



DUS Characterization of Elite Soybean (*Glycine max* (L.) Merrill) Lines for Breeding and Varietal Differentiation

**Shivani Jawarkar ^{a*}, M. K. Shrivastava ^{a++},
Pawan Kumar Amrate ^{a#}, Yogendra Singh ^{a†}, Amit Kumar ^a,
Ravleen Kaur ^a, Jayesh Sarkar ^a and Vikrant Khare ^a**

^a Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh-482004, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Soybean (*Glycine max* L.) is a globally important legume crop valued for its protein-rich seeds and agronomic versatility. This study aimed to characterize 55 soybean genotypes using Distinctness, Uniformity, and Stability (DUS) descriptors to assess morphological diversity and identify traits relevant for breeding and varietal registration. A study conducted at the Seed Breeding farm JNKVV, Jabalpur, in kharif 2023 and kharif 2024, and 50 genotypes, in addition to 5 checks (JS 20-98, JS 20-34, JS 20-69, JS 335 and JS 20-116) were grown in RCBD. Genotypes were evaluated for hypocotyl pigmentation, leaf morphology, pod pubescence and color, and seed attributes under

⁺⁺ Principal Scientist, GPB;

[#] Scientist, Plant Pathology;

[†] Scientist, Plant Biotechnology;

*Corresponding author: E-mail: shivanijawarkar@jnkvv.org;

field conditions. Highly polymorphic traits such as anthocyanin pigmentation, leaflet shape, and pod pubescence showed significant variation, offering reliable markers for parent selection and varietal differentiation. Growth habit was predominantly indeterminate, with limited representation of determinate types. Seed trait analysis revealed that 98.2% of genotypes had medium-sized seeds (10.1–13.0 g/100 seeds), and 70.9% exhibited spherical seed shapes were preferred for uniformity and processing. Yellow seed coats were dominant (94.5%), with 78.2% showing shiny lustre, enhancing market appeal and storability. Hilum color was predominantly black (70.9%), aiding in varietal classification. The observed uniformity in seed size and growth habit reflects current selection trends, while the diversity in pigmentation and pubescence traits highlighted untapped genetic variation. These findings support targeted hybridization and molecular mapping strategies for genetic improvement of soybean. Incorporating large-seeded and determinate type genotypes could broaden the breeding base and enhance adaptability. Breeding programs should integrate highly polymorphic morphological traits with market-preferred seed characteristics to develop resilient, high-yielding cultivars suited for diverse agro-climatic zones.

Keywords: Soybean; DUS; pod pubescence; hilum colour; anthocyanin pigmentation.

1. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is one of the most important legume crops globally. Often referred to as a “wonder crop,” it is celebrated for its versatility, nutritional richness, and economic significance. Commonly known as the golden bean, super legume, or miracle bean, soybean offers high protein content (36.1–41.2%), substantial edible oil yield (16.8–20.2%), and a range of essential minerals, amino acids, vitamins (A, B, C, and D), and antioxidants (Amrate et al., 2020; Banerjee et al., 2023).

Globally, Brazil leads in soybean cultivation with 39.17 million hectares, followed by the United States, Argentina, China, and India. In India, soybean ranks as the third most cultivated oilseed crop, covering approximately 12.1 million hectares (Amrate, 2024). The crop originated in East Asia, particularly Central China, and is grown during the kharif season. It belongs to the family Fabaceae and subfamily Papilionaceae (Mehra et al., 2020; Upadhyay et al., 2022). The genus *Glycine* includes around 30 species, with two annual species under the subgenus *Soja*: *Glycine max* (cultivated soybean) and *Glycine soja* (wild soybean). While *Glycine max* is widely cultivated for its oil and protein, *G. soja* retains primitive traits such as twining growth habit, small black seeds, and hard seed coats (Hymowitz & Singh 1987).

Indian soybean cultivars exhibit limited genetic diversity, which poses challenges for crop improvement (Agarwal et al., 2013; Mehra et al., 2020). Characterizing soybean genotypes is essential for enhancing performance and expanding the genetic base (Banerjee et al.,

2022). Germplasm serves as the cornerstone of breeding programs, providing the raw material for developing improved varieties. The primary goal of plant breeding is to enhance specific traits by creating new genotypes from existing genetic resources (Mishra et al., 2024). This requires the collection and evaluation of germplasm based on morphological traits.

