03, NRC-96-02-02, AMS-50-B, AMS-115, Cat-1113, EC-2581, EC-39491, EC-118443, EC-391336, JS-20-35, JS-20-55, JS-20-59, JS-20-74, JS-20-76, JS-20-83, JSM-224, JSM-258, Delhi-1, Delhi-2, Delhi-5, Delhi-11, Delhi-12, Delhi-20,Delhi-21 and Delhi-2

The lowest group Cluster VI included 5 genotypes namely-97-52, NRC-2014-0-4-10-1-1-1, NRC-2014-0-4-10-1-1-1, NRC-2014-0-4-10-1-2-2, and NRC-2014-B-1-8-1-5-4-1.

The results were supported by the findings of Shrivastava *et al*. (2001) [9], Vart *et al*. (2002) [13], Sihag *et al*. (2004) [10], Singh *et al*. (2007) [11], Patil *et al*. (2011) [6], Tyagi and Sethi (2011) [12], Venkateswarlu and Sirisha (2011) [14], Reni and Rao (2013) [8], Adsul and Monpara (2014) [1], Malek *et al*. (2014) [3], Pushpendra *et al*. (2016) and Mili *et al*. (2017) [4, 7].

Table 1: Genotypes included in different clusters based on cluster analysis for seed yield and its contributing traits of soybean genotypes

Cluster Number	No. of genotypes	Name of genotypes
Cluster I	32	RSC-10-15, JSM-117-4, NRC-2008-F-6, NRC-2009-9, VS-2004-14, VS-2005-19, VS-2005-21, NRC-95-06-03, NRC-96-02-02, AMS-50-B, AMS-115, Cat-1113, EC-2581, EC-39491, EC-118443, EC-391336, JS-20-35, JS-20-55, JS-20-59, JS-20-74, JS-20-76, JS-20-83, JSM-224, JSM-258, Delhi-1, Delhi-2, Delhi-5, Delhi-11, Delhi-12, Delhi-20,Delhi-21 and Delhi-22
Cluster II	38	NRC-20, PK-472, JS-93-05, NRC-2012-G-J-14-1, NRC-2012-E-2-5-1-2, NRC-2012-C-4-13-2, NRC-2012-A-3-2-1-1, NRC-2012-F-1-18-3, NRC-2011-E-4-11-1-1, NRC-2009-15, AMS-39-2-1, EC-685243, JS-20-72, JSM-227, MAUS-703, PI-283327, PRAB-1, Delhi-3, Delhi-4, Delhi-6, Delhi-7, Delhi-7, Delhi-9, Delhi-10, Delhi-13, Delhi-14, Delhi-14, Delhi-15, Delhi-16, Delhi-18, Delhi-19, Delhi-23, Delhi-24, Delhi-25, Delhi-26, NRC-95-10-03, JS-20-30, JS-20-74 and JS-20-87

