Genetic Diversity Analysis in Soybean with Reference to Pod Shattering

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The genetic divergence analysis using Mahalanobis D^2 statistics was carried out in 196 soybean germplasm lines based on the 20 quantitative characters. Estimation of contribution of various characters towards the genetic divergence revealed that individual pod weight was the single largest contributing characters followed by the pod shattering, which is the serious problem in soybean. The 196 germplasm lines were grouped in 11 clusters, of which cluster I accommodated more than 50% of the genotypes. On the contrary four solitary clusters were formed. The 12 shattering resistant genotypes which are identified in the present investigation are distributed in five different clusters indicating the diversity between them and can be utilised in future breeding programme.

Key Words: Genetic Diversity, Pod Shattering, Soybean

A clear understanding of the extent of variability prevalent for each character in germplasm, would imply the scope for improving the character through selection. But in hybridization programme where selection of genetically diverse parents is important to get wide array of recombinants, the knowledge of genetic diversity among the entries of germplasm is necessary. In order to assess the diversity in the germplasm, Mahalanobis D^2 analysis was utilized. The technique has been used in assessing the genetic diversity (Arunachalam and Jawahar, 1967) and proved to be the best tool for selecting the diverse parents for hybridization (Bhatt, 1973).

Pod shattering is an undesirable trait in soybean, known to increase under high temperature and low humidity conditions. The *rabi*/summer season provides the best climate for expression of pod shattering and selection the resistant genotypes. Therefore, the present investigation was carried out to identify the pod shattering resistant genotypes in soybean and to assess the genetic diversity between them.

Materials and Methods

The experiment was conducted with 196 soybean germplasm lines in *rabi*/summer 1999 (December sown). The season was characterized by the high temperature and low relative humidity during the crop maturity, which was conducive for the better expression of pod shattering and associated traits. The experiment was laid out in balanced lattice design with two replications in a single row of 3m with spacing of 45 cm and 15 cm inter- and intra-rows. Observations on six plant growth, four yield attributing and 10 pod characters were recorded. The plant growth characters were days to flower initiation, days to flower termination of main stem, day to maturity, plant height an branches/plant, however, degree of indeterminate growth habit was calculated in day as the difference between days to flower initiation and days to flower termination of main stem. The yield attributing traits were cluster/plant, pods/plant, 100-seed weight (g) and seed yield/plant (g). Pod characters were recorded on the five two-seeded and five three-seeded randomly selected pods. The characters were pod length (mm), pod width (mm), pod thickness (mm), ratio of pod thickness with pod width (PT:PW), ratio of pod thickness with pod length (PT:PL) and seeds/pod. The moisture content of pods at physiological maturity (%), individual pod weight (mg) and seed to pod shell ratio was recorded from the composite sample of 25 pods collected at physiological maturity. However, pod shattering (%) was recorded on the seventh day after maturity as the ratio of number of shattered pods to total number of pods/plant on five randomly selected plants and expression as per cent. Angular transformed values of pod shattering was used for the statistical analysis.

The genetic divergence analysis was done following method suggested by Mahalanobis (1928), however grouping of the genotypes was done as suggested Rao (1960). The per cent contribution of the characters to the genetic diversity was estimated on rank basis of difference value. The Rank 1 is given to the character exhibiting highest mean different and rank 20 to the character possessing the lowest mean difference. Accordingly, the variable that contributes more towards the divergence was identified by ranking of character-wise D^2 value and adding the rank for each character for all the entries. The percentage contribution of each character was calculated by taking 19110 = 100.

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Results and Discussion

Evaluation of Genotypes

Mean pod shattering during *rabi*/summer was 51.87% with the range of 1.2% 9 CGP-67-A) to 95.6 (EC-51150-B). Twelve shattering resistant (below 7% shattering) genotypes were identified, of which ten *viz.*,-EC-14396, CGP-67-A, G-101, NRC-12A, GA-95-A, Himso-107, VLS-38, CGP-268 an GP-7340-A are yellow seeded and WC-7 and EC-7033-A are black seeded genotypes.

