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DUS characterization of indigenous and exotic soybean [*Glycine max* (L.) Merrill] germplasm in North Western Himalayas

Ronika Thakur*, Vedna Kumari, Jyoti Kumari, Diksha Khajuria, Aradhana Kumari and Rishita Kapoor
Department of Genetics and Plant Breeding,
Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh, India

*Corresponding author e-mail: ronikathakur7@gmail.com

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Abstract

Distinctness, Uniformity, and Stability (DUS) characterization plays a crucial role in ensuring accurate identification and differentiation of plant varieties and genotypes. In the present study, 320 indigenous and exotic soybean accessions were morphologically characterized using 20 DUS descriptors during *kharif*, 2022. The characters *viz*., flower color, anthocyanin pigmentation, pod pubescence, and growth habit were identified as prominent for identification of a variety. Principal component analysis revealed that the initial two components explained 24.47% of the overall multi variate variation. Cluster analysis identified four distinct clusters with 16, 14, 267, and 23 genotypes, signifying substantial diversity within the germplasm. This knowledge of frequency distribution analysis under the framework of DUS characterization will guide researchers in taking decisions, ensuring varietal stability and upholding the integrity of plant variety protection systems along with facilitating the characterization, preservation and utilization of beneficial genes in the germplasm for soybean improvement.

Keywords: DUS, genetic resources, germplasm, Soybean

Soybean [*Glycine max* (L.) Merrill] is one of the most important seed legumes on the earth popularly known as the 'wonder crop' due to its high oil (20%), protein content (40%), iso-flavonoids, folic acid, saponins exhibiting several anti-oxidants, anti-diabetic, and anti-inflammatory properties along with its ability to replenish the soil by fixing nitrogen. Out of total 89% of imported crude edible oil, 21% is contributed by soybean oil (Anonymous 2018). In soybean improvement programmes, efforts are being made to develop high yielding (Li *et al*. 2020), abiotic tolerant (Buezo *et al*. 2019), biotic resistant (Tripathi *et al*. 2022), nutritionally rich (Zhang *et al*. 2020), and stable cultivars (Abdelghany *et al.* 2021) to meet the growing demand. Till date, more than 130 varieties have been developed for the different climatic conditions in India (Sivabharathi *et al*. 2022). 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 do not change over generations. Varietal identification is the foundation of seed production, seed certification and maintaining the genetic identity throughout the supply chain and securing quality assurance through grow out test (Singh *et al*. 2021).

Germplasm is the basic material for every crop improvement programme and plays a critical role in crop improvement (Rana *et al.* 2023). The more variation in the available germplasm, higher is the probability of identifying superior genotypes. A collection has limited application until it has undergone a thorough evaluation and characterization which includes a system of recording and storing data that can be readily retrieved and available to others for planning breeding programmes (Soharu *et al*. 2022). Greater variety improves genetic potential and provides greater choices for selection, resulting in the successful completion of a breeding program. Qualitative traits can accurately characterise varieties and genotypes since they are more stable over generations and hence, they are authentic and reliable for the characterization of germplasm and varieties as well (Sekhon and Sharma 2019). In soybean, attributes such as pod pubescence, seed coat colour, shape, size and hilum colour etc. are efficiently used to differentiate the genotypes using DUS descriptors to produce superior varieties.

In India, DU Stesting is implemented by the Protection of Plant Varieties and Farmers' Rights Act 2001 (PPV&FRA) where the information regarding novelty, distinctness, uniformity, and stability are the basic mandates for protection. Novelty refers to the newness of a variety while distinctness, indicates the clearly distinguishable one or more essential characteristics such as morphological, quality, agronomic character, or molecular trait from any other existing varieties. The variety/germplasm is deemed uniform if it is sufficiently uniform in its relevant characteristics, it should be pure and phenotypically similar. In addition, stability indicates that essential characters should remain unchanged under different agro-climatic conditions. The requirement of DUS is assessed and based on characteristics/descriptors which are feature of whole plant or part of plant. These traits could be morphological, molecular, biochemical or of any other type. Characterization is the process of describing a plant using descriptors. Morphological characterization is based on qualitative characteristics (shape, flower color) and pseudo-qualitative characteristics (pubescence, pigmentation). Keeping in view the prime importance, the present study was conducted to characterise the soybean germplasm lines (indigenous and exotic) and study distinctness among each other to utilize them in future soybean breeding program as per the requirements.

