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DUS characterization of elite improved lines of mungbean [*Vigna radiata* (L.) Wilczek] using agro-morphological traits

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Abstract

Any variety or hybrid must be characterized in order to determine its novelty for the registration and notification. Genotypes can be differentiated and their genetic variety quantified using a catalog that is created through morphological characterization of the genotypes. Following the recommendations PPV&FR-2007, GOI, DUS (Distinctness, Uniformity and Stability) guidelines, current study was carried out under field conditions that encourage periodic growth and expression for all descriptors of mungbean. Therefore, in present study a collection of 106 diverse genotypes of mungbean were characterized using thirteen agro-morphological traits during the *Kharif* 2021 in RBD design with two replications. Study revealed ample and exploitable amount of variation among all the diverse genotypes for all the traits studied.

Keywords: DUS, *Vigna radiata* (L.) Wilczek, agro-morphological traits

Introduction

Among major pulse crops, mungbean (*Vigna radiata* L., Wilczek) belongs to Family Leguminosae, subfamily Papilionoideae, and tribe Fabaceae) occupies third position after chickpea and pigeonpea, which is thought to be native to the Indo-Burman region (Kumar and Kumar, 2014) [9]. It is mainly a self- pollinated, diploid (2n=2x=22), short- duration pulse crop with relatively small genome size of 579 Mb/1C (Sabatina *et al.*, 2021) [16]. As a leguminous crop it is important in term of both nutrition and economic because they play a significant role symbiotic soil nitrogen fixation and sustainable agriculture (Sharma, *et al.*, 2023) [18]. In India, mungbean was grown over an area of 5.13 m ha, with production of 3.19 m tonnes and productivity 601 kg/ha (Anonymous, 2022) [1]. It plays an important role in sustaining soil fertility by improving the physical and biological properties of the soil (Rohilla, *et al.*, 2022) [15]. Mungbean is a crucial and reasonably priced source of dietary protein in Asia, particularly for people with limited resources, and is essential in decreasing protein deficiency, especially in developing nations (Selvi *et al.*, 2006) [17]. It is the cheapest source of easily digestible, good-quality protein (25.10%), fiber (13.40%), total amino acids (21-25%) and and carbohydrates (59-65%), apart from these mungbean is also a rich source of vitamin A (83 mg/100 g), riboflavin (0.15 mg/100 g), thiamine (0.72 mg/100 g), nicotinic-acid (2.4 mg/100 g) (Vairam *et al.*, 2016; Joshi *et al.*, 2022) [16, 6]. Mung beans are extensively grown during the *kharif* season in the arid and semi-arid region of India. But now, due to the availability of short-lived varieties, the area and production is increasing under summer season (Versha *et al.*, 2023) [22].

As the demand of growing population is increasing day by day but area under food crops (cereals and pulses) is limited. So, to mitigate the demand of growing population the production and productivity of pulses like mungbean must be increased. Despite the potential for increased consumption of mungbean to alleviate hidden hunger, progress is still needed to increase production and yields lag behind grains (Sharma *et al.*, 2023) [18]. Although many high-yielding varieties of mungbean have been developed over few last decades, but they needed help to overcome the hurdles in improving production due to their vulnerability to biotic and abiotic stress, narrow genetic base and low harvest index (Rohilla *et al.*, 2022) [15]. Seed yield in mungbean is a multiplex quantitative trait influenced by many other morphological, physiological traits and G x E interaction. So, it is necessary to characterize lines to understand the variability that exists between them before lines with similar traits are grouped and used in breeding programme (Piyada *et al.*, 2010) [10].

Normal morphological descriptions of lines by plant breeders are not sufficient to convey a complete picture of the lines, underscoring the need for standardized genotype characterization methods described by an appropriate authority such as PPV & FRA (Protection of Plant Varieties and Farmers Rights) (Janghel *et al.*, 2020) [5]. The DUS characteristics (Distinctiveness, Uniformity and Stability) have been recommended by the Plant Variety Protection and Farmers' Rights Authority (PPV & FRA) for classifying the lines for their protection and certification. Draft national testing recommendations for mung bean DUS testing provide the necessary characteristics to compare potential varieties with current varieties and the information obtained is required when filling out applications (Singh *et al.*, 2006) [19]. Characterizing and assessing the variance in the best improved green gram lines is critical to improving both qualitative and quantitative traits, as well as protection. So keeping in mind all above aspects, present investigation was carried out to assess variability among germplasm and genotype classification for mungbean improvement, using DUS (distinctness, uniformity, and stability) descriptions.

