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Research Note

Morphological characterization and new variation in compound leaf of mungbean (*Vigna radiata* L. Wilczek) genotypes

Shivangi Rahangdale*, S.K. Singh, J.P. Lakhani, Shailendra Sagar Prajapati and Pratik Kumar

Department of Plant Breeding & Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur-482004, (M.P.), India
***E-Mail:** shivangirahangdale@gmail.com

Abstract
The present investigation was executed under field conditions that favour normal growth and expression for all descriptors. A collection of 40 mungbean genotypes were characterised for 21 agro-morphological traits during the summer 2021 and 2022. The experimental material was evaluated in three replications in RCBD and observations were recorded as per DUS guidelines. The phenotypic assessment showed polymorphism for the characters such as hypocotyl anthocyanin coloration, stem colour, leaf shape, leaf colour, leaf vein colour, petiole colour, flower petal colour, pod position, pod colour, pod curvature, seed colour, seed size *etc*. Some special character including yellow seed colour of local germplasm 'yellow-mung' diversified the crop. Furthermore, an increased number of leaflet *viz.* quadrifoliate and pentafoliate compound leaf variations were also observed rather than the normal trifoliate compound leaf of mungbean. The standard descriptors can be used as a marker to characterize the crop species for utilization of germplasm and conservation programmes.

Keywords: characterization, compound leaf, DUS, greengram, polymorphism

After chickpea and pigeonpea, Mungbean (*Vigna radiata* (L.) Wilczek), which is native to India or the Indo-Burma region, is the third-most significant self-pollinated, short-duration grain legume crop. It is thought that the primary source of mungbean genetic diversity is in central Asia (Kumar and Kumar, 2014). Mungbean has a relatively small (579 Mb) genome with 22 chromosomes in the 2n set (Parida *et al.,* 1990; Kang *et al.,* 2014). It is also referred to as greensoy, greengram, greenbean, mashbean, and goldengram (Markam *et al.,* 2018). Mungbean is a crucial and affordable source of food protein throughout Asia, especially for the underprivileged, and is crucial in reducing protein deficiency, especially in emerging nations (Selvi *et al.,* 2006). It has an excellent place for balanced diets since it has a relatively high proportion of easily digestible good quality protein (24%) with less flatulence and a high iron content (40-70 ppm) (Selvi *et al.,* 2006; Vairam *et al.,* 2016). The majority of the world's greengram comes from India, and it is grown in almost every state of India. According to 3rd advance estimates- 2021-2022, the overall production of pulses in India is to be 27.75 million tonnes. In India, the total mung bean production is 2.85mt out of which 1.48mt is produced in *kharif* and 1.37mt in *rabi* and it accounts for 10% of all pulse production (Anonymous, 2022). Besides its rapid growth and early maturity, mungbean possesses an ability to improve soil fertility by fixing the atmospheric nitrogen (50-109Kg/ha) in symbiotic association with rhizobium bacteria (Paramesh *et al.,* 2016).

To group lines with related traits and use them in breeding programmes, lines must first be characterised in order to understand their diversity (Lee *et al.,* 2004; Piyada *et al.,* 2010). Agro-morphological characteristics are typically utilised to identify lines since they are simple to spot with the unaided eye during physical purity maintenance. Therefore, in the era of intellectual property rights for the protection of lines as well as quality seed production and certification, characterization utilising Distinctness, Uniformity, and Stability (DUS) is of considerable significance (Janghel *et al.,* 2020). These descriptors are easy to use, affordable and not don not involve complicated laboratory procedures. In order to increase both qualitative and quantitative characteristics as well as protection, it is crucial to characterise and assess variation in the elite improved lines of greengram. In light of these considerations, the current experiment was carried out to describe the mungbean germplasm in accordance with DUS descriptors in order to evaluate the variability parameters among germplasm and grouping of genotypes for mungbean improvement.

The experiment was carried out on the site of Breeder Seed Production Unit, JNKVV, Jabalpur (M.P.) during *summer*-2021 and *summer*-2022. The experimental material comprising of 40 genotypes of mungbean was evaluated in three replications in Randomized Complete Block Design (RCBD) for the morphological characterization. The genotypes were sown in four rows, each of two meter length, with a row to row spacing of 45cm.

Observations on 21 morphological characters were recorded at specified stages of the crop growth period when the traits under study had full expression *i.e.,* different growth stages. At the unfolded cotyledonary stage, the anthocyanin coloration was visible (5-10 days after sowing). At the days to 50% flowering stage, the traits, growth and plant behaviours, stem and leaf features were documented. Pod characters like colour, curvature, position and length were recorded at maturity stage of the pod. After the crop was harvested, characteristics of the seeds, such as colour, coat lustre, shape and size were determined. As per the DUS guidelines of Protection of Plant Varieties & Farmers' Rights Authority (2007), morphological features were observed. The Royal Horticultural Society (RHS) colour chart was used to evaluate colour attributes. The SAS software programme (version 9.2) was used to analyse the morphological data in order to estimate the Euclidian genetic distance between paired genotypes and perform genotype clustering.

