SELECTION OF SUPERIOR GERMPLASM LINES FOR SOYBEAN BASED ON MORPHOLOGICAL CHARACTRS FOR HYBRIDISATION

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Fifty genotypes including both indigenous and exotic soybean (*Glycine max*) genotypes were evaluated for genetic divergence to identify the likely desirable and potential parents in soybean breeding programme. Genetic divergence was studied for morphological characters like growth habit, flower colour, pubescence density, leaflet shape, leaf colour, pod colour and seed coat colour. Anderson meteroglyph analysis method was used for computing genetic divergence. All the 50 genotypes were grouped into nine clusters. The contribution of characters like growth habit, pubescence density, leaflet shape and pod colour were higher as compared to chasracters like flower colour, leaf colour and seed coat colour. The two characters growth habit and pubescence density contributed more to variations among the genotypes, the parents should be selected for hybridization on the basis of these characters.

Keywords : Clustering; Morphological characters; Soybean.

Introduction

Soybean (Glycine max (L) Merril) ranks on the top of the list of oilseed crops on the global scale. However, overall improvement in the yield, oil and protein content in soybean remains the task with the plant breeders. This can be achieved through selection, efficiency of which mainly depends upon the extent of variability existing in the above material. In self-pollinated crops crop species like soybean, germplasm is available in the form multitude of homozygous lines. Limited mating flexibility resulting from the normal population and biparental mating system necessitates critical choice of parents in breeding programme. Out of methods adopted for selection of parents, methods based on measurement of divergence enables evaluation of parents without actual crossing and grouping the parental material into few clusters in a significant pattern. The grouping of parental materials into clusters can be done on basis of morphological, biometrical and molecular characters. In this study an attempt has been made to select the superior line of soybean by clustering on the basis of morphological characters.

Materials and Methods

Fifty soybean genotypes including both indigenous and exotic lines were raised in Completely Randomized Block Design with three replication at the Farm of Botany Section, College of Agriculture, Nagpur, during *Kharif* 2000. Observations on nine morphological characters viz. growth habit, flower colour, pubescence density, leaflet shape, leaf colour, pod colour and seed coat colour. The data recorded were subjected to meteroglyph analysis as proposed by Anderson¹. All the morphological characters were visually scored and categorized in to different groups, the data recorded on the pubescence density and pod colour (the most variable characters) were converted into mean scores index by using the following formulae -

*	(1 x No. of plants in grade 1)
Mean	$+(2 \times No. of plants in grade 2)$
Score =	$+(3 \times No. of plants in grade 3)$
Index	$+(4 \times No. \text{ of plants in grade 4})$
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Total number of plants scored

and used for plotting X and Y axis, respectively, and representing the genotype in the form of a glyph.

Result and Discussion

The 50 soybean genotypes including exotic and indigenous widely varied from one another with respect to different morphological characters (Table 1). The meteroglyph analysis between the genotypes for all the seven morphological characters also indicated the presence of considerable variation among

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Table 1. Morphological characters of fifty soybean genotypes.

