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Morphological Diversity and characterization of Mungbean (*Vigna radiata* L. Wilczek) Genotypes using Distinctiveness, Uniformity and Stability Descriptors

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ABSTRACT: The challenge in the study of crop diversity is to screen and characterize the germplasm for knowing the traits present in it. Therefore, the thirty mungbean [*Vigna radiata* (L.) Wilczek] genotypes collected from S.D.A.U. were morphologically characterized using PPV & FRA descriptors during *kharif*, 2019. Descriptors like, hypocotyl colouration, plant habit, time of flowering, stem colour, plant growth habit, leaf lobes, leaf vein colour, leaf colour, leaf size, flower colour, premature pod colour, pod position, plant height, pod curvature, pod colour, pod length, seed lustre, seed colour, seed size and seed shape showed sufficient variation among genotypes during different growth stages of the crop. UPGMA dendrogram was prepared by using similarity co-efficient. It revealed maximum similarity in LM-353 and LM-385 while, LM-584 showed most divergence with GP-229-B, No-223(1) and LM-1 genotypes. Thus, the contribution of this research will help the researchers to utilize the PPV & FRA descriptors for the purpose of registration, maintenance, protection and diversity study of the genotypes in mungbean.

Keywords: Diversity, DUS descriptors, Morphological characteristics, Mungbean, Similarity co-efficient, UPGMA Dendrogram, Variations.

INTRODUCTION

Indian vegetarian diet prefers pulses as the second choice next to cereal. Pulses are called as the vegetable for wealthy people and meat for the poor people due to its high protein content. But, per capita availability of pulses is only 42 g/person/day against the World Health Organization (WHO) recommendation of 80 g/person/day. The non-availability of high yielding varieties which can tolerate environmental fluctuations to greater extent is the major limiting factors for pulses production and productivity in our country. Among all the pulse in India, mungbean is the leading crop. Mungbean is a self-pollinated plant and having a cleistogamous flower. Greengram is a diploid which has 2n = 2x = 22 chromosomes. The center of origin for mungbean might be Hindustan and Central Asiatic region. It is also known as moong, mashbean, goldengram, greengram, greenbean and greensoy. Mungbean is extensively grown during kharif (under rainfed condition of semi-arid and arid regions of India) and during summer season (under irrigated condition). Southern and eastern regions of India cultivate mungbean in rabi season. Crop duration of moong 60 to 75 days (short duration). It has low input requirement, low moister requirement, wider adaptability. Root nodules of mungbean have *Rhizobium* which fix atmospheric nitrogen symbiotically.

Mungbean has high level of lysine but level of methionine and cystine (sulphur containing amino acids) are low (Jaiwal *et al.*, 2001). Apart from major nutritional value, mungbean also contain 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) (Anonymous, 2018). Genetic diversity is important for crop improvement as well as its conservation, evaluation and utilization (Anumalla *et al.*, 2015; Wang *et al.*, 2015). Also different light treatments, induce variability in *Vigna radiata* (Srivastava, 2020). An experiment was carried out to estimate the genetic parameters like variability, heritability and genetic advance, character association and path analysis for seven quantitative characters (Jyothsna *et al.*, 2016).

Information regarding parental germplasm is necessary for selection and it is possible by screening and characterizing the germplasm. Variety characterisation is done traditionally by first sowing the seeds in the field and then doing the grow out test to examine plants from vegetative to maturity stage. Till date, DUS descriptions of various cultivars are unknown. In case

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of mungbean gene pool, exhaustive characterization is helpful for development of superior or promising varieties. The desired characteristics of the ideal mungbean variety are resistant to diseases and insect pests, resistance to pod shedding, synchronous maturity, larger seeds, higher seed quality and yield.