Contribution of Different Characters Towards Genetic Divergence

The analysis for estimating the contribution of various characters towards the expression of genetic divergence (Table 1) indicats that individual pod weight was the single character which contributed most towards genetic divergence. Though the individual pod weight varied between the node of the same plant (Nakamura *et al.*, 1987), its highest contribution certainly indicates that this character is the basic component of genetic divergence in soybean. Pod shattering which is a serious problem in soybean, contributes next to that of the individual pod weight. The contribution of pods/plant and plant height are also considerable, but the contributions of other character were meager. Kumar and Nandarajan (1994) also reported that pods/plant and plant height were secondary important traits responsible for genetic divergence in soybean.

Tabel 1. Per cent contribution of 20 characters towards soybean genetic divergence

Character	Number of times ranked first	per cent contribution
Days to flower initiation	9	0.04
Days to flower termination	48	0.25
Degree of indeterminate growth habit	10	0.05
Days to maturity	33	0.17
Plant height	554	2.89
Branches/plant	0	0.00
Clusters/plant	12	0.06
Pods/plant	1048	5.48
Seeds/pod	0	0.0
Moisture contents of pods at physiological maturity	57	0.29
Individual pod weight	15373	80.44
Seed to pod shell ratio	0	0.0
Pod length	0	0.0
Pod width	0	0.0
Pod thickness	0	0.0
PT:PL	0	0.0
PT:PE	0	0.0
Seed yield/plant	1	0.0
Pod shattering	1964	10.27
Total	19110	100.00

Grouping of Genotypes into Various Cluster

The 196 genotypes were grouped into 11 cluster based on D^2 values (Table 2). Cluster I accommodated for more than 50% genotypes. This indicates that considerable portion of the germplasm was redundant but the intra-cluster distance was moderate, indicating sufficient diversity between them. In contrast to that, four solitary clusters were formed indicating that these genotypes were diverse from others. The 22 black/brown-seeded genotypes got distributed in four cluster. Cluster I accommodated 11, whereas cluster III had seven and cluster IV had three such genotypes. Remaining one block seeded genotypes was the member of cluster V. The four spreading genotypes were grouped in cluster I (BR-3) and cluster IV (WC-7, EC-7033-A and G-56). This indicates existence of sufficient diversity among the black/brown seeded genotypes. The two shattering resistant checks *viz.*, -Bragg and JS-335 fall in cluster I, whereas Himso-1520 was in cluster II. Two highly susceptible checks Monetta and Block soybean were the members of cluster I and V, respectively. However, MACS-58 (moderately resistant) and JS80-21 (moderately susceptible) checks belongs to cluster III. The resistant genotypes which were identified in the present study are distributed in five different clusters. This suggested the sufficient diversity between them and can be utilized in future breeding programmes.

Intra- and Inter-cluster Distances

The average intra- and inter-cluster distances are presented in Table 3. Cluster XI had the highest intra-cluster distance of 81.64 followed by cluster IV (63.79), cluster III (63.15) and cluster I (62.68). the other intra-cluster distances were 54.41, 48.83 and 37.45 for cluster number II, VI and respectively.

The inter-cluster distances ranged from 53.07 (between two single member cluster VIII and IX) to 606.9 (between cluster VI and XI). Cluster V and XI were the next best diverse clusters as the distance between them was 586.9. Cluster I was closely related to cluster VII (103.2) and cluster II (110.6). Cluster X (119.6) was the next proximal cluster followed by cluster III (125.7). Cluster XI was the farthest from cluster I with D^2 value of 383.6. Cluster II was nearest the cluster IV (111.3) and farthest from cluster VI (332.9). Like wise cluster III was nearest with cluster VII (94.75) and maximum diverse with cluster XI (490.8). The inter-cluster distance between cluster IV with other cluster indicated the lowest distance with VIII (102.4) and highest distance with cluster VI

