Characterization of Soybean [*Glycine max* (L.) Merrill] Genotypes based on DUS Traits

R.C. Sivabharathi[1], A. Muthuswamy[2], K. Anandhi[3] and L. Karthiba[3]*
[1]PG Research Scholar, Department of Plant Breeding and Genetics,
Tamil Nadu Agricultural University, Coimbatore (Tamil Nadu), India.
[2]Associate Professor, Agricultural College and Research Institute, Karur (Tamil Nadu), India.
[3]Assistant Professor, Department of Pulses,
Tamil Nadu Agricultural University, Coimbatore (Tamil Nadu), India.

(Corresponding author: R.C. Sivabharathi*)

ABSTRACT: The challenge in the present study is to characterize the sixty-nine soybean genotypes based on the DUS test given by PPV&FR for the fourteen qualitative and four quantitative traits. The qualitative traits include 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 lustre, seed hilum colour, presence and absence pod pubescence and seed cotyledon colour and the quantitative traits are days to 50% flowering, plant height, days to maturity and seed size. Pod pubescence and seed cotyledon were found to be a monomorphic trait for all the sixty-nine genotypes. The study revealed that flower colour and hypocotyl pigmentation were found to be directly linked. JS 95-60 and MACS 29 were two genotypes observed as late flowering. PK 1024 was the only genotype with lancealote leaf shape. Cluster analysis depicted that the 69 genotypes could be grouped into four major clusters each with two sub clusters. The similarity coefficient ranges from 0.75 to 0.77. The genotypes in cluster I and IV were observed to have wide variation. Thus, the contribution of this research will help the researchers to utilize the genotypes in cluster I and cluster IV for the crop improvement programmes.

Keywords: Cluster, Dendrogram, Descriptors, DUS, Qualitative traits.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is called "Miracle crop" or "Golden bean" because it contributes significantly as both oilseed and leguminous crop in terms of total production and international trade (Chung and Singh 2008). It belongs to the family Fabaceae and subfamily Papilionaceae. World soybean production in 2021 – 22 is estimated as 385.527 million tonnes. Brazil ranks first in soybean production with 144 million tonnes followed by the United States, Argentina, China and India (Anonymous, 2022a). Production in India accounts 12.90 million tonnes cultivated under 12.81 million hectares with the productivity of 1007 kg/ha in 2020-21 (Anonymous, 2021). Madhya Pradesh and Maharashtra contributes 89 per cent of soybean production in India. In 2021-22, the world production volume of soybean oil amounted to 60.27 million metric tonnes (Anonymous, 2022b). This demonstrates that soybean oil production is rising quickly around the world as a result of its high nutritional value as a food source for both people and livestock, as well as its importance as a source of edible oil with industrial applications. Soy seeds contain 38–43 per cent protein, while 17–19 per cent oil (Chung and Singh 2008). Furthermore, 100g of soybeans had 432 calories, 10.5g of fat, and 426mg of vitamins (A, B, and D). In addition to this, soybean also contains 240mg of calcium, 690mg of phosphorus, and 11.5mg of iron (Nagraj, 1995).

The characterization based on distinctness, uniformity, stability and novelty is prerequisite. The varietal characterization of a genotype should be precisely explained, accepted and should have standard method of observation. In addition, it should be least or less affected by the environment (Raut, 2003). Emphasis on characterization, varietal identification and genetic purity assessment of soybean genotypes is very important to the field functionaries, certification officers, seed production officers and seed growers for regulating quality of the seed. It is also favorable for plant breeder to assess relationship between yield and its various components, which will facilitate selection

of desirable characteristics (Jain *et al.,* 2015). Identification of genotypes based on morphological characteristics is the most extensively used method. In case of no variation observed among the genotypes with qualitative traits, quantitative traits can be taken into observation to get precise results (Raut, 2003). Therefore, the present study is focused on the characterization of soybean genotypes for both qualitative and quantitative traits. The quantitative and qualitative data were analyzed by GGT 2.0 Software (Kujane *et al*., 2019). The dendrogram was constructed using UPGMA tree clustering (Ramteke *et al*., 2015). In this aspect, genotypes with similar traits were grouped into single cluster based on qualitative and quantitative traits which can be used for the selection of genotypes with wide variation for the future breeding programmes.