Characterization of 40 elite improved lines of greengram was carried out using DUS descriptors. Seventeen descriptors out of 21 *viz.,* hypocotyl anthocyanin coloration, flowering initiation, plant type, plant growth habit, stem colour, leaf shape, leaf colour, leaf vein colour, petiole colour, flower petal colour, pod position, mature pod colour, pod curvature, seed colour, seed lusture, seed shape and seed size differed significantly, indicating a large and exploitable amount of genetic variability for the individual elite germplasm profile development for identification and protection. Similar result was recorded by Katiyar *et al.* (2006). They also reported no variation for traits leaflet lobes, stem pubescence, pod pubescence and pod colour. Singh *et al.* (2014) and Sabatina *et al*. (2021) also exploited DUS characterization in greengram for identification and distinguishing the genotypes from each other.

On the basis of scores of 21 descriptors, the 40 genotypes were categorized in various groups and the distribution frequency is presented in **table 1** and a graphical representation of some morphological traits showing high variability has been presented in **Fig. 1**. Anthocyanin colouration is normally considered as an important morphological marker in greengram to discriminate the lines into two groups based on their presence or absence (Singh *et al.,* 2014). In the present investigation, 10 genotypes were without pigmentation and 30 genotypes showed anthocyanin colour indicating the existence of variation among the lines and can be used as selection criteria for identification of the lines at the seedling stage (**Fig. 2**).

At the post seedling stage, stem colour, petiole colour, leaf shape, pod colour may be taken as identification traits. On the basis of stem colour, 90% of genotypes were found with green stem, whereas 7.50% and 2.50% genotypes were found with purple and green with purple splashes stem colour, respectively. Stem pubescence was present in all of the genotypes, whereas none of the genotypes had leaflet lobes. So, these traits are not useful for the identification and purity maintenance of breeding material.

Leaf characters like leaflet lobes, shape, colour, size and vein colour play an important role in the yielding ability of the genotypes, as the leaves are the points of food synthesis and transpiration site of the plants. All the genotypes had ovate leaf shape except Urdi Local, which have lanceolate leaf shape (**Fig. 3**). On the basis of leaf colour, 80% of genotypes were found with green colour leaf, while 20% of genotypes had dark green coloured leaf. Leaf vein colour had wide variations and was found as green, greenish purple and purple colour in 27.50%, 67.50% and 5.00% genotypes, respectively (**Fig. 4**). Similarly, on the basis of petiole colour 35%, 60% and 5% genotypes were categorized into green, green with purple splashes and purple colour, respectively.

The genotypes under study recorded yellow and light yellow coloured flower petals in 42.5% and 57.5% cases respectively (**Fig. 5**). Among the genotypes studied, 65 % were of medium duration(40-50 days), 32.50% were early flowering (<40 days) and one genotype

Table 1. Frequency distribution of morphological and seed traits in mungbean genotypes

S. No.	Traits	Class	Note/ Score	Frequency	Percentage	Name of genotypes
1	Hypocotyl: Anthocyanin	Absent	1	10	25.00	TJM-140, TJM-196, LGG-460, Shikha, Kanika, Virat, Yellow Mung, IPM-430-1, PKVAM-4, PM-1623
		Present	9	30	75.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-136, TJM-137, TJM-141, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, PDM-139, SML-668, GAM-5, MH-421, Ganga-8, Hum-1, Urdi Local, Pusa Vishal, Pusa B-51, MH-903, TM-96-25
2	Flowering initiation	Early	3	13	32.50	TJM-140, TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-136, TJM-141, TJM-143, TJM-155, TJM-160, TJM-235, TJM-236
		Medium	5	26	65.00	TJM-137, TJM-144, TJM-145, TJM-146, TJM-196, TJM-231, TJM-232, PDM-11, PDM-139, LGG-460, SML-668, Shikha, Kanika, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Urdi Local, Yellow Mung, Pusa Vishal, Pusa B-51, MH-903, PKVAM-4, PM-1623, TM-96-25
		Late	7	1	2.50	IPM-430-1
3	Plant type	Erect	3	0	0.00	-
		Semi-erect	5	37	92.50	TJM-37, TJM-111, TJM-115, TJM-134, TJM-136, TJM-137, TJM-140, TJM-141, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-196, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, PDM-139, LGG-460, SML-668, Shikha, Kanika, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Yellow Mung, Pusa Vishal, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, PM-1623
		Spreading	7	3	7.50	TJM-124, Urdi Local, TM-96-25
4	Plant growth habit	Determinate	1	3	7.50	TJM-141, Pusa B-51, TM-96-25
		Semi-determinate	2	12	30.00	TJM-37, TJM-124, TJM-134, TJM-236, Ganga-8, Hum-1, Urdi Local, Yellow Mung, Pusa Vishal, MH-903, PKVAM-4, PM-1623
		Intermediate	3	7	17.50	TJM-143, TJM-145, TJM-155, PDM-11, SML-668, GAM-5, MH-421
		Semi-indeterminate	4	18	45.00	TJM-111, TJM-115, TJM-136, TJM-137, TJM-140, TJM-144, TJM-146, TJM-160, TJM-196, TJM-231, TJM-232, TJM-235, PDM-139, LGG-460, Shikha, Kanika, Virat, IPM-430-1
5	Stem colour	Green	1	36	90.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-136, TJM-137, TJM-140, TJM-141, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-196, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, PDM-139, LGG-460, Shikha, Kanika, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Yellow Mung, Pusa B-51, IPM-430-1, PKVAM-4, PM-1623, TM-96-25
		GWPS	2	1	2.50	Pusa Vishal
		Purple	3	3	7.50	SML-668, Urdi Local, MH-903
6	Stem pubescence	Absent	1	0	0.00	--
		Present	9	40	100	All 40 genotypes under study

