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Genetic divergence in soybean *Glycine max* L. Merrill

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Abstract
The present investigation was carried out to determine the genetic diversity of hundred soybean genotypes. The genetic divergence studies grouped hundred genotypes into six clusters. The cluster VI showed the maximum intra cluster distance hence belonging to this cluster could be utilized as parent in future breeding programme to get better recombinants. Maximum inter-cluster distance was recorded between clusters III and VI, followed by cluster I and VI clusters I and V. Hence, it would be advisable to choose parents from these clusters having different gene pools for important genes to be combined in improved genotypes through hybridization programme.

Keywords: Soybean *Glycine max*, genetic diversity

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. The wide diversity in the tested soybean accessions indicates that there is a considerable potential for the improvement of soybean for both agronomic and quality traits. Genetic divergence is of greatest interest to the plant breeder as it plays a vital role in framing a successful breeding programme. The genetically diverse parents are likely to produce high heterotic effects and desirable segregates.

Materials and Methods
The experimental materials of the study was consisting hundred diverse genotypes of soybean laid out in Research *cum* Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India, during *kharif* 2014 and *kharif* 2015 were grown in an Randomized Complete Block design with three replications. All the agronomical package of practices was adopted and necessary observation were recorded for the genetic divergence studies. The observations were recorded on thirteen quantitative and qualitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, pod bearing length (cm), number of seeds per pod, number of seeds per plant, hundred seed weight (g), protein content (%), oil content (%), harvest index (%) and seed yield per plant (g). The D² analysis was carried out for all the thirteen characters to access genetic divergence using Mahalanobis D² statistics (1936). The genotypes were grouped on the basis of minimum generalized distance using the Tocher's method (Rao, 1952).

Results and Discussion
Based on D² statistics and Tocher's method, the hundred genotypes were grouped into six clusters with variable number of entries revealing the presence of variable amount of diversity in the material (Table 1). The cluster III and VI contained 14 genotypes each, while, cluster I consisted of 19 genotypes. Cluster II consisted of 16 genotypes, whereas, cluster V consisted of 8 and cluster IV consisted maximum number of 29 genotypes.

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Table 1: Grouping of soybean genotypes in different clusters

Cluster number	Number of genotypes included	Name of genotypes
I	19	JS 2, JS 20-34, JS 335, JS 76-205, JS 95-60, Lee, MACS 1140, MACS 57, Monetta, NRC 2, PK 327, PK 416, PK 472, PS 1042, RKS 113, RSC 12-03, Shilajeet, SL 295 and SL 525.
II	16	DS 228, Hardee, IS 9, JS 90-41, MACS 1407, MACS 450, MAUS 61, MAUS 81, NRC 37, NRC 7, NRC 93, PS 1092, PS 1225, PS 564, RSC 12-02 and RSC 12-06.
III	14	VL Soya 59, LSb 1, JS 93-05, JS 71-05, Hara soya, Alankar, VL Soya 47, VL Soya 2, RSC 10-15, RAUS 5, PUSA 24, NRC 12, MACS 1340 and MACS 1336.
IV	29	Birsa Soya 1, Bragg, DS 98-14, Improved Pelican, JS 72-44 (Gaurav), JS 75-46, JS 79-81, Kalitur, KB 79, KHSB 2, MACS 124, MACS 13, MAUS 1, MAUS 2, MAUS 32, MAUS 7, MAUS 504, MAUS 71, PS 1029, Punjab 1, PUSA 6, PUSA 20, PUSA 22, RSC 11-06, RSC 12-04, TAMS 38, TAMS 98-21, Type 49 and VL Soya 21.
V	8	JS 80-21, MACS 1460, MACS 58, RKS 18, RSC 10-29, RSC 11-05, RSC 12-05 and RSC 12-07.
VI	14	CG Soya-1, RSC 10-70, RSC 10-71, RSC 11-03, RSC 11-04, RSC 11-07, JS 97 52, MAUS 61-2, PS 1024, RSC 10-05, RSC 10-17, RSC 10-30, RSC 10-46 and RSC 10-52.

The intra cluster distances were measured that the genotypes within the cluster have smaller average distance (intra cluster distance) than the inter cluster distance. The different combinations of different cluster distances are presented in Table 2 & Fig:1. The results of cluster analysis indicated that the highest intra-cluster distance was observed for cluster III (3.594) followed by cluster II (2.853), cluster V (2.771), cluster IV (2.741), cluster I (2.483) and cluster VI (2.226). Moreover, the highest inter cluster distance was measured between clusters III and VI (4.929), followed by cluster I and VI (4.606), clusters I and V (4.334), clusters IV and VI (4.142), clusters III and V (4.029), clusters IV and V (3.573), clusters III and IV (3.391), clusters I and II (3.243), clusters V and VI (3.229), clusters II and III (3.217), clusters II and IV (3.175), clusters I and III (3.013), II and VI (2.803.) The lowest inter cluster distance was measured between clusters I and VI (2.648).