Materials and Methods

One hundred six genotypes of mungbean were morphologically evaluated at Pulses Section Research Farm, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, India during *Kharif* 2021. All the recommended agronomic package and practices were followed to raise a good crop. Each genotype was grown in a row of 4m length with row to row 30 cm and plant to plant 10 cm spacing in Randomized Block Design (RBD) with three replications. The experimental site situated at 29.10° N latitude and 75.46° E longitude at an elevation of 215. 2 meter above mean sea level. Mungbean genotypes were evaluated based on their morphological traits as per DUS guidelines provided by the PPV & FRA, GOI for mungbean. For plant growth habit and pod bearing habit, data were collected as visual observations in a single assessment on a group of plant or plant part. Data for the days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, biological yield (g), harvest index (%), seed yield per plant (g) and 100-seed weight were taken from five randomly selected plants from each replication by visual observations.

Results and Discussion

As a prerequisite for varietal identification recognition, the classification of 106 improved genotypes of greengram was done using DUS descriptors. Study revealed ample and exploitable amount of variation among all the diverse genotypes for all the traits studied. These results were in agreement with previous findings by Kaur *et al.*, 2017 [7]; Rohilla *et al.*, 2022 [22] and Rahangdale *et al.*, 2023 [14] who also found highly significant variability among the genotypes for almost all studied traits. Based on scores for thirteen descriptors, these different 106 genotypes have been classified into different groups and their frequency of distribution is presented in Table 1.

Time of 50% flowering and days to maturity that is observed on the plot basis varied from genotypes to genotypes. Based on these observation flower initiated at early duration (<40 days) was demonstrated by 67% of genotypes, whereas about 27% genotypes exhibited flowering at medium duration (40-45 days) and remaining genotypes started flowering in the late duration (>45 days). Likewise, early maturity (60-70 days) was documented to about 95% of total genotypes, where as only 5% genotypes exhibited late maturity (>70 days). These results clearly demonstrated that early flowering exhibited early maturity. As, early flowering and maturity is useful to plant breeding programme because it transfers the vegetative phase energy to the reproductive phase early, and this probably aids in the enhancement of seed yield (Sharma *et al.*, 2023) [18]. Jain *et al.* (2002) [4]; Patel *et al.* (2019) [12] also reported the usefulness of flower characterization of mungbean accession.

Likewise, another descriptor used for characterization of mungbean genotypes is number of branches per plant. More number of branches per plant regarded as a useful criterion for characterization because more number of branches having robust stature provide a better chance for better return *i.e.*, yield. In present investigation maximum genotypes (77) having more number of branches (>3), whereas some genotypes (27) exhibited 2-3 branches per plant and very low genotypes (2) having less than 2 branches per plant.

Characterization of mungbean genotypes based on plant height classified the total genotypes into three categories (Short, medium and tall). Assessment of this character is based at fully mature pod stage. In our study maximum plant (71) were observed to medium in height (50-70cm) followed (27) by tall (>70cm) and only 8 genotypes are short in stature (<70). For plant height, more height is desirable in the tall genotype, whereas less height is desirable in dwarf types because dwarf genotypes can withstand in logging conditions. Similar results were in accordance with the previous results of Khajudparn and Tantasawat (2011) [8] and Patel *et al.* (2019) [12] in mungbean where, they also observed the similar pattern of plant height.

Regarding plant growth habit, all the 106 genotypes were morphologically classified in three groups *viz.*, erect, semi-erect and spreading type plant growth habit. Data was collected at the 50% flowering stage by observation of a group of plants. In our study, 13 genotypes were found erect, 60 semi-spreading and 33 genotypes were found spreading. Generally, erect plant varieties are typically preferred because they receive the greatest amount of sunlight absorption for photosynthesis by consistently exposing all leaves, which would also increase dry matter production and a simultaneous increase in yield (Escuro *et al.*, 1971) [2]. Similar observation of plant type was observed by Kaur *et al.* (2017) [7] and versha *et al.* (2022) [22] in their study of five and twenty high yielding genotypes of mungbean, respectively.