Morphological characterization, guided by the Distinctiveness, Uniformity, and Stability (DUS) criteria under the Protection of Plant Varieties and Farmers’ Rights Act (2001), remains a fundamental approach for assessing genetic diversity (Upadhyay et al. 2022; Ramteke et al., 2012). It offers a cost-effective and practical method for evaluating phenotypic traits (Govindaraj et al., 2015). Studying morphological variation among soybean genotypes provides valuable insights for targeted selection and breeding strategies (Asati et al., 2023; Yadav et al., 2023; Salgotra & Chauhan, 2023). In this context, the present study aimed to classify soybean genotypes based on their morphological traits to support breeding programs focused on developing improved varieties.

2. MATERIALS AND METHODS

The experiment was conducted during the *Kharif* 2023 and *Kharif* 2024 at the Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur. Jabalpur, in eastern Madhya Pradesh, lies within the Satpura Plateau agro-climatic zone, between 23.10°–23.25° N latitude and 79.55°–80.05° E longitude. The region has a subtropical climate with seasonal variation. During Kharif, temperatures range from 24.5°C to 36.8°C, and annual rainfall averages ~1,200

mm, mostly from June to September. The experimental site featured deep black cotton soil (Vertisols) with high moisture retention and fertility. These conditions supported optimal soybean growth and reliable expression of morphological traits. A total of 55 elite soybean genotypes were evaluated using a randomized complete block design (RCBD) with three replications. Each genotype was sown in 2 meter long rows, with a row-to-row spacing of 45 cm and plant-to-plant spacing of 7-8 cm. Five widely cultivated varieties namely; JS 20-98, JS 20-34, JS 20-69, JS 335 and JS 20-116-were included as checks.

Morphological data were recorded from whole plot of each genotype. Observations for fifteen traits were taken at physiological maturity or different stages when the complete expression of characters were observed (Table 1). The genotypes were characterized for various characters such as Hypocotyl pigmentation; Growth type; Growth habit; Leaf shape; Leaf size; Intensity of green color in leaves; Flower color; Pod pubescence; Pod pubescence color; Pod color; Seed size; Seed shape; Seed coat color; Hilum color; Seed coat lustre. These traits were selected based on their relevance to phenotypic variability and potential utility in soybean breeding programs, as described in previous studies (Upadhyay et al. 2022; Banerjee et al. 2022).

3. RESULTS AND DISCUSSION

A total of 55 soybean genotypes were evaluated for fifteen morphological traits as per DUS guidelines (Table 1). Substantial phenotypic variation was observed across hypocotyl pigmentation, growth type and habit, flower and leaf traits, pod characteristics and seed morphology indicating a rich pool of genetic diversity suitable for breeding programs.

3.1 Variation for Hypocotyl Pigmentation

Out of 55 genotypes, 24 (43.6%) exhibited anthocyanin pigmentation in the hypocotyl, showing purplish coloration, while 31 genotypes had green hypocotyls (Fig. 1). This trait is governed by the W1 locus and is linked to flavonoid biosynthesis pathways, particularly malvidin derivatives (Murai et al. 2016). Anthocyanin-rich hypocotyls are associated with enhanced seedling vigor and stress tolerance, making them valuable for early-stage resilience breeding.

Similar results for variation in pigmentation on hypocotyl are also reported by Upadhyay et al. 2022 in exotic germplasm of soybean, among the studied genotypes colored hypocotyl was predominant.

3.2 Growth Type and Habit

Semi-determinate growth type and semi-erect growth habit was observed in all 54 genotypes (98.2%). These traits are agronomically desirable for lodging resistance and compatible with mechanized harvesting (Kim et al., 2022). The predominance of semi-determinate architecture reflects breeder selection for adaptability and yield optimization.

Upadhyay et al. (2022) studied forty-eight exotic genotypes of soybean and observed that 47 genotypes had semi-determinate growth types. For growth habit traits, semi-erect growth habit was predominant. Barela et al. (2022) and Jhariya et al. (2025) also studied soybean germplasm and results showed that semi-determinate growth habit as well as semierect growth habit are predominant.