Materials and Methods

The experimental material comprised of 320 soybean germplasm lines including 24 checks received for multilocation germplasm evaluation trial under All India Co-ordinated Research Project (AICRP) in soybean from ICAR-Indian Institute of Soybean Research, Indore, Madhya Pradesh. The experiment was carried at experimental farm of the Department of Genetics and Plant Breeding, CSKHPKV, Palampur, Himachal Pradesh during *kharif*, 2022. The site is located at 32°09' N latitude and 76°55' E at the altitude of 1290 m above sea level with a precipitation of 2500 mm annually. The pH of the soil is acidic from 5.0-5.6.The material was grown in randomised block design in two replications withrow length, spacing and plot size of 2 m, 45 × 15 cm and 1.80 m^2,respectively.The recommended agronomic management practices were followed to raise the crop. The data on twenty traits *viz*., hypocotyl anthocyanin pigmentation, flower colour, plant growth, leaf shape, leaf size, leaf colour, growth habit, pod colour, pod pubescence, podding, seed shape, colour of testa, seed coat color, hilum colour, colour of hilum funicle, seed weight (g) and seed cotyledon colour were recorded as per the national DUS guidelines except for days to 50% flowering, days to 75% maturity and plant height (cm) calculated on relative basis for DUS characterisation. The recorded data was analysed using Microsoft Excel for frequency distribution. The UPGMAa simple agglomerative hierarchical clustering method based on Euclidean similarity index was used to construct the cluster dendrogram. Principal component analysis was worked out using PAST software version 4.03. To estimate the diversity present among the genotypes, the phenotypic frequencies of these traits were employed to estimate the Shannon's Diversity Index (H) using PAST software version 4.03.

Results and Discussion

Distribution of qualitative traits

The results indicated presence of sufficient variability among the genotypes investigated for different traits (Table1). Soybean generally have purple or white flowers conditioned by a dominant/recessive allele of the W1 locus. The W1gene pleiotropically conditions hypocotyl color; soybean with purple flowers have purple hypocotyl, whereas those with white flowers have green hypocotyl. However, in present studyout of 320 accessions, 226 were anthocyanin pigmented and 230 had purple flower while only 90 were white flowered. Leaves are the primary organs of photosynthesis and assimilation in plants. In this study, 12%, 49% and 39% of total genotypes were having small, medium and large sized leaf, respectively. Moreover, the leaf intensity of green color varied from light (15%),

Table 1. Classification of soybean genotypes based on various characters

Sr.no	Characters	Descriptors	Frequency	% contribution	Sr. no.	Characters	Descriptors	Frequency	% contribution
1.	Hypocotyl: anthocyanin coloration	Present	226	71			Medium	144	45
		Absent	94	29			Light	88	27.5
2.	Plant: growth type	Determinate	64	20	13.	Seed: size (100 seed weight)	Small (<10g)	26	8
		Semi-determinate	189	59			Medium (10-13g)	139	44
		Indeterminate	67	21			Large (>13g)	155	48
3.	Plant: time of flowering (days)	Early (<50)	6	2	14.	Seed: shape	Spherical	114	35.62
		Medium (50-75)	290	91			Spherical flattened	185	57.8
		Late (>75)	24	7			Elongated	1	0.31
4.	Leaf: shape of lateral leaflet	Lanceolate	17	5			Elongated flattened	20	6.25
		Triangular	-	-	15.	Seed: ground color of testa (excluding hilum)	Yellow	256	80
		Pointed ovate	199	62			Yellow green	42	13
		Rounded ovate	104	33			Green	2	0.62
5.	Leaf: size of lateral leaflet	Small	37	12			Brown	4	1.25
		Medium	158	49			Black	16	5
		Large	125	39	16.	Seed coat: lustre	Shiny	102	32
6.	Leaf: intensity of green color	Light	49	15			Indeterminate	173	54
		Medium	120	38			Dull	45	14
		Dark	151	47	17.	Seed: hilum color	Grey	-	-
7.	Plant: growth habit	Erect	76	24			Yellow	-	-
		Semi-erect	151	47			Brown	141	44
		Semi-erect to horizontal	93	29			Imperfect black	30	9
8.	Flower: color	White	90	28			Black	149	47
		Violet	230	72	18.	Plant: time of maturity in days			
							Early (<100)	-	-
9.	Pod: presence of hairs	Present	289	90			Medium (101-125)	122	38
		Absent	31	10			Late (>125)	198	62
10.	Pod: color of hairs	Grey	34	12	19.	Seed: cotyledon color	Yellow	318	99.37
		Tawny	255	88			Green	2	0.63
11.	Plant: height (cm)	Short (<50)	-	-	20.	Seed: Colour of Hilum Funicle			
							Same as testa	257	80
		Medium (50-70)	14	4			Different to testa	63	20
		Tall (>70)	306	96					
12.	Podding	Heavy	88	27.5					

medium (38%) to dark (47%). Leaf shape could be associated with other characteristics such as presence, number, and size of trichomes in plants. The variation in leaf shape was categorized into lanceolate (5%), triangular (0%), pointed ovate (62%) and rounded ovate (33%) types. The presence of abundant variation in leaf shape is an important symbol of level of genetic diversity and evolutionary status which can facilitate utilization of germplasm evaluation and classification for the soybean germplasm (Yan *et al*. 2014). The present study indicated three types of plant growth in soybean determinate (20%), semi-determinate (59%) and indeterminate (21%). Plant growth of these types is similar during the vegetative growth phase until reproductive phase.