Cluster III	59	NRC-2, MAUS-47, PS-10-92, PK-416, NRC-2012-F-1-18-1, NRC-2012-M-127-3, NRC-2012-M-127-2-4, NRC-2012-12-1-9, NRC-2011-C-5-5, NRC-2011-B-1-8-1-43, NRC-2011-1-14-10, NRC-2011-F-1-15, NRC-2011-G-3-13, NRC-2011-E-2-1-9-1, NRC-2008-G-1-12, NRC-2008-B-3-17, NRC-2008-D-5-3, NRC-2008-F-1, NRC-2008-B-1-9-1, NRC-2008-G-1-8-2, NRC-2008-B-2-6-2, NRC-2007-A-2-3, NRC-2008-G-2-6, NRC-2008-J-8-1-1, NRC-2009-2, NRC-2009-3, NRC-2009-5, NRC-2009-8, NRC-2009-10, NRC-2009-11, NRC-2009-12, NRC-2009-13, NRC-2009-14, NRC-2006-F-2-2, NRC-2006-M-6, NRC-2007-B-1-19, NRC-2007-B-2-4, NRC-2007-4-1-36, NRC-95-02-03, VS-2157, VS-495, VS-2002-9, VS-2004-9, VS-2004-18, VS-2004-13, VS-2173, VLS-47, VS-2005-22, NRC-95-03-01, AMS-148, Cat-2502, EC-100027, EC-125738, EC-232019, EC-389148, EC-389148, EC-685256, GP-448 and JS-20-81
Cluster IV	67	JS-335, Bragg, JS-80-21, Indira soya-9, Birsa soya 1, PK-10-24, MACS-58, SL-599, JS-15-14, JS-79-263, JS-80-54, SL-328, PB-1, EC-389179, EC-391167, TS-99-76, PS-564, Shilajeet, PK-317, PS-1024, PK-515, Himso-15-63, KB-165, TS-128-5, NRC-56, TS-148, SL-518, NRC-57, MACS-756, DS-98-14, PK-13-14, JS(SH)96-31, MACS-798, DS-228, MACS-693, MACS-694, PK-12-25, JS(SH)94-21, PK-327, EC-391181, SL-517, B-5-97-12, Himso-15-21, MAUS-144, PS-1476, MAUS-145, MAUS-71, RAUS-5, MAUS-61-2, RSC-10-01, RSC-10-17, NRC-2012-E-2-10-1-1, NRC-2012-E-2-6-4-1, NRC-2006-A-23, NRC-2007-A-3-1, NRC-2006-A-7, NRC-2006-I-1, Cat-1368, EC-107416, GP-393, HIMSO-175, JS-20-47, JS-20-47, NRC-2014-M-2-1-3, NRC-2014-K-3-9-1-3-2, NRC-2014-Q-1-9-1-2 and NRC-2014-M-2-1-5
Cluster V	33	PK-10-29, JS-92-14, PK-12-41, JS-95-60, JS-98-21, MMS-36, EC-34117, B-458, JS-90-41, JS-18-13, JS-82-180, RSC-10-02, RSC-10-16, RSC-10-18, RSC-10-29, RSC-10-46, NRC-2012-B-1-8-1-4-1-1, NRC-2012-G-3-16-2, NRC-2012-F-25-4, NRC-2012-M-127-1, NRC-2012-4-1-2-2-5, NRC-2012-J-2-2-1, NRC-2012-I-1-6, NRC-2011-A-3-7, NRC-2011-A-3-10, NRC-2011-C-N-11, NRC-2011-F-1-23, NRC-2011-A-3-22, NRC-2011-A-3-6, NRC-2009-6, NRC-2006-C-7, NRC-2007-L-1-5 and NRC-2007-J-3
Cluster VI	5	JS-97-52, NRC-2014-0-4-10-1-1-1,NRC-2014-0-4-10-1-1-1, NRC-2014-0-4-10-1-2-2, NRC-2014-B-1-8-1-5-4-1
Cluster VII	39	RSC-10-04, RSC-10-05, RSC-10-30, NRC-2008-B-3-21-1, NRC-2008-B-2-2-2, NRC-2009-1, NRC-2009-4, NRC-2007-C-1-5, NRC-2007-12-7-2, NRC-2007-1-3, NRC-95-05-03, NRC-2006-4-1-2, NRC-2006-4-13, NRC-2006-J-7, VLS-2, VS-2005-28, VS-2005-37, NRC-95-03-03, NRC-95-03-02, NRC-96-05-03, NRC-95-08-01, AMS-60-2-34, AMS-MB-5-18, Cat-2722, Cat-3299, EC-15966, EC-34078, EC-685250, EC-685255, JS-20-42, JS-20-78, NRC-2014-G-1-2-1-5, NRC-2014-N-3-10-4-4-1, NRC-2014-K-1-7-2-3-2, NRC-2014-P-8-2-3-1-1, NRC-2014-R-1-5-1-3-3, NRC-2014-N-2-7-3-1-1, JS-20-71 and JS-20-79