3.3 Flower Color Types

Violet flowers were present in 24 genotypes, while 31 genotypes had white flowers (Fig. 2). Flower colour is a stable varietal marker controlled by loci such as W1 and W47 (Sundaramoorthy et al., 2015). Its utility in varietal identification and purity assessment is well documented.

Akin result for variation in flower colour were also recorded by Dhaliwal et al. (2020) in soybean genotype. Violet flower colour was predominant colour suggesting it important in soybean varietal identification. Similar results are also reported by Singh et al. (2021).

3.4 Leaf Traits

Variation in leaf morphology was evident among the 55 soybean genotypes. Leaf size ranged from small to large, with 17 genotypes exhibiting small leaflets, 24 medium-sized and 14 large (Fig. 3). Medium-sized leaflets were the most prevalent (43.6%), offering a balance between photosynthetic efficiency and optimal canopy architecture (Li et al 2024). In terms of leaf shape, the pointed ovate form was dominant, observed in 72.7% of genotypes, followed by lanceolate (23.6%) and round ovate shapes

(3.6%). These morphological differences influence light interception, canopy structure, and overall plant vigor. Additionally, 17 genotypes displayed dark green foliage, which may reflect higher chlorophyll content and enhanced photosynthetic capacity, traits that are advantageous for biomass accumulation and stress resilience.

Similar results for leaf characters were also observed by Barela et al. (2022) and Upadhyay et al. (2022). Anand et al., 2024 evaluated 165 lines for leaf morphology and found similar observation.



Fig. 1 a) Pigment present; b) Pigment absent



Fig. 2. types of flower colour; A . Violet flower, B. White flower

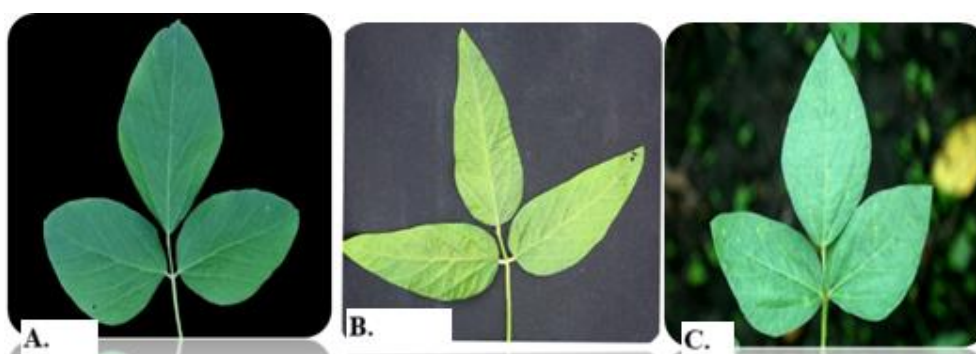


Fig. 3. Leaf shape of lateral leaflet; A. Round ovate, B. Lanceolate, C. Point ovate

Table 1. Characterization and frequency distribution of Morphological and Seed Traits (As per DUS guideline)

