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Research Note

Unveiling genetic diversity in soybean germplasm: A comprehensive snalysis through DUS characteristics

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Abstract
Morphological characterization and diversity estimation are essential in plant breeding. In this endeavour, the researcher performed a visual assessment of 17 phenotypic DUS listed traits of 100 soybean accession in *Kharif* 2019-2020. Seven traits were dimorphic, while ten traits were polymorphic. Shannon's diversity indices were estimated using Microsoft excel. The index ranged from 0.06 to 1.72, with a mean value of 0.693. Seed peroxidase activity (g) obtained the highest value. Of the 100 accessions, few were unique as they could be distinguished based on a single trait, while the majority were very closely related. Cluster analysis revealed that the 100 accessions were grouped into four major clusters—similar genotypes concerning different traits clustered in the same clusters and vice versa.

Keywords: Soybean, DUS, Morphological Characterization, Shannon's Diversity Index.

Glycine max (*L.) Merrill*, a wonder crop, is also known as the "yellow jewel" of the twenty-first century that contains approximately 20 per cent of good quality oil, a very high amount of protein (around 40 per cent), and 25% per cent carbohydrates. Soybean serves as an excellent vegetable oil and protein source for human use and animal feed (USDA,2009). The contents of these metabolites are affected by both environmental and genetic factors. It has been reported that soybean originated in North-eastern China in the 11th century BC or earlier (Fukuda, 1933; Singh, 2010). In developing new varieties, genetic resources act as the key. Nearly 1.7 lakhs soybean accessions with some duplications are present worldwide, which can aid in genetic improvement (Nelson, 2009). Indian soybean germplasm collections are meager, with nearly 3000 germplasm accessions at ICAR NBPGR and about 2500 accessions at ICAR-IISR Indore. For varietal registration under PPV&FRA (2001), Distinctness, Uniformity, and Stability testing is critical.

The morphological characterization is essential in describing and classifying accessions. Success of breeding program mainly depends upon the magnitude of genetic variability. (Zubair *et al.,* 2007). To assess genetic diversity, a database of distinguishing features is required. These databases can be created using morphological characterization. Hence characterization of varieties or genotypes is an efficient way of identifying, grouping and avoiding duplication (Das and Kumar, 2012). It is crucial to characterize the collection's diversity to use, maintain, and increase germplasm collections efficiently and effectively. Germplasm serves as the base for any crop improvement program. Germplasm collection, evaluation, and cataloguing are the need of the hour for the soybean breeding program. cluster analysis in DUS testing and morphological characterization is a powerful tool for understanding genetic diversity, guiding breeding programs, ensuring regulatory compliance, and making informed decisions for sustainable agriculture.

However, not enough attempts have been made to evaluate the available soybean germplasm for efficient breeding programs. Therefore, the present study will help characterize more morphological traits in specific germplasm for planning the soybean improvement program. Viewing the importance of genetic diversity, a study for assessing soybean genotypes was undertaken.

DUS characterization was conducted for the hundred soybean accessions. The material was raised in an Augmented Plot Design I during the *Kharif* season of 2019-20 at the All India Coordinated Research Project on Soybean, JN Agriculture University, Jabalpur, India (Latitude: 23º14 N, Longitude: 79º56 E, Altitude: 411.5 m). The germplasm, including various indigenous and exotic collections, was received from ICAR-IISR, Indore, India. Four released varieties (JS 20-34, JS 335, JS 20-98, and NRC 86) were used as checks.

Each accession was sown in 4m row length with 50 x 6-8 cm^2 crop geometry. Recommended cultural practices were observed to take care of the germplasm. Based on the DUS test, the data were recorded for 17 morphological characters (**Table 1**). Data were registered on five plants, and then the average was worked out. The Phenotypic frequencies were worked out and were used to estimate Shannon's Diversity Index (H) (Negassa,1985) to check out the available diversity.

$$H= -\Sigma [p_i X \log p_i]$$

Where, p_i is the portion of the total number of entries belonging to the i^{th} class.

Cluster analysis was conducted using Statgraphics Centurion XIX software, and Pearson correlation coefficients (r) were evaluated using the package Corrplot.

The germplasm accessions were classified following the 'k-means clustering' model as explained by Macqueen (1967) and Forgy (1965). K-means cluster analysis was performed OPSTAT.

The distinctiveness test used visual scoring for 17 characters observed (**Table 1**). Seven characters were dimorphic viz. hypocotyl pigmentation, growth habit, growth type, leaf shape, flower colour, presence of hairs on pods, and colour of hilum funicle. The other ten characters showed polymorphic variation.

