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Research Article

Characterization of soybean [*Glycine max*(L.) Merrill] genotypes using DUS descriptors

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Abstract

A total of 70 soybean genotypes from the Ramaiah gene bank including five checks were evaluated for 14 qualitative and four quantitative traits based on DUS guidelines given by PPV& FR. Sixty-five genotypes and five check varieties were subjected to cluster analysis and were grouped into four major clusters with an average similarity of 77%. Cluster I consisted of 41 genotypes, cluster II had 15 genotypes, cluster III had nine genotypes and cluster IV had five genotypes. The study revealed an association between anthocyanin pigmentation in hypocotyl and flower colour. MACS 1254 was identified as the only genotype with a yellow green seed coat among 70 genotypes. According to the DUS, two genotypes viz., JS 76-1194 and JS (SH) 91-93 showed a lanceolate leaf shape. The distinct genotypes identified in the present study could be used in the breeding programme for the improvement of soybean.

Keywords: Soybean, Characterization, DUS, Qualitative traits, Cluster.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is an economically important legume crop (2n=40) and their seed contains 40% protein, 20% cholesterol-free oil and it replenishes the soil by fixing nitrogen (Chung and Singh, 2008). Soybean is the world's major contributor of vegetable protein and oil and as such, they are known as the "golden bean" or "miracle crop." Soybean is indigenous to northeast Asia, particularly China. It belongs to the family Fabaceae and subfamily Papilionaceae. The cultivated soybean (*Glycine max*) descended from the presently known wild ancestor *Glycine usariensis* (Pawale *et al.*, 2019). World soybean production in 2021–22 is estimated at 385.524 million tonnes (Anonymous, 2022). Brazil ranks first in soybean production followed by the US, Argentina, China, and India. Soybean production in India accounts for 12.90 million tonnes cultivated under 12.81 million hectares with the mean yield of 1007 kg/ha in 2020-21 (Anonymous, 2021). Maharashtra and Madhya Pradesh dominated the

soybean production in India which contributes to 89 per cent of the total production in India (Anonymous, 2021).

In India, till date more than 100 varieties have been developed under the domestic breeding programme for the different climatic conditions of the country. DUS testing can assist in identifying whether a novel variety is unique from existing varieties of the same species and whether the features that produce distinctness are expressed consistently and whether these characters do not change over generations. Plant breeders, seed inspectors, researchers and other client's benefits from the characterization of a newly developed variety since it helps them meet their specific needs. Qualitative characters are more stable (Raut, 2003) hence, they are authentic for the characterization of varieties. The purpose of this study was to characterize the soybean genotypes in terms of their qualitative and quantitative traits. DUS

test was carried out for the eighteen traits based on the PPV&FR, 2001 guidelines. Cluster analysis was carried out in the present study as it helps in examining the phenotypic variation.

MATERIALS AND METHODS

The experimental material consisted of 70 soybean genotypes obtained from the Ramaiah gene bank including five check varieties: NRC 132, NRC 142, NRC 147, MACS 1460 and CO (Soy) 3. Of these, NRC 132, NRC 142 and NRC 147 were obtained from the Indian Institute of Soybean Research, Indore. MACS1460 was provided by the Agharakar Research Institute, Pune. CO (Soy) 3 is released from the Tamil Nadu Agricultural University, Coimbatore. The list of soybean genotypes under study is given in **Table 1**. The experiment was conducted at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore and the experimental plot was located at the latitude of 11.0232 °N and the longitude of 76.9293 °E. The altitude of the experimental location is 426.72 m above MSL. The soil type is red soil. The experiment was laid down in augmented block design II with 3 m row length and 30 cm x 10 cm spacing during *rabi*, 2021–22. DUS (Distinctness, Uniformity, and Stability) characterization was performed on the soybean

cultivars based on 14 qualitative traits, viz., anthocyanin pigmentation on hypocotyl, plant growth type, leaf shape, leaf colour, plant growth habit, flower colour, pod pubescence colour, pod colour, seed shape, seed colour, seed luster, seed hilum colour, presence and absence of pod pubescence and seed cotyledon colour and four quantitative characters viz, days to 50% flowering, plant height, days to maturity and seed size. The genotypes were scored for each trait based on the note values of the DUS characters given by PPV & FR, 2001. The morphological data were subjected to cluster analysis using GGT 2.0 Software (Kujane *et al.*, 2019). The dendrogram was constructed using UPGMA tree clustering.