MATERIALS AND METHODS

The present study was carried out at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore during *rabi,* 2021-22 using augmented block design II. The experimental plot was at the latitude of 11.0232 °N, the longitude of 76.9293 °E and the altitude at 426.72m above MSL. Each genotype was raised in 3m length with spacing of 30 × 10cm. The experiment was carried out with 69 genotypes enlisted in Table 1, including five check varieties *viz.,* NRC 132, NRC 142, NRC 147, MACS 1460 and CO (Soy) 3. Observations were recorded for fourteen qualitative traits and four quantitative traits. The qualitative traits were anthocyanin pigmentation on hypocotyls, plant growth type, leaf shape, leaf colour, plant growth habit, flower colour, pod pubescence colour, pod colour, seed shape, seed colour, seed lustre, seed hilum colour, presence and absence of pod pubescence and seed cotyledon colour and the quantitative traits were days to 50 per cent flowering, plant height, days to maturity and seed size (Table 2). The genotypes were evaluated for each trait based on note values of the DUS characters as per the Protection of Plant Varieties and Farmers Rights, 2001 (Table 3). The eighteen traits of 69 genotypes were subjected to cluster analysis using GGT 2.0 software (Kujane *et al.,* 2019).

Table 1: List of soybean genotypes used for study.

Sr. No.	Genotypes	Source/Origin
1.	CO 2	Department of Pulses, Tamil Nadu Agricultural University, Tamil Nadu, India
2.	CSB 0809	China
3.	CSB 0811	China
4.	EC 18736	Collected by Sh. H. B. Singh P.I.O and Mr. P. P.Khanna for Nepal
5.	JS 20-01	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
6.	JS 20-09	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
7.	JS 76119	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
8.	JS 89-24	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
9.	JS 95-60	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
10.	JS 95-98	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
11.	JS 97-52	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
12.	JS 98-21	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
13.	JS 98-61	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
14.	JS 98-68	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
15.	JS 99-12	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
16.	JS(SH)92-46	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
17.	JS(SH)93-37	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
18.	JS(SH)93-44	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India
19.	MACS 1188	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
20.	MACS 1259	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
21.	MACS 1281	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
22.	MACS 145	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
23.	MACS 565	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
24.	MACS 610	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
25.	MACS 629	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
26.	MACS 693	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
27.	MACS 694	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
28.	MACS 715	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
29.	MACS 798	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
30.	MACS 94-2	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
31.	MACS 985	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
32.	MAUS 39	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
33.	MAUS 414	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
34.	MAUS 417	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
35.	MAUS 52-1	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
36.	MAUS 55	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
37.	JS(SH) 8554	Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur, Madhya Pradesh, India

38.	MAUS 71-07	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
39.	NRC 2006-M-6	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
40.	NRC 2007-G-1-13	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
41.	NRC 2007-I-3	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
42.	NRC 2007-K-7-2	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
43.	VLS 69	ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarkhant
44.	PK 1243	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
45.	MAUS 59	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
46.	MAUS 60	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
47.	MAUS 61	Vasantrao Naik Marathwada Agricultural University (MAU), Parbhani, Maharastra
48.	NRC 76	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
49.	NRC 78	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
50.	NRC 79	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
51.	VLS 70	ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, Uttarkhant
52.	WC 37	-
53.	WC 67	-
54.	PK 1000	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
55.	PK 1303	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
56.	PK 257	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
57.	PK 768	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
58.	PK 1011	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
59.	PK 1014	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
60.	PK 1024	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
61.	PK 1038	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
62.	PK 1125	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
63.	PK 1146	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
64.	PK 1225	Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarkhand
65.	NRC 132	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
66.	NRC 142	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
67.	NRC 147	National Research Center for Soybean (NRCS), Indore, Madhya Pradesh
68.	MACS 1460	Maharastra Association for the cultivation of Science' Agharkar Research Institute, Pune, Maharastra
69.	CO (Soy) 3	Department of Pulses, Tamil Nadu Agricultural University, Tamil Nadu, India

Table 2: Classification of the 69 soybean genotypes based on DUS traits.