Once soybean begin to flower, indeterminate plants continue to develop leaves on the main stem and branches throughout flowering while determinate plants cease growth on the main stem at the R1 stage but leaves continue to develop on branches until the beginning seed (R5) growth stage. Soybean pubescence/ trichomecoloris a trait that is visually assessed. This trait plays an important role in insect resistance, drought tolerance, and other stresses (Li *et al*. 2022) and being expressed only at maturity when leaves have senesced, as the trichome colorare not visible when a full canopy cover is present. In the present study, 289 genotypes showedpod pubescence with 255 and 34 genotypes having tawny and grey coloured pubescence. Seed coat color is an important attribute determining outward appearance of soybean seed, which exists in a range of colors from yellow, yellow green, green, brown and black. The differences in seed color are contributed differentially to the variations in the contents of carotenoid and chlorophyll components. Soybean genotypes with different seed colors have been used for evaluating and improving seed chemical compositions such as isoflavone, fatty acids, carbohydrates, protein and oil. Compared with yellow seeds of most grown soybean varieties, black/brown seeds usually accumulate flavonoids and anthocyanins having antioxidant properties (Song *et al*. 2016). Majority of genotypes (80%) in this experiment were having yellow seed coat color while only 13% were yellow green, 0.62% green, 1.25% brown and 5% were having black seed coat. Therefore, this trait can be useful as phenotypic marker in soybean breeding programme due to convenience for observation and for the nutritionalimprovement.

Soybean seeds can be shiny/luster, intermediate or dull varying with their surface properties. Seeds with dull luster have abundant seed surface protein such as hydrophobic protein from soybean (HPS) which act as an allergen that causes asthma in persons allergic to soybean dust (Gijzen *et al*. 2003). The results of our experiments indicated 54%, 32% and 14% of total genotypes were intermediate, shiny/luster and dull in seed coat luster. Seed hilum color acts as an important descriptor for DUS characterization of soybean genotypes. In soybean, the hilum, which connects the pod wall with the seed coat, provides a pathway for delivering nutrients and photosynthates to the developing embryo and is therefore, important for seed development (Zhao *et al*. 2021). Plant seeds with intact hilum exhibit relatively high seed vigor, whereas plants with injured hilum produce poor quality seeds thus, result in significant yield losses, possibly due to bacterial infections and reduced nutrient flows. Most of the genotypes (47%) under study exhibited black seed hilum followed by brown (44%) and imperfect black (9%). However, none of the genotypes were having grey and yellow seed hilum color. Plant height is a key trait in soybean breeding because it affects lodging, seed yield and quality. Majority of genotypes (96%) in the current study were tall however, 4% were of medium height. Seed weight is one of the most important agronomic traits in soybean for yield improvement. Besides yield, it is also positively correlated with seed germination, viability and vigor. The present investigation sorted 48.43% genotypes into largest category, 43.43% in medium and 8.12% were classified as small.

Flowering time and maturity traits play key roles in economic soybean production. In present study only 2% of total genotypes were early flowering while 91% and 7% were medium and late flowering, respectively. Furthermore, out of 320 genotypes only 38% were medium maturity while 62% were late in maturity. Hence, medium flowering and maturing genotypes could be selected from the existing germplasm for utilizing in soybean breeding programmes for developing medium duration high yielding varieties which can also be utilized as in intercrop for boosting the soybean production and productivity of India especially Himachal Pradesh. A general grouping of soybean accessions for essential DUS descriptors has been shown in Figure 1A and 1B.