Traits		Classes	Genotypes	Frequency
Hypocotyl: Anthocyanin pigmentation	10-15 Days after sowing	Present	AGS 163, AUKS 203, DS 1510, JS 335, EC 350664, NRC 257, JS 21-74, JS 21-75, JS 24-23, JS 25-01, JS 25-02, JS 25-03, JS 22-12, JS 23-09, NRC 256, AMS 56, AMS 269, NRC 166, NRC 190, JS20-53, NRC 264, NRC 268, NRC 270, JS 335	24
		Absent	DS 1547, DS 3109, NRC 259, PS 1696, RSC 1175, JS 23-02, JS 24-25, JS 24-26, JS 25-06, JS 25-08, JS 21-72, JS 21-13, DS 1318, RVSM 2012-04, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, JS 25-55, NRC 150, JS 20-79, JS 25-50, JS 25-52, JS 20-34, JS 20-69, JS 20-98, JS 20-116	31
Growth type	About 77 % pods attained full length	Determinate	JS 20-34	1
		Semi-determinate	AGS163, AUKS203, DS 1510, DS 1547, DS 3109, EC 350664, NRC 257, NRC 259, PS 1696, RSC 1175, JS 21-74, JS 21-75, JS 23-02, JS 24-23, JS 24-25, JS 24-26, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 25-08, JS 21-72, JS22-12, JS 22-16, JS 23-09, NRC 256, JS21-13, AMS 56, AMS 269, DS 1318, NRC 166, NRC 190, RVSM 2012-04, JS20-53, JS20-89, JS 22-01, JS21-77, JS30-12, JS30-13, JS30-15, JS30-16, NRC 138, NRC 264, JS 25-55, NRC 268, NRC 270, NRC 150, JS20-79, JS 25-50, JS 25-52, JS 20-69, JS 20-98, JS 20-116, JS 335	54
Growth habit	About 50% plants have at least one flower open	Erect	JS 20-34	1
		Semi erect	AGS 163, AUKS 203, DS 1510, DS 1547, DS 3109, EC 350664, NRC 257, NRC 259, PS 16-96, RSC 1175, JS 21-74, JS 21-75, JS 23-02, JS 24-23, JS 24-25, JS 24-26, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 25-08, JS21-72, JS 22-12, JS 22-16, JS 23-09, NRC 256, JS 21-13, AMS 56, AMS 269, DS 1318, NRC 166, NRC 190, RVSM 2012-04, JS20-53, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, NRC 264, JS 25-55, NRC 268, NRC 270, NRC 150, JS 20-79, JS 25-50, JS 25-52, JS 20-69, JS 20-98, JS 20-116, JS 335	54
Flower colour	About 50% plants have at least one flower open	White	DS 1547, DS 3109, NRC 259, PS 1696, RSC 1175, JS 23-02, JS 24-25, JS 24-26, JS 25-06, JS 25-08, JS21-72, JS21-13, DS 1318, JS21-13, RVSM 2012-04, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, JS 25-55, NRC 150, JS 20-79, JS 25-50, JS 25-52, JS 20-34, JS 20-69, JS 20-98, JS 20-116	31
		Violet	AGS 163, AUKS 203, DS 1510, JS 335, EC 350664, NRC 257, JS21-74, JS 21-75, JS 24-23, JS 25-01, JS 25-02, JS 25-03, JS 22-12, JS 23-09, NRC 256, AMS 56, AMS 269, NRC 166, NRC 190, JS20-53, NRC 138, NRC 264, NRC 268, NRC 270	24
Leaf size of lateral leaflet	About 50% plants have at least one flower open	Small	DS 1510, DS 1547, EC 350664, NRC 257, AMS 269, DS 1318, NRC 190, JS 22-01, JS 21-77, NRC 138, NRC 264, NRC 150, JS 22-12, JS 20-34, JS 335, JS 22-16, JS 23-09	17
		Medium	AGS 163, AUKS 203, DS 3109, PS 1696, RSC 1175, JS 21-74, JS 23-02, JS 24-23, JS 24-25, JS 24-26, JS 25-01, JS 25-02, JS 25-06, JS 21-72, NRC 256, NRC 166, JS 20-53, JS 20-89, JS 30-12, NRC 270, JS 20-79, JS 25-52, JS 20-69, AMS 56	24
		Large	JS 25-50, NRC 268, JS 25-55, JS 30-13, JS 30-15, JS 30-16, NRC 259, JS 21-75, JS 25-03, JS 25-08, JS 21-13, RVSM 2012-04, JS 20-116, JS 20-98	14
Leaf shape of	About 50% plants	Lanceolate	AGS 163, DS 1547, PS 1696, JS 21-75, JS 24-23, JS 24-25, JS 25-01, JS 25-06, AMS 56, AMS 269,	13