For the categorization of genotypes for number of clusters per plant, genotypes having less than seven clusters kept in low cluster group, seven to ten clusters in medium group and more than ten clusters carrying genotypes were kept in high cluster group. Genotypes in low, medium and high group were six, 34 and 66, respectively. The trait, pod bearing habit was classified into three groups *viz.*, pod bearing above the canopy, intermediate pod bearing and pods not visible. Among one hundred six genotypes pod bearing in 60 genotypes was of above canopy type and intermediate in 40 genotypes while in six genotypes pods were not visible

More pods per plant are associated with a higher yield. So based on number of pods per plant descriptor these 106 mungbean genotypes were classified into three groups *i.e* low number of pods (<15), medium (15-20) and high (>20) pods. Ninety-one genotypes were grouped in high category, 14 in medium while only one genotype in low category. So, ultimately more number of pods gives more yield. These results were in agreement with previous findings by Kaur *et al.* (2017) [7], Patel *et al.* (2019) [12] and Mounika *et al.* (2020) [11] in mungbean.

Similarly, more number of seeds per pod aids in the enhancement of seed yield. So our study based on this trait classified the genotypes as less (<8), medium (8-10) and high (>10) number of seeds per pod and genotypes in each category were 19, 29 and 58, respectively. Based on the 100 seed weight, mungbean genotypes were grouped as small (<3 gram), medium (3-5 gram) and large seed size (>5 gram) groups. Maximum number of genotypes were in large seed group *i.e.* 85 followed by the 20 genotypes in small category while only one genotype SML 668 had the large size seeds. Similar observation of usefulness of seed parameters were observed by Khajudparn and Tantasawat (2011) [8] and Rahangdale *et al.* (2023) [14] in mungbean and Harini *et al.* (2022) [3] in lentil.

Another one descriptor *i.e.* Biological yield per plant was classified in three categories *viz.*, low (<40 g), medium (40-60 g) and high (>60 g) dry plant weight per plant. In low category 12 genotypes were found; 86 genotypes in medium group and eight genotypes were found in high biological yield category. Likewise, the trait seed yield per plant was categorized into three groups *viz.*, low (< 8 gram), medium (8-10 g) and high (>10 g) seed yield per plant in gram. Total genotypes in low, medium and high category were 19, 45 and 42, respectively. More biological yield and seed yield per plant is significant because these traits were positively associated with more economic yield. Similar result was found by Khajudparn and Tantasawat (2011) [8] and Sunayana *et al.* (2017) [20] in 14 high yielding genotypes of mungbean; Kumar and Shrikant (2016) [10] in cowpea and Patel *et al.* (2019) [12] in mungbean, where they observed same consonance of results with our finding.

Table 1: Morphological characterization of mungbean genotypes using DUS descriptor