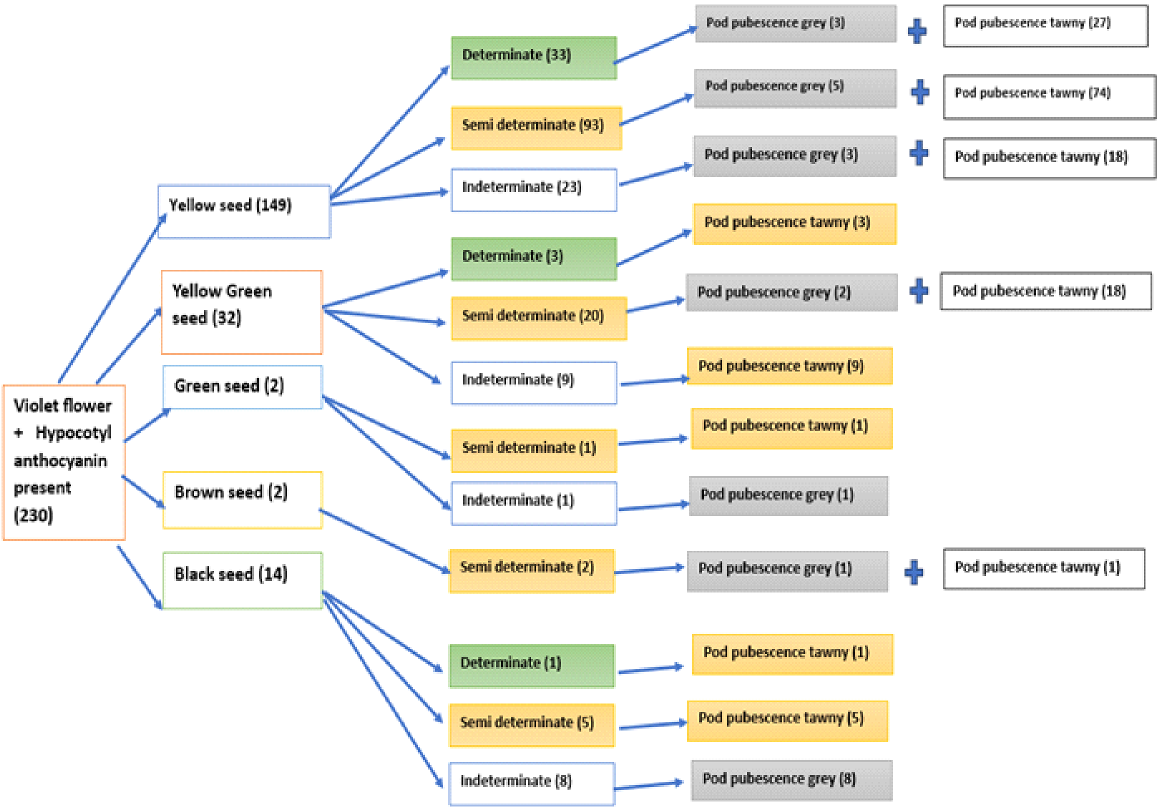

Fig. 1A Grouping of soybean accessions based on essential DUS characters

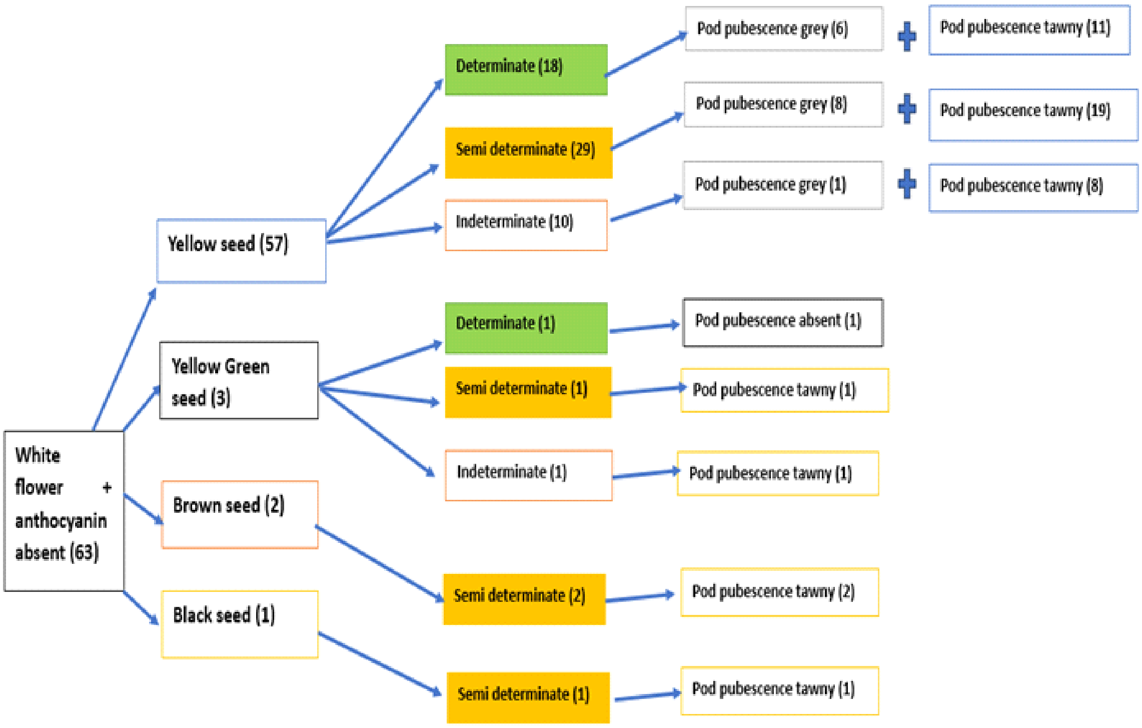

Fig. 1B Grouping of soybean accessions based on essential DUS characters

Soybean diversity analysis based on morphological descriptors traits

Diverse parents are the prime requirement of any hybridization programme (Sekhon *et al*. 2019). The Shannon's diversity indices estimated for 20 morphological traits ranged from 0.0375 to 1.069 with a mean value of 0.6946. The H index of the trait podding was observed to be highest (1.069) among all the traits while seed cotyledon had minimum value of 0.0375 as soybean genotypes exhibited no variability for these traits (Table 2). Thus, high diversity can be revealed in the morphological characters studied by diversity index. These findings align with similar observations reported by various researchers in different crops *viz*., Ashinie *et al*. (2020) in Ethiopian cowpea; Asati *et al*. (2023) in chickpea and Pachori *et al*. (2023) in soybean.

Cluster analysis

Cluster analysis based on Euclidean distance grouped the 320 germplasm lines into four main clusters. The first cluster contained two subgroups, with the first subgroup including two soybean genotypes (GW30 and GW32) while second sub group had 14 genotypes. The second cluster consisted of 14 soybean genotypes with two sub clusters one being mono-genotypic (GW53). The third main cluster was the largest with 267 soybean genotypes with two sub clusters having 240 and 27 genotypes each. The fourth cluster contained 23 soybean genotypes (Table 3 and Figure 2). Therefore, present study concludes that for several qualitative traits, the accessions in different clusters are diverse and can be helpful in the crosses successfully for distinct traits that might helpful in plant breeding programme (Sharma *et al.