Intra and Inter-cluster distances

The estimate of average intra and inter-cluster distances were represented in Table 4.6 and Fig. 4.2. The maximum intra-cluster distance was obtained for cluster VI (5.415) followed by cluster IV (3.156), cluster VII (2.711), cluster me (2.697) and cluster III (2.497). The minimum intra-cluster distance (2.491) was shown by cluster II. The intra cluster distance varied from 2.49 to 5.41. The highest inter cluster distance values were observed between cluster VI and III (8.096) followed by cluster VI and II (7.927), cluster VI and IV (7.823), cluster VI and V (7.281), cluster VII and VI (5.737), cluster VI and I (5.665), cluster IV and I (4.553), cluster III and I (4.365), cluster VII and II (3.625), cluster V and I (3.596), cluster VII and I (3.407), cluster IV and II (3.286), cluster II and I (3.218), cluster IV and II (2.956), cluster VII and V (2.840), cluster V and IV (2.824), cluster III and II (2.712), cluster VII and III(2.694) and cluster V and III (2.572).
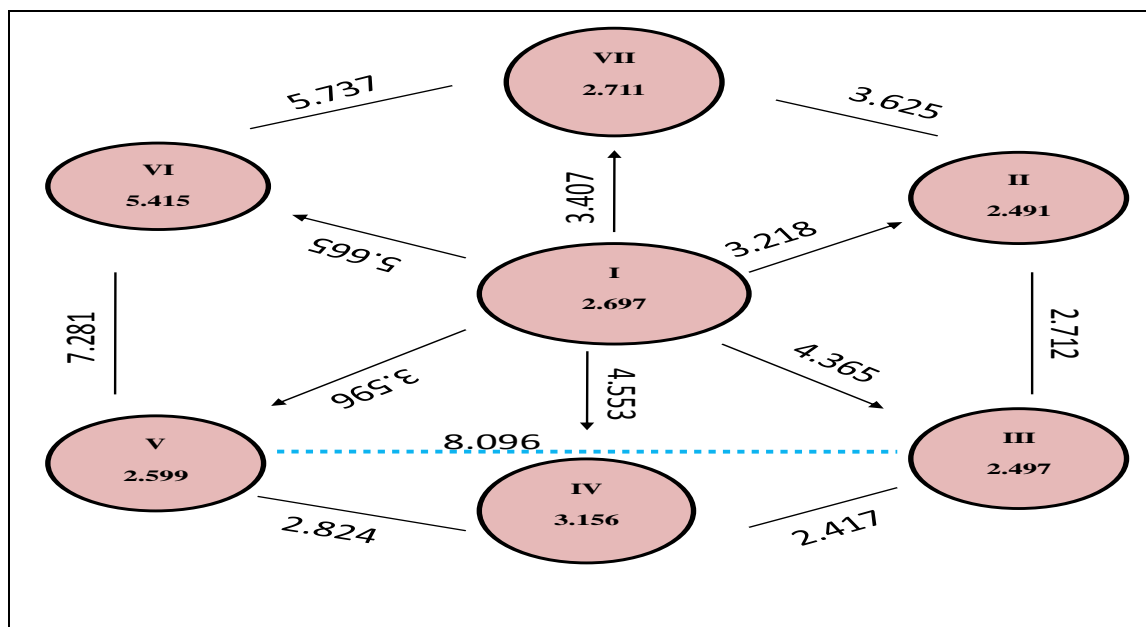

Fig. 1: Cluster diagram showing intercluster distance and distance between the cluster members from the cluster centroid (value in circles)

Table 2: Estimation of average intra (bold) and inter cluster distance in quantitative characters for seven clusters in soybean germplasm accessions

Cluster	I	II	III	IV	V	VI	VII
I	2.697	3.218	4.365	4.553	3.596	5.665	3.407
II		2.491	2.712	3.286	2.956	7.927	3.625
III			2.497	2.471	2.572	8.096	2.694
IV				3.156	2.824	7.823	3.174
V					2.599	7.281	2.840
VI						5.415	5.737
VII							2.711

The lowest inter-cluster D^2 value was found between cluster IV and III (2.471). The inter cluster distance varied from 2.471 to 8.096. Intra and inter-cluster distance are presented in Table 4.6. All the intercluster distances were larger than the intra-cluster distance indicating the presence of wider diversity among genotypes of distance groups. Most of the germplasm are traditional but they showed high variability between them which was revealed from the results of intra and inter-cluster distance values. The highest intra cluster value was 5.415 and the highest inter-cluster value was 8.096, which clearly indicated variability existed in the germplasm of different clusters. It is, therefore, suggested that the genotypes belonging to cluster pairs separated by large inter-cluster distance. In this respect, the highest intercluster distance was observed between cluster VI and III.

Intra-cluster means
The intra-cluster group means for thirteen quantitative characters are given in Table 4.4 which revealed marked differences between the seven clusters in respect of cluster means for different characters.

