Study of Genetic Divergence in Soybean Germplasm

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Abstract
The objectives of this study were to evaluate the genetic variation in soybean by means of 120 accessions received from NBPGR New Delhi and DSR Indore along with 5 checks *viz.*, SL 688, PS 1347, PS 1092, Bragg, PS 1042. The adjusted mean of genotypes were subjected to Hierarchical Cluster Analysis (HCA) and the genotypes were grouped based on 40 % dissimilarity level. The 120 genotypes including 5 checks were grouped in 9 clusters based on hierarchical cluster analysis. The distribution pattern of accessions in clusters showed that accessions from different locations were clustered together in one cluster and also accessions from the same region were grouped under different clusters. This suggests that there is no parallelism between genetic diversity and geographical diversity. Inter and intra clustering distance was also calculated to determine extent of diversity among and between the clusters. Greater intra-cluster distance shows greater diversity among the accessions of the same cluster whereas less intra-cluster distance shows that these accessions are closely related and less variable with respect to their mean values.

Introduction

Soybean (*Glycine max* (L.) Merrill) popularly known as "Golden Bean" or "Miracle crop" is a member of Papilionaceae family. Cultivated Soybean is a diploid crop having chromosome number of 2n=40. It is basically a leguminous crop but widely used as an oilseed crop. Considering the potential of soybean crop, there is a need of improvement to develop varieties suited to specific agro-ecological conditions and also for specific end use. Genetic diversity is a major factor that determines the prospects of yield improvement in future. Knowledge of genetic diversity within a crop and correlation among the yield contributing characters is pre requisite for the long term success of a breeding program and maximizes the exploration of germplasm resources. Importance of genetic diversity in crop production is to be best appreciated by realizing the current and future food security needs of country as well as world. Genetic diversity and heterotic pool are the basis of plant breeding and genetic engineering. In addition to this new gene pool also provides building blocks for further improvement. Genetic diversity is essential if high level of productivity is to be achieved and sustained. In order to meet the growing needs of varietal improvement for higher productivity, it is essential to preserve, assemble, develop and document the entire array of crop germplasm. Planned utilization of genetic diversity present in land races, cultivar and wild relative's for any of the economically important traits aims at pyramiding of genes for higher productivity, better quality, and resistance to biotic and abiotic stresses to ultimately develop high yielding varieties.

Thus, genetic divergence among parents is of paramount importance in selecting parental genotypes for crossing programmes. More the diverse parents greater are the chances of achieving heterotic F_1's and a broad spectrum variability in segregating generation. Further these new lines represent a new array of genes and the analysis of yield and yield contributing traits *viz.*, total dry matter weight, harvest index and seed yield etc. along with additional morphological parameters would be of immense importance.

Material and method

The experiment was conducted at N E Borlaug Crop Research Centre, G B Pant University of Agriculture and Technology Pantnagar, Udham Singh Nagar, Uttarakhand. Experimental material of the investigation comprised of 120 genotypes along with 5 checks *viz.*, SL 688, PS 1347, PS 1092, Bragg and PS 1042. The experiment was conducted in augmented design (Federer, 1956) with four blocks. Each block planted with thirty genotypes and five checks. Each accession planted in a single row of 4 m length with row to row distance 45 cm and plant to plant distance 5-7 cm. Standard package and practices were followed to raise the healthy crop. The observations were

recorded on five randomly selected competitive plants from a single row of each germplasm line for yield and yield contributing traits namely days to 50% flowering, days to maturity plant height, number of branches per plant, number of node per plant, number of pods per plant, number of pod cluster per plant, plant population, 100 seed weight, dry matter weight per plant (g) and seed yield per plant (g). On the whole row basis the observations were recorded for days to 50 % flowering and maturity, whereas on the composite sample basis 100-seed weight, were recorded and derived character like harvest index also calculated.

The analysis of variance for augmented design was done using the method given by Federer (1956) as described by Federer and Ragavarao (1975) and Petersen (1985) and Hierarchical Euclidean cluster analysis (Ward, 1963) were used for clustering of genotypes.