Traits		Classes	Genotypes	Frequency
lateral leaflet	have at least one flower open		NRC 166, JS 21-77, NRC 264	
		Pointed ovate	AUKS 203, DS 1510, DS 3109, EC 350664, NRC 257, NRC 259, RSC 1175, JS 21-74, JS 23-02, JS 24-26, JS 25-02, JS 25-03, JS 25-08, JS 21-72, JS 22-12, JS 22-16, JS 23-09, NRC 256, JS21-13, DS 1318, NRC 190, RVSM 2012-04, JS 20-53, JS 20-89, JS 22-01, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, JS 25-55, NRC 150, JS 20-79, JS 25-50, JS 25-52, JS 20-69, JS 20-98, NRC 268, NRC 270, JS 335	40
		Round ovate	JS 20-34, JS 20-116	2
Leaf intensity of green colour	About 50% plants have at least one flower open	Green	JS 25-08, JS 25-01, JS 23-02, NRC 259, AGS 163, AUKS 203, DS 1510, DS 1547, DS 3109, EC 350664, RSC 1175, PS 1696, JS 24-23, JS 24-25, JS 25-02, JS21-72, JS 23-09, NRC 256, AMS 269, DS 1318, NRC 190, RVSM 2012-04, JS20-53, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, JS 25-55, NRC 268, NRC 150, JS 25-52, JS 20-34, JS 20-69, JS 20-98, JS 335	38
		Dark green	NRC 257, JS21-74, JS 21-75, JS 24-26, JS 25-03, JS 25-06, JS 22-12, JS 22-16, JS 21-13, AMS 56, NRC 166, JS 20-89, NRC 264, NRC 270, JS 20-79, JS 25-50, JS 20-116	17
Pod Pubescence	About 77 % pods attained full length	Pubescent	AGS 163, AUKS 203, DS 1510, DS 1547, EC 350664, NRC 259, PS 1696, JS 23-02, JS 24-25, JS 24-26, JS 25-08, JS 21-72, JS 22-16, JS 21-13, DS 1318, RVSM 2012-04, JS 20-53, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, JS 25-55, NRC 150, JS20-79, JS 25-50, JS 25-52, JS 20-69, JS 20-98	32
		Glabrous	DS 3109, NRC 257, RSC 1175, JS 21-74, JS 21-75, JS 24-23, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 22-12, JS 23-09, NRC 256, AMS 56, AMS 269, NRC 166, NRC 190, NRC 264, NRC 268, NRC 270, JS 20-34, JS 20-116, JS 335	23
Pod: Pubescence colour	About 77 % pods attained full length	Tawny brown	AGS 163, AUKS 203, DS 1510, DS 1547, EC 350664, NRC 259, PS 1696, JS 23-02, JS 24-26, JS 25-08, JS 21-72, JS 22-16, JS 21-13, DS 1318, RVSM 2012-04, JS 20-53, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, JS 25-55, NRC 150, JS20-79, JS 25-50, JS 25-52, JS 20-69, JS 20-98	30
		Gray	JS 24-25	1
		Absent	DS 3109, NRC 257, RSC 1175, JS21-74, JS21-75, JS 24-23, JS 25-01, JS 22-12, JS 23-09, AMS 56, NRC 264, NRC 268, NRC 270, NRC 166, NRC 190, AMS 269, NRC 256, JS 25-02, JS 25-03, JS 25-06, NRC 257, JS 20-116, JS 335, JS 20-34	24
Pod: Colour	About 50 % of pods are ripe		AGS 163, EC 350664, NRC 259, JS 25-02, JS 25-03, JS 25-08, JS 23-09, JS21-13, DS 1318, JS 22-01, NRC 268, JS 21-77, JS 30-13, JS 25-55, JS20-79, JS 25-50, JS 25-52	17
		Yellow Brown	AUKS 203, DS 1510, DS 1547, DS 3109, NRC 257, PS 1696, RSC 1175, JS 23-02, JS21-72, JS 22-12, JS 22-16, NRC 166, NRC 190, RVSM 2012-04, JS20-53, JS20-89, JS 30-12, JS 30-16, NRC 138, NRC 150, JS 20-34, JS 20-69, JS 20-98, JS 335	24
		Black	JS21-74, JS21-75, JS 24-23, JS 24-25, JS 24-26, JS 25-01, JS 25-06, NRC 256, AMS 56, AMS 269, JS 30-15, NRC 264, NRC 270, JS 20-116	14
Seed size	Harvested seed	Small (<10.0 gm)	EC 350664	1
		Medium (10.1-	AGS 163, AUKS 203, DS 1510, DS 1547, DS 3109, NRC 257, NRC 259, PS 1696, RSC 11-75, JS21-	54