Sr. No.	Qualitative Characters	Descriptors	NOTE	Absolute Frequency	Relative Frequency (%)
A.	Hypocotyl: Anthocyanin pigmentation	Absent Present	1 9	09 60	13.04 86.96
B.	Flower: Colour	White Purple	1 2	09 60	13.04 86.96
C.	Leaf: Shape	Lanceolate Pointed ovate Rounded ovate	1 2 3	01 59 09	01.45 85.51 13.04
D.	Leaf: Colour	Green Dark green	1 2	62 07	89.86 10.14
E.	Plant: Growth habit	Erect Semi-erect	1 2	57 12	82.61 17.39
F.	Plant: Growth type	Determinate Semi-determinate Indeterminate	1 2 3	15 24 30	21.74 34.78 43.48
G.	Pod: Pubescence	Absent Present	1 9	00 69	00.00 100.00
H.	Pod: Pubescence colour	Grey Tawny	1 2	11 58	15.94 84.06
I.	Pod: Colour	Yellow Brown Black	1 2 3	13 50 06	18.84 72.46 08.70
J.	Seed: Colour	Yellow Yellow green Green Black	1 2 3 4	68 00 00 01	98.55 00.00 00.00 01.45
K.	Seed: Lustre	Shiny Dull	1 9	45 24	65.22 34.78
L.	Seed: Shape	Spherical Elliptical	1 2	41 28	59.42 40.58
M.	Seed: Hilum colour	Yellow Grey Brown	1 2 3	00 05 50	00.00 07.25 72.46

		Black	4	14	20.29
		Variegated	5	00	00.00
N.	Seed: Cotyledon colour	Yellow	1	69	100.00
		Green	2	00	00.00
O.	Plant: Height (cm)	Short (< 40 cm)	3	39	56.52
		Medium (41-60 cm)	5	29	42.03
		Tall (>60 cm)	7	01	01.45
P.	Days to maturity	Early (< 95 days)	3	50	72.46
		Medium (96–105 days)	5	18	26.09
		Late (> 105 days)	7	01	01.45
Q.	Seed: Size(100 seeds weight)	Small (=10.0g)	3	38	55.07
		Medium (10.1-13.0g)	5	30	43.48
		Large (>13.0g)	7	01	01.45
R.	Days to 50% flowering	Early(< 35 days)	3	01	01.45
		Medium (36–45 days)	5	66	95.65
		Late(> 45 days)	7	02	02.90

Table 3: Characterization of the 69 soybean genotypes as per DUS guidelines.