Result and Discussion

Characters days to 50% flowering, number of nodes per plant, number of pod clusters per plant, and 100 seed weight showed highly significant difference among check varieties. The significant difference indicates that these traits showed significant variation with the blocks. Significant differences among varieties were recorded for days to 50 % flowering, days to maturity, plant height, and number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant and 100 seed weight. The presence of variability gives an ample scope for improvement in population through various breeding approaches. Vavilov (1950) stated that wider the range of variability, greater is the chances for improvement with respect to different desirable traits through selection.

Cluster formation based on HCA

The 120 genotypes including 5 checks (**Table 1**) were grouped in 9 clusters (**Table 2**) based on hierarchical cluster analysis, cluster IX had the highest number of genotypes (40) followed by Cluster V with 34 accessions, Cluster III with 13 accessions, cluster VII with 12 accessions, cluster VI with 11 accessions,, cluster IV and VIII with 5 accessions each, cluster I with 4 accessions and Cluster II with only 1 accession/genotype. Finally the dendrogram prepared based on HCA (**Figure 1**).

Table 1 List of germplasm accessions of soybean received from NBPGR New Delhi and directorate of DSR Indore

S. No	Genotype	S. No.	Genotype	S. No.	Genotype	S. No	Genotype
1	AGS 25	31	CAT 315	61	CAT 2652	91	JS 20-80
2	AMS 115	32	CAT 3150	62	EC 329156	92	JS 20-81
3	CAT 1263	33	CAT 3166	63	EC 39536	93	JS 20-85
4	CAT 147	34	CAT 3174	64	EC 457198	94	JS 20-86
5	CAT 1487	35	CAT 3218	65	EC 65772	95	JSM 127
6	CAT 1502	36	CAT 3219	66	G 141	96	JSM 224
7	CAT 1582	37	CAT 322	67	G 3	97	JSM 227
8	CAT 165	38	CAT 3229	68	G5P22 (IR)	98	JSM 288
9	CAT 1734	39	CAT 3230	69	GP 116	99	PS 1241
10	CAT 1788	40	CAT 3243	70	GP 465	100	PK 515
11	CAT 1892	41	CAT 3284	71	GP 499	101	Cat. 2660
12	CAT 195	42	CAT 3299	72	JS 20-48	102	Cat. 2891
13	CAT 2007 A	43	CAT 3327	73	JS 20-50	103	Cat. 2755
14	CAT 7048	44	CAT 3391	74	JS 20-72	104	Cat. 2722
15	CAT 2430	45	CAT 3406	75	JS 20-82	105	Cat. 685
16	CAT 2502	46	CAT 3412	76	JS 79-302	106	Cat. 2388
17	CAT 2503	47	CAT 357	77	JSM 284	107	Cat. 2722
18	CAT 2511	48	CAT 44	78	JS 288	108	Cat. 2503
19	CAT 2562	49	CAT 503	79	PK 747	109	Cat. 2809
20	CAT 2698	50	CAT 537	80	PP6 (PI)	110	Cat. 2387 A
21	CAT 2705	51	CAT 585	81	PKS 54	111	Cat. 1113
22	CAT 2722	52	CAT 592	82	Sizta 194	112	SKY/AK 1403
23	CAT 2746	53	CAT 675	83	SL 29-51	113	Cat. 357
24	CAT 2755	54	CAT 683	84	SL 599	114	Cat. 3414
25	CAT 2758	55	CAT 7048	85	VGM 70	115	Cat. 586
26	CAT 2809	56	CAT 710	86	Cat. 2899	116	Cat. 751
27	CAT 2857A	57	CAT 716	87	Cat. 79	117	Cat. 646
28	CAT 2891	58	CAT 772	88	Cat. 2399	118	EC 18745
29	CAT 2928	59	CAT 778	89	Cat. 3230	119	EC 94625
30	CAT 2931	60	CAT 79	90	Cat. 3174	120	EC 7040

Table 2 Distribution of soybean accessions in different clusters based on Hierarchical Cluster Analysis

