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GENETIC DIVERGENCE IN SOYBEAN FOR PHYSIOLOGICAL AND YIELD ATTRIBUTES UNDER RAINFED CONDITION

JAYLAL

Department of Plant Breeding and Genetics, Birsa Agricultural University
Ranchi 834006

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ABSTRACT

Forty genotypes of soybean were grouped in nine clusters on the basis of chlorophyll components and seven clusters with respect to yield attributes. The genotypes KD 1, DS 2, MACS 153 and MACS 189 had distinct identity with respect to chlorophyll components and yield attributes. Crossing between genotypes of the clusters I and IX for chlorophyll components along with carotene content and cluster V (DS 8) as well as cluster VI (KB 38, BR 16) for seed yield and yield attributes is suggested.

Key words: Cluster analysis, Chlorophyll components, Genetic divergence, Soybean.

Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically diverse parents in any breeding programme, is essential to create new genetic stock. Earlier workers showed the importance of study of genetic divergence for yield and yield attributes [1, 2] and for chlorophyll components with carotene content [3]. In the present investigation, genetic diversity in a set of 40 soybean genotypes has been assessed by multivariate analysis for yield and chlorophyll components along with carotene content.

MATERIALS AND METHODS

Forty genotypes belonging to different agroclimatic regions (Table 1) were sown in randomized block design with 3 replications at Ranchi. Each genotypes was sown in 3 rows, 3 m long, at a distance of 45 cm between rows. Chlorophyll and carotene content were estimated by the standard methods [4–7]. Leaf samples were taken from flower initiation node (FIN) i.e. 4th node and other node (ON). The data were recorded on 5 random competitive plants in each treatment from each replication for 8 metric traits of yield and yield attributes and eight chlorophyll components and carotene content. Pooled data for each set of eight characters were taken for analysis. The analysis of genetic divergence was carried out using Mahalanobis' D^2 statistics. The genotypes were grouped in clusters by the Toucher's method as described by Rao [8] and Mahalanobis [9] separately on the basis of yield attributes, chlorophyll components and carotene content.

RESULTS AND DISCUSSION

The Wilk's test revealed highly significant differences (χ^2 values = 242.31) for all the characters (Table 2). Forty genotypes were grouped into nine clusters (Table 3). The lines from Himachal Pradesh, Junagarh, Ludhiana, New Delhi, Dharwar and Pune were spread over clusters I and II; I, II and III; I and VI; I and VIII; I and VIII; and I, II VII, respectively,

Table 1. Distribution of 40 genotypes of soybean on the basis of yield attributes and chlorophyll components along with carotene per cent and yield

Cluster	Number of genotypes	Genotypes with origin (chlorophyll and carotene %)	Number of genotypes	Genotypes (yield attributes)
I	26	Birsa Soybean-1, BR 16, BR 17 (BAU, Bihar), Bragg (USA), DS 8, DS 9, DS 10 (IARI, New Delhi), HIMSO 1520, HIMSO 1533 (HPAU, H.P.), J 323, (GAU, Junagarh), JS 71-5, JS 81-303, JS 81-607, JS 81-714 (JNKVV, Jabalpur), KD 2 (UAS, Dharwar), MACS 13 (Pune), PK 416, PK 472, PK 879, PK 884, PK 885 (GBPUAT, Pantnagar), SH 84-25, (HAU, Hissar), SL 141, SL 142 (PAU, Ludhiana), VLS 7, VLS 8 (VPKAS, Almora)	23	Birsa Soybean-1, DS 9, DS 10, HIMSO 1520, HIMSO 1532, HIMSO 1533, J 75-27-51, J 140, J 323, JS 81-607, JS 81-714, KB 34, PK 472, PK 838, PK 879, PK 884, PK 885, SL 140, SL 141, SL 142, UGM 21, VLS 7, VLS 8
II	5	HIMSO 1532 (HPAU, H.P.), KB 34, KB 38 (UAS, Bangalore), MACS 153, MACS 189 (Pune)	7	JS 71-5, JS 81-303, KD 2, MACS 189, MACS 153, PK 416, SH 84-25
III	1	J 140 (GAU, Junagarh)	3	KD 1, DS 2, MACS 141
IV	1	J 75-27-51 (GAU, Junagarh)	3	BR 17, Bragg, MACS 13
V	2	PK 838, PK 863 (GBPUAT, Pantnagar)	1	DS 8
VI	1	SL 140 (PAU, Ludhiana)	2	KB 38, BR 16
VII	1	MACS 141 (Pune)	1	PK 863
VIII	2	KD 1 (UAS, Dharwar, DS 2 (IARI, New Delhi)		
IX	1	UGM 21 (TNAU, Coimbatore)		