Sr. No.	Traits	State	Genotypes	Frequency of genotypes
1	Days to 50% flowering	Early (<40 days)	MH 565, IPM 312-394, EC 581523, IPM 205-7, SML 1018, SML 1082, IPM 2-03, MH 521, MH 560, MH 729, ML 1628, PDM 96-262, SML 1194, TMB 131, AKM 9904, HUM 7, IPM 409-4, IPM 410-3, Pusa 9531, SHIM 12-1, SML 1023, IPM 02-17, IPM 02-19, MH 921, Pusa Vishal, SML 668, COGG 13-19, IC 15276, IPM 06-5, IPM 312-19, KM 2211, ML 735, Pusa 1542, Pusa 1642, 2KM 117, IPM 03-2, M 605, MH 539, 2KM 101, MH 98-1, ML 2037, ML 759, NDMZ 215-1, Pusa 1142, Pusa 1502, Pusa 1601, Samrat, TMB 163, Asha, M 395, ML 1451, ML 776, PANT M-5, Pusa 0871, RMG 991, TRCM 155-1, 2KM 111, GM- 9926 YMV, HUM 16, IPM 302-2, KM 2241, KM 2328, ML 1907, NBPGR 150, Pusa 0672, Pusa 1141, Pusa 1501, Pusa Ratna, SML 1115, SML 1781, TMB 196	71
		Medium (40-45 days)	IPM 02-14, 2KM 101, 2KM 115, IC 39574, OUM 11-5, PM 11-51, PM 99-3, 2KM 112, ML 1108, NDMZ 13-11, COGG 13-14, GANGA 8, NDMZ 15-2, PLM 62, VGG-1, 2KM 138, COGG 1102, COGG-8, IC 103196, NDMZ 13-12, PLM 76, PLM 24, 2KM 216, EC 251552, EC 393410, EC 470096, EC 581523B, HUM 27, VGG-2	29
		Late (>45 days)	EC 399233, CH 210-3, EC 393407, EC 30400, ADGG 13034, EC 470090	6
2	Days to maturity	Early (<60 days)	IPM 409-4, IPM 205-7	2
		Medium (60-70 days)	IPM 410-3, MH 560, MH 565, MH 521, IPM 312-394, 2KM 117, IC 15276, IPM 06-5, IPM 2-03, EC 470096, IPM 312-19, KM 2241, MH 921, HUM 7, IPM 03-2, MH 539, COGG-8, EC 581523, HUM 16, IPM 02-19, MH 729, COGG 13-19, GANGA 8, HUM 27, 2KM 101, MH 98-1, 2KM 112, IPM 02-14, M 395, 2KM 111, GM- 9926 YMV, IPM 02-17, M 605, 2KM 216, AKM 9904, ML 1108, ML 1628, 2KM 138, EC 581523B, IC 39574, ML 1451, 2KM 101, 2KM 115, KM 2211, IC 103196, IPM 302-2, ML 1907, COGG 1102, EC 30400, KM 2328, Asha, EC 251552, EC 470090, CH 210-3, ADGG 13034, EC 393410, EC 399233, COGG 13-14, EC 393407,ML 2037, ML 735,ML 759, ML 776, NBPGR 150, NDMZ 13-11,NDMZ 13-12, NDMZ 15-2, NDMZ 215-1, OUM 11-5, PANT M-5, PDM 96-262, PLM 24, PLM 62, PLM 76, PM 11-51, PM 99-3, Pusa 0672, Pusa 0871, Pusa 1141, Pusa 1142, Pusa 1501, Pusa 1502, Pusa 1542, Pusa 1601, Pusa 1642, Pusa 9531, Pusa Ratna, Pusa Vishal, RMG 991, Samrat, SHIM 12-1, SML 1018, SML 1023, SML 1082, SML 1115, SML 1194, SML 1781, SML 668, TMB 131, TMB 163, TMB 196	101
		Late (> 70 days)	TRCM 155-1, VGG-1, VGG-2	3
3	Number of branches per plant	Low (<2 branches)	HUM 27, IPM 06-5	2
		Medium (2-3 branches)	HUM 16, IPM 205-7, EC 581523B, IPM 02-14, KM 2328, ML 1907, SML 1018, KM 2241, Pusa 1642, IC 103196, IPM 409-4, Pusa 1501, SML 1115, GM- 9926 YMV, IPM 302-2, IPM 312-394, SML 668, 2KM 216, EC 470090, IC 39574, IPM 02-17, MH 921, NBPGR 150, 2KM 111, IPM 410-3, ML 735, SML 1781	27
		High (>3 branches)	NDMZ 215-1, PM 99-3, SHIM 12-1, IC 15276, M 605, NDMZ 13-11, SML 1194, 2KM 138, COGG-8, GANGA 8, COGG 13-19, M 395, MH 565, MH 98-1, ML 1628, Pusa Ratna, COGG 13-14, Pusa 1502, Pusa 1542, TMB 131, CH 210-3, HUM 7, MH 539, MH 560, NDMZ 15-2, PLM 76, Pusa Vishal, SML 1082, RMG 991, TMB 163, EC 393410, EC 399233, 2KM 101, ML 1108, OUM 11-5, Pusa 9531, 2KM 101, PDM 96-262, Pusa 0672, TRCM 155-1, AKM 9904, Asha, COGG 1102, ML 1451, NDMZ 13-12, Pusa 0871, Pusa 1601, SML 1023, 2KM 112, 2KM 115, IPM 312-19, ML	77