The violet flower colour was associated with the presence of hypocotyl anthocyanin pigmentation. Sixty-three of the accession bore exhibited the presence of anthocyanin pigmentation along with violet-coloured flowers, while thirty-seven carried white-coloured flowers. Hypocotyl pigmentation was absent in these genotypes. The study revealed that hypocotyl pigmentation and flower colour could be used as critical morphological markers to ascertain varietal distinctiveness amongst genotypes. (Dhaliwal *et al.,*2020). All the accessions displayed semi-determinate and semi-erect type growth habits, except JS 20-34, which had determinate and erect growth habits and growth types.

Three leaf traits, *viz.,* the shape, size, and leaf colour intensity, were recorded. Two out of three designated classes of leaf shape were recorded in the accessions under study. Thirty-four genotypes bore rounded ovate leaves, while the rest had pointed ovate leaves. Size of the leaves is another important leaf trait that distinguished eleven genotypes with large leaflets from the rest of the genotypes; seventy-five have medium-sized lateral leaflets while fourteen have small-sized leaves. Fifteen genotypes bore light green coloured leaves; thirty-seven bore dark green leaves distinct from the rest of the genotypes based on leaf colour intensity. All the other forty-eight genotypes had a medium green colour intensity on leaves.

Three pod traits, i.e., the presence of hairs, the colour of hairs, and the intensity of brown colour on pods, were included in this study. Most of the genotypes had hairs on the pods, contrary to the eighteen on which hairs were absent. The absence of colours on the hairs of the pod was observed in eleven genotypes rest had tawny or grey colours. (**Table 1 & 2**). Fifty-two genotypes had medium intensity and were distinct from those with a light colour (24 genotypes) and dark colour (24genotypes) pods.

Seed traits are crucial for DUS characterization as these are more stable since they are less affected by the environment. In the present investigation, seven seed traits were studied. In seed testa colour, two genotypes, namely JS 20-29, EC 391181, were yellow-green, and two genotypes viz. EC-389153 and UPSL 152 were green. Four genotypes, namely EC 294003, UPSM 77, TGX 849-D-13-4, and DE 201, were black, and two genotypes 23-11A(Z-18), EC 457336, were brown. Rest all were yellow. All the genotypes in the present study were grouped into three classes of seed size: small, medium, and bold. A maximum number of genotypes (81) had medium-sized seeds; six were bold, and 13 were undersized. Seed shape and lustre were also polymorphic. Seed hilum colour is a polymorphic trait and highly stable. In the present study, four out of five designated classes of hilum colour were observed. Fourteen genotypes had grey hilum, 46 had brown, eight had imperfectly black, while 32 genotypes had black hilum. Most of the genotypes (90) had the same funicle colour as the hilum, while ten genotypes had a different funicle colour. Only 12 genotypes did not show any peroxidase activity, while others had variation in peroxidase activity.

From studying these characters, we can quickly identify different genotypes of soybean. So, as to these characters as an identification key. A similar characterization pattern

Table 1. Frequency distribution along with Shannon-weaver diversity index for 17 morphological traits of soybean genotypes

S.No.	Trait	Classes	Score	Number of genotypes	Frequency (%)	Shannon's Diversity Index
1	Hypocotyl colouration	Present	9	63	63	0.65
		Absent	1	37	37	
2	Growth habit	Determinate	1	1	1	0.06
		Semi-determinate	2	99	99	
		Indeterminate	3	00	00	
3	Growth type	Semi erect to horizontal	3	00	00	0.06
		Semi-erect	2	99	99	
		Erect	1	01	01	
4	Leaf shape	Lanceolate	1	00	00	0.57
		Pointed ovate	2	76	76	
			3	24	24	
5	Leaf size	Small	1	14	14	0.73
		Medium	2	75	75	
		Large	3	11	11	
6	Leaf intensity of green	Light	1	15	15	1.1
		Medium	2	48	48	
		Dark	3	37	37	
7	Flower colour	White	1	37	37	0.66
		Violet	2	63	63	
8	Pods: presence of hairs	Present	1	82	82	0.47
		Absent	2	18	18	
9	Pod: Colour of Hairs	Tawny	2	67	67	0.84
		Grey	1	22	22	
		Absent	3	11	11	
10	Pod: brown color intensity at maturity	Dark	3	24	24	1.1
		Medium	2	11	11	
		Light	1	24	24	
11	Seed: ground colour of testa	Black	4	04	04	0.46
		Green	3	02	02	
		Yellow-green	2	02	02	
		Yellow	1	90	90	
		Brown	5	02	02	
12	Seed size	Small	1	13	13	0.61
		Medium	2	81	81	
		Bold	3	06	06	
13	Seed shape	Spherical	1	16	16	1.28
		Spherical flattened	2	46	46	
		Elongated	3	20	20	
		Elongated flattened	4	18	18	
14	Seed coat lusture	Shiny	1	26	26	0.98
		Intermediate	2	56	56	
		Dull	3	18	18	
15	Hilum colour	Grey	1	14	14	1.19
		Yellow	2	00	00	
		Brown	3	46	46	
		Intermediate black	4	08	08	
		Black	5	32	32	
16	Colour of Hilum funicle	Different to tseta	1	10	10	0.32
		Same as testa	2	90	90	
17	Seed : Peroxidase Activity	0	0	12	12	1.72
		1	1	24	24	
		2	2	23	23	
		3	3	20	20	
		4	4	11	11	
		5	5	10	10	