Table 2: Estimates of intra (diagonal and bold) and inter cluster distances among six clusters

Clusters	I	II	III	IV	V	VI
I	**2.483**	3.243	3.013	2.648	4.334	4.606
II		**2.853**	3.217	3.175	3.374	2.803
III			**3.594**	3.391	4.029	4.929
IV				**2.741**	3.573	4.142
V					**2.771**	3.229
VI						**2.226**

Diagonal & bold values shows intra- cluster distance

Mean performance of individual cluster for different characters are presented in (Table 3.) for days to 50 percent flowering cluster II possessed the highest mean value of 45.12 days followed by cluster VI (44.79), VII (45.57), IV (44.15) and cluster V (42.93). Moreover, the lowest mean value of 39.48 for days to 50 percent flowering was recorded for

cluster III. The cluster IV possessed maximum mean value for days to maturity (103.86) followed by VI (102.24), II (101.81), III (99.14) and V (97.67) while, lowest mean value for days to maturity was recorded in cluster I (95.78). The cluster V exhibited the highest mean value of 75.79 for plant height followed by cluster VI (71.96), IV (58.05), IV (59.45), and II (54.73), However, cluster I (46.21) possessed the lowest plant height. Cluster VI having the highest mean value (3.90) for number of primary branches per plant followed by clusters V (3.80), IV (3.60), I (3.58), III (3.44), whereas, cluster II (3.41) exhibited the lowest mean value for number of primary branches per plant.

Intra and inter cluster distance along with cluster mean value is of paramount importance for selection of parents for hybridization programme. In present study, the pattern of distribution of hundred genotypes in various clusters revealed that there is considerable genetic diversity in the material. In the present investigation, 100 genotypes were grouped in to six clusters. The highest intra cluster distance was observed for cluster III consisting of 14 genotypes. The maximum inter cluster distance was measured between clusters III and VI followed by cluster I and VI, I and V, IV and VI and III and V.

As cluster III showed the maximum intra-cluster distance as compared to other clusters indicating genetic divergence among the genotypes belonging to this cluster. Hence, VL Soya 59, LSb 1, JS 93-05, JS 71-05, Hara soya, Alankar, VL Soya 47, VL Soya 2, RSC 10-15, RAUS 5, PUSA 24, NRC 12, MACS 1340 and MACS 1336 could be utilized as parent in future breeding programme to get better recombinants. These results are in general agreement with the findings of Mili *et al.* (2017) [4], Pushpendra *et al.* (2016) [6], Nimnual *et al.* (2016) [5], Barh *et al.* (2014) [1], Kachhadia *et al.* (2014) [2], Tyagi *et al.* (2012) [8].

Table 3: Mean performance of different clusters for yield and its component traits.

Clusters number	1	2	3	4	5	6	7	8	9	10	11	12	13
I	40.45	95.78	46.21	3.58	39.57	30.07	2.39	94.53	10.92	38.10	20.42	51.44	10.30
II	45.12	101.81	54.73	3.41	52.99	35.91	2.42	127.83	11.25	38.43	19.88	48.12	14.34
III	39.48	99.14	47.43	3.44	39.33	32.00	2.46	96.63	13.10	39.52	18.70	47.10	12.73
IV	44.15	103.86	58.05	3.60	36.78	39.35	2.40	88.35	10.35	38.08	19.66	47.45	9.16
V	42.93	97.67	75.79	3.80	48.27	48.71	2.45	118.77	10.54	40.28	18.74	48.17	12.49
VI	44.79	102.24	71.96	3.90	54.43	44.80	2.54	138.19	10.98	37.83	20.72	47.95	15.13
Per cent contribution to variation	18.8	22.3	2.7	1.2	1.8	8.9	1.2	1.5	8.6	1.8	2.4	28.3	0.6