S. No.	Traits	Class	Note/ Score	Frequency	Percentage	Name of genotypes
7	Leaflet: lobes	Absent	1	40	100	All 40 genotypes under study
		Present	9	0	0.00	--
8	Leaf shape	Deltoid	1	0	0.00	--
		Ovate	2	39	97.50	All genotypes except Urdi Local
		Lanceolate	3	1	2.50	Urdi Local
		Cuneate	4	0	0.00	--
9	Leaf colour	Green	1	32	80.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-140, TJM-141, TJM-143, TJM-144, TJM-145, TJM-155, TJM-196, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, PDM-139, LGG-460, SML-668, Shikha, Kanika, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Yellow Mung, Pusa Vishal, IPM-430-1, PKVAM-4, TM-96-25
		Dark Green	2	8	20.00	TJM-136, TJM-137, TJM-146, TJM-160, Urdi Local, Pusa B-51, MH-903, PM-1623
10	Leaf vein colour	Green	1	11	27.50	Shikha, Kanika, Yellow Mung, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, PM-1623, TM-96-25, TJM-143, PDM-139
		Greenish Purple	2	27	67.50	TJM-37, TJM-111, TJM-115, TJM-134, TJM-136, TJM-137, TJM-140, TJM-141, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-196, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, LGG-460, SML-668, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Urdi Local
		Purple	3	2	5.00	TJM-124, Pusa Vishal
11	Petiole colour	Green	1	14	35.00	TJM-235, TJM-236, PDM-11, PDM-139, LGG-460, Shikha, Kanika, Yellow Mung, Pusa Vishal, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, TM-96-25
		Green with purple splashes	2	24	60.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-136, TJM-137, TJM-140, TJM-141, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-196, TJM-231, TJM-232, Virat, GAM-5, MH-421, Ganga-8, Hum-1, PM-1623
		Purple	3	2	5.00	SML-668, Urdi Local
12	Flower: Petal colour	Yellow	3	17	42.50	TJM-124, TJM-137, TJM-140, TJM-141, TJM-143, TJM-155, LGG-460, Shikha, MH-421, Ganga-8, Urdi Local, Yellow Mung, Pusa Vishal, Pusa B-51, IPM-430-1, PKVAM-4, PM-1623
		Light Yellow	5	23	57.50	TJM-37, TJM-111, TJM-115, TJM-134, TJM-136, TJM-144, TJM-145, TJM-146, TJM-160, TJM-196, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, PDM-139, SML-668, Kanika, Virat, GAM-5, Hum-1, MH-903, TM-96-25
13	Premature pod colour	Green	1	40	100	All 40 genotypes under study
		GWPS	2	0	0.00	--
14	Pod pubescence	Absent	1	0	0.00	--
		Present	9	40	100	All 40 genotypes under study
15	Pod position	Above Canopy	1	16	40.00	TJM-37, TJM-115, TJM-134, TJM-136, TJM-141, TJM-143, TJM-144, TJM-145, LGG-460, SML-668, GAM-5, MH-421, Ganga-8, Hum-1, Pusa B-51, PKVAM-4
		Intermediate	2	23	57.50	TJM-111, TJM-124, TJM-137, TJM-140, TJM-146, TJM-155, TJM-160, TJM-196, TJM-231, TJM-232, TJM-235, TJM-236, PDM-11, PDM-139, Shikha, Kanika, Virat, Yellow Mung, Pusa Vishal, MH-903, IPM-430-1, PM-1623, TM-96-25
		Not visible	3	1	2.50	Urdi Local