According to PVP & FR Act (2001), Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA) have suggested to use DUS (Distinctiveness, Uniformity and Stability) descriptors for characterization of the lines for their protection and registration. For mungbean, draft national test guidelines for DUS testing have appropriate characteristics to compare candidate variety to the common varieties and obtained information is require while doing application (Singh et al. 2006). Thus, in our experiment, thirty genotypes were characterized using PPV & FRA descriptors to know the extent diversity present in these genotypes.

MATERIALS AND METHODS

Experimental site and material. Experiment was taken in *kharif*, 2019 at Agronomy Instructional Farm, S.D.A.U., Sardarkrushinagar. The investigation site represents typical sub-tropical climate include semi-arid and arid condition. Thirty genotypes of mungbean were selected from the enormous genetic resources available at the Pulses Research Station, S.D.A.U., Sardarkrushinagar.

Experimental details. The complete sets of 30 genotypes were planted in Randomized Block Design (RBD) with four replications. Plant spacing was 45 cm \times 10 cm. Each genotype was sown in a 3 m length (single row) plot.

Study of descriptors. All descriptors were selected and recorded as per guidelines to conduct DUS test by PPV and FRA (Anonymous, 2007). Total 23 descriptors were studied at various life stages of crop. Distinctiveness and uniformity of descriptors were recorded by four types of assessment methods. List of studied DUS descriptors, stages of observation and methods of assessment is given in Table 1.

Scoring as well as data analysis for diversity study. Data on 23 morphological characteristics were used to draw a single link dendrogram. NTSYSpc version 2.02i (Rohlf, 1997) was used for data analysis. Method of Sneath and Sokal (1973) were used to transform ordinal scale of data of morphological characteristics into binary characters depending on the variations available in each character. Scoring of '0' and '1' were given for absence as well as presence of phenotypes respectively. By using method of Jaccard (1908), the set of gathered data were used for cluster analysis which is depending on the values of similarity coefficient. To make dendrogram, SAHN (Sequential Agglomerative Hierarchical Nonoverlapping) clustering was done on similarity coefficient matrices gained from observations using the UPGMA (Unweighted Pair Group Method with Arithmetic Averages).

Sr. No.	DUS descriptors	Stage of observation	Method of assessment						
1.	Hypocotyl: Anthocyanin colouration	Cotyledons Unfolded	VS						
2.	Time of flowering	50% plants with minimum one open flower	VG						
3.	Plant: Habit	50 % flowering	VG						
4.	Plant: Growth habit	50 % flowering	VG						
5.	Stem: Colour	50 % flowering	VG						
6.	Stem: Pubescence	50 % flowering	VG						
7.	Leaflet: Lobes (terminal)	50 % flowering	VG						
8.	Leaf: Shape (terminal)	50 % flowering	VG						
9.	Leaf: Colour	50 % flowering	VG						
10.	Leaf: Vein colour	50 % flowering	VG						
11.	Leaf: Size (at 5 th node from the base)	50 % flowering	VG						
12.	Flower: Colour of petal (standard)	50 % flowering	VG						
13.	Pod: Colour of premature pod	Fully developed green pods	VG						
14	Plant: Height	Fully developed green pods	MS						
15.	Pod: Pubescence	Fully developed green pods	VS						
16.	Pod: Position	VG							
17.	Pod: Length (mature pod)	Harvest maturity	MS						
18.	Pod: Curvature of mature pod	Harvest maturity	VG						
19.	Pod: Colour	Harvest maturity	VG						
20.	Seed: Colour	Mature seeds	VG						
21.	Seed: Lustre	Mature seeds	VG						
22.	Seed: Shape	Mature seeds	VG						
23.	Seed: Size (weight of 100 seeds)	Mature seeds	MG						
VS	: Individual plants or parts of pla	nt were assessed by taking visual observat	ions						
VG	: Group of plants of parts of plants of each genotype were assessed by taking visual observations								
MS	: Observations were taken by measuring number of individual plants or parts of plants								
MG	: Single observations were taken by measuring a group of plants or parts of plants								

Table 1: List of DUS Descriptors, stages of observation and methods of assessment.