			2037, ML 759, PM 11-51, EC 581523, IPM 02-19, MH 521, ML 776, PLM 24, VGG-1, VGG-2, EC 393407, IPM 2-03, MH 729, PANT M-5, Pusa 1142, Samrat, Pusa 1141, 2KM 117, EC 30400, EC 470096, ADGG 13034, KM 2211, PLM 62, EC 251552, IPM 03-2, TMB 196	
4	Plant height	Short (<50 cm)	IPM 312-394, TMB 131, IPM 312-19, HUM 27, SML 1023, MH 521, IPM 02-19, Pusa 1642	8
		Medium (50-70 cm)	IPM 409-4, IPM 205-7, KM 2241, MH 565, EC 393407, IPM 2-03, IPM 02-14, PDM 96-262, IPM 02-17, NDMZ 13-12, IC 103196, SHIM 12-1, IC 15276, IPM 06-5, SML 1115, SML 1018, MH 729, 2KM 138, TMB 196, IPM 410-3, 2KM 101, NDMZ 215-1, GANGA 8, 2KM 112, MH 921, EC 251552, M 395, TMB 163, EC 581523, SML 1194, Samrat, EC 393410, NDMZ 15-2, EC 581523B, ML 2037, PM 99-3, IPM 03-2, MH 539, MH 560, MH 98-1, PLM 24, NBPGR 150, OUM 11-5, GM- 9926 YMV, SML 1082, IC 39574, IPM 302-2, RMG 991, VGG-1, NDMZ 13-11, AKM 9904, 2KM 117, COGG-8, ML 1907, Pusa Ratna, SML 1781, PLM 62, TRCM 155-1, ML 1628, EC 399233, 2KM 111, EC 470090, Pusa 9531, ML 759, Pusa 1502, EC 470096, COGG 13-19, M 605, SML 668, Pusa 1542, PANT M-5	71
		Tall (>70 cm)	2KM 101, KM 2211, HUM 7, COGG 1102, EC 30400, KM 2328, Pusa 1501, 2KM 216, Pusa 1141, HUM 16, ML 1451, Pusa 1142, Pusa 1601, Pusa 0871, CH 210-3, 2KM 115, Pusa 0672, ADGG 13034, VGG-2, PLM 76, ML 735, ML 776, PM 11-51, Asha, ML 1108, COGG 13-14, Pusa Vishal	27
5	Plant growth habit	Erect (<300)	EC 3934077, GM- 992 YMV, HUM 27, IPM 03-2, IPM 312-4, IPM 205-7, KM 22-11, ZKM 138, ZKM 216, KM 2328, MH 921, ML 776, Pusa 1642	13
		Semi-spreading (300-600)	Asha, AVM 9904, COGG-8, COGG 1102, EC 30400, EC 251552, EC 399233, EC 393410, EC 581523, EC 581523B, Ganga 8, HUM 16, IC 15276, IC 39557, IC 031096, Pusa 1701, IPM 02-19, IPM 06-5, IPM 302-2, IPM 409-4, IPM 410-3, IPM 312-19, KM 2241, ZKM 112, ZKM 115, ZKM 117, M 395, M 60, COGG 13-19, MH 98-1, MH 565, MH 709, MH 729, ML 735, ML 759, COGG 13-14, ML 1108, ML 1451, ML 1628, ML 2037, NDMZ 13-11, NDMZ 15-2, Pusa 1831, NDMZ 215-1, NBPGR 150, OUM 11-5, PANT M-5, Pusa 1141, Pusa 1502, Pusa 1601, Pusa Ratna, Pusa Vishal, SHIM 12-1, SML 688, SML 1115, SML 1194, SML 1781, PBM 163, PBM 196, TRCM 155-1, VGG-1, VGG-2, NKM 15-12	60
		Spreading (>600)	ADGG 13034, CH 210-3, EC 470090, EC 470096, IPM 02-14, IPM 02-3, IPM 02-17, ZKM 101, OUM 1105, ZKM 111, MH 521, MH 539, MH 560, TMB 131, ML 1907, NDMZ 13-12, PM 99-3, PM 11-51, PDM 96-262, PLM 24, PLM 62, PLM 76, Pusa 0672, Pusa 0871, Pusa 9531, Pusa 1142, Pusa 1501, Pusa 1542, RMG 991, Samrat, SML 1018, SML 1023, SML 1082, HUM 7	33
6	Number of clusters per plant	Low (<7)	EC 393407, EC 393410, EC 251552, HUM 27, IPM 205-7, SML 1781	6