Table 2. Categorization of soybean genotype based on morphological characters

Genotype	HC	PGT	PGH	LS	LSZ	LC	FC	P: POH	PC	POD CL	SSZ	SS	TC	SCL	HC	FC	PA
K-53	9	2	2	3	2	2	2	1	2	2	2	2	1	2	5	2	3
EC 109540	9	2	2	2	2	2	2	1	2	2	1	2	3	2	3	1	2
UGM 75	9	2	2	3	2	2	2	1	2	2	2	3	3	2	5	1	4
MACS 303	9	2	2	2	2	2	2	1	2	3	2	3	1	2	4	1	2
TNAU 20022	9	2	2	2	2	2	2	1	2	3	2	2	4	2	5	1	0
EC 528640	9	2	2	2	2	2	2	1	2	1	2	2	2	2	3	1	2
EC-389153	9	2	2	3	1	2	2	1	2	3	2	1	1	3	3	1	3
UPSL 152	1	2	2	2	2	2	1	1	1	3	2	2	1	3	4	1	2
JS 20-34	9	2	2	2	2	1	2	1	2	2	1	4	1	1	1	1	0
JS 97-52	1	2	2	2	1	3	1	1	2	2	2	3	1	2	5	1	4
NRC 2007A	1	2	2	2	2	1	1	1	1	2	2	2	1	3	5	1	5
NRC 80-1	1	2	2	2	2	2	1	1	2	3	2	1	1	2	3	1	4
JS 20-01	9	2	2	2	1	3	2	1	2	2	2	4	1	2	4	1	3
EC 396065	9	2	2	2	1	2	2	1	2	3	2	4	1	2	1	1	2
DCB 137	1	2	2	2	2	3	1	1	1	1	1	1	1	2	3	1	1
EC 457214	9	2	2	2	2	2	2	1	2	3	1	1	1	3	5	1	1
DE 201	9	2	2	2	2	1	2	1	2	2	2	2	4	1	5	2	0
EC 457336	1	2	2	2	1	3	1	1	2	2	3	4	5	1	3	2	0
AGS 12	9	2	2	3	2	3	2	2	3	3	2	2	1	2	3	1	2
F4P20	1	2	2	3	2	2	1	1	1	1	2	2	1	2	5	1	1
EC 103336	9	2	2	2	2	3	2	1	2	2	2	4	1	1	1	1	2
NRC 86	9	2	2	2	2	3	2	1	2	1	2	1	1	2	3	1	4
EC 106998	9	2	2	2	2	1	2	1	2	1	2	2	1	2	3	1	1
SL 752	9	2	2	3	2	1	2	2	3	3	1	2	1	1	5	1	2
SQL 37	9	2	2	2	2	2	2	1	1	2	2	4	1	1	1	1	3
WT 88	1	2	2	3	3	2	1	2	3	2	2	4	1	2	5	1	2
EC 538830	1	2	2	3	2	3	1	1	2	1	1	2	1	2	5	2	1
NRC 2006M	1	2	2	2	2	2	1	1	2	2	2	1	1	2	3	1	0
EC16213	9	2	2	2	1	2	2	1	2	2	2	2	1	1	5	1	2
JS 20-52	1	2	2	2	1	2	1	1	2	2	2	1	1	2	5	1	3
PS 1475	1	2	2	2	2	2	1	1	2	3	2	3	1	1	5	2	4
EC 389179B	1	2	2	2	2	1	1	1	1	2	2	2	1	3	4	1	1
JSM 227	9	2	2	3	2	2	2	2	2	1	2	3	1	2	3	1	0
SL 2951	9	2	2	2	1	1	2	1	2	2	1	4	1	2	3	1	2
EC 389099	9	2	2	2	1	1	2	1	2	1	2	3	1	1	1	1	1
JS 20-69	1	2	2	2	1	2	1	1	1	2	1	2	1	2	5	2	1
JSM 195	1	2	2	2	2	3	1	1	1	2	2	1	1	2	3	1	2
EC 291397	9	2	2	2	1	2	2	1	2	2	2	3	1	2	1	1	2
PS 1336	1	2	2	2	2	2	1	1	2	3	2	2	1	2	3	1	3
EC 294003	9	2	2	2	2	2	2	1	2	2	2	4	4	2	5	2	0
EC 291451	9	2	2	2	2	2	2	1	2	1	2	3	1	1	1	2	1
EC 24091	9	2	2	2	3	3	2	1	2	2	2	4	1	1	1	1	1
RSC 14	1	2	2	2	2	3	1	1	2	2	2	2	1	2	3	1	2
EC 325103	9	2	2	3	3	3	2	1	2	3	2	2	1	2	3	1	3
JSM 285	9	2	2	3	2	3	2	2	1	1	2	2	1	1	5	1	1
EC 33872B	9	2	2	2	2	2	2	1	2	2	2	2	1	2	5	1	4
SQL 1	9	2	2	2	2	2	2	1	2	2	1	3	1	1	5	2	1
JSM 232	1	2	2	3	3	3	1	2	1	3	2	2	1	2	3	1	1
JSM 222	9	2	2	2	3	3	2	1	1	3	1	1	1	2	3	1	2
JSM 245	1	2	2	3	3	3	1	2	3	3	2	2	1	2	3	1	1
PS 1467	1	2	2	3	2	3	1	2	3	3	2	2	1	2	5	1	0
SL (E)1	9	2	2	2	3	3	2	1	2	1	3	2	1	2	3	1	3