1. Days to 50% flowering
2. Days to maturity
3. Plant height (cm)
4. Number of primary branches per plant

5. Number of pods per plant
6. Pod bearing length (cm)
7. Number of seeds per pod
8. Number of seeds per plant

9. 100 seed weight (g)
10. Protein content (%)
11. Oil content (%)
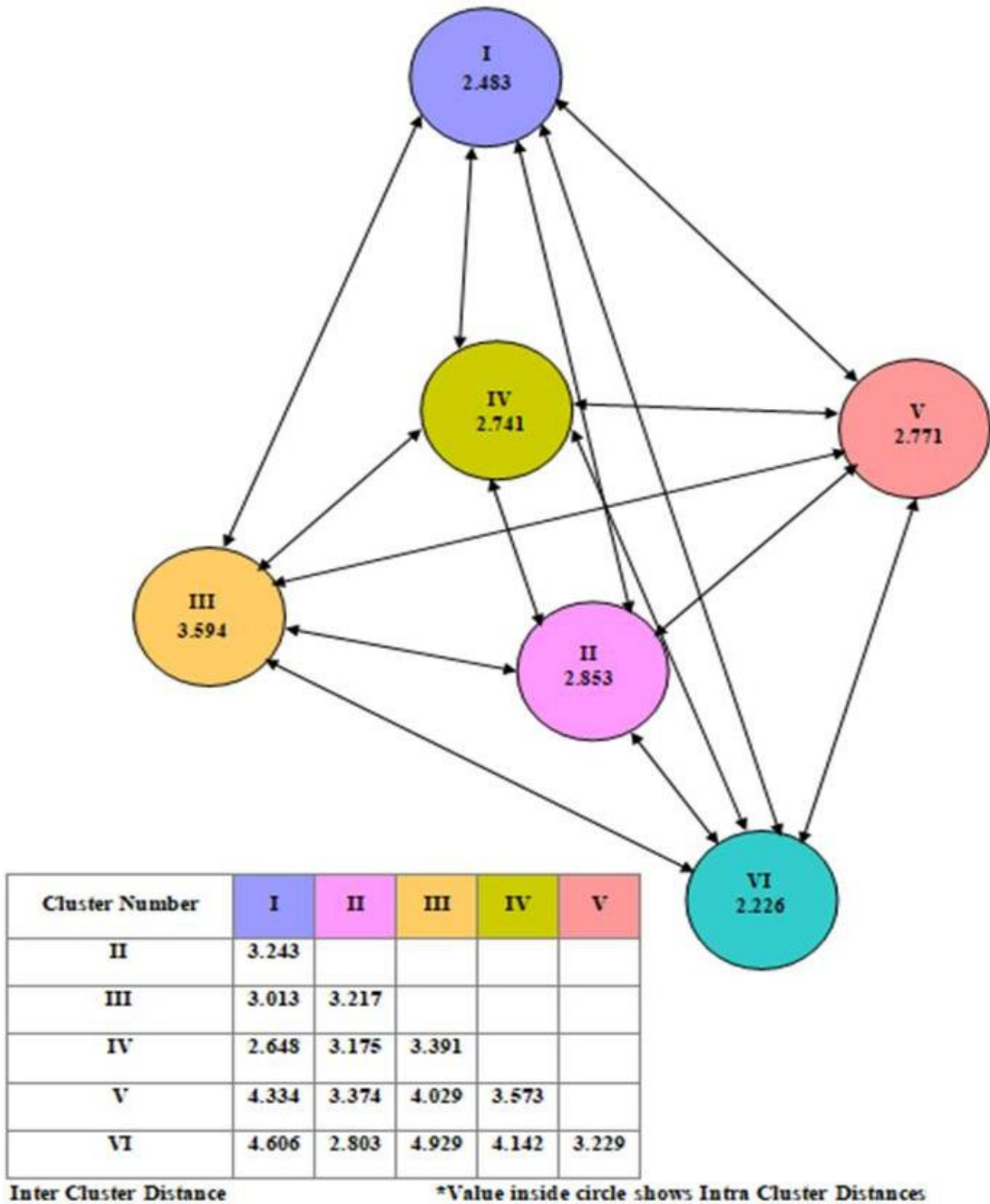12. Harvest index (%) 13. Seed yield per plant (g)

Cluster Number	I	II	III	IV	V
II	3.243				
III	3.013	3.217			
IV	2.648	3.175	3.391		
V	4.334	3.374	4.029	3.573	
VI	4.606	2.803	4.929	4.142	3.229

Inter Cluster Distance   *Value inside circle shows Intra Cluster Distances

Fig 1: Cluster diagram showing inter-cluster & intra-cluster distances between six clusters

Conclusion
In the present investigation maximum inter cluster distance was observed between clusters I and cluster VI. Hence, it would be advisable to choose parents from these two clusters for hybridization. The diverse clusters may have different gene pools for important genes to be combined in improved genotypes. Other important clusters were cluster I and cluster VI, showing greater divergence, from where parents could be selected for further hybridization programme. Thus the results of present investigation clearly indicate that parents from diverse group can easily be selected for different economic traits.

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