* 2013). The first principal component (PC1) was most important and explained 13.16% of total variation which was mainly contributed by seed hilum color, seed ground color of testa, podding, seed color of hilum funicle and seed shape. The principal component (PC2) contributed 11.31% of total variation through growth habit, plant growth, leaf shape, leaf size and leaf color. The third principal component (PC3) explained 9.21% of the total variation which was mainly contributed by seed hilum color, leaf color and leaf shape. PC4 contributed 7.65% of the total variation through pod pubescence color, plant height, growth habit and leaf size. PC5 contributed 6.61% of total variation through 100-seed weight, seed shape and leaf size. PC6 contributed 5.76 % of the total variation which was mainly contributed by seed ground color of testa, seed color of hilum funicle and seed lustre. PC7 contributed 5.35% of total variation through seed coat lustre, leaf shape and seed hilum color.

Principal Component Analysis

Principal component analysis (PCA) allows us to summarize and visualize the information in a data set containing observations described by multiple inter-correlated quantitative variables. PCA reduces the dimensionality of a multi variate data and extracts the important information from a multi variate data and express this information as a set of few new variables called principal components (Singh *et al.* 2024). These new variables correspond to a linear combination of the

Table 2.Shannon's diversity index based on morphological characters studied in soybean

Character	Shannon index	Character	Shannon index
Anthocyanin coloration	0.6055	Seed shape	0.8758
Plant growth type	0.9603	Seed ground color of testa	0.6813
Leaf shape	0.8166	Seed coat lustre	0.9728
Leaf size	0.9651	Seed hilum color	0.9389
Leaf intensity of green color	1.01	Seed cotyledon	0.03795
Plant growth habit	1.055	Seed color of hilum funicle	0.496
Flower color	0.5941	Plant height	0.1797
Pod pubescence	0.3182	Seed weight	0.9324
Pod pubescence color	0.3622	Days to 50% flowering	0.358
Podding	1.069	Days to75% maturity	0.6647

Table 3. Grouping of 320 soybean genotypes into various clusters based on qualitative traits