Sr. No.	Genotypes	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1.	CO 2	9	2	2	1	1	1	9	1	1	1	1	1	4	1	3	3	3	5
2.	CSB 0809	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	5	3	5
3.	CSB 0811	9	2	2	1	1	3	9	2	2	1	1	1	3	1	5	7	3	5
4.	EC 18736	9	2	2	1	1	2	9	2	2	9	4	2	4	1	5	5	3	5
5.	JS 20-01	9	2	2	1	1	1	9	2	2	1	1	2	4	1	3	3	5	5
6.	JS 20-09	9	2	3	1	2	1	9	1	2	1	1	1	4	1	3	3	5	5
7.	JS 76119	9	2	2	1	1	3	9	2	2	9	1	1	4	1	3	3	3	5
8.	JS 89-24	9	2	2	1	1	2	9	2	2	9	1	2	3	1	5	3	3	5
9.	JS 95-60	9	2	3	1	1	3	9	2	2	9	1	1	3	1	5	3	3	7
10.	JS 95-98	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	3	3	5
11.	JS 97-52	1	1	3	1	1	1	9	2	1	1	1	2	4	1	3	3	3	5
12.	JS 98-21	9	2	2	1	1	3	9	2	2	1	1	1	3	1	5	3	3	5
13.	JS 98-61	9	2	2	1	1	3	9	2	2	1	1	2	3	1	7	3	3	5
14.	JS 98-68	1	1	2	1	2	1	9	1	2	1	1	1	4	1	3	3	5	5
15.	JS 99-12	9	2	2	1	1	3	9	2	2	9	1	1	3	1	5	5	3	5
16.	JS(SH)92-46	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	5	3	5
17.	JS(SH)93-37	9	2	2	1	1	3	9	2	1	1	1	2	3	1	5	3	5	5
18.	JS(SH)93-44	9	2	2	1	1	3	9	2	2	1	1	1	3	1	5	3	5	5
19.	MACS 1188	1	1	2	2	2	1	9	1	2	1	1	1	4	1	3	3	5	5
20.	MACS 1259	9	2	3	1	1	1	9	1	2	1	1	2	2	1	3	3	3	5
21.	MACS 1281	9	2	2	1	1	2	9	1	2	1	1	1	4	1	3	3	5	5
22.	MACS 145	9	2	2	1	1	2	9	2	2	1	1	1	3	1	3	5	3	5
23.	MACS 565	9	2	2	1	1	3	9	2	2	9	1	1	3	1	3	5	3	5
24.	MACS 610	9	2	2	1	1	2	9	2	2	1	1	1	3	1	3	5	3	5
25	MACS 629	9	2	2	1	1	2	9	2	2	1	1	2	3	1	5	5	5	7
26.	MACS 693	9	2	2	1	1	3	9	2	1	9	1	1	3	1	3	5	3	5
27.	MACS 694	9	2	2	1	1	3	9	2	2	1	1	1	3	1	3	5	3	5
28.	MACS 715	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	5	3	5
29.	MACS 798	9	2	2	1	1	3	9	2	2	9	1	1	3	1	5	5	3	5
30.	MACS 94-2	9	2	2	1	1	3	9	2	2	1	1	1	3	1	3	5	3	5
31.	MACS 985	9	2	3	1	1	2	9	1	2	1	1	1	4	1	3	5	5	5
32.	MAUS 39	9	2	2	1	1	3	9	2	2	1	1	1	3	1	5	5	3	5
33.	MAUS 414	9	2	2	1	1	3	9	2	9	1	1	2	3	1	5	3	3	5
34.	MAUS 417	9	2	2	2	1	2	9	2	2	1	1	2	3	1	3	3	5	5
35.	MAUS 52-1	9	2	2	1	1	2	9	2	2	1	1	1	3	1	3	3	5	5
36.	MAUS 55	9	2	2	1	1	3	9	2	2	9	1	1	3	1	3	5	5	5
37.	JS(SH) 8554	9	2	2	1	1	2	9	2	1	1	1	2	3	1	3	3	5	5
38.	MAUS 71-07	9	2	2	1	1	3	9	2	2	1	1	2	3	1	3	3	3	5
39.	NRC 2006-M-6	1	1	2	1	2	1	9	2	2	9	1	1	3	1	3	3	3	5
40.	NRC 2007-G-1-13	1	1	2	1	2	2	9	2	2	1	1	2	4	1	3	5	3	5
41.	NRC 2007-I-3	9	2	2	1	1	3	9	2	2	9	1	2	3	1	3	3	3	5
42.	NRC 2007-K-7-2	9	2	2	1	2	1	9	2	2	1	1	1	3	1	3	3	5	5
43.	VLS 69	9	2	2	1	1	3	9	2	3	9	1	2	3	1	3	3	3	5
44.	PK 1243	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	3	3	5
45.	MAUS 59	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	3	3	5
46.	MAUS 60	9	2	2	1	1	2	9	2	3	9	1	1	3	1	5	3	3	5
47.	MAUS 61	9	2	2	1	1	1	9	2	3	9	1	2	3	1	3	3	5	5
48.	NRC 76	9	2	2	1	1	3	9	2	2	9	1	2	3	1	5	3	5	5
49.	NRC 78	9	2	2	2	2	1	9	1	1	1	1	1	2	1	3	3	5	5
50.	NRC 79	1	1	3	2	2	1	9	1	1	1	1	2	2	1	3	3	5	5