S. No.	Traits	Class	Note/ Score	Frequency	Percentage	Name of genotypes
16	Pod colour	Brown	1	24	60.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-143, TJM-144, TJM-196, PDM-11, LGG-460, SML-668, Shikha, Kanika, Virat, Ganga-8, Urdi Local, Yellow Mung, Pusa Vishal, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, PM-1623, TM-96-25
		Black	2	16	40.00	TJM-136, TJM-137, TJM-140, TJM-141, TJM-145, TJM-146, TJM-155, TJM-160, TJM-231, TJM-232, TJM-235, TJM-236, PDM-139, GAM-5, MH-421, Hum-1
17	Pod curvature	Straight	1	32	80.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-136, TJM-137, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-196, PDM-11, PDM-139, LGG-460, SML-668, Shikha, Kanika, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Urdi Local, Yellow Mung, Pusa Vishal, MH-903, IPM-430-1, PM-1623, TM-96-25
		Curved	3	8	20.00	TJM-140, TJM-141, TJM-231, TJM-232, TJM-235, TJM-236, Pusa B-51, PKVAM-4
18	Seed colour	Yellow	1	1	2.50	Yellow Mung
		Light Green	2	26	65.00	TJM-37, TJM-111, TJM-115, TJM-137, TJM-143, TJM-144, TJM-145, TJM-155, TJM-160, TJM-196, TJM-232, TJM-236, PDM-11, PDM-139, LGG-460, Shikha, Kanika, Ganga-8, Hum-1, Pusa Vishal, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, PM-1623, TM-96-25
		Yellowish Green	3	6	15.00	TJM-124, TJM-146, SML-668, Virat, GAM-5, MH-421
		Brownish Green	4	6	15.00	TJM-140, TJM-141, TJM-231, TJM-235, TJM-134, TJM-136
		Dark Green	5	1	2.50	Urdi Local
19	Seed lusture	Shiny	1	35	87.50	TJM-37, TJM-111, TJM-115, TJM-124, TJM-136, TJM-137, TJM-140, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-160, TJM-196, TJM-232, TJM-236, PDM-11, PDM-139, LGG-460, SML-668, Shikha, Kanika, Virat, GAM-5, MH-421, Ganga-8, Hum-1, Urdi Local, Yellow Mung, Pusa Vishal, Pusa B-51, MH-903, IPM-430-1, PM-1623, TM-96-25
		Dull	2	5	12.50	TJM-134, TJM-141, TJM-231, TJM-235, PKVAM-4
20	Seed shape	Oval	1	26	65.00	TJM-37, TJM-111, TJM-115, TJM-124, TJM-134, TJM-136, TJM-137, TJM-140, TJM-141, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-196, TJM-231, TJM-232, TJM-235, PDM-139, SML-668, Kanika, GAM-5, Urdi Local, Yellow Mung, Pusa Vishal, PM-1623
		Drum Shaped	3	14	35.00	TJM-160, TJM-236, PDM-11, LGG-460, Shikha, Virat, MH-421, Ganga-8, Hum-1, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, TM-96-25
21	Seed size	Small	3	6	15.00	TJM-37, PDM-139, Shikha, Hum-1, Yellow Mung, TM-96-25
		Medium	5	25	62.50	TJM-111, TJM-115, TJM-124, TJM-134, TJM-140, TJM-143, TJM-144, TJM-145, TJM-146, TJM-160, TJM-196, TJM-236, PDM-11, LGG-460, Kanika, Virat, MH-421, Ganga-8, Urdi Local, Pusa Vishal, Pusa B-51, MH-903, IPM-430-1, PKVAM-4, PM-1623
		Large	7	9	22.50	TJM-136, TJM-137, TJM-141, TJM-155, TJM-231, TJM-232, TJM-235, SML-668, GAM-5