RESULTS AND DISCUSSION

Variation through DUS descriptors. Morphological characteristics give idea about the amount of genetic variability. Twenty-three DUS descriptors were recorded in 30 mungbean genotypes and variations were noticed in 20 descriptors (Table 2 and Plate I to Plate III). It shows the usefulness of these descriptors in differentiating the genotypes.

Anthocyanin colouration of hypocotyl was absent in seven genotypes and present in the remaining genotypes. This is the useful trait for differentiation and Intellectual property protection of genotypes. Mounika *et al.* (2020), Katiyar *et al.* (2008); Mukherjee and Pradhan (2002) had found similar results.

Genotype No-223(1), LM-1 and GM-4 were early flowering; genotype LM-584 and CM-512 were late flowering while rest of the genotypes were medium day flowering. Eight genotypes showed indeterminate plant habit and twenty-two genotypes showed determinate plant habit. Three types of growth habits were recorded at 50% flowering. Majority of the genotypes had erect growth habit.

Stem colour showed variation among the genotypes. The genotypes, PIMS-1, A-59-7, GP-229-B, SML-68, M.GP-124-B, LM-141, LM-578, No-223(1), LM-584, CM-512, LM-2, PS-10, LM-359 and GM-4 showed green stem colour while LM-389 exhibited purple stem colour. The other genotypes recorded green stem with purple splashes.

The descriptors, stem pubescence, leaf shape (terminal) and pod pubescence showed no variation among the genotypes. All the genotypes showed presence of stem and pod pubescence with ovate leaf shape indicating they are least useful in characterization for these genotypes. Similar result was obtained for stem pubescence and pod pubescence by Mounika *et al.* (2020).

Leaflet lobes were present in the genotypes, LAM-GG-127, LM-554, LM-584 and LM-359, while absent in other genotypes. The genotypes GP-229-B, M.GP-124-B, LM-141, MBC-5, LM-554, LM-578, No-223(1), LM-1, PS-10, TT8E \times 345 and LM-350 showed green leaf colour while remaining genotypes recorded dark green colour. Leaf vein colour showed three types. Genotype M.GP-124-B and GM-4 showed green leaf vein while other genotypes were divided into either greenish purple or purple leaf vein group.

Leaf size of the genotype, M.GP-124-B was small while, large leaf size was noticed in the genotypes, Guj-1, A-59-7, A-61-1, SML-68, LM-141, LM-584, CM-512, LM-389, LM-7, LM-359, TT8E \times 345, LM-385, LM-353, GM-4 and GAM-5. Rest of the genotypes showed medium leaf size.

Light yellow flower was noticed in Guj-1 and LM-141, while flowers of other genotypes were yellow colour. Jain *et al.*, (2002) showed the importance of flower characteristics in characterization of greengram genotypes.

Colour of premature pod was recorded when green pods were fully developed. Ten genotypes showed green colour pods while twenty genotypes showed green pods with pigmented suture.

Pod position was intermediate in LM-584 and CM-512, while rest of the genotypes showed above canopy pod position.

Plant height is a useful attribute and cultivars like GP-229-B, M.GP-124-B, LM-578, No-223(1), LM-1, PS-10, LM-359 and LM-34 Showed medium plant height (50 cm-70 cm) and rest of the genotypes had >70 cm height.

Pod colour of LM-34 was brown. MBC-5, No-223(1) and CM-512 showed black pods and the remaining genotypes showed blackish brown pods.

Curvature of mature pod was straight for the genotypes, SML-68, MBC-5, LM-584, LM-359 and LM-309 while other genotypes showed pods which were slightly curved at beak.

The genotypes, GM-4 and GAM-5 showed medium pod length (8-10 cm) while, other genotypes showed short pod length (<8 cm).

Further, yellow seed colour was noticed in MBC-5. Genotypes, A-61-1, GP-229-B and LM-389 showed mottled seed colour and rest of the genotypes showed green seeds.

