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Research Article

GENETIC DIVERGENCE STUDIES IN SOYBEAN (*Glycine max* L. MERRILL)

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Abstract- An experiment was conducted during kharif 2013 on forty genotypes of soybean to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The data were recorded on eleven important quantitative traits from the genotypes grown in randomized block design with three replications. The forty soybean genotypes were grouped into six clusters. The cluster III was the largest cluster with thirteen genotypes. Highest inter cluster distance was observed between cluster I & cluster VI followed by between V & VI and V and VI respectively. The genotypes JS 20-89 having diverse genetic base for yield contributing components (cluster VI) was identified for yield characters primary branches per plant (3.67), number of pods per plant (111.67), number of seeds per pod(2.78), number of three seeded pods per plant(95.33), harvest index (35.21) and seed yield per plant. Whereas genotypes RVS 2000-4, KDS 72, NRC 107, RVS 2002-22, RVS 2002-19, MAUS613 can be used for shorter maturity duration and plant height (cluster I) was identified for early maturity with early flowering habit and average plant height. Genotypes included in these two clusters can be utilized for future crop improvement programm.

Keywords- Soybean, Genetic diversity, Inter and intra cluster distance

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Introduction

Soybean(*Glycine max* L. Merrill)is an important source of high quality protein and oil. It is however, characterized by low yield only because of low yield varieties, lodging and pod shattering, which are major production constrains. Soybean has the highest protein content of all other food crops and is second only to ground nut in terms of oil content. Assessing genetic diversity of cultivated crop plants is very important to select better genotypes for a hybridization program. Genetic diversity is always important in any breeding programme to create new genetic stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. To analyze genetic diversity in any population methods have relied on pedigree data, morphological data, agronomic performance data, biochemical data, and more recently molecular (DNA-based) data. For reasonably accurate and unbiased estimates of genetic diversity, adequate attention has to be devoted to utilization of various data sets using clustering procedures and other multivariate methods in analyses of data. The divergence can be studied by technique using D2 statistics developed by Mahalanobis [1]. It is based on multivariate analysis and grouped into various cluster. This is considered as the most effective method to assess the genetic diversity present among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the genotypes and to identify the diverse genotypes for future.

Material and Methods

Forty genotypes of soybean from different AICRP centers of the country were tested in randomized block design with three replications at Rajmata Vijayaraje Scindia Krishi VishwaVidyalaya, College of Agriculture, Gwalior, India, during kharif 2013. Each genotype was grown in a 3 row plot of 4 m long with row to row 30 and plant to plant 5 cm spacing. Observations were recorded on five randomly tagged plants for days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, number of three seeded pods per plant, number of two seeded pods per plant, 100 seed weight (g), harvest index and seed yield per plant (g). Wilks criteria were used to test the significance of differences in mean values of all the 10 characters. Genetic diversity was studied using Mahalanobis's D^2 analysis. Intra and inter-cluster distances and mean performance of the clusters for the characters were also computed.

Results and discussion

The analysis of variance for the experimental design showed highly significant differences among genotypes for all the characters studied. Based on D^2 values 40 genotypes were grouped into VI clusters [Table-1]. The cluster III was the largest and consisted of 13 genotypes followed by clusters I which had 10 genotypes.

Table-1 *Distribution of 40 genotypes into different clusters*

S. No	Cluster No.	No. of genotypes	Name of genotype
1	I	10	SL 995, NRC 111, MACS 1410, JS 20-53, HIMSO 1685, DSb 23-2, KBS 100-2021, VLS 87, BAUS 96, RSC 10-04
2	II	8	PS1539, DS 2047, JS 20-79, NRC 98, PS 1543, NRC 96, NRC 97, MACS 1420
3	III	13	KDS726, DS 3050, SL 983, DS 2961, RKS 109, AMS 1001, MACS 1419, RKS 111, BAUS 27, DSb 25, MAUS 613, KDS 743, MACS 1370
4	IV	2	RSC 10-17, PS 1540
5	V	6	RVS 2000-4, KDS 72, NRC 107, RVS 2002-22, RVS 2002-19, MAUS613
6	VI	1	JS 20-89

The cluster II had 8 genotypes, cluster IV had 2 genotypes cluster V

had 6 genotypes and cluster VI had 1 genotype. This suggested the presence of high degree of divergence among genotypes.