Table 2. Canonical vectors and contribution of quantitative characters in soybean for chlorophyll, carotene content and yield attributes

Character	Canonical vectors			Contribution (%) to diversity (D^2)
	Z_1	Z_2	Z_3	
A. Chlorophyll components and carotene content:				
Chlorophyll a (FIN)	0.07	- 0.20	0.10	8.05
Chlorophyll a (ON)	- 0.01	0.04	- 0.01	0.00
Chlorophyll b (FIN)	0.01	- 0.02	- 0.00	0.00
Chlorophyll b (ON)	0.02	- 0.02	- 0.04	0.00
Carotene content (FIN)	- 0.02	0.03	- 0.01	0.00
Carotene content (ON)	0.26	- 0.99	- 0.14	23.45
Total chlorophyll (FIN)	1.07	0.26	- 0.12	43.90
Total chlorophyll (ON)	- 0.14	0.08	- 1.13	24.60
Contribution to variability (%)	51.89	32.93	11.09	
Total variability	95.90			
B. Quantitative characters:				
100-seed weight	0.11	- 0.12	- 0.01	1.07
Seeds per pod	- 0.02	- 0.01	- 0.07	1.00
Pods per plant	- 0.02	0.01	- 0.03	4.00
Pods per cluster	1.03	0.23	- 0.04	50.02
Days to maturity	0.09	- 0.04	- 0.08	2.30
Branches per plant	0.00	- 0.37	- 0.75	16.41
Leaflets per plant	- 0.23	0.23	0.19	4.60
Seed yield per plant	0.22	- 0.77	0.41	20.60
Contribution to variation (%)	65.16	18.77	10.84	
Total variation	94.77			

on the basis of chlorophyll components alongwith carotene content (Table 1). The clustering pattern of the lines suggested that geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of varieties for hybridization should be based on genetic diversity rather than geographic diversity [10]. In contrast, all lines from Bihar (3), Jabalpur (4) and Almora (2) were grouped into a single cluster, viz. I, indicating genetic similarly among lines coming from different geographic area, as was also observed by Jeswani et al. [11].

On the basis of the present study it can be suggested that though geographic diversity may not necessarily be an index of genetic diversity, due attention should be paid to geographic diversity if sufficient genetic diversity has to be accumulated in the germplasm or lines [12].

The constellations obtained by D^2 analysis were also confirmed by canonical analysis (Table 2). The first three canonical vectors accounted for 95.9% of total genetic divergence, maximum intracluster distance was observed in cluster VIII and minimum in cluster V. The highest intercluster distance was observed between clusters I and IX (60.3) and lowest between III and IV (8.0) (Table 3). Hybridization between genotypes falling in the most distant clusters I and IX should result in maximum hybrid vigour and eventually desirable segregates or desirable combinations leading to development of useful genetic stocks and varieties.

Table 3. Mean intra- (in bold) and intercluster distance (D^2 values) in soybean for chlorophyll components along with carotene content and yield with yield attributes (in parentheses)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**11.9** **(31.4)**	23.9 (45.4)	17.4 (76.8)	20.7 (43.9)	35.4 (44.8)	18.2 (110.3)	21.6 (47.6)	40.2	60.3
II		**10.6** **(31.2)**	21.3 (54.9)	26.9 (54.3)	55.9 (50.4)	30.6 (84.1)	26.9 (59.9)	40.3	55.4
III			**0.0** **(20.5)**	7.9 (63.1)	44.9 (94.2)	15.8 (39.1)	25.7 (74.1)	41.4	23.7
IV				**0.0** **(23.3)**	44.9 (68.1)	19.5 (96.2)	32.5 (47.2)	48.6	15.4
V					**9.6** **(0.0)**	34.8 (123.3)	40.9 (79.2)	55.3	40.9
VI						**0.0** **(10.3)**	21.5 (109.1)	35.8	25.4
VII							**0.0** **(0.0)**	20.6	15.7
VIII								**15.4**	16.9
IX									**0.0**