Traits		Classes	Genotypes	Frequency
		13.0 gm)	74, JS21-75, JS 23-02, JS 24-23, JS 24-25, JS 24-26, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 25-08, JS21-72, JS 22-12, JS 22-16, JS 23-09, NRC 256, JS21-13, AMS 56, AMS 269, DS 1318, NRC 166, NRC 190, RVSM 2012-04, JS20-53, JS20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, NRC 264, JS 25-55, NRC 268, NRC 270, NRC 150, JS20-79, JS 25-50, JS 25-52, JS 20-69, JS 20-98, JS 20-116, JS 335, JS 20-34	
		Large (>13.0 gm)	0	
Seed shape	Harvested seed	Spherical	AGS 163, DS 1510, DS 1547, DS 3109, EC 350664, NRC 257, NRC 259, PS 1696, JS 23-02, JS 24-25, JS 24-26, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 25-08, JS 23-09, NRC 256, JS21-13, AMS 56, AMS 269, NRC 166, NRC 190, RVSM 2012-04, JS20-53, JS 20-89, JS 22-01, JS 21-77, JS 30-12, NRC 138, NRC 264, NRC 268, NRC 270, JS20-79, JS 25-52, JS 20-69, JS 20-98, JS 20-116, JS 335	39
		Elliptical	AUKS 203, RSC 1175, JS 21-74, JS 21-75, JS 24-23, JS 21-72, JS 22-12, JS 22-16, DS 1318, JS 30-13, JS 30-15, JS 30-16, JS 25-55, NRC 150, JS 25-50, JS 20-34	16
Seed: The ground colour of testa	Harvested seed	Yellow	AGS 163, AUKS 203, DS 1510, DS 1547, EC 350664, NRC 257, NRC 259, PS 1696, RSC 1175, JS21-74, JS 21-75, JS 23-02, JS 24-23, JS 24-25, JS 24-26, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 25-08, JS 21-72, JS 22-12, JS 22-16, JS 23-09, NRC 256, JS 21-13, AMS 56, AMS 269, DS 1318, NRC 190, RVSM 2012-04, JS 20-53, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, JS 30-15, JS 30-16, NRC 138, JS 25-55, NRC 268, NRC 270, NRC 150, JS20-79, JS 25-50, JS 25-52, JS 20-34, JS 20-69, JS 20-98, JS 20-116, JS 335	52
		yellow-green	DS 3109, NRC 166, NRC 264	3
Seed coat luster	Harvested seed	Shiny	AGS 163, AUKS 203, DS 1510, DS 1547, EC 350664, NRC 257, NRC 259, PS 1696, JS21-74, JS21-75, JS 23-02, JS 24-25, JS 25-01, JS 25-02, JS 25-03, JS 22-12, JS 22-16, JS 23-09, NRC 256, JS 21-13, AMS 56, AMS 269, DS 1318, NRC 166, NRC 190, RVSM 2012-04, JS 20-89, JS 22-01, JS 21-77, JS 30-12, JS 30-13, NRC 138, NRC 264, JS 25-55, NRC 268, NRC 270, NRC 150, JS20-79, JS 25-50, JS 25-52, JS 20-98, JS 20-116, JS 335	43
		Dull	DS 3109, RSC 1175, JS 24-23, JS 24-26, JS 25-06, JS 25-08, JS 21-72, JS 20-53, JS 30-15, JS 30-16, JS 20-69, JS 20-34	12
Hilum colour	Harvested seed	Black	AUKS 203, DS 1510, DS 1547, DS 3109, JS 24-23, EC 350664, NRC 257, NRC 259, PS 1696, RSC 1175, JS 21-74, JS 21-75, JS 25-01, JS 25-02, JS 25-03, JS 25-06, JS 25-08, JS 21-72, JS 22-12, JS 22-16, JS 23-09, AMS 56, AMS 269, DS 1318, NRC 190, RVSM 2012-04, JS 20-53, NRC 256, JS 21-77, JS 30-15, JS 30-16, NRC 138, NRC 268, NRC 150, JS 20-34, JS 20-69, JS 20-98, JS 20-116, JS 335	39
		Brown	AGS 163, JS 23-02, JS 24-25, JS 24-26, JS 21-13, NRC 166, JS 20-89, JS 22-01, JS 30-12, JS 30-13, JS 25-55, NRC 264, NRC 270, JS 20-79, JS 25-50, JS 25-52,	16

3.5 Pod Characters

Pod morphology varied notably among the soybean genotypes. A majority of genotypes (58.2%) exhibited pubescent pods, with tawny brown being the predominant pubescence color (93.8%) (Fig. 5). Pod pubescence plays a critical role in pest resistance and moisture regulation, contributing to improved field performance under variable environmental conditions (Barela et al., 2022). In terms of pod color, brown pods were most common (43.6%), followed by yellow (30.9%) and black (25.5%) (Fig. 6). This variation reflects underlying genetic diversity and may influence consumer preferences, market classification, and seed coat development. The presence of multiple pod color types within the germplasm pool suggests potential for selection based on both agronomic and commercial traits.