Four cultivars, *viz.* LM-584, LM-389, LM-34 and LM-309 exhibited dull type seed lusture and rest 26 genotypes showed shiny seeds.

Seed shape is a useful trait. Four varieties (No-223(1), LM-584, LM-389 and LM-34) exhibited drum shaped seeds and others were oval shaped.

Weight of 100 seeds were <3 g for PIMS-1, LAM-GG-127, M.GP-124-B, LM-141, LM-554, LM-578, LM-584, LM-359, LM-34, LM-385, LM-350 and LM-353 while, remaining genotypes showed 3 to 5 g seed weight.

Result revealed sufficient amount of variability based on DUS descriptors. Results were supported by Kaur *et al.* (2017) for stem pubescence, leaf colour, flower colour, pod pubescence, pod colour and seed lustre; with the results of Mounika *et al.* (2020) for leaflet lobe, premature pod colour, leaf shape, pod position, pod pubescence, pod length, seed lustre, seed shape and seed size; with the results of Katiyar *et al.* (2008) for anthocyanin colour, terminal leaf shape, growth habit, stem colour, plant habit, stem pubescence, leaf colour, leaf size, leaf vein colour, plant height, time of flowering and flower colour.

Study of diversity by constructing single link dendrogram using DUS descriptors. Similarity coefficient of Jaccard were estimated on the basis of 23 DUS descriptors ranged from 0.2703 (between LM-584 and GP-229-B, LM-584 and No-223(1), LM-584 and LM-1) to 1.000 (between LM-353 and LM-385). Similarity indices 1.000 indicated most similar genotypes while, LM-584 showed most divergence with GP-229-B, No-223(1) and LM-1 genotypes.