Table 2. Clustering pattern of 196 soybean genotypes

Cluster number	Number of genotypes	Genotypes
I	108	EC-14396, CGP-67-A, G-101, CGP-85-1, EC-4-A, EC-7033, CGP-927-A, EC-109923, G-95-A, CGP-43, RPSP-227, Pusa-16-A, VLS-9, **EC-11093, G-1080, EC118420, EC-118420-A, BR-3*, IC-18736, AGS-28, CG-103, WC-66-A, CGP-43-B, R2-T21-C,** WC-58, EC-51160-B, EC-51160, AGS-56-B-A, AGS-56-B, AGS-56, IC-100956, G-58, AGS-48, IC-39506, EC-10954, CGP-2426-B, CGP-2426-A, K-202, CGP-927-A-A, CGP-2426-B-A, EC—10954-A, G-78-A, G-58-A, AGS-56-B-C, NIC-19836, CGP-927-B, EC-34092, CGP-253-A, Pusa-16, VLS-45-A, G-75, G-124, G-7340-A, T-35, BR-8, G-22, BS-86-75, G-1412, WC-66, IC-28-A, JS-335, G-130-A, ***Monetta*, Bragg,*** g-1080, CGPB-84, PK-1197, AGS-80, G-140, IC-118233, Line-24, G-147-A, SL-238, KB-83, GP-284, CGP-1405, G-1374, EC-14396-A, ADG-41-A, EC-23-A, WC-23, G-101-A, R2-T38, EC-289073, CGP-268, CGP-1042, GL-38-A, EC-16, IC-47657, CGP-188, CGP-188-A, G-124B, EC-118237-A, JS-1, M-558, WC-16-A, G-147, 94-4, EC-63, WC-4, EC-35657, IC-49859, CGP-85-1.
II	35	NRC-12-A, G-158, EC-391515, G-158-A, CGP-2653, CGP-67, G-156-A, GP-7340-A, PK-262-A, JS-2, TAS-90, IC-11645, IC-104877, G-92-A, EC-104817, R2-T31-B, RSC-2, RSC-3, MACS-45-2, CGPB-84-C, CGPB-84-A, G-540, EC-246, HIMCO-1520, G-92, L-449, G-48, IPS-94, G-237, CGP-108, GP-108, GP-7340-A, EC-118237, G-95, EC-141383, WC-4-A.
III	32	G-74, G-55-1, **EC-109545-A, IC-15997, G-1074, GL-38, G-48-A, G-7340, EC-280129,** EC-39026, AGS-38, G-32, AGS-56-B-B, EC-11843, UGM-20, IC-39506-A, G-124-A, NIC-19836-A, Gaurav, khsB-2, Hardee, IC-28, EC-11893, MACS-58, Ankur, CGP-188-B, G-172-A, WC-15, EC-34083, JS80-21, WC-12-A, WC-12.
IV	6	NRC-12C, PK-262, NRC-12-B, Himso-107, PK-1165, ADG-41.
V	2	6g-78, ***Black Soybean****
VI	7	**WC-7*, EC-7033-A, G-156*,** G-494, CGP-924-B, G-130, G-237-A.
VII	1	1-32
VIII	1	PK-472
IX	1	VLS-38
X	1	EC-109545
XI	2	G-26, AVRDC-20.

Bold = Black seeded genotypes, Bold* = Black seeded spreading genotypes, Italic & Bold = Resistance checks, Italic & Bold* = Susceptible checks

Table 3. Average intra- and inter-cluster distances between 11 clusters in soybean

Cluster*	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**62.68**	110.6	125.7	200.9	214.4	250.7	103.2	285.4	312.1	119.6	383.6
II	10.52	**54.51**	211.0	111.3	305.1	332.9	170.2	192.8	219.5	155.3	290.7
III	11.21	14.52	**63.15**	306.0	111.3	159.6	93.75	393.2	419.6	145.8	490.8
IV	14.17	10.55	17.49	**63.79**	401.2	425.5	260.0	102.4	131.3	233.3	197.1
V	14.64	17.46	10.54	20.03	**37.45**	102.1	160.8	489.8	515.7	216.6	586.6
VI	15.83	18.24	12.63	20.62	10.10	**48.83**	170.8	514.5	537.6	211.5	606.9
VII	10.16	13.04	9.68	16.12	12.68	13.07	**0.00**	348.1	373.4	64.45	441.1
VIII	16.89	13.88	19.82	10.12	22.13	22.68	18.65	**0.00**	53.07	318.1	108.6
IX	17.66	14.81	20.48	11.45	22.71	23.18	19.32	7.28	**0.00**	344.9	97.96
X	10.93	12.46	12.07	15.27	14.71	14.54	8.02	17.83	18.57	**0.00**	406.6
XI	19.58	17.05	22.15	14.03	24.22	24.63	21.00	10.42	9.89	20.16	**81.64**