Anand et al. 2024 studied pod morphology in 165 soybean lines and observed pod pubescence in 106 genotypes. Pod hairiness was predominantly pubescent while investigating 90 soybean genotypes, with 76 lines exhibiting trichome-covered pods a trait often linked to insect resistance (Barela et al., 2022). Pod pubescence colour showed tawny brown as the most frequent expression, recorded in 67.77% of genotypes, followed by grey and absence of pubescence.

It was also studied by Mishra et al (2025) they evaluated soybean genotypes and also observed similar results for pod morphology.

3.6 Variation in Seed Traits

Seed morphology among the evaluated soybean genotypes revealed consistent patterns aligned with breeding and market standards. Most genotypes (98.2%) possessed medium-sized seeds ranging from 10.1 to 13.0 g per 100 seeds, which confirm to agronomic norms for optimal yield and handling (Fig. 6). Only one genotype exhibited small seeds, indicating limited variability in seed size. In terms of shape, spherical seeds were predominant (70.9%), followed by elliptical forms (29.1%). Spherical seeds are generally preferred for uniformity, ease of processing, and mechanical sowing (Shrestha et al. 2023). Seed coat colour was largely uniform, with 94.5% of genotypes displaying yellow coats and a minority (5.5%) showing yellow-green hues. Yellow seed coats are favoured in commercial markets due to their visual appeal and consumer acceptance. In the RIL population studied by Yang et al. (2023) yellow hilum was the predominant colour, observed in 58.70% of genotypes. Other hues included brown (24.16%), light brown (9.34%), dark brown (3.85%), black (1.67%), light yellow (1.10%), and rare variants like yellow-green and green (each 0.55%).



Fig. 4. Pubescence colour of pod; A. Grey, B. Absent, C. Tawny



Fig. 5. Variation for pod colour; A. Black, B. Yellow, C. Brown

Seed shape is one of the important descriptors for evaluating soybean genetic resources, with elliptic Fourier descriptors proving useful in quantifying morphological diversity for breeding programs (Sammour 2014). This aligns well with our finding that spherical seeds were predominant (70.9%), followed by elliptical forms (29.1%) and adds weight by referencing established methodology for pod shape analysis.

In the study conducted by Barela et al. (2022), morphological characterization of 90 soybean genotypes revealed distinct patterns in seed traits that are valuable for varietal identification and breeding. The predominant seed size observed was medium, present in 64.44% of genotypes, while spherical flattened seed shape was most common, found in 77.77% of the lines. The seed coat colour was predominantly yellow (84.44%), and intermediate seed coat lustre was observed in 77.77% of genotypes, indicating a balanced surface texture across the germplasm. Hilum colour varied among genotypes, with imperfect black being the most frequent

(63.33%), followed by brown (34.44%) and black (2.22%). These seed characteristics, along with other DUS descriptors, provide a robust framework for genotype differentiation and can support targeted breeding strategies aimed at improving soybean yield and adaptability. Similar result were also reported by Asati et al., 2023 in soybean.

In this study the predominance of semi-determinate and semi-erect types, medium seed size, and yellow shiny seed coats reflects current breeding priorities. However, the limited presence of large seeds and non-yellow testa types suggests opportunities for introgression to meet evolving market demands. Traits like anthocyanin pigmentation, pod pubescence, and leaflet shape offer high polymorphism and can serve as effective markers for parent selection and varietal differentiation. Integrating these morphological markers with molecular tools will enhance precision in varietal release and protection.