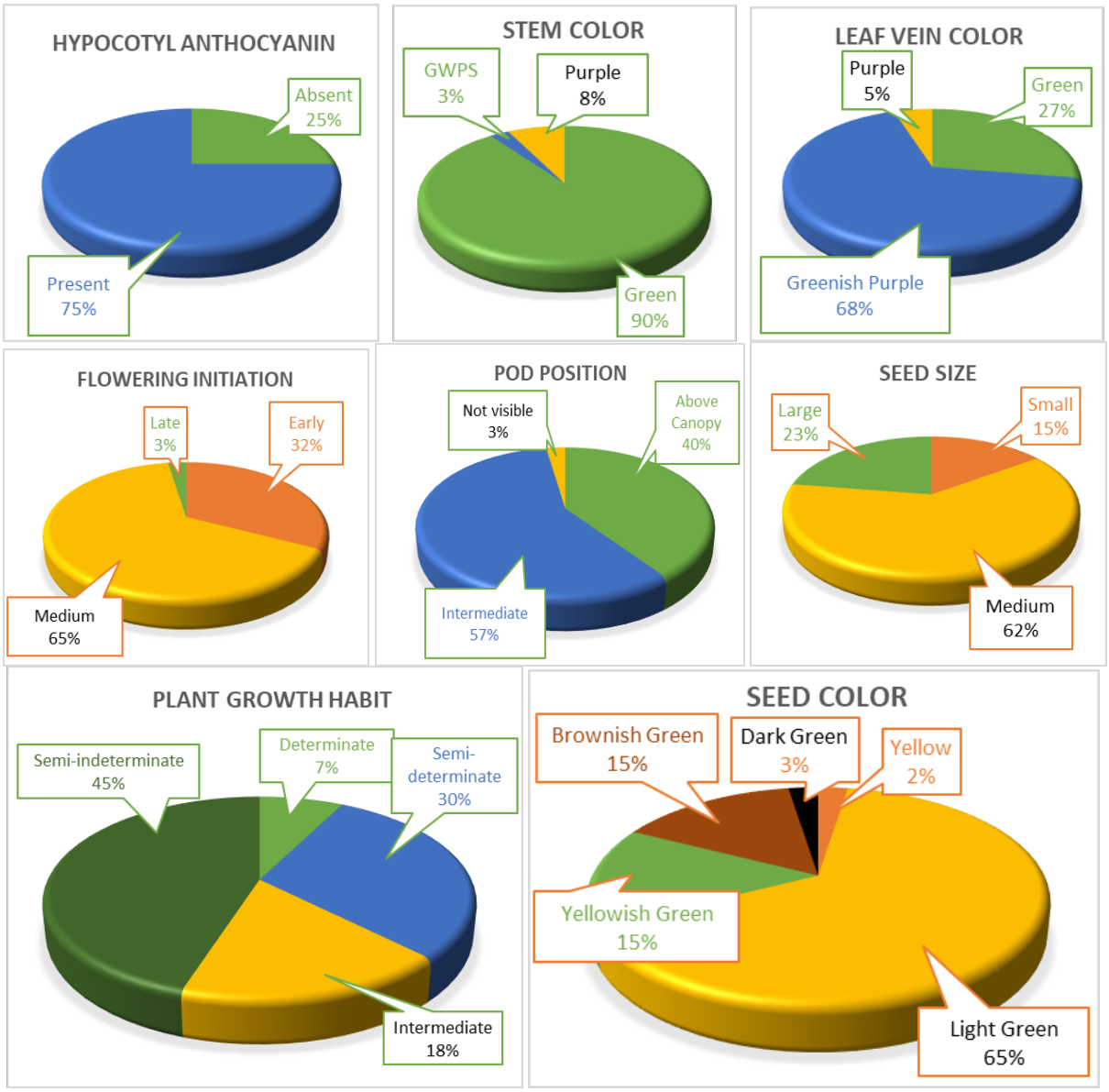

Fig. 1. Frequency distribution pie chart for different morphological traits

(IPM-430-1) was late flowering. Jain *et al.* (2002) reported the usefulness of flower characteristics in characterization of mungbean germplasm. On the basis of plant type, 92.50% of genotypes were found with semi-erect type and only 7.50% were spreading type, while none of the genotypes were recorded for erect plant type. Normally, erect plant types are preferred as they provide good growth and are preferable for machine harvest also. Thus, there is a need to incorporate this trait. Plant growth habit showed a variation of 45% semi-indeterminate, 30% semi-determinate, 17.5% indeterminate and only 7.50% determinate genotypes.

Pod characters such as premature pod colour, pod pubescence, pod position, mature pod colour, pod curvature are useful in the identification of the genotypes and also influence the yielding ability of the plant. All the genotypes were similar in green premature pod colour and presence of pod pubescence, hence both traits had no use in discriminating the genotypes in the present material. Pod position was above canopy for 40% of the genotypes and 57.5% of them had intermediate position, while only one genotype (2.50%) had not visible position of pod (**Fig. 6**). On the basis of matured pod colour, 60% of genotypes were grouped under brown pod colour