		Medium (7-10)	ML 735, IC 103196, EC 470090, EC 581523, EC 399233, TMB 131, TMB 163, 2KM 115, IPM 2-03, Pusa 0871, ML 1108, SML 668, Pusa Ratna, CH 210-3, EC 30400, TMB 196, HUM 7, 2KM 138, KM 2328, M 395, IPM 409-4, SML 1018, PM 99-3, Asha, PLM 24, IC 15276, MH 521, ADGG 13034, 2KM 117, 2KM 216, TRCM 155-1, EC 581523B, COGG 13-14, Pusa 1142	34
		High (>10)	IC 39574, M 605, IPM 312-394, Pusa Vishal, 2KM 112, GM- 9926 YMV, IPM 302-2, KM 2211, ML 2037, PANT M-5, PLM 62, SML 1082, IPM 410-3, KM 2241, ML 759, IPM 06-5, NDMZ 15-2, SHIM 12-1, IPM 02-14, ML 1907, Pusa 0672, 2KM 101, IPM 312-19, MH 98-1, 2KM 111, ML 776, VGG-2, COGG-8, PM 11-51, SML 1194, MH 921, RMG 991, SML 1023, HUM 16, Pusa 1141, Pusa 1642, GANGA 8, Pusa 9531, IPM 02-19, Pusa 1501, COGG 13-19, SML 1115, VGG-1, Pusa 1601, IPM 03-2, PLM 76, Pusa 1542, MH 539, Pusa 1502, NDMZ 13-11, PDM 96-262, IPM 02-17, 2KM 101, MH 729, ML 1628, Samrat, COGG 1102, MH 560, OUM 11-5, NDMZ 215-1, NBPGR 150, MH 565, ML 1451, AKM 9904, NDMZ 13-12, EC 470096,	66
7	Pod-bearing habit	Above canopy	2KM 111, 2KM 115, 2KM 117, 2KM 138, COGG 1102, COGG-8, EC 470090, EC 470096, EC 581523, HUM 27, HUM 7, IC 103196, IC 15276, IC 39574, IPM 02-14, IPM 02-19, IPM 03-2, IPM 06-5, IPM 2-03, IPM 205-7, IPM 312-19, IPM 312-394, IPM 409-4, IPM 410-3, KM 2241, MH 521, MH 539, MH 560, MH 565, MH 709, MH 729, MH 98-1, ML 1451, ML 1628, ML 1907, ML 2037, ML 759, NBPGR 150, NDMZ 13-11, NDMZ 13-12, NDMZ 15-2, OUM 11-5, PDM 96-262, PLM 24, PLM 76, PM 11-51, Pusa 0672, Pusa 0871, Pusa 1142, Pusa 9531, Samrat, SHIM 12-1, SML 1018, SML 1023, SML 1115, SML 668, TMB 131, TMB 163, TMB 196, VGG-2	60
		Intermediate	2KM 101, 2KM 112, 2KM 216, AKM 9904, Asha, CH 210-3, COGG 13-14, COGG 13-19, EC 251552, EC 393407, EC 399233, EC 581523B, GANGA 8, GM- 9926 YMV, HUM 16, IPM 02-17, IPM 302-2, KM 2211, KM 2328, M 395, M 605, MH 921, ML 1108, NDMZ 215-1, PANT M-5, PLM 62, PM 99-3, Pusa 1141, Pusa 1501, Pusa 1502, Pusa 1542, Pusa 1601, Pusa Ratna, Pusa Vishal, RMG 991, SML 1082, SML 1194, SML 1781, TRCM 155-1, VGG-1	40
		Not visible	ADGG 13034, EC 30400, EC 393410, ML 735, ML 776, Pusa 1642	6
8	Number of pods per plant	Low (<15)	EC 393407	1
		Medium (15-20)	EC 251552, EC 393410, EC 399233, HUM 27, EC 30400, EC 470090, EC 581523, TMB 163, TMB 131, CH 210-3, SML 668, ML 1108, IC 103196, M 395	14
		High (>20)	PM 99-3, ML 735, Pusa Ratna, Pusa 0871, TMB 196, EC 581523B, IPM 205-7, 2KM 138, IC 15276, SML 1018, HUM 7, OUM 11-5, IPM 409-4, ADGG 13034, NDMZ 13-11, PLM 24, 2KM 117, MH 521, 2KM 101, KM 2328, TRCM 155-1, M 605, NDMZ 215-1, Samrat, IPM 02-17, KM 2241, COGG 13-14, NBPGR 150, ML 1907, MH 921, NDMZ 13-12, KM 2211, COGG 13-19, Asha, IPM 2-03, ML 2037, NDMZ 15-2, PDM 96-262, IPM 312-19, IPM 302-2, IPM 312-394,	91