Sr. no.	Cluster no.	No. of genotypes	List of genotypes
1	Cluster 1	16	GW102, GW284, GW57, GW152, GW236, GW126, GW237, GW7, GW132, GW9, GW151, GW183, GW306, GW110, GW30 and GW32
2	Cluster 2	14	GW53, GW125, GW284, GW150, GW278, GW300, GW149, GW220, GW383, GW19, GW143, GW302 and GW22
3	Cluster 3	267	GW25, JS 20-69, GW83, GW39, GW181, GW43, GW84, GW117, GW81, GW87, GW108, MACS 1407, GW37, GW140, GW38, GW46, GW113, GW96, GW105, SL 1074, GW221, GW222, GW138, JS 97-52, NRC 37, GW146, RVSM 2011-35, GW42, GW204, GW211, GW61, GW13, GW95, GW99, GW97, GW100, GW153, GW106, GW131, GW162, GW133, GW285, GW147, GW149, GW148, GW179, GW163, GW54, GW64, GW70, GW68, GW207, GW191, GW283, GW74, GW288, GW358, GW88, GW143, GW145, GW214, GW312, DSB 34, GW175, GW111, GW320, GW313, Palam Soya 1, GW268, SL 955, GW296, GW115, GW116, GW145, GW233, RKS 113, GW184, GW89, GW160, GW155, AMS 2014-1, GW150, GW45, GW154, GW158, GW159, VLS 89, GW17, NRC 130, GW253, GW192, GW202, GW66, GW267, GW374, GW197, RSC 11-07, GW62, GW193, GW208, GW176, GW260, GW259, GW258, GW198, GW209, GW210, GW215, NRC 138, GW3, GW279, GW373, GW190, GW369, GW201, GW226, GW180, GW248, GW69, GW223, GW186, GW199, GW189, VLS 63, KDS 753, GW275, GW372, GW20, GW49, GW146, GW378, GW200, GW234, GW263, GW85, GW238, GW187, GW195, GW225, GW270, GW272, GW264, GW318, GW276, GW319, GW286, GW196, GW265, GW48, GW232, GW263, GW85, GW238, GW187, GW195, GW225, GW270, GW272, GW264, GW318, GW276, GW319, GW316, GW286, GW196, GW265, GW48, GW297, GW14, GW28, GW213, GW134, GW60, GW120, GW365, GW382, GW4, GW75, RKS 113, GW177, GW144, GW218, GW16, GW128, GW129, GW130, GW59, GW254, GW34, GW203, GW15, GW23, GW63, GW50, GW112, GW107, GW119, GW135, GW144, GW139, GW142, GW377, GW245, GW291, GW368, JS 20-116, GW101, GW103, GW123, GW94, GW148, GW182, GW247, GW376, GW224, GW231, GW242, GW249, GW250, GW271, GW244, GW251, GW217, GW161, GW185, GW360, GW361, GW287, GW289, GW290, GW362, GW118, GW305, GW310, GW295, GW6, GW301, GW314, GW157, PK 472, GW44, GW51, GW65, GW76, GW212, GW67, GW280, GW299, GW47, GW58, GW219, GW273, GW77, GW257, GW26, GW36, GW206, GW27, GW55, GW266, GW78, GW304, GW164, GW71, GW124, GW379, GW86, GW31, NRC 128, GW80, GW87, GW79 and GW52
4	Cluster 4	23	GW90, VLS 63, GW24, GW10, GW12, GW147, GW18, GW8, GW252, GW317, GW281, GW311, GW315, PS 26, GW240, GW282, GW303, GW370, GW293, GW309, JS 71-05, GW292, GW294 and GW298