Table 2. Continued

Genotype	HC	PGT	PGH	LS	LSZ	LC	FC	P: POH	PC	POD CL	SSZ	SS	TC	SCL	HC	FC	PA
PK 701	9	2	2	3	2	2	2	2	2	3	2	2	1	2	3	1	2
PK 1038	9	2	2	2	2	1	2	1	2	2	2	4	1	3	3	1	5
RKS 54	1	2	2	2	2	3	1	1	1	1	1	2	1	1	5	1	4
EC 33940	9	2	2	2	2	2	2	1	2	2	2	2	1	1	3	1	2
G2225	9	2	2	2	2	3	2	1	2	1	1	2	1	2	3	1	3
JS 20-29	1	2	2	2	2	3	1	1	1	2	2	2	2	3	3	1	5
G4P15	9	2	2	2	2	3	2	2	3	2	2	2	1	1	3	1	2
GP 465	1	2	2	2	3	3	1	1	2	3	2	2	1	3	3	1	3
TGX 849-D-13-4	9	2	2	2	2	2	2	1	2	2	2	2	4	3	5	2	0
MACS 171	1	2	2	2	2	2	1	1	1	3	2	1	1	2	3	1	2
JS 20-98	1	2	2	2	2	3	1	1	2	1	2	1	1	1	5	1	3
TG X 849-813	9	2	2	2	2	3	2	1	2	1	2	2	1	3	3	1	0
KB-17	9	2	2	2	2	1	2	1	2	2	2	3	1	2	3	1	1
KDS 256	1	2	2	2	2	3	1	1	1	1	2	4	1	2	5	1	3
LEE-54	9	2	2	2	2	2	2	1	2	2	2	4	1	1	3	1	2
JS 96-31	1	2	2	2	2	3	1	1	2	2	3	3	1	2	3	1	3
TNAU 20024	9	2	2	3	2	3	2	2	2	3	2	2	1	2	3	1	4
PK 258	9	2	2	3	2	3	2	2	3	2	2	1	1	2	3	1	2
EC 468597	9	2	2	3	2	2	2	2	3	3	2	2	1	2	5	1	1
EC 572160	9	2	2	2	1	2	2	1	2	2	2	3	1	3	3	1	3
NRC 37	9	2	2	2	2	2	2	1	2	2	2	4	1	1	1	1	3
EC 391181	9	2	2	2	2	2	2	1	2	1	2	4	1	1	1	1	1
VGM 70	9	2	2	2	1	3	2	1	1	2	2	1	1	2	3	1	3
VLS 75	9	2	2	2	2	2	2	1	1	1	2	3	1	1	1	1	4
EC 391316	9	2	2	2	2	2	2	1	2	2	2	3	1	1	1	1	5
SL 682	9	2	2	2	2	3	2	1	1	3	1	1	1	3	3	1	4
PI 204336	9	2	2	2	2	3	2	1	2	2	2	2	1	2	4	1	0
UGM 70	9	2	2	2	2	3	2	1	1	2	3	3	1	1	3	1	1
LEE 96	9	2	2	2	2	1	2	1	2	1	2	3	1	2	1	1	1
TG X 1488-9-1D	9	2	2	2	3	2	2	1	1	2	2	2	1	2	3	1	5
GP566	1	2	2	2	2	2	1	1	1	2	2	2	1	2	3	1	3
PS1421	9	2	2	2	2	1	2	1	2	2	2	4	1	2	1	1	1
VLS 11	9	2	2	2	2	2	2	1	2	1	2	2	1	2	3	1	3
UPSM 77	1	2	2	2	3	3	1	1	2	2	2	2	1	2	3	1	0
EC 350664	9	2	2	2	2	3	2	1	2	2	2	2	1	2	4	1	2
EC 377883B	9	2	2	2	2	2	2	1	2	1	3	3	1	3	4	1	1
JS 20-34	1	2	2	3	1	1	1	2	3	3	2	2	1	2	5	1	5
G.C. 84051-32-1	9	2	2	2	2	2	2	1	1	1	2	4	1	1	1	1	1
J.S. 20-50	1	2	2	3	2	1	1	2	2	2	2	3	1	3	3	1	1
MACS-7102	9	2	2	3	2	2	2	2	3	3	2	1	1	2	3	1	2
20-40B(Z-9)	1	2	2	3	3	1	1	1	2	2	2	2	1	3	5	1	5
20-148 (Z-15)	1	2	2	2	2	1	1	1	2	2	2	3	1	3	5	1	4
23-10B(Z-17)	1	2	2	2	2	2	1	1	2	2	2	3	1	2	5	1	5
23-11A(Z-18)	1	2	2	2	2	2	1	1	2	2	2	2	5	3	5	1	5
J.S. 20-34	1	1	1	3	2	2	1	2	2	2	2	1	1	1	5	1	5
JS 335	9	2	2	3	2	3	2	2	3	1	2	2	1	1	3	1	3
J.S. 20-98	1	2	2	2	2	2	1	1	2	2	2	2	1	1	5	1	2
NRC 86	9	2	2	2	2	3	2	1	2	3	3	4	1	3	4	1	3