			COGG-8, 2KM 216, IPM 02-14, SML 1082, Pusa 1142, SHIM 12-1, IC 39574, IPM 06-5, MH 729, ML 1451, ML 759, ML 776, PLM 62, SML 1781, GM- 9926 YMV, IPM 03-2, MH 98-1, 2KM 111, Pusa Vishal, 2KM 112, HUM 16, 2KM 101, PANT M-5, 2KM 115, Pusa 0672, IPM 02-19, SML 1023, Pusa 1141, PM 11-51, Pusa 1501, EC 470096, SML 1194, GANGA 8, IPM 410-3, ML 1628, Pusa 1601, Pusa 1642, VGG-1, SML 1115, VGG-2, Pusa 9531, Pusa 1502, Pusa 1542, RMG 991, MH 539, MH 565, PLM 76, AKM 9904, COGG 1102, MH 560	
11	biological yield per plant (g)	Low (<40)	EC 393410, EC 470090, EC 393407, SML 1018, EC 251552, EC 30400, IPM 205-7, EC 399233, TMB 163, EC 581523, IPM 409-4, SML 1023	12
		Medium (40-60)	CH 210-3, NDMZ 13-11, HUM 27, HUM 7, IC 15276, SHIM 12-1, ML 759, MH 521, 2KM 101, ML 1108, GM- 9926 YMV, TMB 131, SML 1082, Pusa 1542, Pusa 0672, TMB 196, IPM 410-3, COGG 13-14, EC 470096, 2KM 138, 2KM 216, SML 668, KM 2328, COGG-8, KM 2241, 2KM 117, IPM 2-03, IPM 02-19, SML 1194, MH 560, PLM 24, AKM 9904, PLM 76, M 395, Pusa 1642, OUM 11-5, COGG 1102, Samrat, PANT M-5, NBPGR 150, ML 735, IPM 302-2, ML 776, Pusa Vishal, NDMZ 15-2, PLM 62, M 605, MH 565, IC 103196, 2KM 112, Pusa RATNA, COGG 13-19, IPM 06-5, EC 581523B, KM 2211, Pusa 1601, IPM 02-17, Pusa 0871, Pusa 1501, NDMZ 13-12, ADGG 13034, VGG-1, NDMZ 215-1, IC 39574, IPM 03-2, IPM 312-394, HUM 16, IPM 312-19, 2KM 111, Pusa 9531, PM 11-51, TRCM 155-1, RMG 991, ML 1451, PM 99-3, 2KM 115, IPM 02-14, Asha, SML 1781, PDM 96-262, Pusa 1502, SML 1115, Pusa 1142, 2KM 101, MH 539, ML 1907	86
		High (>60)	GANGA 8, Pusa 1141, MH 921, MH 98-1, MH 729, ML 2037, VGG-2, ML 1628	8
12	Seed yield per plant (g)	Low (<8)	EC 393407, EC 393410, EC 470090, GM- 9926 YMV, COGG-8, EC 399233, EC 251552, SML 1082, SML 668, TMB 196, EC 30400, CH 210-3, COGG 1102, COGG 13-14, COGG 13-19, HUM 27, OUM 11-5, ML 759, ML 735	19
		Medium (8-10)	Pusa 0672, NDMZ 215-1, NDMZ 13-11, PANT M-5, 2KM 216, PLM 76, VGG-1, KM 2328, TMB 163, SHIM 12-1, HUM 7, PLM 24, IC 103196, IC 15276, 2KM 138, ML 776, ADGG 13034, EC 581523, M 605, TMB 131, 2KM 101, PLM 62, Samrat, NBPGR 150, Pusa 1542, KM 2241, M 395, IC 39574, KM 2211, NDMZ 15-2, Pusa 0871, Pusa 1642, SML 1018, IPM 205-7, PM 99-3, Pusa RATNA, IPM 302-2, 2KM 112, 2KM 117, EC 581523B, 2KM 115, RMG 991, Asha, TRCM 155-1, ML 1108	45