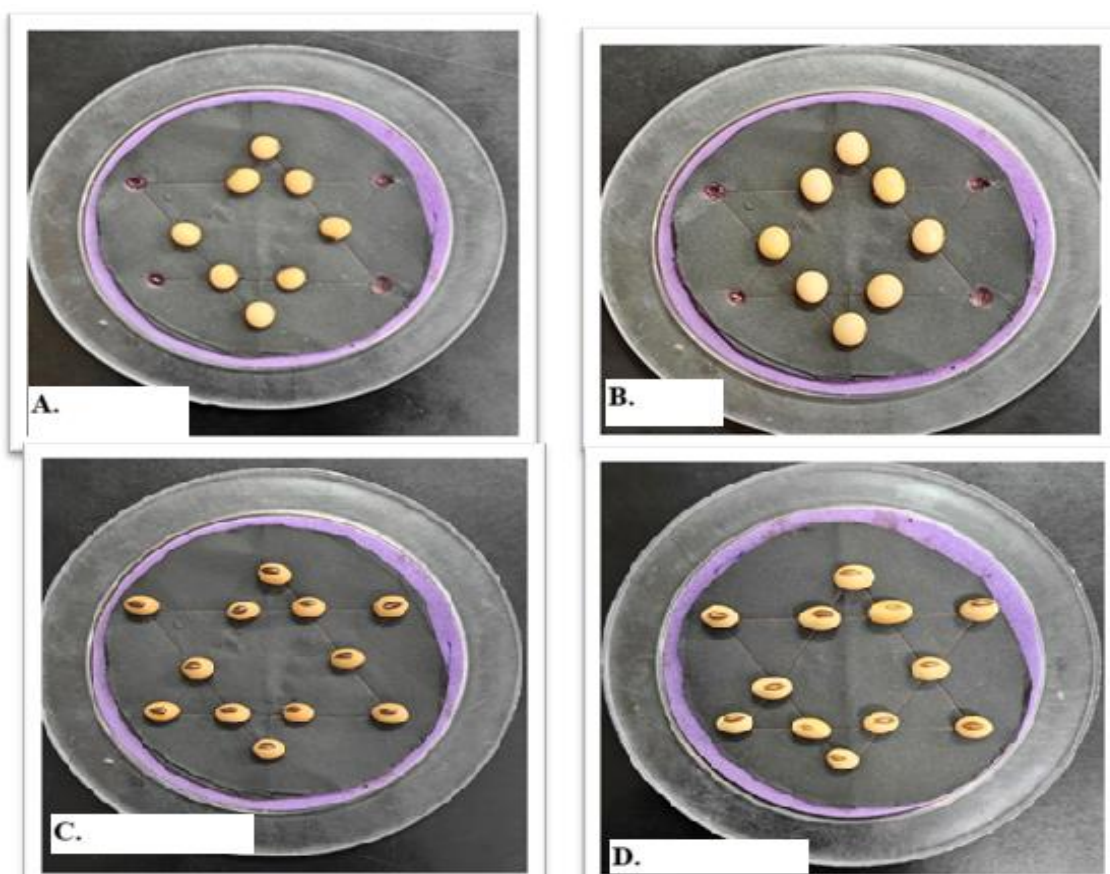


Fig. 6. variation for seed colour and hilum colour A. Spherical shaped seed, B. Elliptical shaped seed, C. Black coloured hilum, D. Brown coloured hilum

4. CONCLUSIONS

The comprehensive DUS-based evaluation of 55 soybean genotypes revealed substantial morphological diversity across key traits, including hypocotyl pigmentation, leaf morphology, pod pubescence and colour and seed characteristics. High polymorphism traits such as anthocyanin pigmentation on hypocotyl, leaflet shape and colour and pod pubescence colour were emerged as robust markers for parent selection and varietal differentiation, offering strategic value for breeding programs. Notably, 98.2% of genotypes exhibited medium-sized seeds (10.1–13.0 g/100 seeds) and 70.9% had spherical seed shapes, indicating strong directional selection for agronomic uniformity and processing efficiency. Yellow seed coats were dominant (94.5%), with 78.2% showing a shiny lustre, traits that align with commercial preferences for marketability and storability. Hilum colour, predominantly black (70.9%), further supports varietal classification efforts. These findings provide a foundation for targeted hybridization, molecular mapping, and cultivar registration, and underscore the importance of integrating both high-polymorphism and market-relevant traits in soybean improvement strategies. Future efforts may benefit from coupling morphological data with molecular markers and agro-physiological performance to enhance selection accuracy and breeding efficiency.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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