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Sr.	Genotypes	Growth	Flower	Pube-	Leaflet	Leaf	Pod	Seed coat
No:		habit	colour	scence	shape	colour	colour	colour
1.	EC-241401	Indeterminate	Purple	Normal	Normal	Green	L Brown	Black
2.	EC-118057	Indeterminate	Purple	Normal	Broad	D Green	Brown	Black
3.	ÉC-2515	Determinate	Purple	Normal	Broad	Green	Straw	Yellow
4.	EC-3853	Indeterminate	Purple	Sparse	Broad	L Green	Brown	Yellow
5.	EC-39147	Indeterminate	Purple	Normal	Small	Green	Straw	Yellow
6.	EC-118036	Determinate	Purple	Sparse	Broad	L Green	Straw	Yellow
7.	EC-351469	Determinate	Purple	Normal	Broad	L Green	L Brown	Yellow
8.	AMS98-9	Determinate	Purple	Sparse	Broad	L Green	Straw	Yellow
9.	EC-385314	Determinate	Purple	Normal	Broad	Green	L Brown	Yellow
10.	EC-37933	Semi-determinate	Purple	Normal	Broad	Green	Straw	Yellow
11.	EC-385323	Determinate	Purple	Dense	Broad	L Green	Straw	Yellow
12.	EC-39179	Determinate	Purple	Normal	Broad	Green	Straw	Yellow
13.	EC-385319	Determinate	Purple	Sparse	Broad	D Green	Straw	Yellow
14.	AMS98-20	Determinate	Purple	Sparse	Broad	L Green	Straw	Yellow
15.	PKV-1	Determinate	Purple	Dense	Broad	Green	L Brown	Yellow
16 .	EC24-1997	Indeterminate	Purple	Normal	Broad	L Green	Straw	Yellow
17.	EC-241600	Semi-determinate	Purple	Normal	Normal	Green	L Brown	Yellow
18.	EC-2409333	Semi-determinate	Purple	Dense	Broad	Green	Straw	Yellow
19.	EC-250616	Semi-determinate	Purple	Normal	Broad	D Green	Straw	Yellow
20.	EC-250587	Semi-determinate	Purple	Normal	Normal	Green	L Brown	Yellow
21.	EC-29051	Indeterminate	Purple	Normal	Normal	Green	L Brown	Yellow
22.	W-63	Determinate	Purple	Normal	Broad	Green	Brown	Green
23.	W-141	Determinate	Purple	Normal	Broad	Green	L Brown	Yellow
24.	W-72	Determinate	Purple	Normal	Broad	L Green	L Brown	Yellow
25.	NS-24	Determinate	White	Normal	Small	Green	Straw	Yellow
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	Sr.	Genotypes	Growth	Flower	Pube-	Leaflet	Leaf	Pod	Seed coat
	No.		habit	colour	scence	shape	colour	colour	colour
the second s	26.	NS-33	Determinate	White	Normal	Broad	L Green	Straw	Yellow
and the second	27.	NS-86	Determinate	Purple	Normal	Small	Green	L Brown	Yellow
	28.	NS-88	Determinate	White	Normal	Broad	Green	Straw	Yellow
	29.	NS-89	Determinate	White	Normal	Small	Green	Straw	Yellow
	30.	NS-93	Determinate	White	Dense .	Broad	Green	L Brown	Yellow
	31.	NS-94	Determinate	White.	Normal	Broad	D Green .	L Brown	Yellow
	32.	NS-97	Determinate	Purple	Sparse	Broad	Green	Straw	Yellow
	33.	NS-98	Determinate	Purple	Normal	Small	Green	Straw	Yellow
	34.	NS-99	Determinate	Purple	Dense	Broad	Green	Straw	Yellow
	35.	IC-96356	Determinate	Purple	Sparse	Broad	D Green	Straw	Yellow
	36.	IC-112938	Indeterminate	Purple	Sparse	Normal	Green	Straw	Yellow
	37.	IC-118296	Determinate	Purple	Glabrous	Broad	Green	Straw	Yellow
	38.	ICC-4403	Determinate	Purple	Normal	Broad	Green	Straw	Yellow
	39.	IC-96297	Semi-determinate	Purple	Normal	Broad	Green	L Brown	Black
	40.	G-07	Indeterminate	Purple	Sparse	Broad	Green	L Brown	Black
	41.	G-59	Determinate	Purple	Normal	Normal	Green	Brown	Green
	42.	G-89	Semi-determinate	White	Dense	Normal	Green	L Brown	Yellow
	43.	JS-335	Determinate	Purple	Glabrous	Broad	Green	Straw	Yellow
	44.	JS-80-21	Determinate	Purple	Normal	Broad	Green	L Brown	Yellow
	45.	NIC-19858	Determinate	Purple	Dense	Broad	Green	Brown	Yellow
	46.	NIC-19868	Determinate	Purple	Normal	Broad	Green	Straw	Yellow
2000	47.	Bragg	Determinate	White	Normal	Normal	Green	L Brown	Yellow
	48.	NS-77	Determinate	Purple	Normal	Broad	Green	L Brown	Yellow
	49.	Dsb-1	Determinate	White	Sparse	Normal	Green	D Brown	Yellow
	50.	RCS-2	Determinate	Purple	Normal	Broad	Green	Straw	
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Fig. 1. Grouping of genotypes into clusters based on morphological characters.