The analysis for estimating the contribution of chlorophyll components and carotene content towards the expression of genetic divergence (Table 3) indicated that carotene content (ON) 23.45%, total chlorophyll (FIN) 43.90% and total chlorophyll (ON) 24.60% contributed maximum to the total genetic divergence in the material. These physiological attributes accounted for more than 90% of total divergence in the collection. It is clear that these are the basic physiological parameters which need greater attention.

Analysis of variance showed significant differences among the strains for all the characters, indicating the existence of genetic diversity among the varieties. The dispersion between the variables was also highly significant as tested by Wilk's criterion. Therefore, further analysis to estimate D^2 values was done and on the basis of the relative magnitude of D^2 values, and all the 40 genotypes were grouped into seven clusters (Table 1). The highest intercluster distance was between V and VI (123.3) (Table 3). Hybridization between genotypes falling in the most distant clusters V (DS 8) and VI (KB 38, BR 16) should result in maximum hybrid vigour and eventually desirable segregates. Also, based on mean performance, genetic distance and clustering pattern, hybridization involving genotypes from the clusters VI (KB 38, BR 16) and VII (PK 863) should result in desirable combinations leading to development of usual genetic stocks and varieties.

The cluster constellations obtained by D^2 analysis were also confirmed by canonical analysis (Table 2). The canonical vectors corresponding to the three largest roots (λ_1, λ_2 and λ_3) provided the three best orthogonal vectors Z_1, Z_2 and Z_3. Maximum variability was accounted for only by Z_1 (65.16%) and nearly 94.77% by the first three vectors. A comparison of the values of the first three canonical vectors for the genotypes also supports the existance of considerable variability between genotypes. Number of pods per cluster in Z_1 (1.03) and Z_2 (0.22), and seed yield per plant in Z_1 (0.22) and Z_3 (0.41) had maximum positive values. Number of seeds per pod had negative values in Z_1, Z_2 and Z_3. Thus, canonical analysis also confirms the existence of substantial genetic divergence.

The analysis of the contribution of various characters in the expression of genetic divergence (Table 2) indicated that pods per cluster (50.02%), branches per plant (16.40%), and seed yield per plant (20.60%) contributed maximum to the total genetic divergence in the collection. It is clear that these characters are the basic attributes of plant architecture which need greater attention, as they accounted for more than 85% of total divergence in the materials. Mahto and Verma [13] reported similar observations for siliquae per plant, seeds per siliqua and seed yield per plant in Indian mustard under rainfed condition. Ranga Rao et al. [14] reported that seed yield per plant and capitula per plant contribute more towards diversity in the safflower collections studied under two environments. Mahto et al. [15] reported test weight, seed yield per plant, plant height and days to maturity to be the basic attributes in sesame. Mahto [16] had observed number of branches and seed yield per plant as basic attributes in soybean.

MACS 153 and MACS 189 were clubbed in cluster II on the basis of chlorophyll components and carotene content, and yield and its attributes. The genotypes KD 1, and DS 2 were grouped in clusters VIII and III on the basis of chlorophyll components and yield attributes, respectively. The present study revealed that considerable genetic diversity is present among the entries for yield and its attributes. Six clusters were superior: clusters I and IX for chlorophyll components, II and V for chlorophyll components and carotene content, V and VI for yield, and VI and VII for yield attributes. Intercrossing between genotypes of these diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars. Clustering was more elaborate on the basis of chlorophyll components and carotene content than based on yield and its attributes as chlorophyll components were spread over nine clusters and yield attributes over seven clusters.

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