* Main diagonal (bold) = inter-cluster D^2 value; Upper diagonal = inter-cluster D^2 value; Lower diagonal = inter-cluster D value

(425.4). Cluster V with cluster and cluster VI with cluster VII and closely related. Cluster VII had lowest distance with cluster x (64.45) and maximum with cluster XI 441.1 Cluster X with the farthest from cluster VIII and IX.

According to Arunachalam *et al.*, (1984) the optimum level of genetic divergence between the parents gives the best heterosis and better segregants. However, Shwe *et al.*, (1972) and Sichkar *et al.*, (1988) suggested that hybridization between highly divergent parent generate promising breeding material.

The method suggested by Arunchalam *et al.*, (1984) was used to classify the genetic divergence present in the germplasm using the intra-and inter-cluster distance. The procedure consisted of the estimation of mean and standard deviation of intra- and inter-cluster distance (D value) and classified into four divergence classes (DC1, DC2, DC3, DC4). As in the present study 11 clusters were formed, of which four contained single variety. Obviously intra-cluster D values for these clusters were zero. Thus, there were 55 inter-cluster, but only seven were intra-cluster D value. 62 D values ranged from 6.11 t 24.63 with the mean of 14.76 and standard deviation of 5.00. Thus, four divergence classes are than DC1 = 24.77 to 19.77, DC = 14.76 to 19.76, DC3=9.75 to 14.75 and DC4 = 9.74 to 4.74.

Cluster classification based on these divergence classes are presented in Table 4. It is evident from the table that, of the 55 inter- cluster distances, 13 come under the divergence class 1, 15 and 24 inter cluster distances come under the divergence class 2 and 3respectively. However, only three inter cluster distances represent the divergence classes (DC-2 and DC-3) from the other clusters. However, cluster III and VII represent all the four divergence class distance with other clusters.

Twelve shattering resistant genotypes were distributed in five different clusters, i.e. cluster I, II, IV, VI and IX. These clusters belong to divergence class DC2 and DC3, except the cluster VI from IV and IX comes under DC1. Moreover the genotypes belongs to cluster VI work black seed genotypes.

Individual D^2 values between the genotypes indicated that EC-14396, CGP-67-A, G-0101 were close, but Bragg had optimum diversity with others in cluster I, whereas NRC-12-A and EC-3911515 had optimum distance in cluster II. Intermitting of these genotypes or crossing with Himso-107 (cluster IV) and VLS 38 (Cluster IX) may give better chance for developing shattering resistance genotypes.

Cluster Mean Analysis

The study of clusters mean value of 11 clusters indicated considerable differences for the characters studies (Table 5). After leaving out the solitary clusters, the range of variation for days to flower initiation, seeds/pod, PT:PL and PT:PW were low among the multi-member clusters. The characters *viz.*- days to flower termination, degree of indeterminate growth habit, 100-seed weight, moisture content of pod at physiological maturity, seed to pod shell ratio, pod length, pod width and pod thickness exhibited moderate variations. The high range of variation was observed for days to maturity, plant height, branches/plant, cluster/plant individual pod weight, seed yield and pod shattering among the different clusters.

The variations observed in cluster mean also point out the degree of variability. In the present investigation, clusters I, II, IX had early flowering initiation genotypes, whereas cluster I, II, IV, VIII, IX and XI had early flowering termination genotypes than the population mean. Cluster I, IV, VIII, IX and XI had lower degree for indeterminate growth habit. The genotypes included in clusters I, IX and XI recorded early maturity. Above

Table 4. Classification of inter-cluster distances into four divergence classes*

Divergence class	Divergence cluster	
	From	To
DC1	III	VIII, IX, XI
	IV	V, VI
	V	VIII, IX, XI
	VI	VIII, IX, XI
	VII	XI
	X	XI
DC2	I	VI, VIII, IX, X
	II	V, VI, IX, XI
	III	IV
	IV	VII, X
	VII	VIII, IX
	VIII	X
	IX	X
DC3	I	II, III, IV, V, VII, X
	II	III, IV, VII, VIII, X
	III	V, VI, X
	IV	VIII, IX, XI
	V	VI, VII, X
	VI	VII, X
	VIII	XI
	IX	XI
DC4	III	VII
	VII	X
	VIII	IX