		High (>10)	Pusa 1502, Pusa 1601, 2KM 111, Pusa 1141, SML 1115, IPM 409-4, SML 1781, Pusa Vishal, IPM 02-17, Pusa 1142, SML 1023, PDM 96-262, EC 470096, ML 1451, ML 1907, VGG-2, IPM 2-03, MH 521, NDMZ 13-12, IPM 02-19, IPM 02-14, PM 11-51, IPM 312-19, Pusa 9531, SML 1194, IPM 410-3, Pusa 1501, AKM 9904, MH 539, GANGA 8, MH 98-1, MH 921, IPM 06-5, HUM 16, ML 2037, MH 729, IPM 312-394, IPM 03-2, 2KM 101, MH 560, ML 1628, MH 565	42
13	Harvest Index (%)	Low (<15)	COGG-8, COGG 13-19, GM- 9926 YMV, COGG 1102, SML 668, NDMZ 215-1, TMB 196	7
		Medium (15-20)	VGG-1, SML 1082, EC 393407, OUM 11-5, COGG 13-14, ADGG 13034, ML 735, VGG-2, Pusa 1141, PANT M-5, IC 103196, IC 39574, PLM 76, EC 399233, PM 99-3, Asha, KM 2211, 2KM 115, M 605, Pusa 0871, CH 210-3, Pusa 1502, ML 776, Pusa 1142, RMG 991, SML 1115, ML 1907, 2KM 216, KM 2328, TRCM 155-1, ML 1628, PLM 24, EC 393410, PLM 62, SML 1781, HUM 27, MH 98-1, ML 759, PDM 96-262, ML 2037, MH 921, Pusa 0672, 2KM 111, MH 729, GANGA 8, NBPGR 150, NDMZ 15-2, Samrat, ML 1451, Pusa RATNA, EC 470090, 2KM 138, MH 539, EC 581523B, EC 251552, M 395, Pusa 1601, IPM 02-14, 2KM 112, KM 2241, Pusa 1642, IPM 02-17, SHIM 12-1, PM 11-51, EC 30400, IPM 302-2, IPM 312-19, Pusa 9531, TMB 131, NDMZ 13-12	70
		High (>20)	Pusa 1542, NDMZ 13-11, 2KM 101, 2KM 101, HUM 16, IC 15276, HUM 7, Pusa 1501, 2KM 117, Pusa Vishal, IPM 312-394, TMB 163, IPM 03-2, IPM 06-5, IPM 2-03, EC 581523, EC 470096, ML 1108, IPM 02-19, AKM 9904, SML 1194, IPM 410-3, MH 521, MH 565, IPM 205-7, MH 560, SML 1023, IPM 409-4, SML 1018	29

Conclusion

In present study all 13 morphological DUS descriptors showed trimorphic variation among all studied 106 genotypes of mungbean. This result indicates that there is a surprisingly large genetic diversity among these genotypes, which could allow the assignment of different morphological traits. These morphological DUS characterization data serve as a useful resource for the study of mungbean genotypes and creates opportunities for their use in traditionally as well as in molecular breeding for trait and gene identification, respectively. This significant variation, which, if used for detection and exploitation, could simplify the registration of the genotypes at PPVFRA, since these distinguishing features are found in the genotypes.

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