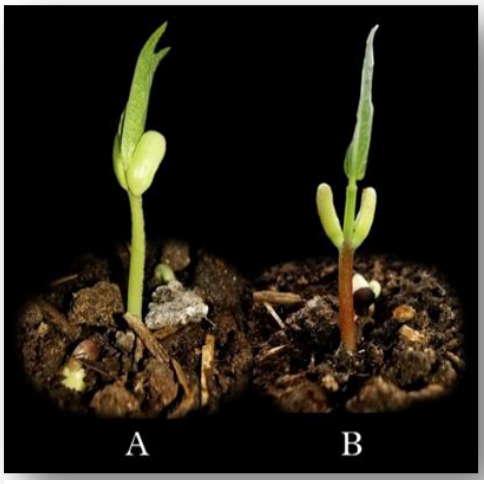

Fig. 2. Anthocyanin coloration of hypocotyl (A) Absent (B) Present

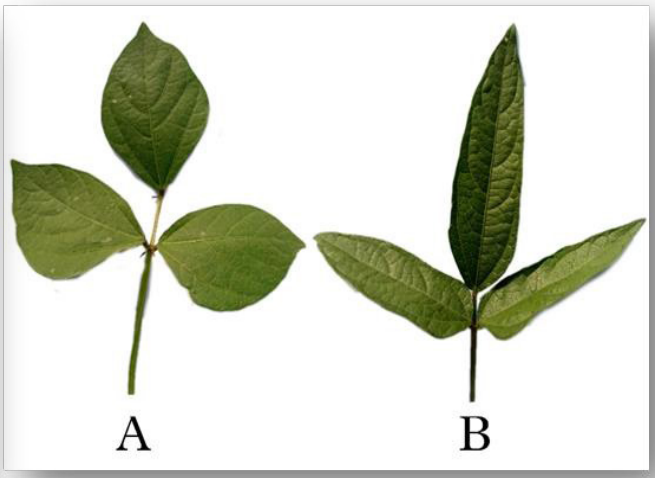

Fig. 3. Shape of leaf (A) Ovate (B) Lanceolate

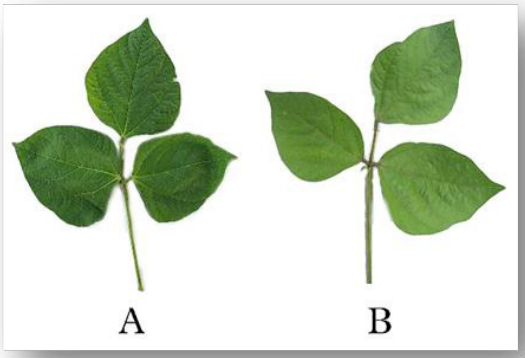

Fig. 4. Vein colour of leaf (A) Green (B) Purple

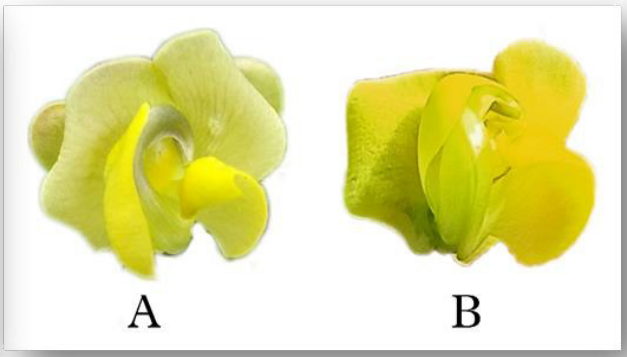

Fig. 5. Colour of petal (A) Light Yellow (B) Yellow

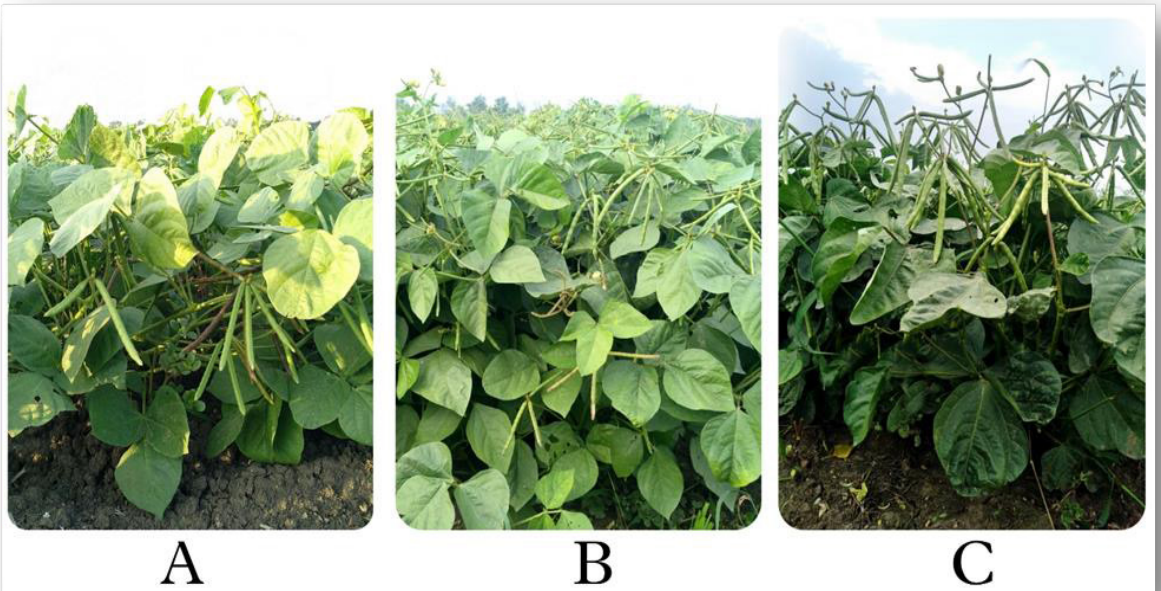

Fig. 6. Pod position in plant (A) Below canopy (not visible) (B) Intermediate (C) Above canopy