RESULTS AND DISCUSSION

Qualitative characters are used as the markers for the advanced breeding methods. The research on inheritance and linkage studies of qualitative character was reviewed by Raut (2003). Satyavathi *et al.* (2004) substantiate that the colour of hair, seed colour and flower colour in soybean were the most stable characters across different climatic zones. The relative and absolute frequencies were calculated for 70 genotypes and the results are depicted in **Table 2**. The DUS test conducted in 70 genotypes clearly differentiated each other based

Table 1. List of soybean genotypes used in the study

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1	CLARK	25	MACS 1140	49	VLS 75
2	CO 1	26	MACS 1148	50	PK 25
3	CSB 0804	27	MACS 1238	51	PK 258
4	CSB 0806	28	MACS 1254	52	PK 727
5	CSB 0808	29	MAUS 109	53	PK 1028
6	EC 18678	30	MAUS 144	54	PK 701
7	JS 76-1194	31	MAUS 17	55	NRC 29
8	JS 90-21	32	MAUS 2	56	NRC 34
9	JS 90-29	33	MAUS 20	57	NRC 42
10	JS 92-22	34	MAUS 311	58	NRC 43
11	JS 98-63	35	MAUS 34	59	NRC 44
12	JS 99-128	36	JS(SH) 2001-04	60	NRC 45
13	JS 99-72	37	JS(SH) 2002-14	61	NRC 46
14	JS 99-76	38	JS(SH) 89-2	62	JS 87-12
15	JS 99-77	39	MAUS 68	63	CSB 0810
16	JS 99-83	40	MAUS 81	64	NRC 82
17	JS(SH)18608	41	NRC 21	65	PK 7247
18	JS(SH)89-49	42	NRC 25	Checks	
19	JS(SH)90-91	43	VLS 53	66	NRC 132
20	JS(SH)91-93	44	PK 1158	67	NRC 142
21	JS(SH)99-14	45	PK 1223	68	NRC 147
22	MACS 1039	46	NRC 80-1	69	MACS 1460
23	MACS 1126	47	NRC 84	70	CO (Soy) 3
24	MACS 1139	48	NRC 95-06-03		

Table 2. Classification of the soybean genotypes based on DUS characters

S.No.	Qualitative characters	Descriptors	Absolute frequency	Relative frequency (%)
1.	Hypocotyl: Anthocyanin pigmentation	Absent	14	20.00
		Present	56	80.00
2.	Plant: Growth type	Determinate	23	32.86
		Semi-determinate	24	34.28
		Indeterminate	23	32.86
3.	Days to 50% flowering	Early(< 35 days)	01	01.43
		Medium (36–45 days)	68	97.14
		Late(> 45 days)	01	01.43
4.	Leaf: Shape	Lanceolate	02	02.86
		Pointed ovate	54	77.14
		Rounded ovate	14	20.00
5.	Leaf: Colour	Green	64	91.43
		Dark green	06	08.57
6.	Plant: Growth habit	Erect	51	72.86
		Semi-erect	19	27.14
7.	Flower: Colour	White	14	20.00
		Purple	56	80.00
8.	Plant: Height (cm)	Short (< 40cm)	45	64.29
		Medium (41-60cm)	24	34.28
		Tall (>60cm)	01	01.43
9.	Pod: Pubescence colour	Grey	16	22.86
		Tawny	54	77.14
10.	Pod: Colour	Yellow	24	34.29
		Brown	41	58.57
		Black	05	07.14
11.	Days to maturity	Early (< 95 days)	50	71.43
		Medium (96–105 days)	19	27.14
		Late (> 105 days)	01	01.43
12.	Seed: Size (100 seeds weight)	Small (=10.0g)	30	42.86
		Medium (10.1-13.0g)	39	55.71
		Large (>13.0g)	01	01.43
13.	Seed: Shape	Spherical	41	58.57
		Elliptical	29	41.43
14.	Seed: Colour	Yellow	69	98.57
		Yellow green	01	01.43
		Green	0	00.00
		Black	0	00.00
15.	Seed: Lustre	Shiny	50	71.43
		Dull	20	28.57
16.	Seed: Hilum colour	Yellow	01	01.43
		Grey	06	08.57
		Brown	45	64.29
		Black	18	25.71
		Variegated	0	00.00
17.	Pod: Pubescence	Absent	0	00.00
		Present	70	100.00
18.	Seed: Cotyledon colour	Yellow	70	100.00
		Green	0	00.00

on the eighteen traits as given in **Table 3**. The flower colour and anthocyanin pigmentation in hypocotyl were found to be correlated. Gupta *et al.* (2010) also observed the same result of correlation in soybean. Genotypes with white coloured flowers showed non-

pigmented hypocotyls, whereas purple coloured flowers showed pigmentation in their hypocotyls. Hypocotyl with anthocyanin pigmentation was found in 56 genotypes, while those without pigmentation were found in 14 genotypes (**Fig. 1**). The flower colour is controlled