Sr. No.	Name of genotypes	Hypocotyl: Anthocyaninc olouration	Time of flowering	Plant: Habit	Plant: Growth habit	Stem: Colour	Stem: Pubescence	Leaflet: Lobes (terminal)	Leaf: Shape (terminal)	Leaf: Colour	Leaf: Vein colour	Leaf: Size (at 5 th node from the base)	Flower: Colour of petal (standard)	Pod: Colour of premature pod	Plant: height	Pod: pubescence	Pod: Position	Pod:Leng h (mature pod)	t Pod: Curvature of mature pod	Pod: Colour	Seed: Colour	Seed: Lustre	Seed: Shape	Seed: Size (weight of 100 seeds)
1.	Guj-1	1	1	0	2	1	1	0	1	1	1	2	1	0	2	1	0	0	1	1	1	0	0	1
2.	PIMS-1	1	1	1	0	0	1	0	1	1	1	1	0	1	2	1	0	0	1	1	1	0	0	0
3.	A-59-7	1	1	1	0	0	1	0	1	1	2	2	0	0	2	1	0	0	1	1	1	0	0	1
4.	A-61-1	1	1	1	0	1	1	0	1	1	1	2	0	1	2	1	0	0	1	1	2	0	0	1
5.	LAM-GG-127	1	1	0	0	1	1	1	1	1	2	1	0	1	2	1	0	0	1	1	1	0	0	0
6.	GP-229-B	1	1	0	1	0	1	0	1	0	1	1	0	0	1	1	0	0	1	1	2	0	0	1
7.	SML-68	0	1	0	0	0	1	0	1	1	1	2	0	0	2	1	0	0	0	1	1	0	0	1
8.	M.GP-124-B	0	1	0	0	0	1	0	1	0	0	0	0	0	1	1	0	0	1	1	1	0	0	0
9.	LM-141	0	1	1	2	0	1	0	1	0	1	2	1	0	2	1	0	0	1	1	1	0	0	0
10.	MBC-5	1	1	0	0	1	1	0	1	0	2	1	0	1	2	1	0	0	0	2	0	0	0	1
11.	LM-554	1	1	0	1	1	1	1	1	0	2	1	0	1	2	1	0	0	1	1	1	0	0	0
12.	LM-578	1	1	0	0	0	1	0	1	0	1	1	0	1	1	1	0	0	1	1	1	0	0	0
13.	No-223 (1)	0	0	0	0	0	1	0	1	0	1	1	0	0	1	1	0	0	1	2	1	0	1	1
14.	LM-584	1	2	1	0	0	1	1	1	1	2	2	0	0	2	1	1	0	0	1	1	1	1	0
15.	CM-512	0	2	1	1	0	1	0	1	1	1	2	0	1	2	1	1	0	1	2	1	0	0	1
16.	LM-2	1	1	0	0	0	1	0	1	1	1	1	0	1	2	1	0	0	1	1	1	0	0	1
17.	LM-1	1	0	0	0	1	1	0	1	0	2	1	0	1	1	1	0	0	1	1	1	0	0	1
18.	LM-389	1	1	0	0	2	1	0	1	1	1	2	0	1	2	1	0	0	1	1	2	1	1	1
19.	PS-10	1	1	0	0	0	1	0	1	0	1	1	0	1	1	1	0	0	1	1	1	0	0	1
20.	LM-7	1	1	1	0	1	1	0	1	1	2	2	0	1	2	1	0	0	1	1	1	0	0	1
21.	LM-359	1	1	0	0	0	1	1	1	1	1	2	0	1	1	1	0	0	0	1	1	0	0	0
22.	LM-34	1	1	0	1	1	1	0	1	1	1	1	0	1	1	1	0	0	1	0	1	1	1	0
23.	TT8E × 345	1	1	1	0	1	1	0	1	0	2	2	0	1	2	1	0	0	1	1	1	0	0	1
24.	LM-385	1	1	0	0	1	1	0	1	1	2	2	0	1	2	1	0	0	1	1	1	0	0	0
25.	LM-350	1	1	0	0	1	1	0	1	0	1	1	0	1	2	1	0	0	1	1	1	0	0	0
26.	LM-353	1	1	0	0	1	1	0	1	1	2	2	0	1	2	1	0	0	1	1	1	0	0	0
27.	Chaklama-2	1	1	0	1	1	1	0	1	1	1	1	0	1	2	1	0	0	1	1	1	0	0	1
28.	LM-309	1	1	0	0	1	1	0	1	1	1	1	0	0	2	1	0	0	0	1	1	1	0	1
29.	GM-4	0	0	0	0	0	1	0	1	1	0	2	0	0	2	1	0	1	1	1	1	0	0	1
30.	GAM-5	1	1	0	1	1	1	0	1	1	2	2	0	1	2	1	0	1	1	1	1	0	0	1
		0: Absent [Plate I-A]	0: Early (<40 days)	0: Determinate [Plate I-C]	0: Erect [Plate I-E]	0: Green [Plate I-A]	0: Absent	0: Absent [Plate I-L]	0: Deltoid 1: Ovate [Plate I-N and O]	0: Green [Plate I-P]	0: Green [Plate I-Q]	0: Small [Plate II-A]	0: Yellow [Plate II-B]	0: Green [Plate II-C]	0: Short (<50 cm)	0: Absent	0: Above canopy [Plate II-D]	0: Short (<8 cm)	0: Straight [Plate II-F]	0: Brown [Plate II-I]	0: Yellow [Plate II-L] 1: Green [Plate II-M]	0: Shiny [Plate II-O]	0: Oval [Plate II-Q]	0: Small (<3g)
		1: Present [Plate I-B]	1: Medium (40 to 50 days) 2: Late (>50 days)	1: Indeterminate [Plate I- D]	1: Semi-erect [Plate I-A] 2: Spreading [Plate I-A]	1: Green with purple [Plate 1-F] 2: Purple [Plate 1-G]	l: Present [Plate]-K]	1: Present [Plate I-M]	2: Lanceolate 3: Cuneate	1: Dark green [Plate I-P]	1: Greenish purple [Plate I-R] 2: Purple [Plate I-S]	1: Medium [Plate II-A] 2: Large [Plate II-A]	1: Light yellow [Plate II-B]	1: Green with pigmented suture [Plate II-C]	1: Medium (50cm-70 cm) 2: Long (>70 cm)	1: Present [Plant II-H]	1: Intermediate [Plate 1-E] 2: Not visible	1: Medium (8-10 cm) 2: Long (>10 cm)	1: Slightly curved at beak [Plate II-G] 2: Curved	1: Blackish brown [Plate IL-J] 2: Black [Plate II-K]	2: Mottled [Plate II-N] 3: Black	1: Dull [Plate II-P]	1: Drum shaped [Plate II-R]	1: Medium (3-5 g) 2: Large (>5 g)