Cluster	No. of Entry	Entry Number
I	4	91, 92, 93, 94
II	1	71
III	13	10, 13, 15, 19, 30, 49, 54, 62, 67, 73, 81, 86, 115
IV	5	4, 51, 52, 61, 82
V	34	12, 22, 32, 33, 38, 42, 43, 45, 47, 68, 74, 75, 80, 86, 87, 88, 90, 97, 98, 102, 103, 104, 106, 107, 108, 109, 110, 111, 112, 113, 114, 117, 119, 120
VI	11	3, 8, 23, 25, 44, 57, 58, 60, 89, 96, 99
VII	12	7, 18, 20, 31, 37, 39, 63, 79, 83, 84, 85, 105
VIII	5	4, 21, 46, 66, 76
IX	40	1, 2, 5, 9, 11, 14, 16, 17, 24, 26, 27, 28, 29, 34, 35, 36, 40, 41, 48, 50, 53, 55, 56, 58, 64, 69, 70, 72, 77, 78, 95, 100, 101, 116, 118, 121, 122, 123, 124, 125
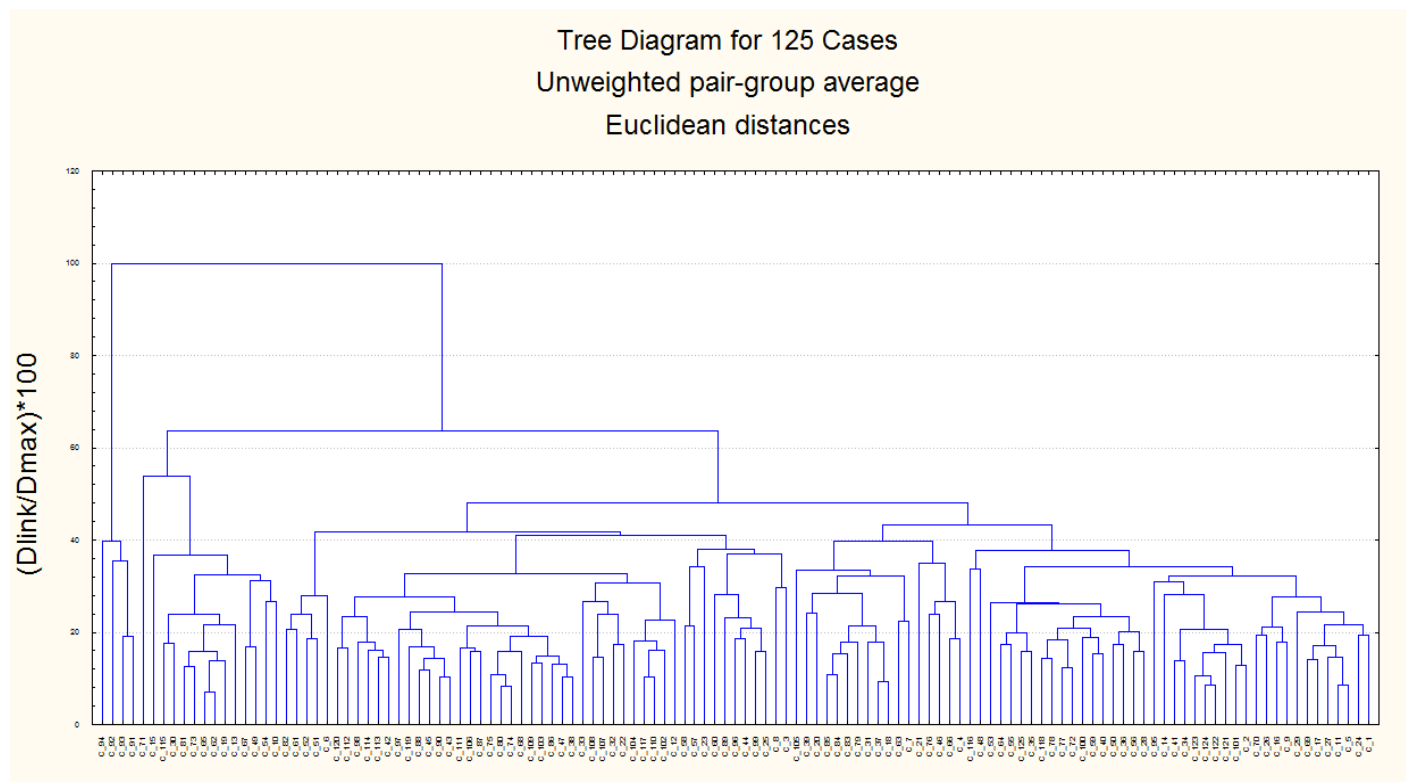
Figure 1 Dendrogram of 125 accessions of soybean based on hierarchical cluster analysis