Table 3. Characterization of the 70 genotypes as per DUS guidelines

S. No.	Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	CLARK	P	Pu	Ro	G	Se	Id	Gy	Y	Sn	Y	El	Bl	S	E	M	M	P	Y
2	CO 1	P	Pu	Po	G	Er	Sd	T	Bl	Sn	Y	Sp	Br	S	E	M	M	P	Y
3	CSB 0804	P	Pu	Ro	G	Se	D	Gy	Y	Sn	Y	Sp	Bl	M	E	M	M	P	Y
4	CSB 0806	P	Pu	Ro	G	Se	D	Gy	Y	Sn	Y	Sp	Y	S	E	M	M	P	Y
5	CSB 0808	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Br	S	M	Sm	M	P	Y
6	EC 18678	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	El	Br	S	E	Sm	M	P	Y
7	JS 76-1194	A	W	Ln	G	Er	Sd	T	Br	DI	Y	El	Bl	S	E	Sm	M	P	Y
8	JS 90-21	P	Pu	Po	G	Er	Sd	T	Y	DI	Y	El	Br	M	E	Sm	M	P	Y
9	JS 90-29	P	Pu	Po	G	Er	Sd	T	Br	DI	Y	El	Br	S	E	Sm	M	P	Y
10	JS 92-22	P	Pu	Po	G	Er	Id	T	Y	Sn	Y	Sp	Gy	TI	E	Sm	M	P	Y
11	JS 98-63	P	Pu	Po	G	Se	D	T	Y	Sn	Y	El	Br	S	E	M	M	P	Y
12	JS 99-128	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	S	M	Sm	Lt	P	Y
13	JS 99-72	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	S	M	M	M	P	Y
14	JS 99-76	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	S	M	M	M	P	Y
15	JS 99-77	A	W	Po	G	Er	Sd	T	Y	Sn	Y	El	Bl	S	M	Sm	M	P	Y
16	JS 99-83	P	Pu	Po	G	Er	Id	T	Br	DI	Y	El	Br	M	M	Sm	M	P	Y
17	JS(SH)18608	P	Pu	Po	G	Er	Sd	T	Br	DI	Y	El	Br	M	M	M	M	P	Y
18	JS(SH)89-49	P	Pu	Po	G	Er	Id	T	Br	DI	Y	El	Br	M	M	M	M	P	Y
19	JS(SH)90-91	P	Pu	Po	G	Er	Sd	T	Y	Sn	Y	Sp	Br	S	M	Sm	M	P	Y
20	JS(SH)91-93	P	Pu	Ln	G	Er	Id	T	Br	Sn	Y	El	Br	M	M	M	M	P	Y
21	JS(SH)99-14	A	W	Ro	G	Se	D	Gy	Y	Sn	Y	El	Gy	S	E	M	M	P	Y
22	MACS 1039	P	Pu	Po	G	Se	D	Gy	Y	Sn	Y	El	Br	S	E	M	M	P	Y
23	MACS 1126	P	Pu	Ro	G	Se	D	Gy	Y	DI	Y	El	Br	S	E	M	M	P	Y
24	MACS 1139	P	Pu	Po	G	Se	D	Gy	Y	Sn	Y	Sp	Bl	S	E	M	M	P	Y
25	MACS 1140	P	Pu	Po	G	Er	D	Gy	Y	Sn	Y	El	Bl	S	E	M	M	P	Y
26	MACS 1148	A	W	Po	Dg	Er	D	T	Y	DI	Y	El	Br	S	E	Sm	M	P	Y
27	MACS 1238	A	W	Po	Dg	Se	D	Gy	Y	Sn	Y	Sp	Bl	S	E	M	M	P	Y
28	MACS 1254	P	Pu	Ro	G	Se	D	Gy	Y	Sn	Yg	El	Bl	S	E	L	M	P	Y
29	MAUS 109	P	Pu	Po	G	Er	Id	T	Br	DI	Y	Sp	Br	S	M	M	M	P	Y
30	MAUS 144	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	El	Bl	M	M	M	M	P	Y
31	MAUS 17	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Br	M	M	M	M	P	Y
32	MAUS 2	P	Pu	Po	G	Er	Sd	T	Br	DI	Y	El	Br	M	M	Sm	M	P	Y
33	MAUS 20	P	Pu	Po	G	Er	Id	T	Y	Sn	Y	El	Gy	M	M	Sm	M	P	Y
34	MAUS 311	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	M	M	Sm	M	P	Y
35	MAUS 34	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	M	E	M	M	P	Y
36	JS(SH) 2001-04	A	W	Ro	G	Er	D	Gy	Br	Sn	Y	El	Bl	S	E	M	M	P	Y
37	JS(SH) 2002-14	P	Pu	Po	G	Er	D	T	Br	Sn	Y	El	Bl	S	E	M	M	P	Y
38	JS(SH) 89-2	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Bl	M	E	Sm	M	P	Y
39	MAUS 68	P	Pu	Ro	Dg	Er	D	Gy	Y	Sn	Y	Sp	Bl	S	E	M	M	P	Y
40	MAUS 81	P	Pu	Po	G	Er	Sd	T	Bl	DI	Y	Sp	Br	S	E	Sm	M	P	Y
41	NRC 21	P	Pu	Po	G	Er	Sd	T	Bl	Sn	Y	Sp	Br	M	E	M	M	P	Y
42	NRC 25	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Bl	S	M	M	M	P	Y
43	VLS 53	P	Pu	Po	G	Se	Id	T	Br	DI	Y	El	Br	M	E	Sm	M	P	Y
44	PK 1158	P	Pu	Po	G	Er	Sd	T	Br	DI	Y	El	Br	M	E	Sm	M	P	Y
45	PK 1223	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Br	M	E	Sm	M	P	Y