Days to 50 % flowering
In case of character days to 50 % flowering, the highest cluster mean was obtained for cluster IV (46.56), cluster VI (45.80), cluster II (43.10), cluster V (42.81), cluster VII (41.42) cluster I (40.44) and cluster III(39.23) were flowering in descending order.

Days to Maturity
In case of character days to maturity, the highest cluster mean was obtained for cluster IV (101.47) followed by cluster VII (99.50), cluster VI (98.40), cluster I (98.28), cluster III (98.19), cluster II (96.14), while cluster V (91.03) showed the lowest cluster mean value

Plant Height (cm)
The cluster mean for plant height (cm) was the highest for cluster VI (88.43) while cluster VII had (69.22). The plant height (cm) cluster IV, cluster V, cluster III, cluster I and cluster II were recorded 65.49, 55.77, 56.72,44.02 & 40.25 respectively.

No. of primary branches per plant
The cluster mean for number of primary branches per plant was the highest for cluster I (3.92) followed by cluster II (3.91), cluster IV (3.68), cluster V (3.55), cluster VI (2.99), and cluster VII (2.95) while the lowest cluster mean was observed for cluster III (2.88).

Pod bearing length (cm)
The cluster mean for number of pods bearing nodes was the highest for cluster VI (72.09) followed by cluster VII (55.19), cluster IV (48.11), cluster III (41.26), cluster V (37.28), and cluster me (32.58) while the lowest cluster mean was observed for cluster II (23.00).

Number of pod bearing nodes
The cluster mean for number of pods bearing nodes was the highest for cluster V (10.38) followed by cluster IV (10.13), cluster III (9.20), cluster I (8.39), cluster VII (8.27), cluster II (7.73) while the lowest cluster mean was observed for cluster VI (7.51).

Number of pods per plant
The cluster mean for number of pods per plant was the highest for cluster VI (75.60) followed by cluster VII (54.45), cluster I (51.92), cluster V (119.55), cluster II (36.39), cluster III (36.12) while the lowest cluster mean was observed for cluster IV (35.34).

Number of seeds per pod
The cluster mean for number of seeds per pod was the highest for cluster VI (3.26) followed by cluster me (3.24), cluster II (2.76), cluster IV (2.61), cluster V (2.52), and cluster VII (2.44) while the lowest cluster mean was observed for cluster III (2.36).

Table 3: Cluster mean for thirteen quantitative characters of 273 soybean genotypes

S. No	Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
	No of Germplasm	**32**	**38**	**59**	**67**	**33**	**5**	**39**
1.	Days to 50 % flowering	40.44	43.10	39.23	46.56	42.81	45.80	41.42
2.	Days to maturity	98.28	96.14	98.19	101.47	91.03	98.40	99.50
3.	Plant height (cm)	44.02	40.25	56.72	65.49	55.77	88.43	69.22
4.	Number of primary branches per plant	3.92	3.91	2.88	3.68	3.55	2.99	2.95
5.	Pod bearing length(cm)	32.58	23.00	41.26	48.11	37.28	72.09	55.19
6.	Number of pod bearing nodes	8.39	7.73	9.20	10.13	10.38	7.51	8.27
7.	Number of pods per plant	51.92	36.39	36.12	35.34	47.64	75.60	54.45
8.	Number of seeds per pod	3.24	2.76	2.36	2.61	2.52	3.26	2.44
9.	Number of seeds per plant	167.25	99.13	85.04	91.78	119.55	238.30	132.34
10.	100 seed weight(g)	11.29	11.53	10.57	9.70	9.89	11.65	10.48
11.	Seed yield per plant(g)	18.87	11.36	8.96	8.83	11.81	26.88	13.82

| 12. | Protein content (%) | 38.21 | 38.29 | 37.33 | 38.26 | 38.28 | 32.88 | 37.10 |
| 13. | Oil content (%) | 19.40 | 19.32 | 18.58 | 20.14 | 18.95 | 22.37 | 18.93 |

Number of seeds per plant
The cluster mean for number of seeds per plant was the highest for cluster VI (238.30) followed by cluster I (167.25), cluster VII (132.34), cluster V (119.55), cluster II (99.13), cluster IV (91.78) while the lowest cluster mean was observed for cluster III (85.04).

100 seed weight (g)
The cluster mean for 100 seed weight (g) was the highest for cluster VI (11.65) followed by cluster II (11.53), cluster I (11.29), cluster III (10.57), cluster VII (10.48), cluster V (9.89), while the lowest cluster mean was observed for cluster IV (9.70).