Inter and intra-cluster distance

The number of clusters represents the number of groups in which genotypes classified. The distance between two clusters is the measure of the degree of diversification. The greater the distance between two clusters the greater the divergence and vice-versa. The genotypes falling in the same cluster are more likely to be related than those belonging to another cluster. In other words the genotypes grouped in one cluster are less divergent than those which are placed in different cluster. The intra and inter cluster distances calculated for different clusters have been presented in **Table 3** and discussed below.

Highest intra-cluster distance was recorded for cluster III (40.11) followed by cluster I (38.59), cluster VI (36.75), cluster IX (36.3), and cluster VIII (32.06). The lowest intra-cluster distance was observed for cluster II (0.0) followed by cluster IV (27.23), cluster VII (29.98), cluster V (30.76). Greater distance among the members of a cluster implies that there is wide range of variability still present for the concerned character. If we lower down the dissimilarity level there will be further dissolution of the existing cluster. On the other hand clusters with less intra-cluster distance shows that these accessions are closely related and less variable with respect to their mean values.

The inter-cluster distance was highest between cluster I and cluster VI (138.06) followed by cluster I and cluster IV (132.36) on the other hand lowest inter-cluster distance was estimated between cluster VII and cluster VIII (44.07) thereafter by cluster VII and cluster IX (45.08).

Table 3 Intra (diagonal) and inter -cluster (Off-diagonal) distances based on Hierarchical Cluster Analysis of soybean germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	38.59	116.77	91.45	132.36	124.77	138.06	93.91	111.95	101.42
II		0	64.87	106.73	130.61	130.23	96.72	75.18	101.75
III			40.11	67.18	79.02	86.75	52.97	49.11	55.23
IV				27.23	46.12	46.18	52.25	48.38	49.76
V					30.76	45.5	54.34	70.8	47.32
VI						36.75	57.44	67.27	62.57
VII							29.98	44.07	45.08
VIII								32.06	56.72
IX									36.3

Highest inter-cluster distance between cluster I and cluster VI revealed that these two clusters and members of these clusters are distinctly related to each other. More the inter-cluster distance more will be the diversity between the genotypes which provide ample opportunity to select a number of donors to carry out hybridization programmes for the improvement of desirable traits in the soybean.

We can proceed with the hybridization programme by making cross between distinctly related genotypes having desired traits in order to get more number of transgressive segregants. Then selection is practiced to select genotype having desired traits.

Cluster Mean for Different Clusters

The cluster mean for different traits under study was computed and presented in **Table 4**. The Table clearly revealed that the clusters were exhibited differences for various morpho-agronomic characters. This allows the identification of suitable donors for different traits and suggested the inclusion of these donors in various hybridization programmes.

Table 4 Cluster means for different characters studied on soybean germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
Days to 50% flowering	43.95	55.75	52.27	50.47	47.36	52.53	54.63	57.11	48.84
Days to maturity	96.80	117.20	113.70	114.5	109.94	107.4	113.48	115.64	110.32
Plant height (cm)	72.93	100.87	79.98	79.65	62.21	90.68	90.64	101.02	61.43
Number of branches per Plant	6.11	12.87	7.8	5.71	4.66	4.38	5.85	6.72	5.73
Number of nodes per plant	32.65	124.55	73.41	59.55	33.92	39.91	44.56	72.67	52.35
Number of pod clusters per plant	27.15	60.45	48.27	47.09	26.13	23.30	31.05	44.01	33.96
Number of Pods per plant	175.65	130.52	110.53	56.12	58.78	46.14	93.75	84.86	85.2
Plant population	33.6	28.50	29.79	33.7	34.11	33.39	31.31	32.94	30.87
100-seed weight(g)	6.28	9.22	6.77	7.07	7.83	7.83	7.61	6.91	8.04
Dry matter weight per plant (g)	59.78	52.28	43.57	28.53	32.24	31.36	37.95	41.81	40.93
Harvest index (%)	31.92	29.57	34.25	33.38	31.74	32.94	32.97	30.86	33.57
Seed yield per plant (g)	18.81	15.58	14.84	9.40	10.14	10.22	12.52	12.87	13.69