46	NRC 80-1	A	W	Po	G	Se	D	T	Y	Sn	Y	Sp	Br	S	E	M	M	P	Y
47	NRC 84	A	W	Po	G	Er	D	T	Br	Sn	Y	Sp	Br	S	E	M	M	P	Y
48	NRC 95-06-03	A	W	Po	G	Er	Sd	Gy	Y	DI	Y	Sp	Br	S	E	Sm	M	P	Y
49	VLS 75	A	W	Po	Dg	Se	D	T	Br	Sn	Y	Sp	Br	S	E	M	M	P	Y
50	PK 25	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Bl	M	E	M	M	P	Y
51	PK 258	P	Pu	Po	G	Er	Id	T	Br	DI	Y	Sp	Br	M	E	M	M	P	Y
52	PK 727	A	W	Ro	G	Se	D	T	Br	Sn	Y	Sp	Br	S	E	M	M	P	Y
53	PK 1028	A	W	Ro	G	Er	D	T	Br	DI	Y	Sp	Br	S	M	Sm	M	P	Y
54	PK 701	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	S	E	M	M	P	Y
55	NRC 29	P	Pu	Po	G	Er	Id	T	Br	DI	Y	El	Br	M	E	Sm	M	P	Y
56	NRC 34	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	S	M	Sm	M	P	Y
57	NRC 42	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	M	E	M	M	P	Y
58	NRC 43	P	Pu	Po	G	Er	Sd	T	Bl	Sn	Y	Sp	Br	S	E	M	M	P	Y
59	NRC 44	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	Sp	Br	S	E	Sm	M	P	Y
60	NRC 45	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	M	E	Sm	M	P	Y
61	NRC 46	P	Pu	Po	G	Er	Sd	T	Br	Sn	Y	El	Br	S	E	Sm	M	P	Y
62	JS 87-12	P	Pu	Ro	G	Se	D	Gy	Y	Sn	Y	Sp	Gy	S	E	M	M	P	Y
63	CSB 0810	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	Sp	Br	S	Lt	Sm	M	P	Y
64	NRC 82	P	Pu	Ro	Dg	Se	D	Gy	Br	Sn	Y	El	Gy	S	E	M	M	P	Y
65	PK 7247	P	Pu	Po	G	Er	Id	T	Br	Sn	Y	El	Br	M	E	Sm	M	P	Y
66	NRC 132 (C)	A	W	Ro	G	Er	D	T	Y	DI	Y	Sp	Bl	S	E	M	M	P	Y
67	NRC 142 (C)	P	Pu	Ro	G	Se	Sd	T	Y	DI	Y	El	Bl	S	E	M	M	P	Y
68	NRC 147 (C)	P	Pu	Po	G	Se	Sd	T	Y	Sn	Y	Sp	Bl	S	E	S	M	P	Y
69	MACS 1460 (C)	A	W	Po	G	Se	D	Gy	Bl	Sn	Y	Sp	Gy	S	E	M	E	P	Y
70	CO (Soy) 3 (C)	P	Pu	Po	Dg	Er	Id	T	Br	DI	Y	Sp	Br	M	E	S	M	P	Y