Table 2: Study of DUS descriptors for thirty mungbean genotypes.

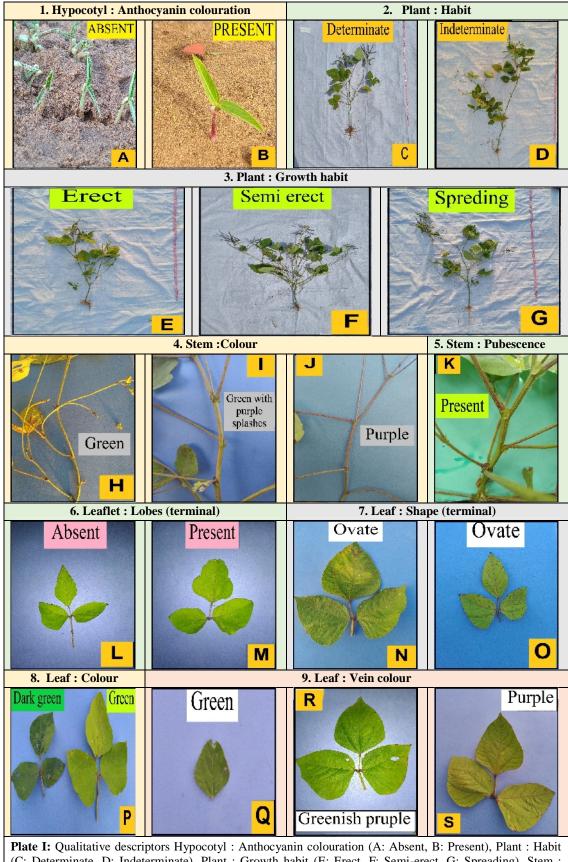
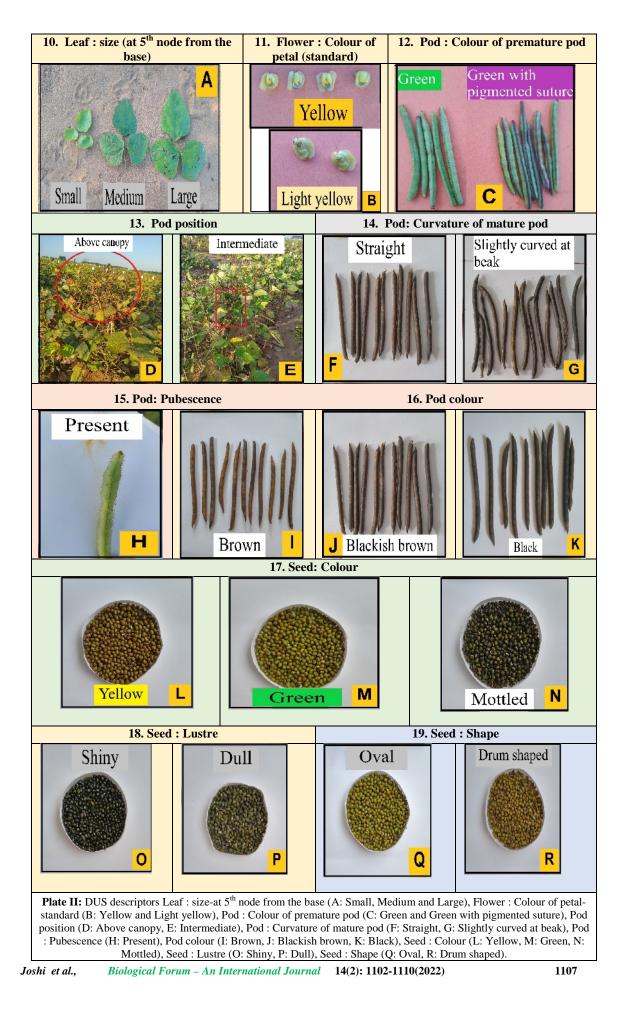