Here:
HC= Hypocotyl colour; FC= Flower colour; TC= Ripe seed: the ground colour of testa; PGT= Plant Growth type; P: POH= Pod: the presence of hairs ; SCL= Ripe seed: seed coat lusture; PGH= Plant Growth habit; PC= pod: the colour of hairs; HC= Ripe seed: hilum colour; LS = Leaf shape;POD CL= Pod: intensity of brown colour; FC= Ripe seed: colour of hilum funicle; LSZ = Leaf size of lateral leaflet; SSZ= Ripe seed: seed size; PA= Ripe seed: colouration due to LC= Leaf intensity of green colour; SS= Ripe seed: seed shape ;peroxidase activity

was adopted by Satyavathi *et al.* (2004), Gupta *et al.* (2010), Ramteke and Murlidharan (2012), Badkul *et al.* (2014), Mishra *et al.* (2016), Dubey *et al.* (2018), and Dhaliwal *et al.* (2020) taking distinguished morphological traits. In soybean, the published literature also corroborates these assertions. The characteristics such as flower colour, presence/absence of pod hair, the colour of hair, and seed colour were found to be the most stable across various agro-climatic zones of India (Satyavathi *et al.,* 2004, Gupta *et al.,* 2010).

Shannon's diversity indices : Diversity is the need of the hour in designing any breeding program. The Shannon's diversity indices estimated for 17 morphological characters (**Table 1**) ranged from 0.06 to 1.72, with a mean value of 0.693. Seed peroxidase activity (g) obtained the highest diversity index, 1.720. In contrast, plant growth habit received the lowest diversity index value of 0.06, and plant growth type as accessions exhibited no variability for these traits. Thus, high diversity can be revealed in the morphological characters studied by diversity index values revealed. Therefore, productive utilization of germplasm accessions can account for improvements in these traits.

Cluster analysis for distinctiveness: The cluster analysis identified distinct subgroups displaying the variation. The cluster analysis suggests that the 100 accessions were clustered into four major groups (**Fig. 1**). The first cluster has 37 genotypes and is subdivided into two sub-clusters (**Fig. 1**). The second cluster had 45 genotypes further subdivided into two sub-clusters. Seventeen genotypes belonged to the third cluster, and JS 20-34 belonged to the fourth cluster. Similar genotypes concerning different traits were put in the same clusters and vice versa.