Among the nine clusters, highest value was recorded as 101.02 cm for cluster VIII for the plant height while minimum (61.43 cm) for cluster IX. For the number of branches per plant, cluster II (12.87) has the highest mean whereas the lowest mean value was observed in cluster VI (4.38). Cluster II recorded the highest mean value (60.45) for number of pod clusters per plant while cluster VI (23.3) showed the lowest value of 6.3 for number of pod clusters per plant. For number of pods per plant highest mean was recorded in cluster I (175.65) followed by cluster II (130.52), cluster III (110.53), cluster VII (93.75), cluster IX (85.2), cluster VIII (84.86), cluster V (58.78), cluster IV (56.12) and cluster VI with the lowest mean value of 46.14. For 100 grain weight, cluster mean value was recorded highest for cluster II (9.22g) and lowest for cluster I (6.28g). For Harvest index cluster III recorded the highest mean value of 34.25% and lowest mean value was found for cluster II (29.57%). The mean value for seed yield per plant was recorded highest for cluster I (18.81g) and lowest for cluster IV (9.4g). Mean values for other clusters were observed as 15.58g (cluster II), 14.84g (cluster III), 10.14g (cluster V), 10.22g (cluster VI), 12.52g (cluster VII), and 12.87g (cluster VIII) and 13.69g cluster IX.

Among all the clusters, cluster II showed highest cluster mean for the maximum number of trait followed by cluster I, and cluster VIII indicating presence of most promising genotypes in them. Selection of parents for

hybridization could be made from these clusters to get desirable recombinants in order to improve the yield of soybean.

Cluster II included most of the accessions having highest mean values for yield contributing characters like number of branches per plant, nodes per plant, pod cluster per plant and 100 seed weight. Cluster I was reported genotypes with earliness in flowering, highest dry matter per plant and highest seed yield per plant. Therefore accessions of cluster I and II can be included in the breeding program as donor for improving these yield and yield contributing traits. It also comprised of accessions with more plant height, which could be used as donors to bred tall varieties.

Identification of Suitable donors for different traits

Yield is a complex character and also the result of interactions of several yield contributing characters. To formulate any successful breeding programme it is not only desirable to select parents based on their yield potential and combining abilities but the identification of principal yield contributing traits also deserve due attention. There may not be genes for yield *per se* but for their components, the multiplicative interaction of which results in ultimate yield. The improved genetic donors may be employed for accumulating the desirable genes as well as combining additional desirable traits in an otherwise good variety. Germplasm may serve as a valuable genetic source for which a careful screening and evaluation is a must. The critical analysis revealed that some of the germplasm accessions of soybean, particularly the accessions better than the best check could be utilized as donor for different yield contributing traits in order to breed for high yielding varieties. Character wise donors identified for yield and its contributing traits are presented in **Table 5** and described below.

Table 5 List of suitable donors for different yield and yield contributing traits identified in studied soybean germplasm

Sr. No.	Character		Donor
1	Days to 50% flowering	Early	JS 20-72, CAT 2722,PP6(PI), JS 20-81
		Late	CAT 147, CAT 3412, JS 79-302
2	Days to maturity	Early	JS 20-80, JS20-81, CAT 79
		Late	GP499, G141, JS 79-302,CAT 3412
3	Plant height(cm)	Dwarf	CAT 3284, CAT 3166, CAT 44,CAT 195
		Tall	CAT 3412, JS 79-302, G141, GP 499
4	Number of branches per plant		GP 499, G141, JS 79-302,CAT 3412
5	Number of nodes per plant		GP499,CAT 683, CAT 1788, CAT 2430, JS 20-50
6	Number of pod clusters per plant		GP 499,JS 20-50, PKS 54, CAT 503, CAT 2931
7	Number of pods per plant		GP 499, G3, PKS 54, CAT 503,CAT 2007A
8	Plant population		Cat. 1113, SKY/AK 1403, EC 7040, Cat.3414
9	100 seed weight(g)		CAT 2809, CAT 2891, CAT 3284, GP499
10	Dry matter weight per plant (g)		JS 20-80, JS 20-81, GP499
11	Harvest index (%)		CAT 1788, CAT 2007A, CAT 2562
12	Seed yield per plant (g)		JS 20-80, JS 20-81, JS 20-85, CAT 2430, GP 499