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Cluster No.	Total No. of genotypes	Genotypes
Î	18	EC-2515, EC-351469, EC-37933, EC-385323, EC-24-1997, EC-250616, W-141, W-72, W-24, NS-33, NS-88, NS-94, NS-98, ICC-4403, NIC-19868, Bragg, NS-77, RCS-2.
I	11	EC-39147, PKV-1, EC-241600, EC-2409333, EC-250587, NS-89, NS-93, NS-99, G-89, JS-80-21, NIC-19858.
Ш	8	EC-118036, AMS 98-9, EC-3853, AMS 98-20, NS-86, NS-97, IC-112938, Dsb-1.
IV	4	ED-241401, EC-118057, IC-96297, G-59.
V	3	EC-385314, W-63, G-59.
VI	2	EC-39179, EC-29051
VII	2	IC-118296, JS-335
VIII	1	IC-96356
IX	1	EC-385319

 Table 2.
 Distribution of fifty genotypes of soybean in different cluster based on morphological characters.

the genotypes (Fig. 1). On this basis the 50 genotypes evaluated were grouped into nine clusters (Table 2). I was the largest consisting of 18 genotypes, 11 genotypes were grouped in II, III consist of 8 genotypes, four genotypes were grouped into IV, and there were 3 genotypes into V and VI, VII consist of 2 genotypes and VIII and IX consist of only one genotype each viz. IC-96356 and EC-385319 respectively.

The contribution of characters like growth habit, pubescence density, leaflet shape and pod colour were observed to be higher as compared to characters like flower colour, leaf colour and seed coat colour. However, only two morphological characters viz. growth habit and pubescence density have been considered to have economical significance. The growth habit of sovbean genotypes were either determinate semi determinate or intermediate of which determinate type is more favourable to reduce pod shattering. Regarding pubescence density. Halvanker et al.² have reported that majority of soybean varieties have pubescence on their pods though glaberous, curly, sparse and puberluent types may occour. Dense pubescence types may have a beneficial effect in lowering the transpiration rate³. Glaberous pods are susceptible to attack of potato leaf hopper than pubescence pods⁴. As this two characters viz. growth habit and pubescence density are contributing to variations among the genotypes on morphological basis, the parents may be selected for hybridization on the basis of these characters.

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Endang *et al.*⁵ have stated that the clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various characters. Based on high mean values and distance between the clusters the genotype may be selected as parents for hybridization programmes. But, as it is observed in the present study that there are several genotypes included in a widely separated clusters. Under such condition Chaudhary *et al.*⁶ suggested that selection of one type from each cluster and testing

them by a series of diallel analysis may prove to be highly fruitful.

References

- 1. Anderson E 1957, Proc. Ant. Acad. Sci. Wash 43 923
- 2. Halvankar G B, Taware S P and Raut V M 1998, J. Maharashtra agric. univ. 23(2) 170
- 3. Ghorashy S R, Pendleton J W, Bernard R L and Bauer M E 1971, Crop Sci. 11 426
- 4. Broersma D B, Bernard R L and Luckmann W H 1972, J. Econ. Ent. 65 78
- 5. Endang S J, Sri Andani and Hakin Nasoction 1997, Int. Rice Comn. News 20 26.
- 6. Chaudhary B D, Bhatt P N and Singh V P 1975, J. agric. Sci. 45 530