No.	Genotype	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
51.	VLS 70	9	2	3	1	1	2	9	2	3	1	1	2	3	1	3	3	5	5
52.	WC 37	9	2	2	1	1	3	9	2	2	9	1	2	3	1	3	3	5	5
53.	WC 67	9	2	2	2	1	3	9	2	1	1	1	1	3	1	3	3	5	5
54.	PK 1000	9	2	2	1	1	3	9	2	2	9	1	2	3	1	5	3	3	5
55.	PK 1303	9	2	2	2	2	1	9	1	1	1	1	1	2	1	3	3	5	5
56.	PK 257	1	1	2	1	1	2	9	2	2	9	1	2	3	1	3	3	7	5
57.	PK 768	9	2	2	1	1	2	9	2	1	1	1	1	3	1	3	3	5	5
58.	PK 1011	9	2	2	1	1	3	9	2	2	1	1	1	3	1	5	3	5	5
59.	PK 1014	9	2	2	1	1	3	9	2	2	1	1	2	3	1	5	3	3	5
60.	PK 1024	9	2	1	1	1	3	9	2	2	1	1	2	3	1	5	3	3	5
61..	PK 1038	9	2	2	1	1	3	9	2	3	9	1	2	3	1	5	3	5	5
62.	PK 1125	9	2	2	1	1	2	9	2	2	1	1	1	3	1	5	3	3	5
63.	PK 1146	9	2	2	1	1	3	9	2	2	9	1	2	3	1	5	3	5	5
64.	PK 1225	9	2	2	2	1	3	9	2	1	1	1	2	3	1	5	5	5	5
65.	NRC 132	1	1	3	1	1	1	9	2	1	9	1	1	4	1	3	3	5	5
66.	NRC 142	9	2	3	1	2	2	9	2	1	9	1	2	4	1	3	3	5	5
67.	NRC 147	9	2	2	1	2	2	9	2	1	1	1	1	4	1	3	3	3	5
68	MACS 1460	1	1	2	1	2	1	9	1	3	1	1	1	2	1	3	3	5	3
69.	CO (Soy) 3	9	2	2	2	1	3	9	2	2	9	1	1	3	1	5	3	3	5

A. Hypocotyl: anthocyanin pigmentation, B. Flower colour, C. Leaf shape, D. Leaf colour, E. Plant Growth habit, F. Plant growth type, G. Pod pubescence, H. Pod pubescence colour, I. Pod colour, J. Seed lustre, K. Seed Colour, L. Seed shape, M. Seed hilum colour, N. Seed cotyledon colour, O. Plant: Height (cm), P. Days to maturity, Q. Seed size, R. Days to 50% flowering.

RESULT AND DISCUSSION

DUS characterization: Based on DUS guidelines as per PPV&FR (2001), fourteen qualitative and four quantitative traits were visually scored for 69 genotypes. Among eighteen traits, two were monomorphic *viz.,* seed cotyledon colour and pod pubescence and showed no variation for all the 69 genotypes. Eight traits were dimorphic and remaining eight were polymorphic in nature. Dhaliwal *et al.* (2020) also reported that out of 19 traits observed in soybean, only one trait *viz.,* plant growth type was monomorphic, nine traits were dimorphic and remaining nine traits were polymorphic. In the present study, flower colour and hypocotyl pigmentation were found to be correlated. Gupta *et al.* (2010) also observed correlation with flower colour and anthocyanin pigmentation in soybean. All the non-pigmented hypocotyls exhibited white flowers whereas all the pigmented hypocotyls exhibited purple flowers. In contrast, bronze band pigmentation on hypocotyls with certain white flowers when grown on continuous light was observed in soybean by Payne and Sundermeyer (1977). Studies on quantitative traits were also made by Karnwal and Singh (2009); Ramteke *et al.* (2012). The eighteen traits were observed at six different stages *viz.,* cotyledon stage, flowering stage (about 50 percent plants have at least one opened flower), pod setting stage (about 70 percent of pods attained full length 30-50 mm), advance ripening stage (about 50 percent of pods are ripe), full maturity stage (about 90 per cent pods are ripe) and post harvesting stage.

Floral characters: All the genotypes except NRC 2006-M-6, NRC 2007-G-1-13, NRC 79, PK 257, JS 97-52, JS 98-68, MACS 1188, NRC 132 and MACS 1460 bore white flowers and had no pigmentation in hypocotyl and remaining genotypes bore purple flowers and had pigmentation in hypocotyl (Fig. 1, 2). Six gene controls flower colour while two genes control pubescence colour in soybean was reported by Palmer *et al.* (2004); Takahashi *et al.* (2008).
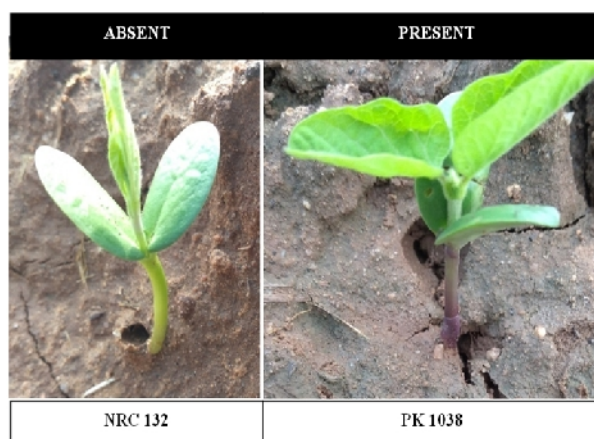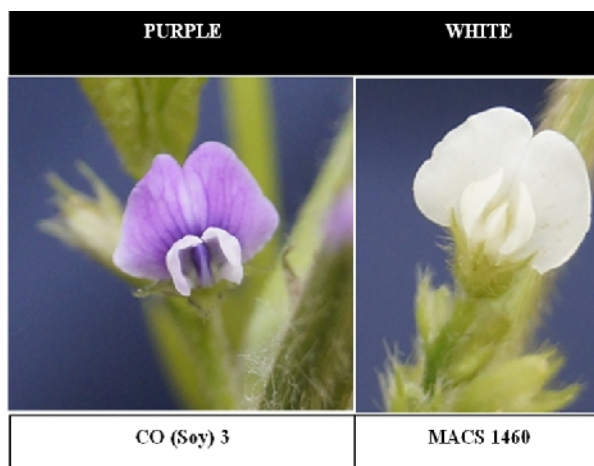