(**Fig. 7**), whereas 40% of genotypes had black pod colour. The curvature of mature pod was straight in 80% of genotypes and curved in 20% of genotypes (**Fig. 8**).

The price of premium quality genotypes of mungbean or consumer acceptance of a variety is decided by the seed characteristics like colour, size and shape (Pratap *et al.,* 2018). Varieties with oval shape, shiny, green coloured grains with medium size are preferable over dull/ brown/ black and drum shaped grains. Seed colour showed pentamorphic variation *i.e.* yellow, light green, yellowish green, brownish green and dark green with 2.5%, 65%, 15%, 15% and 2.5% genotypes respectively (**Fig. 9**). Seed colour determines phytic acid levels . This has been proved by Tajoddin *et al.,* 2011, who reported that yellow seeded genotypes in greengram have low phytic acid content. Majority of the genotypes were shiny seeded (87.5%) , while only five genotypes were dull seeded (12.5%). The seed shape was oval in 65% of genotypes and drum shaped in 35% genotypes. On the basis of 100 seed weight, the seed size was grouped into small, medium and large with 15%, 62.5% and 22.5% genotypes, respectively. Khajudparn and Tantasawat (2011) also discussed the usefulness of seed characters in the characterization of lines in mungbean.

Among the 21 morphological DUS descriptors observed, seed colour trait showed pentamorphic variation; plant growth habit showed tetramorphic variation; six characters *viz.*, flowering initiation, stem colour, leaf vein colour, petiole colour, pod position and seed size showed trimorphic variation; nine characters showed dimorphic variation indicating that the existence of remarkable amount of genetic variability in these genotypes which

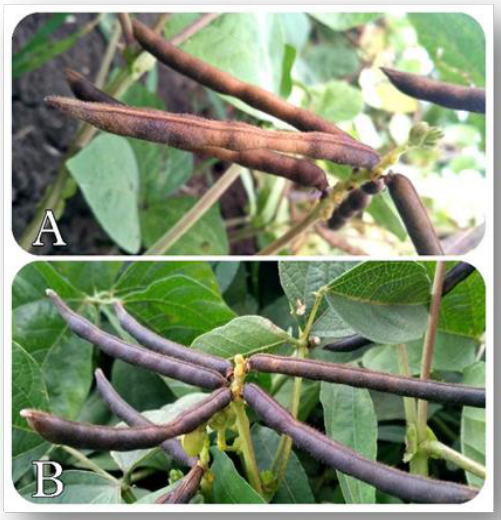

Fig. 7. Mature pod colour (A) Brown (B) Black

Fig. 8. Curvature of mature pod (A) Straight (B) Curved

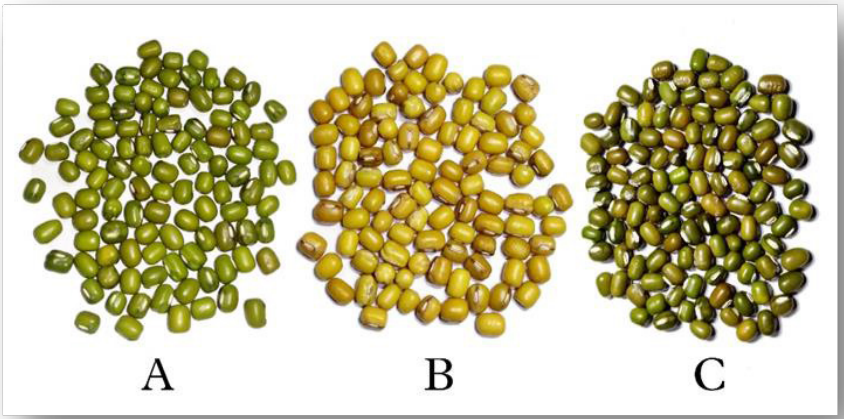

Fig. 9. Seed colour (A) Green (B) Yellow (C) Dark Green

have great potential to assign distinctive morphological profiles from the combination of morphological DUS traits which could be used for elite improved lines identification and characterization as well as the selection of diverse parents in hybridization programme for more heterotic response and generation of better segregants in mungbean breeding.