Highest inter cluster distance was observed between cluster I & cluster VI followed by between V &VI and III and VI respectively [Table-2].Average intra and inter cluster D^2 values among 40 genotypes revealed that the cluster II showed maximum intra cluster D^2 value (5.368) followed by cluster I (4.991) and cluster III (4.507) indicating presence of diversity in these clusters. The inter cluster D^2 values ranged from 77.159 to 7.274. Maximum inter cluster D^2 value 77.159 was observed between cluster I & cluster VI.

The diversity among the genotypes which is measured by inter cluster distances, was adequate for improvement by hybridization and selection [2-3] in the present study the crosses made between the genotypes of clusters separated by large inter-cluster distances [4-5] likely to show high heterosis. Similar findings have been reported by [6]. Minimum inter cluster D^2 value was observed between cluster I and III (7.274) indicating the close relationship among the genotypes included in these two clusters.

The average cluster means for 6 characters [Table-3] revealed that genotypes included in cluster V were of early maturity with early flowering habit. Cluster V genotypes had minimum plant height and shorter duration for maturity however genotypes included in cluster I, II and III were of average plant height. For yield characters the genotypes included in the cluster VI showed highest mean value for primary branches per plant (3.67), number of pods per plant (111.67),number of seeds per pod(2.78), number of three seeded pods per plant(95.33),harvest index (35.21) and seed yield per plant (17.05) [7]. This cluster has one genotype JS 20-89. Selection of genotypes from this cluster for these characters may yield desirable results.

Table-2 *Average intra and inter cluster D^2 values of 40 genotypes of soybean*

Cluster	I	II	III	IV	V	VI
I	4.991	8.323	7.274	28.270	10.068	77.159
II		5.368	14.055	15.148	12.759	40.641
III			4.507	22.677	10.285	71.403
IV				3.119	34.610	41.719
V					3.960	75.186
VI						0.000

Table-3 *The mean values of six characters for 6 clusters in 40 genotypes of soybean*

Cluster	I	II	III	IV	V	VI
Days to 50% flowering	52.97	48.79	51.48	55.33	43.78	51.33
Days to maturity	112.80	110.08	115.41	113.67	97.78	109.67
Plant height (cm)	58.59	68.98	69.23	83.73	54.83	82.13
Number of primary branches	3.30	3.62	3.21	5.67	2.94	3.67
Number of pods/plant	35.83	58.67	33.67	69.33	33.06	111.67
Number of seeds/pod	2.14	2.38	2.54	2.65	2.42	2.78
No. of three seeded pods/plant	5.17	22.38	16.28	37.33	12.56	95.33
No. of two seeded pods/plant	29.30	37.92	14.28	21.33	18.06	28.00
100 seed weight (g)	11.83	12.87	11.25	13.17	12.19	12.79
Harvest index	18.53	21.48	15.58	17.54	18.13	35.21
Seed yield/plant (g)	8.15	11.57	6.65	9.58	7.48	17.05

Cluster II showed highest mean performance for number of two seeded pods per plant(37.92) this cluster also has higher mean performance for 100 seed weight, seed yield per plant and harvest index. Whereas cluster IV showed highest mean performance for 100 seed weight. The grouping pattern did not show any relationship between genetic divergence and geographic diversity which has been the point of debate in the past. Similar observations were reported earlier also[8-10].

Conclusion

It can be concluded from present study that considerable genetic variability was exist in the present material. Selection based on phenotypic performance of yield factors indicates that genotypes JS 20-89 having diverse genetic base for yield contributing components were promising for utilization in further breeding programmes for genetic improvement in seed yield. Whereas genotypes RVS 2000-4, KDS 72, NRC 107, RVS 2002-22, RVS 2002-19, MAUS613 can be used for shorter maturity duration and plant height.

Abbreviations: None declared

Conflict of Interest: None declared

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