1. Anthocyanin pigmentation; 2. Flower colour; 3. Leaf shape; 4. Leaf colour; 5. Plant: growth habit; 6. Plant growth type; 7. Pod pubescence colour; 8. Pod colour; 9. Seed lustre; 10. Seed colour; 11. Seed shape; 12. Seed: hilum colour; 13. Plant height; 14. Days to maturity; 15. Seed size; 16. Days to 50% flowering; 17. Pod pubescence and 18. Seed cotyledon colour. A = Absent, Bl = Black, Br = Brown, D = Determinate, Dg = Dark-green, DI = Dull, E = Early, El = Elliptical, Er = Erect, G = Green, Gy = Grey, Id = Indeterminate, L = Large, Lt = Late, Ln = Lanceolate, M = Medium, P = Present, Po = Pointed ovate, Pu = Purple, Ro = Rounded ovate, S = Short, Sd = Semi-determinate, Se = Semi-erect, Sm = Small, Sn = Shiny, Sp = Spherical, T = Tawny, TI = Tall, W = White, Y = Yellow, Yg = Yellow-green.

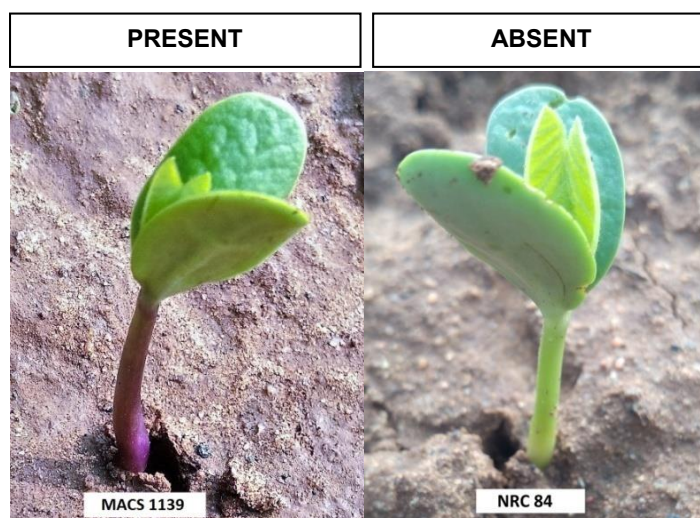


Fig. 1. Variation for hypocotyl colour

by six genes and pubescence colour by two genes (Palmer *et al.*, 2004; Takahashi *et al.*, 2008). White colour flowers were observed in 14 genotypes and purple flowers were observed in 56 genotypes (Fig. 2).

Based on the days to 50% flowering, MACS 1460 was the only one genotype observed to be early as they bloom before 35 days after sowing, 68 genotypes were classified as medium, as these flowers bloom between 36 and 45 days and JS 99-128 was found to be late, as it blooms after 45 days. Ramteke *et al.* (2010) observed similar results of late flowering in VLS 75. According to the DUS, two genotypes viz., JS 76-1194 and JS (SH) 91-93 had lanceolate leaf shapes (Fig. 3). The pointed ovate leaf shape was found in 54 genotypes, whereas the rounded ovate shape was found in 14 genotypes. The

ovate shaped leaves were found to be thick in nature. Out of 70 genotypes, MACS 1148, MACS 1238, MAUS 68, NRC 82, VLS 75 and CO (Soy) 3 had dark green leaves. The remaining 64 genotypes had green colour leaves (Fig. 4).

Determinate plant growth type was observed in 23 genotypes and these genotypes showed thicker leaves than the other two growth types. Twenty-three genotypes were categorized as semi-determinate types. The remaining 24 genotypes were found to be indeterminate and these types recorded more number of pods.