K-means clustering: With K-means clustering, n objects are divided into k clusters, each containing the object with the closest mean. A centroid-based clustering algorithm is K-means. The cluster count, denoted by the "K" is an input parameter. Each data point in collection is assigned to the cluster centre closest to it. The maximum number of distinct clusters produced by this method is k. All 100 germplasm accessions, including four check entries, were categorized into six separate groups using the K-means clustering technique, as shown in **Table 3**. With 23 genotypes, cluster II was the largest, followed by 22 genotypes of cluster I. Our findings are comparable to those of Muhammad *et al.* (2016), Wanga *et al.* (2017), Kaur *et al.* (2018), Sharma *et al.* (2018) and Mohan *et al.* (2019).

Correlations among the different traits studied: The traits under study were estimated for Pearson's correlation coefficients, revealing significant correlations. The trait combinations like hypocotyl colouration and flower colour, plant growth habit and plant growth type, presence of pod hairs and leaf shape, etc., marked significantly strong positive correlations ($p = <0.05$) (**Fig. 2**). The trait combinations like hypocotyl and hilum, flower colours, seed hilum colours, etc., inferred significantly strong negative associations ($p = <0.05$). Among all the trait correlations (**Fig. 2**), hypocotyl colouration strongly correlated with flower colour, validating the morphological observations. Based on their findings, Ramteke and Murlidharan (2012) grouped