Plant leaves are the major photosynthetic organs especially from the shoot apical meristem (SAM). Many studies suggested that there are different genes that play a vital role in regulation processes and molecular mechanism of the compound leaf development. The function of the *LFY* orthologs, *KNOXI genes* to increase the complexity of compound leaf development has also been investigated by researchers in which KNOXI proteins are expressed in leaves and are likely associated with compound leaf development (Champagne *et al.,* 2007 and Wang *et al.,* 2013). Generally, greengram have trifoliate compound leaf structure but in the present investigation, the increased number of leaflets of compound leaf of mungbean was found *viz.* quadrifoliate and pentafoliate compound leaf variations rather than the normal trifoliate compound leaves (**Fig. 11**). Interestingly, heptafoliate-leaf-like mutants similar to the *hel1* mutant in mungbean were also identified and characterized in other legumes, including soybean and cowpea (Fehr, 1972). The *hel1* and *smp1* double mutants were observed with heptafoliate leaves of small size, indicating an epistatic gene interaction between *hel1* and *smp1* in the control of leaflet number. The study on genetic control of compound leaf development in the mungbean found that HEL1 is a key factor to coordinate distinct processes to control the compound leaf development in mungbean and its related non-inverted repeat-lacking clade legumes (Jiao *et al.,* 2019).

Tricotyledonous phenotype was observed in the seedlings of genotype TJM-136, TJM-141, TJM144, TJM-235 and Kanika of mungbean and they produced first true leaves in sets of three (**Fig. 10**) at the first node, rather than two leaves. The progeny test revealed that tricotyledonous phenotypes did not give rise to exclusively tricotyledonous offspring, and the inheritance pattern appeared complicated. Numerous plant species, including the sunflower (Hu *et al.*, 2005), Catharanthus roseus (Rai and Kumar, 2001), tomato (Reynard, 1952; and Kerr, 1985) and mustards (Holtorp, 1944) have been studied by researchers for tricotyledonous seedling phenomenon. In sunflower, tricotyledony mutant appears to be derived from recessive genes of poor penetrance because it could not be fixed after self-pollination for three successive generations and no substantial gain was seen from F_4 to F_5 generation (Hu *et al*., 2005). According to molecular research, the model plant Arabidopsis can develop the tricotyledonous feature when a few mutant genes are present (Azumi *et al.,* 2002; Vernon *et al.,* 2001). Since the function of the cotyledons is to provide nutrients like lipids, proteins, and carbohydrates that the growing plant needs before it reaches the point at which it can make its own supply through photosynthesis, this extra cotyledon may aid the seedlings in becoming established after germination. In tricotyledonous phenotype, one extra cotyledon will give one extra true leaf as three true leaves per node which will provide more leaf area for photosynthesis. So, additional studies are needed to clarify its genetic basis and in the development of a true breeding tricotyledonous line.

In the present investigation, stem pubescence, leaflet lobes, leaf shape, premature pod colour and pod pubescence were almost same for all the lines, so, they may not be useful descriptor for the discrimination or

Fig. 10. Variation found in first true leaf of mungbean seedling

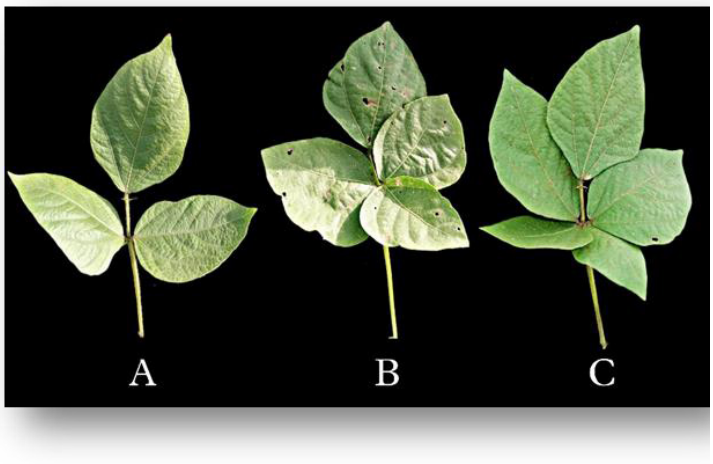

Fig. 11. Variations found in compound leaf phenotype of mungbean. (A) Trifoliate leaf (B) Quadrifoliate leaf and (C) Pentafoliate leaf

identification of the genotypes. Whereas, anthocyanin pigmentation of hypocotyl, plant, leaf, pod and seed characteristics were obserded to have a lot of variability and hence could be exploited for the identification and utilization of genotypes, as reported by Patel *et al.* (2019). Expression of such descriptors could facilitate easy registration of mungbean with distinct characters present in the genotypes.

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