Seed yield per plant (g)
The cluster mean for seed yield per plant (g) was the highest for cluster VI (26.88) followed by cluster I (18.87), cluster VII (13.82), cluster V (11.81), cluster II (11.36), cluster IV (8.83) while the lowest cluster mean was observed for cluster III (8.96).

Protein content (%)
The cluster mean for protein content (%) was the highest for cluster II (38.29) followed by cluster V (38.28), cluster IV (38.26), cluster I (38.21), cluster III (37.33), cluster VII (37.10) while the lowest cluster mean was observed for cluster VI (32.88).

Oil content (%)
The cluster mean for oil content (%) was the highest for cluster VI (22.37) followed by cluster IV (20.14), cluster I (19.40), cluster II (19.32), cluster V (18.95), cluster VII (18.93) while the lowest cluster mean was observed for cluster III (18.58).
Mean performance of different clusters for the characters revealed that medium maturity, dwarf stature, low pod bearing length medium yielding varieties and high protein content were clubbed into cluster II whereas tall height, high pod bearing length (cm), low number of pod bearing nodes, high number of pods per plant, high number of seed per pod, high number of seed per plant, high seed weight content, higher yield, low protein and high oil content were grouped into cluster VI, medium earliness and maturity were grouped in cluster VII, early maturity and average yield were grouped in cluster V. Late earliness and maturity were grouped in cluster IV
High number of primary branches per plant, medium earliness and maturity, high 100 seed weight and high protein content were grouped into cluster I. Medium earliness, maturity, plant height and low 100 seed weight obtained from cluster III. But it was interesting that in the entire cases cluster VI produced highest inter cluster means value with all other clusters. Therefore, the genotypes of cluster VI can be used in hybridization program to produce higher yielding genotypes with all other clusters. Similar finding was supported by several researchers reported were Shrivastava *et al.* (2001) [9] reported the highest inter cluster divergence was observed between cluster III and IV. Sihag *et al.* (2004) [10] genotypes from the same ecogeographic region were classified in different clusters, and genotypes from different eco-

geographic regions were classified into one cluster. Singh *et al.* (2007) [11] To get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI as the inter cluster distance was greater between these clusters. Tyagi and Sethi (2011) [12] the highest inter-cluster distance was observed between II and IV followed by II and VI. Venkateswarlu and Sirisha (2011) [14]. based on inter-cluster distances, the clusters VII, X, VI, X and XII (total 12 clusters) were found as divergent. Hence, selection of genotypes from these clusters namely ICGV 99032 (cluster VI), TCGS 647, JL 220 (cluster VII), ICGV 95477, JL 24, ICGV 99054, ICGV 86699 (cluster X) and ICGV 99029 (cluster XII) for hybridization program may result into good recombinants. Adsul and Monpara (2014) [1] cluster I was the largest with 55 genotypes followed by cluster III containing 17 genotypes and cluster IV containing 16 genotypes. The genotype JS (SH) of cluster XIV, J 606 of cluster X, JS 46-75 of cluster V and Himso 15-48 of cluster XV were identified as genetically diverse parents. Malek *et al.,* (2014) [3] mutants/genotypes from cluster I and cluster II could be used for hybridization program with the mutants of clusters IV and V in order to develop high yielding mutant-derived soybean varieties for further improvement. Pushpendra *et al* studied the maximum genetic divergence was observed between clusters IX and X, whereas lowest genetic divergence was between clusters IV and VII. Mili *et al.,* (2017) [4] highest number of genotypes found in cluster III. The highest intra-cluster distance was found in cluster II and highest inter-cluster distance was found between cluster I and IV followed by I and V.
The wide range of genetic diversity was observed in the present germplasm collection. It is also suggested that said diversity could be utilized for improvement in soybean by best performing lines of different clusters, followed by selection in segregating generations.

Conclusion
Two seventy three soybean germplasm were clustered into main seven groups. Thus the genotypes from different groups can be used as parental stock. The highest inter cluster distance values were observed between cluster VI and III (8.096) indicating that genotypes in V were far diverse from those of VIII. Choosing of genotypes belonging to distant clusters was expected to execute maximum heterosis in crossing and to be used in hybridization program for improvement of quality traits.

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