CSB 0806, CSB 0804, JS 98-63, JS(SH)99-14, MACS 1038, MACS 1126, MACS 1139, MACS 1238, MACS 1254, NRC 80-1, NRC 82, VLS 75, PK 727, JS 87-12

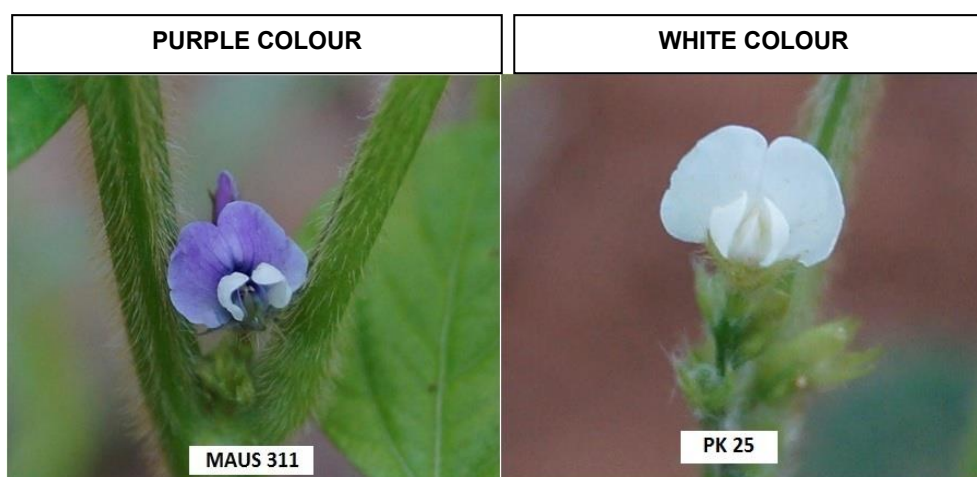


Fig. 2. Variation for flower colour

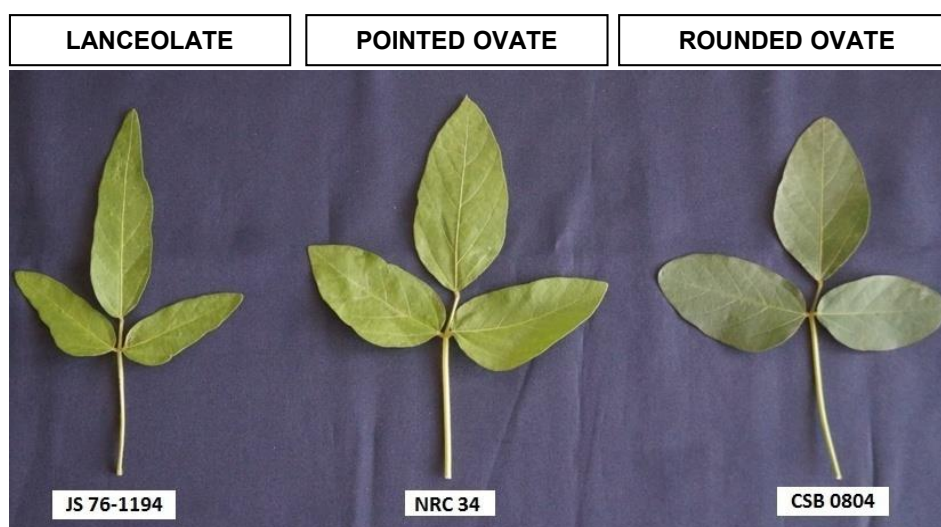


Fig. 3. Variation for leaf shape

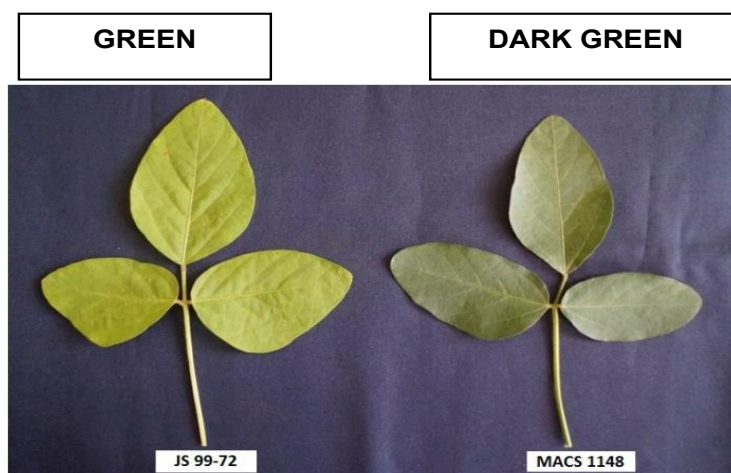


Fig. 4. Variation for leaf colour

and MACS 1460 were the fifteen genotypes that showed semi-erect and determinate in nature. VLS 53 and CLARK were semi-erect and indeterminate in nature. NRC 142 and NRC 147 were semi-erect and semi-determinate in nature. Fifty-one genotypes were classified as erect type. Among the 70 genotypes studied, 45 genotypes were small type (<40cm) and 24 genotypes were medium type (41 to 60cm). JS 92-22 was the only genotype identified as tall (> 60 cm). Singh *et al.* (2021) observed in his study that all seven released varieties of soybean in Himachal Pradesh were categorized as a tall plant. Early maturing genotypes were found in 50 genotypes as they matured in less than 95 days. Medium maturing types were noted in 19 genotypes as they mature in 96-105 days. The genotype CSB 0810 was identified as a late maturing type, as it matures in 112 days. According to Cober and Morrison (2010) eight loci with two alleles at each locus were reported to control the days to maturity and time to flowering through their response to photoperiod in soybean.

CSB 0804, CSB 0806, JS 98-63, JS 99-14, MACS 1039, MACS 1126, MACS 1139, MACS 1140, MACS 1148, MACS 1238, MACS 1254, MACS 68, NRC 80-1, JS 87-12 and NRC 132 were the fifteen genotypes with yellow pod colour and determinate growth type. Yellow pod colour was observed to be semi-determinate and was found in six genotypes viz., JS 90-21, JS 99-77, JS (SH) 90-91, NRC 95-06-03, NRC 142 and NRC 147. The remaining three yellow pod genotypes viz., JS 92-22, MAUS 20 and CLARK showed indeterminate type. Forty-one genotypes had brown pod colour. The remaining five were black in nature (Fig. 5). Grey pod pubescence was found in sixteen genotypes and the remaining 54 genotypes had tawny (brown) pubescence (Fig. 6). Pod pubescence was present in