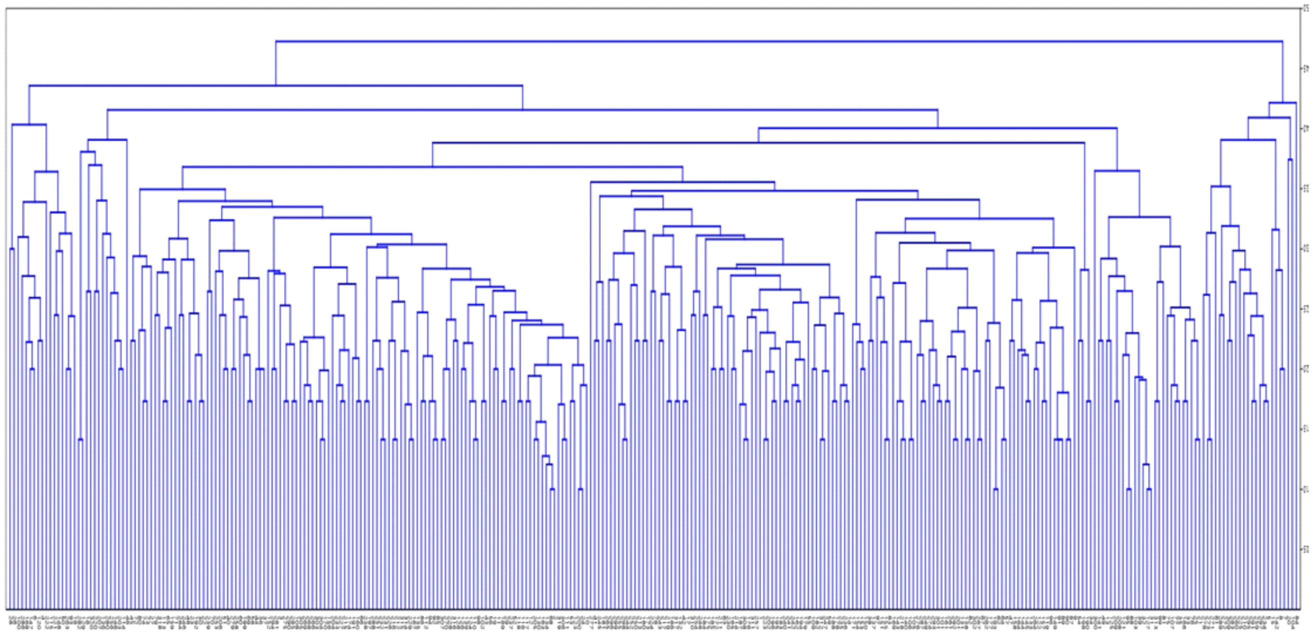

Fig. 2 The clustering pattern of 320 soybean genotypes based on UPGMA

originals. The eigen values determine the number of PCs to retain (Kaiser 1961) and measure the amount of variation retained by each PC. The sum of the eigenvalues is usually equal to the number of variables. Therefore, in present study seven PCs (PC1 to PC7) having eigenvalue greater than one accounted nearly 59.10% of the total variation suggesting these might be used to summarize the original 20 variables in any further analysis of the data. PCA for the first seven principal components of these data are given in Table 4.

Table 4. PCA of studied soybean accessions

	Eigen vectors						
Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**
Anthocyanin	-0.06956	-0.07731	0.076073	0.010031	-0.07146	0.088533	0.10451
Flower Color	0.081162	0.052644	-0.0559	-0.05893	0.039831	-0.11529	-0.09273
Plant Growth	0.17705	0.40852	0.11098	0.12426	-0.1064	-0.01837	-0.27888
Leaf Shape	-0.0102	0.35643	0.21554	-0.06722	-0.28449	-0.15511	0.53555
Leaf Size	-0.10294	0.33039	0.058984	0.23312	0.2973	-0.03882	0.008536
Leaf Color	-0.11396	0.21738	0.32646	-0.52819	0.17611	0.034588	-0.22898
Growth Habit	0.12901	0.56147	0.17064	0.25849	0.007638	-0.04765	-0.21828
Pod Pubescence Color	0.19351	-0.11697	-0.257	0.46592	0.069767	-0.00236	-0.08602
Pod Pubescence	-0.05705	0.036712	0.13644	-0.19794	-0.03562	-0.01337	0.041068
Podding	0.29691	0.064848	-0.19141	0.003802	-0.6614	-0.1762	-0.0067
Seed: Shape	0.2094	0.10087	-0.36497	-0.23767	0.33307	-0.70998	0.19286
Seed: Ground color of Testa	0.51558	0.17721	-0.29261	-0.30995	0.055578	0.48982	0.075211
Seed Coat: Lustre	-0.18895	0.15719	-0.04795	0.092774	0.043672	0.25158	0.62793
Seed: Hilum Color	0.62025	-0.32049	0.62693	0.1051	0.17922	-0.08451	0.2002
Seed: Color of Hilum Funicle	0.2256	0.10598	-0.11283	-0.1143	0.026429	0.25685	0.015582
Seed: Cotyledon Color	0.006023	0.00836	-0.00621	-0.01072	-0.00434	0.008903	-0.00644
Days to 50% flowering	0.038636	0.050359	-0.13334	0.1125	0.12183	0.13137	0.09535
Days to 75 % maturity	-0.00888	-0.04783	0.046721	0.1255	-0.02342	0.074683	-0.07813
Plant height	-0.02182	0.12071	0.063656	0.32436	0.10653	-0.02167	0.10778
100-seed weight	0.070532	0.082002	-0.14457	0.03227	0.4031	0.12034	0.047743
Eigen value	**2.63**	**2.26**	**1.84**	**1.53**	**1.32**	**1.15**	**1.07**
% Variance	**13.16**	**11.31**	**9.21**	**7.65**	**6.61**	**5.76**	**5.35**
% Cumulative variance	**13.16**	**24.47**	**33.68**	**41.34**	**47.94**	**53.72**	**59.10**