Accession JS 20-81 of cluster I and accessions JS 20-72, CAT 2722, PP6 (PI) of cluster V having lowest cluster mean for character days to 50% flowering along with high inter cluster distance between I and V indicated that these accessions could be incorporated in breeding programme for developing early maturing varieties of soybean. Accessions CAT 147, CAT 3412, JS 79-302 of cluster VIII with high cluster mean showed higher days to 50% flowering, so these accessions may be used as donor in breeding programme to develop late flowering or late maturing varieties.

For days to maturity accessions JS 20-80, JS 20-81 were identified to mature earlier and their mean values were also found superior over the best check (PS 1092). Accession Cat. 79 from cluster VI also mature early. The low cluster means of clusters I and V along with high inter cluster distance (138.06) between them suggests that hybridization of these accessions will be fruitfully utilized to get transgressive segregants for this character.

Accessions G3, RKS 54, CAT 503, CAT 2007A of cluster III with cluster mean 48.27 and Accession GP 499 of cluster II with cluster mean 130.52 had more number of pods. The higher cluster means of clusters I and II along with high inter cluster distance (116.77) between them suggests that hybridization of these accessions will be useful to develop varieties having more number of pods per plant.

For shorter plant height no accessions are found superior than best check (PS 1347) however accessions CAT 3284, CAT 3174, CAT 44 belongs to cluster IX(having cluster mean of 61.43) and accessions CAT 3166 CAT 195,

and G5P22(IR) belongs to cluster V (having cluster mean of 62.21), have shortest plant height among 120 accessions. Intermediate inter cluster distance between cluster V and IX revealed that this both cluster are somewhat related to each other, but these accessions could be utilized in hybridization to get better segregants.

For character like 100-seed weight, the accessions GP 499 of cluster II and accessions CAT 165, CAT 2809, CAT 2891, and CAT 3284 of cluster IX having high 100-seed weight and they also shows superiority over the best check (PS 1347). The high inter cluster distances between cluster II and IX indicated that these accessions could be utilized in hybridization programme to get better segregants.

Two genotypes from cluster I (JS 20-80, JS 20-81) shows superiority over best check(PS 1042) and have high cluster mean, one accession from cluster II (GP 499) also showed higher mean values with high cluster mean for dry matter per plant. High inter cluster distance between cluster I and II provide great opportunity to improve dry matter per plant via hybridization between them.

Seed yield per plant was observed higher for JS 20-80 [which also shows superiority over best check (SL 866)] followed by JS 20-81, JS 20-85 of cluster I with high cluster mean. Seed yield per plant is also higher for accession GP 499 with high cluster mean. Considerable high inter cluster distance between cluster I and II indicate that seed yield per plant could be improved through hybridization among these clusters.

Three genotypes from cluster III (CAT 1788, CAT 2007A, CAT 2562) shows high harvest index with high cluster mean. CAT 2562 also shows superiority over best check (Bragg), one accession CAT 2502 of cluster IX also shows high mean value with high cluster mean.

For number of branches per plant accession GP 499 of cluster II and accessions G141, JS 79-302, CAT 3412 of cluster VIII showed high cluster mean along with high mean value. High inter cluster distance between cluster II and VIII indicate that this character will be best improved using hybridization among accessions of these clusters.

For number of branches per plant, number of nodes per plant, number of pod clusters per plant, number of pods per plant, 100-seed weight and dry matter yield per plant GP 499 of cluster II identified as suitable donors. Therefore Gp499 may be proved very useful as donor to improve these characters.

Conclusion

On the basis of present findings, it can be concluded that 125 genotypes grouped into 9 clusters based on 40 % dissimilarity level which shows great diversity among genotypes. Gp499 of cluster II showed greatest diversity among all the 120 genotypes, therefore Gp499 as well as other identified donor of respective characters can be used to improve soybean in future breeding programmes.

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