Fig. 5. Variation for mature pod colour



Fig. 6. Variation for pod pubescence

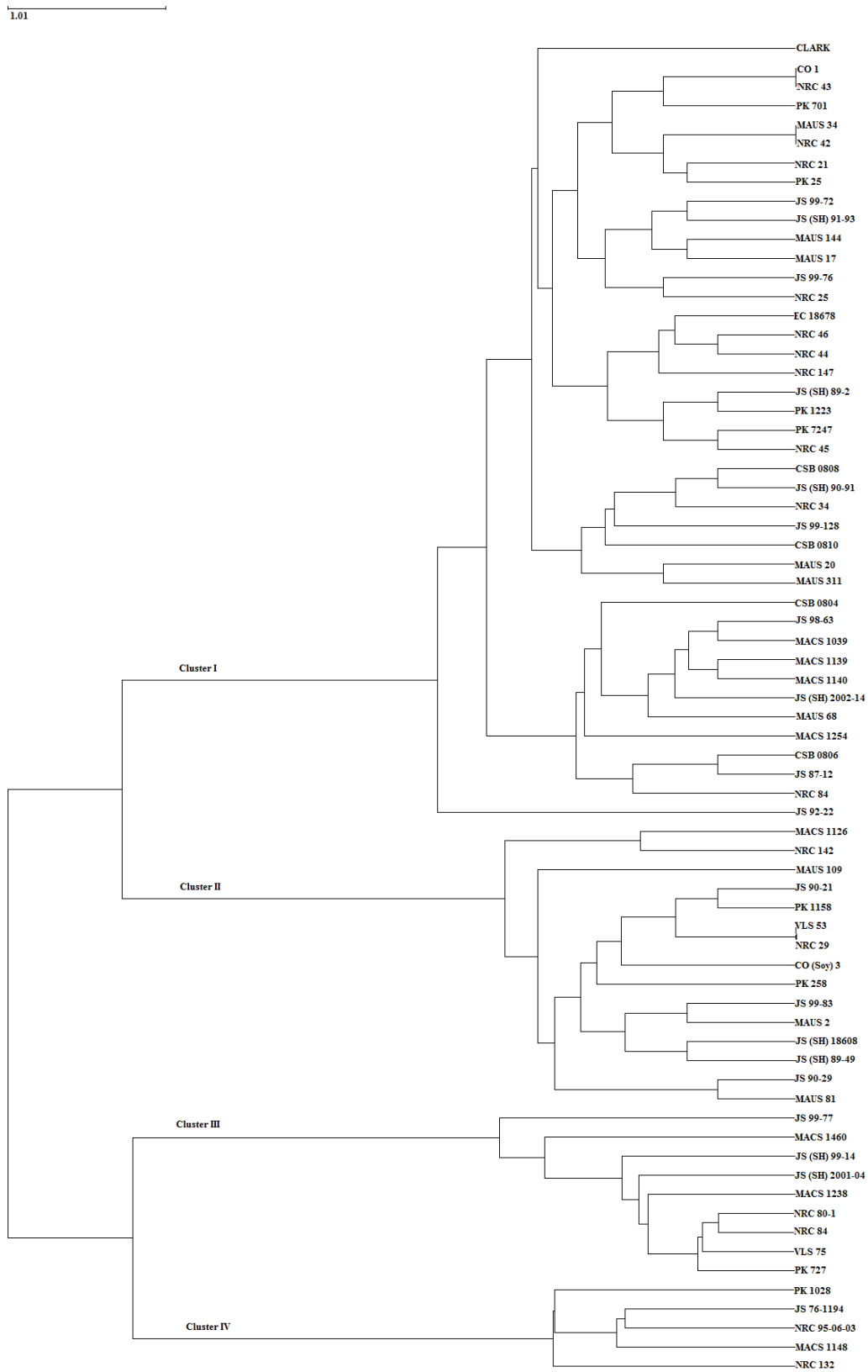


Fig. 7. Clustering of 70 soybean genotypes based on the qualitative and quantitative traits

all 70 genotypes. Chaudhary *et al.* (2021) also reported the presence of pod pubescence in all 236 pigeonpea genotypes. Small seeds were found in 30 genotypes and weighed less than 10 g per 100 seeds, medium seeds were found in 39 genotypes and weighed 10.1 g to 13.0 g, and large seeds were found in one genotype and weighed 14.12 g (*i.e.*, >13.0 g) *viz.*, MACS 1254. Seeds with a spherical shape were found in 41 genotypes, whereas elliptical seeds were found in the 29 genotypes. MACS 1254 was the only genotype with a yellow green seed coat identified in 70 genotypes. Ramteke *et al.* (2012) also observed the same yellow green pattern of seed coat in JS 90-41. The seed coat colour of the remaining 69 genotypes was yellow in colour. A total of 50 genotypes had shiny seed lustre, while 20 genotypes had dull seed luster. Only CSB 0806 had yellow hilum colour, while six genotypes had grey hilum colour, *viz.*, JS 92-22, JS (SH) 99-14, MAUS 20, NRC 82, JS 87-12 and MACS 1460. Brown hilum was found in 45 genotypes, while black hilum was found in 18 genotypes. Variation in hilum colour of soybean was also reported by Yadav and Sharma (2001). Seed cotyledon colour showed no variation as all the 70 genotypes were observed to be yellow in colour.