Plate I: Qualitative descriptors Hypocotyl : Anthocyanin colouration (A: Absent, B: Present), Plant : Habit (C: Determinate, D: Indeterminate), Plant : Growth habit (E: Erect, F: Semi-erect, G: Spreading), Stem : Colour (H: Green, I: Green with purple splashes, J: Purple), Stem : Pubescence (K: Present) Leaflet : Lobesterminal (L: Absent, M: Present), Leaf : Shape-terminal (N and O: Ovate), Leaf : Colour (P: Dark green and Green), Leaf: Vein colour (Q: Green, R: Greenish purple, S: Purple).





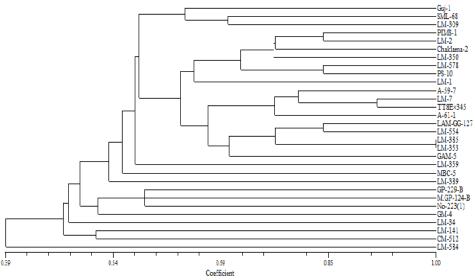


Fig. 1. Distribution of genotypes based on the UPGMA dendrogram of 23 DUS descriptors.

 Table 3: Distribution of genotypes based on the clusters from UPGMA dendrogram from 23 DUS descriptors.

Cluster Sub-cluster			Genotypes	No. of genotypes
A	A1	A1:1	Guj-1, SML-68, LM-309, PIMS-1, LM-2, GM-4, Chaklama-2, LM- 350, LM-578, PS-10, LM-1, LM-7, A-59-7, TT8E×345, A-61-1, LAM-GG-127, LM-554, LM-385, LM-353, GAM-5, LM-359, MBC- 5, LM-389, GP-229-B, M.GP-124-B, No-223(1)	26
		A1:2	LM-34	01
	A2	A2:1	LM-141	01
	AL	A2:2	CM-512	01
В		-	LM-584	01

Waniale *et al.* (2014) found 90 to 100 per cent similarity among the genotypes which shows conformity of result.

The distribution of all the genotypes based on the clusters from UPGMA dendrogram is shown in Fig. 1 and Table 3. Clusters A and B were two main clusters with 39 % similarity. Cluster A was partitioned into A2 and A1 sub-clusters (47 % similarity among them). Sub-cluster A1 was again partitioned into A1:1 (contains 26 genotypes) and A1:2 (contains 1 genotype) sub-clusters with 48 % similarity. Sub-cluster A2 was partitioned into sub-clusters.

A2:1 (contains 1 genotype) and A2:2 (contains 1 genotype) with 52 % similarity. Cluster B had 1 genotype and did not contain any sub-cluster. The results were in accordance with Waniale *et al.* (2014) (studied 35 genotypes and found 5 clusters).

CONCLUSION

Overall, present preliminary characterization of these genotypes helped to use them in future study as a reference genotype and to group them into various categories for specific trait. Also, diversity analysis showed presence of diversity in the genotypes and can be used for future breeding work. Acknowledgement. Special thanks to Pulse research station for providing material and C. P. College of Agriculture along with Directorate of Research, S.D.A.U., Sardarkrushinagar for providing research facility. Conflict of Interest. None.

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