Fig. 1. Variation in hypocotyls colour.

Fig. 2. Variation in flower colour.

Growth characters: Erect type was displayed in most of the genotypes, except CO 2, JS 20-09, JS 98-68, MACS 1188, NRC 2007-G-1-13, NRC 2007-K-7-2, NRC 78, NRC 79, PK 1303, NRC 142, NRC 147 and MACS 1460 that had semi-erect type growth habit (Fig. 3). Singh *et al.* (2021) grouped all the seven released soybean varieties of Himachal Pradesh used in his study under tall stature category. But in our present study, there is a variation in the plant height among the 69 genotypes. Out of 69 genotypes, only one genotype JS 98-61 was observed as tall statured, 29 were noted as medium statured and 39 genotypes were of short stature. Plant growth type is classified into 3 categories *viz.,* determinate, semi-determinate and indeterminate. Determinate type was found in 15 genotypes, semi-determinate in 24 genotypes and indeterminate in 30 genotypes. Days to 50 per cent flowering was observed to be dimorphic. MACS 1460 exhibited early flowering, 66 genotypes were with medium type of flowering and remaining two genotypes *viz.,* JS 95-60 and MACS 629 were observed as late. Early maturing type was observed in 50 genotypes, medium maturing was observed in 18 genotypes and CSB 0811 was the only genotype categorized as late maturing type. Cober and Morrison (2010) reported that days to maturity and time to flowering is controlled by eight loci each with two alleles in soybean.

Leaf characters: Leaf shape was observed to be polymorphic trait. PK 1024 was the only genotype with lancealote leaf shape, 59 genotypes had pointed-ovate shape and nine genotypes had rounded ovate leaf shape.
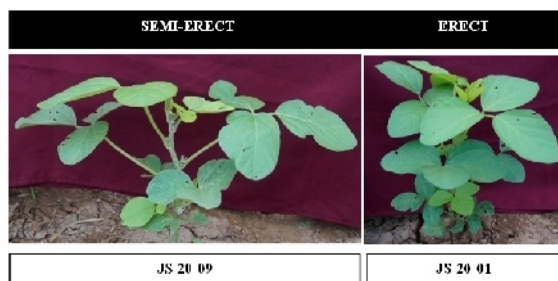
Fig. 3. Variation in Plant growth habit.
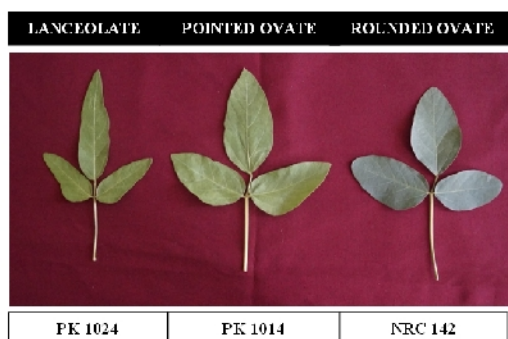
Fig. 4. Variation in leaf shape.

This shows that the variation in the leaf shape was mainly observed between rounded ovate and pointed ovate leaf (Fig. 4). Similar observation in leaf shape of soybean was found by Gupta *et al.* (2010). Green leaf colour was displayed by majority of the genotypes except MACS 1188, MAUS 417, NRC 78, NRC 79, WC 67, PK 1303 and CO (Soy) 3 which were with dark green coloured leaves.