Based on cluster analysis, the 70 genotypes were classified into four clusters *viz.* cluster I, cluster II, cluster III and cluster IV (**Fig. 7**). Dhaliwal *et al.* (2020) also obtained the four clusters in characterizing 22 soybean lines for 19 characters. The trait contributing for the first grouping was anthocyanin pigmentation and flower colour. The similarity coefficient ranged from 0.73 to 0.80. Cluster I, II, III and IV consisted of 41, 15, 9 and 5 genotypes, respectively. Cluster I was the largest with 41 genotypes and cluster IV was the smallest with five genotypes. Ranjani and Jayamani (2021) also reported four clusters formed from 68 genotypes of pigeonpea with a maximum number of genotypes in cluster I and a minimum number of genotypes in cluster IV. The genotypes CO 1 and NRC 43 in cluster I was similar and the genotypes MAUS 34 and NRC 42 in cluster I were also found to be similar. Similarly in cluster II, VLS 53 and NRC 29 were found to be identical.

The study revealed that the flower colour and hypocotyl pigmentation was found to be directly linked. In addition, the presence of pod pubescence and yellow seed cotyledon colour showed no variation for all the 65 genotypes and five varieties. Therefore, the remaining 16 traits were only focused for the distinctness of the genotypes. The genotypes in cluster I and cluster IV had the largest inter cluster distance. Hence, the genotypes in cluster I and cluster IV can be used for future hybridization and crop improvement programmes.

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