The traits with largest absolute value closer to unity within the first PC influence the clustering more than those with lower absolute value closer to zero (Chahal and Gosal 2002). In the present investigation, the first PC had high positive component loading from seed hilum color, seed ground color of testa, podding, seed color of hilum funicle, seed shape, pod pubescence color, growth habit, plant growth, flower color and 100 seed weight and high negative loading from seed coat lustre, leaf color, leaf size, anthocyanin pigmentation, pod pubescence, plant height and leaf shape indicating their positive and negative correlations, respectively with first PC. The variable correlation plot depicts relationship between all variables. In this case, the traits 100-seed weight, cotyledon color, flower color, seed shape, hilum funicle color and podding were having small vector angles between them indicating positive correlation and hence, grouped together in same quadrant. However, seed coat lustre, leaf color and leaf size were negatively correlated variables with pod pubescence color and hence, hilum color and positioned on opposite sides of the plot origin (opposed quadrants). The distance between genotype and the biplot origin is a unique measure of the genotype. For example, the accessions such as GW 294, GW 296, GW95, GW 163, GW 113, GW 287, GW 170, GW 84, GW 42 and GW 139 were with longest vectors having extreme values for one or more traits (Figure 3). Therefore, such genotypes might be useful as parents for these traits in hybridisation programme.

Conclusion

DUS characterization of soybean involves a combination of genetic and phenotypic analysis to assess the distinctiveness, uniformity, and stability of soybean varieties. It is essential for the protection of plant breeders' rights, varietal verification, and ensuring the quality and authenticity of soybean seeds used in agriculture and research. Clustering analysis of qualitative traits in soybean offers a powerful tool for comprehending genetic diversity, trait associations, and relationships among varieties. The results reveal substantial variation within the 320 indigenous and exotic soybean germplasm pool, providing breeders with valuable insights for selecting suitable parents in soybean breeding programs, particularly for traits like earliness, bold seed, and other qualitative attributes. Making DNA fingerprinting a critical process to detect the fundamental distinction between biochemical and molecular markers can be employed. These insights are

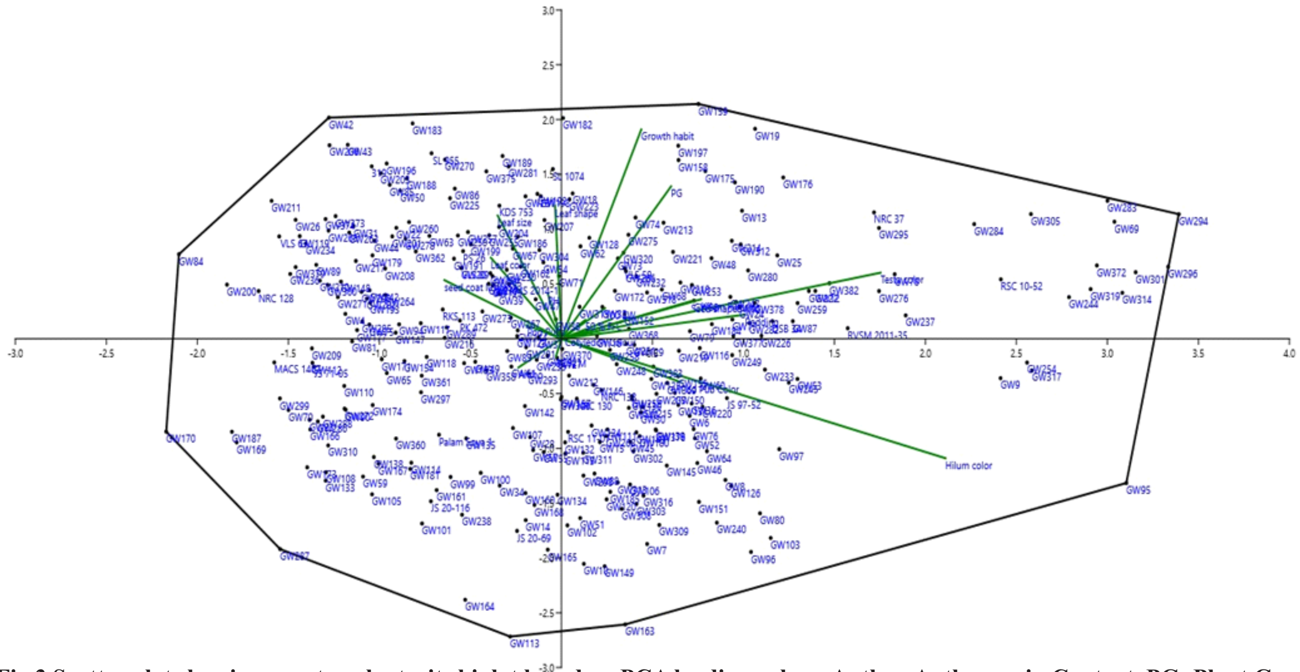

Fig.3 Scatter plot showing genotype by traits biplot based on PCA loading values. Antho= Anthocyanin Content, PG=Plant Growth; 75% M=75 % Maturity, 50% F=50% Flowering, 100-SW= 100-seed weight

valuable for soybean breeding programs, trait prioritization, and the efficient management of genetic resources in plant breeding.

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Conflict of interest: Authors declare no competing interest.

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