* According to Arunachalam *et al.*, (1984)

Table 5. Cluster mean for 20 quantitative characters in soybean

Character	Cluster number										GM
	I	II	III	IV	V	VI	VII	VIII	IX*	X*	XI	
DFI	44.4	44.1	46.3	45.1	47.0	46.2	55.5	47.0	41.5	62.5	45.5	44.93
DFT	58.3	59.1	61.8	56.7	64.8	63.4	75.0	57.0	49.5	81.0	57.3	59.30
DID	13.8	15.0	15.5	11.6	17.8	17.2	19.5	10.0	8.0	18.5	11.8	14.38
DM	94.7	97.0	97.4	97.3	98.3	102.6	103.0	99.0	94.0	112.5	96.0	96.11
PH	34.2	34.1	43.4	27.9	62.3	60.2	72.6	27.6	47.7	56.5	40.7	37.10
BP	2.9	3.3	3.5	2.9	4.4	4.2	5.0	2.1	3.6	6.0	2.6	3.13
CP	17.7	19.1	21.1	16.5	25.3	32.5	35.3	12.4	9.7	46.8	19.6	19.25
PP	42.5	47.9	50.5	41.5	67.3	78.8	101.3	29.0	22.1	141.0	44.4	46.96
SP	2.4	2.5	2.3	2.3	2.3	2.2	2.8	2.2	2.5	2.6	2.5	2.42
SW	11.0	12.3	9.0	13.4	10.3	11.7	15.0	13.9	19.4	5.6	14.4	11.10
MCP	57.0	57.3	56.7	56.4	59.5	56.6	57.3	39.6	59.7	52.7	45.2	56.8
IPW	423.5	527.4	316.4	569.8	315.0	452.0	370.0	705.5	730.0	413.5	803.3	435.5
S:PS	1.6	1.6	1.6	1.7	1.6	1.7	1.9	0.5	1.9	1.9	0.7	1.61
PL	4.17	42.9	39.8	42.6	38.8	40.4	42.0	41.6	52.8	41.5	47.1	41.6
PW	9.3	9.6	8.8	10.0	8.0	8.9	8.9	9.3	10.4	8.9	9.9	9.27
PT	5.4	5.5	4.6	5.6	4.8	4.7	4.9	4.7	5.2	4.9	5.6	5.23
PT:PL	0.130	0.133	0.127	0.117	0.127	0.120	0.102	0.106	0.098	0.118	0.119	0.126
PT:PW	0.582	0.577	0.570	0.526	0.545	0.550	0.455	0.503	0.500	0.551	0.569	0.566
SY	4.3	5.0	4.0	4.5	3.9	5.7	6.5	2.9	5.5	7.9	2.7	4.47
PSh	52.0	48.1	59.5	36.7	86.1	43.1	50.5	48.9	4.0	46.2	55.3	51.87

* Solitary clusters

average plant height was found in most of the clusters, but cluster III and IX had moderate plant height with increased branches/plant. So the cluster I and IV had desirable means for plant growth characters.

For the yield attributing trait cluster III, V and VI had higher means for clusters/plant and pods/plant. 100-seed weight was more in cluster, II, IV, VI, XI and solitary clusters except cluster X. These results imply that cluster VI possessed the desirable mean for yield attributing traits, part from solitary clusters VII and X.

The mean of clusters of important pod characters indicates that individual pod weight was higher in clusters II, IV, VI, VII, IX and XI, whereas clusters II, IV, VII and IX and XI possessed the higher pod length. The higher seed to pod shell ration was observed in clusters IV, VI, VII, IX and X. Although the seven clusters had lower pod shattering than the population mean, a solitary cluster IX had the desirable means for important pod characters. In addition to this cluster IV had mean in desirable direction for plant yield and pod characters. So the genotypes included in this cluster can have more utility value for overall improvement.

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