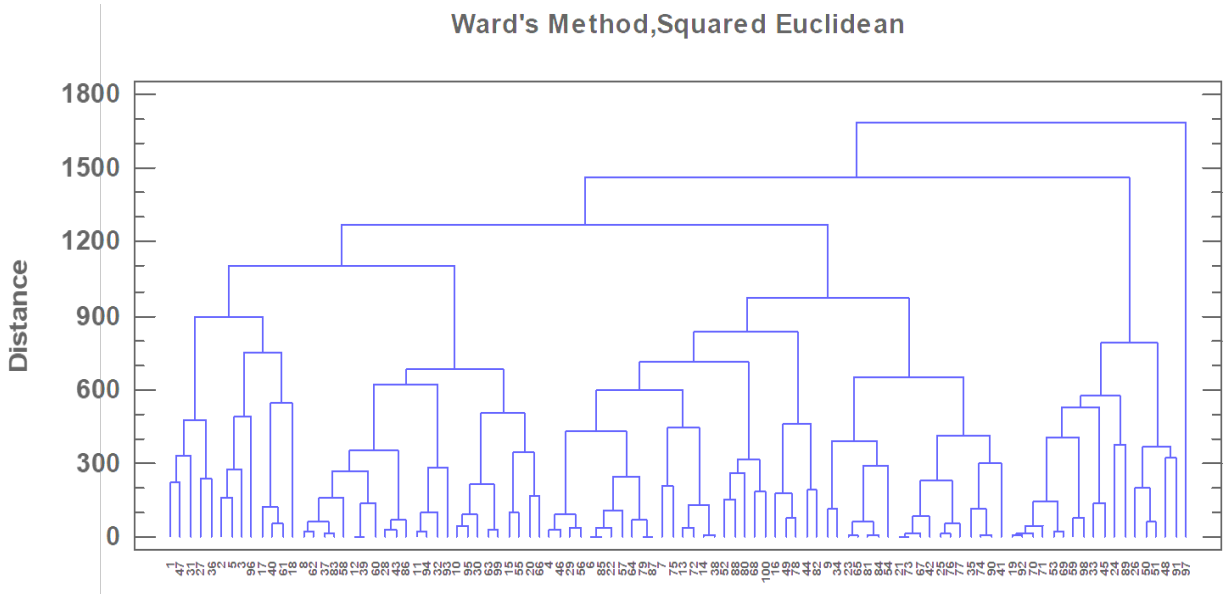

Fig.1. Dendrogram representing distinctiveness of 100 soybean genotypes

Table 3. Distribution of genotypes into 6 clusters as per K-Means Clustering

Clusters	Number of genotypes	Genotypes
1	22	VLS 75, DCB 137, EC 457336, F4P20, UGM 75, MACS 303, NRC 2006M, NRC 37, JS 20-69, JSM 195, PS 1336, RSC 14, JSM 232, JSM 245, JS 20-34, GP 465, JSM 227, JS 96-31, GP566, PS 1467, JS 20-50, JS 95-60,
2	23	K-53, UPSL 152, VGM 70, JS 20-01, AGS 12, NRC 86, EC 325103, EC 33872B, JSM 222, SL (E)1, PK 701, PK 1038, G2225, TNAU 20024, SQL 37, TNAU 20022, PK 258, SL 682, TG X 1488-9-1D, VLS 11, JS 20-50, JS 335, NRC 86
3	15	JS 97-52, JS 20-52, PS 1475, NRC 2007A, NRC 80-1, RKS 54, JS 20-29, JS 20-98, KDS 256, JS 20-34, 20-40B(Z-9), 20-148 (Z-15), 23-10B(Z-17), 23-11A(Z-18), JS 20-34,
4	19	EC-389153, EC 389179B, EC 391181, EC 457214, EC 106998, SL 752, EC16213, MACS 171, JSM 285, SQL 1, EC 33940, G4P15, TG X 849-813, KB-17, WT 88, PI 204336, UGM 70, EC 350664, EC 377883B
5	4	UPSM 77, DE 201, EC 294003, TGX 849-D-13-4,
6	17	EC 391316, EC 3960651, EC 103336, EC 109540, SL 2951, EC 389099, EC 291397, EC 291451, EC 24091, LEE-54, EC 528640, EC 538830, EC 468597, EC 572160, LEE 96, PS1421, GC 84051-32-1

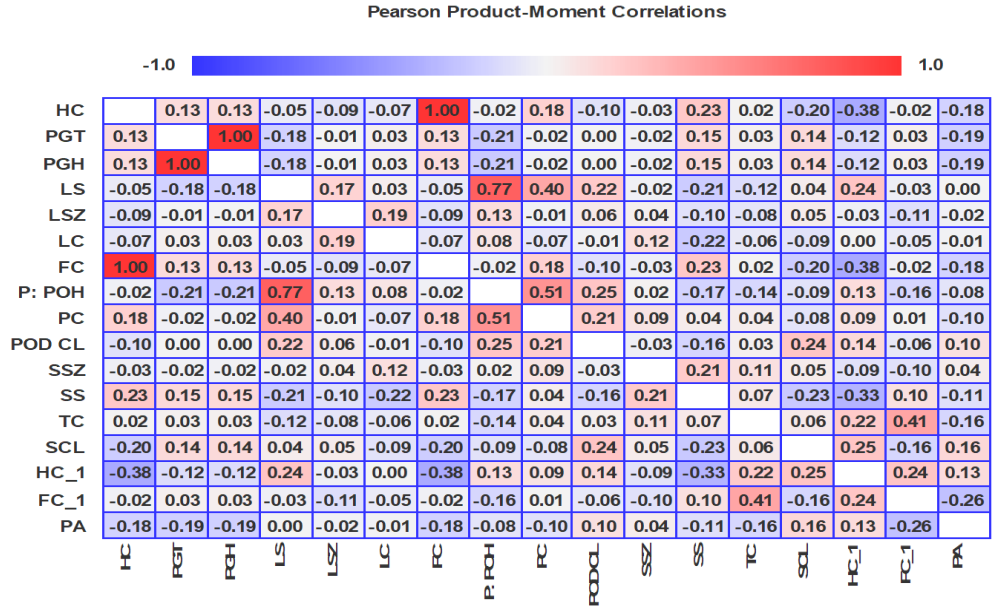

Fig. 2. Represents Pearson's correlation coefficients of the 17 DUS traits as a heat map

Red colour represents positive correlation, and blue colour represents negative correlation.

soybean varieties of India into two significant groups concerning flower colour, i.e., white-flowered and violet-flowered, supporting our work.

Hence, all the traits should be considered collectively to identify a genotype. Analysis revealed a sufficient and desirable variability for most characters, indicating enough scope for selection. Making DNA fingerprinting a critical process to detect the fundamental distinction between biochemical and molecular markers can be employed. The present study will be helpful to the breeders to identify the variable sources to be further used in breeding programs and thus seek protection under the Protection of Plant Varieties and Farmers Rights Act.