Pod characters: Pod pubescence was found to be monomorphic and all the genotypes were observed with pubescence. Almost 50 genotypes had brown pod colour, 13 genotypes had yellow pod colour and the remaining genotypes *viz.,* VLS 69, MAUS 60, MAUS 61, VLS 70, PK 1038 and MACS 1460 had black pod colour. Majority of the genotypes had tawny pod pubescence colour except CO 2, JS 20-09, JS 98-68, MACS 1188, MACS 1259, MACS 1281, MACS 985, NRC 78, NRC 79, PK 1303 and MACS 1460 which were with grey pubescence.

Seed characters: Seed traits are crucial for DUS characterization as these are less influenced by the environment and are thus stable. Across the varying climatic zones, hair colour, flower colour and seed colour in soybean were reported to be the most stable characters by Satyavathi *et al*. (2004). Five seed traits *viz.,* seed size, seed shape, seed coat colour, seed lustre and seed cotyledon colour were noted in the present study and these traits were observed at post harvesting stage. Among the seed traits, seed size and seed hilum colour were polymorphic; seed shape, seed coat colour and seed lustre were dimorphic; and seed cotyledon colour was monomorphic in nature. Seed size was computed on the basis of hundred seed weight. Large-sized seed was observed in only one genotype *viz.,* PK 257, medium sized seed was observed in 30 genotypes and small-sized seed was observed in 38 genotypes. Forty-one genotypes exhibited spherical shaped seeds and the remaining genotypes exhibited elliptical shaped seeds. EC 18736 was the only genotype with black seed coat and remaining 68 genotypes exhibited yellow seed coat (Fig. 5). Ramteke *et al*. (2012) also observed the same type of variation in seed coat of soybean. Difference in seed coat within a species can usually be linked to variation in chromosome number or some aspect of gross morphology in soybean (Newell and Hymowitz, 1978). Seed hilum colour is highly stable and in the present study, three out of five designated classes of hilum colour were observed. MACS 1259, NRC 78, NRC 79, PK 1303 and MACS 1460 were the genotypes with grey hilum, 50 genotypes had brown hilum and fourteen genotypes had black hilum (Fig. 6). Yadav and Sharma (2001) also reported the variation in hilum colour in soybean. Morphological observations for seed lustre were observed to be shiny for all the soybean cultivars reported by Pawale *et al*. (2019). But in this study shiny seeds were observed in 45 genotypes and dull seeds were observed 24 genotypes.
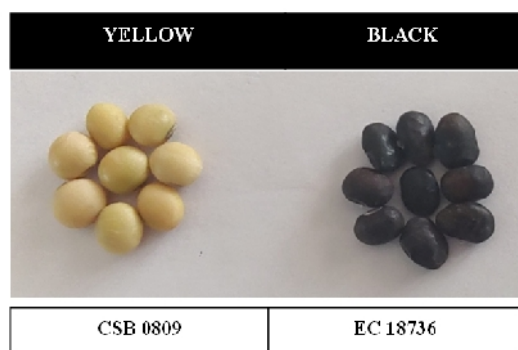
Fig. 5. Variation in seed colour.

Fig. 6. Variation in seed hilum colour.

Cluster analysis: Among the genotypes studied, few genotypes were distinct as they could be classified based on a single trait while majority of the genotypes were closely related. The similarity coefficient ranged from 0.81 to 0.82. Ranjani and Jayamani (2021) grouped 68 pigeonpea genotypes at an average similarity of 80%. The 69 genotypes were grouped into four clusters using UPGMA dendrogram in GGT 2.0 software (Fig. 7). Dhaliwal *et al.* (2020) also reported four clusters in grouping 22 soybean lines for 19 characters. The trait contributing for first grouping was anthocyanin pigmentation and flower colour. The first cluster had 39 genotypes that were subdivided into two sub clusters. The first sub cluster had 17 genotypes and these genotypes were very similar to each other for eight traits and varied for ten traits. The second sub cluster had 22 genotypes were found to be similar to each other for ten traits and showed variation for eight traits.

The second cluster had 21 genotypes that were subdivided into two sub clusters. The first sub cluster had only one genotype EC 18736. The second sub cluster had 20 genotypes and was very similar to each other for seven traits and showed variation for eleven other traits. The third cluster had two sub clusters. The first sub cluster had JS 97-52 and NRC 2007-G-1-13 and had 13 similar traits and varied for five traits. The second sub cluster had JS 98-68, MACS 1188, NRC 79 and MACS 1460 and had 12 similar traits and differed for six traits. The fourth cluster had three genotypes that were further divided into two subcultures. Sub cluster I

had two genotypes *viz.,* NRC 132 and NRC 2007-G-1-13 and these two genotypes had thirteen similar traits and varied for five traits. The sub cluster II had one genotype *viz.,* PK 257.
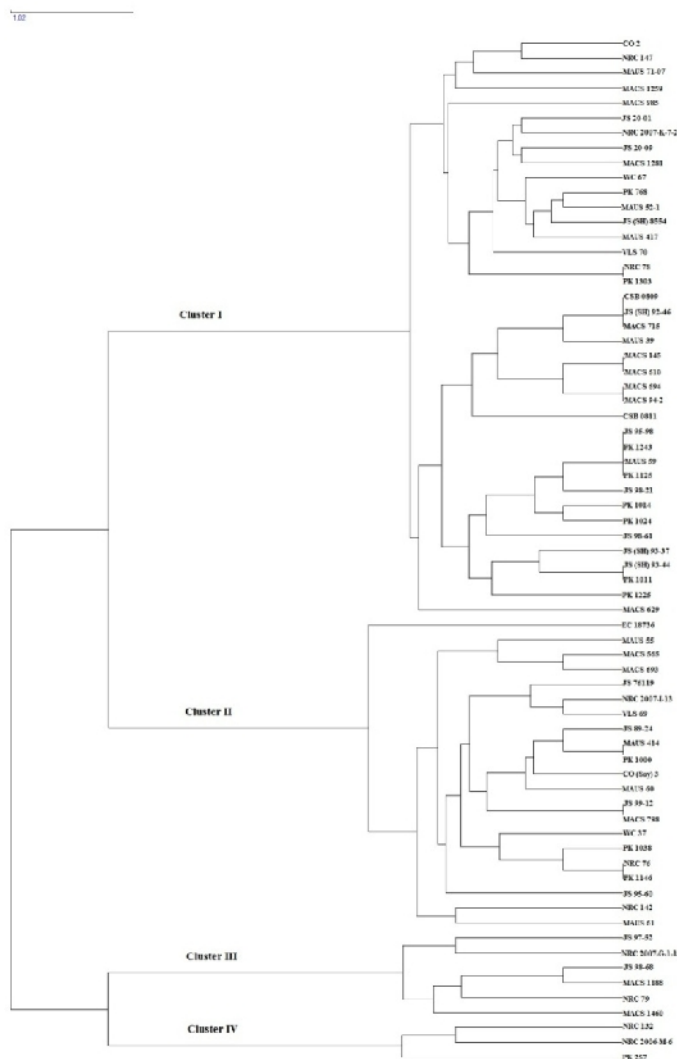

Fig. 7. Dendrogram constructed by cluster analysis of 69 soybean genotypes.

CONCLUSION

Among the 69 soybean genotypes studied, the genotypes CO 2, NRC 147, MAUS 71-07, MACS 1259, MACS 985, JS 20-01, NRC 2007-K-7-2, JS 20-09, MACS 1281, WC 67, PK 768, MAUS 52-1, JS (SH) 8554, MAUS 417, VLS 70, NRC 78 and PK 1303 from cluster I grouped under sub cluster I and the genotypes NRC 132, NRC 2007-G-1-13 and PK 257 in cluster IV in both the sub clusters were found to have wide variation. This study also revealed that traits *viz.,* flower colour, hypocotyl colour, presence and absence of pod pubescence and seed cotyledon colour were found to be reliable. The remaining traits can be focused for the

distinctness of the genotypes. Thus, the present study could be used for the selection of reference varieties for DUS testing of new soybean genotypes. In addition, genotypes with wide variation can be used as parent for crop improvement programmes.

FUTURE SCOPE

DUS characterization is important for cataloguing the genotypes based on their distinctness and utilization of variant genotypes for future crop improvement. Therefore, the genotypes with variation identified in the present study could be used as parent for the future breeding programme.

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