REFERENCES

Badkul, A., Shrivastava, A.N., Bisen, R. and Mishra, S. 2014. Study of principal components analyses for yield contributing traits in fixed advanced generations of soybean [*Glycine max* (L.) Merrill]. *Soybean Research,* **2**: 44-5

Das, A. and Kumar, D. 2012. Genetic evaluation and characterization of jute (*Corchorus* spp. L)

genotypes using DUS parameters. *SAARC Journal of Agriculture,* **10**: 147-153. [Cross Ref]

Dhaliwal, I., Khosla, G., Singh, T.P., Gill, B.S. and Kaushik, P. 2020. DUS Characterization of some Released Varieties and Advanced Breeding Lines of Soybean (*Glycine max* L.) under Punjab Agroclimatic Conditions. *Int.J.Curr.Microbiol.App.Sci.,* **9**(08): 2124-2135. [Cross Ref]

Dubey, Nidhi & Avinashe, H.A. and Shrivastava, A.N. 2018. Genetic parameters and character association studies of soybean genotypes in Madhya Pradesh region. *Annals of Biology*, **34**. 207-211

Forgy, E.W. 1965. Cluster analysis of multivariate data efficiency vs. interpretability of classifications. *Biometrics,* **21**: 768−769.

Fukuda, Y. 1933. Cytogenetical studies on the wild and cultivated Manchurian soybeans (*Glycine max* L.). *Japanese Journal of Botany,* **6**: 489–506.

Gupta, A., Mahajan, V., Khati, P. and Srivastava, A.K. 2010: Distinctness in Indian soybean (*Glycine max*) varieties using DUS characters. *Indian Journal of Agricultural Sciences,* **80**:1081- 4.

Kaur, G., Joshi, A. and Jain, D. 2018. Marker-assisted evaluation of genetic diversity in mung bean (*Vigna radiata* (L.) Wilcezk) genotypes. *Brazilian Archives of Biology and Technology,* **61**: e18160613. [Cross Ref]

Macqueen, J.B. 1967. Some methods for classification and analysis of multivariate observations. Proceedings of 5th Berkeley Symposium. Mathematical statistics and probability. *University of California Press,* **1**: 281−297.

Mishra, S., Jha, A. and Shrivastava, A.N. 2016. Genetic divergence analysis in new breeding genotypes of soybean [*Glycine max* (L.) Merril]. *Indian Journal of Ecology,* **43** (Special Issue): 000-00.

Mohan, S., Sheeba, A. and Kalaimagal, T. 2019. Genetic diversity and association studies in greengram [*Vigna Radiata* (L.) Wilczek]. *Legume Research*, DOI: 10.18805/LR-4176, 1-6. [Cross Ref]

Muhammad, A., Muhammad, A.M., Qamar, U.Z. and Muhammad, A.A. 2016. Uncovering the of mung bean (*Vigna radiata* L. Wilczek) genotypes under saline conditions using k-mean cluster analysis. *Journal of Agriculture and Basic Sciences,* **1**(1): 37−44.

Negassa, M. 1985. Patterns of phenotypic diversity in an ethiopian barley collection and the arussi-bale highland as a center of origin of barley. *Hereditas,* **102**: 139–150. [Cross Ref]

Nelson, R. 2009. Collection, conservation and evaluation of soybean germplasm. In: The

abstract of Proceedings. The eight world Soybean Research Conference. Beijing, China.

Ramteke, Rajkumar and Murlidharan, Pooja. 2012. Characterization of soybean (Glycine max) varieties as per DUS guidelines. *Indian Journal of Agricultural Sciences*, **82**. 572-7.

Satyavathi, C.T., Bharadwaj, C.H., Husain, S.M., Karmakar, P.G., Tiwari, S.P., Joshi, O.P. and Mohan, Y. 2004. Identification key for soybean (*Glycine max*) varieties released or notified in India. *Indian Journal of Agricultural Sciences*, **74**: 215–8.

Sharma, S.R., Singh, D., Kumar, P., Khedar, O.P. and Varshnay, N. 2018. Assessment of genetic diversity in mungbean [*Vigna radiata* (L) wilczek] genotypes. *International Journal of Genetics,* **10**(7): 471−474.

Singh, G. 2010. The soybean: botany, production and uses: The origin and history of soybean, L. J. Qui & R. Z. Chang, 1-23, CAB International. [Cross Ref]

United States Department of Agriculture. (USDA). 2009. National Nutrient Database for Standard Reference Release 18.

Wanga, L., Baib, P., Yuanc, X., Chena, H., Wanga, S., Chenc, X. and Chenga, X. 2017. Genetic diversity assessment is a set of introduced mung bean accessions (*Vigna radiate* L.) *The Crop Journal,* **6**(2): 207−213. [Cross Ref]

Zubair, M., Ajmal, S.U., Anwar, M. and Haqqani, A.M. 2007. Multivariate analysis forquantitative traits in mungbean (*Vigna Radiata (L.) Wilezek). Pakistan Journal of Botany*, **39**(1): 103.