Journal of Agriculture and Food Sciences
Volume 22, Number 2, October 2024, pp 51- 71 .

CHARACTERIZATION OF 20 MUNG BEAN (*VIGNA RADIATA* L.) GENOTYPES IN OWERRI, SOUTH EASTERN NIGERIA

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ABSTRACT

The problem of protein deficit in the diets of individuals in South-eastern Nigeria led to exploring affordable plant-based protein sources, hence, the introduction of Mung bean (Vignaradiata L.) to curb this issue. Mung bean seeds were sown on ridges and the experiment was laid out in Randomized Complete Block Design replicated thrice. Data generated on agronomical and morphological characters were subjected to Analysis of Variance (ANOVA) which revealed significant differences (p<0•05) amongst characters and Duncan's Multiple Range Test (DMRT) was utilized for the separation of means. Results showed higher variations existed in agronomic characters like: days to 50% seedling emergence, seedling vigour, number of pod cluster, plant height at maturity, 10 pod weight(g), 100 seed weight(g), seed yield/plant(g), yield/plant(g) and yield in kg/ha. Considerable variations subsisted for characters including: number of primary branches, plant height at maturity, pod length, and number of seeds per pod. However, low to no variation was present in days to 50% seedling emergence, days to 50% flowering, days to first pod maturity, primary leaflet length and width and terminal leaflet length and width. Euclidean DistanceCluster Analysis grouped the genotypes in six clusters; Cluster IV had maximum genotypes (six), while Clusters V and VI possessed only one genotype in each. The closest intra-cluster distance was observed between Tvr1172 and Tvr125 and the maximum inter-cluster distance existed between Tvr10 and Tvr161. We recommend that more research should be done in other agricultural areas to give more universally acceptable findings.

Keywords: Agronomic, characters, cluster, morphological, variations
https://dx.doi.org/10.4314/jafs.v22i2.5

INTRODUCTION

Mung bean (*Vignaradiata*L.) alternatively called green gram, classified in the order Fabales; family Fabaceae is economically the most important crop of the genus Vigna, and is characterized by rapid maturation under warm conditions, low water requirement and excellent soil fertility enhancement via nitrogen fixation (Yagoob et al., 2014). Achieving a gain in yield through breeding requires collection, characterization, and evaluation of germplasm, as the first step in identifying genotypes with the desired characteristics. Exploring the phenotypic diversity is a prerequisite in selecting suitable parents for genetic improvement of crops in a plant breeding program (Abna et al., 2012; Basnet et al., 2014). Characterizing germplasm facilitates the formation of groups with like traits, subsequently providing knowledge about those traits that may be used to differentiate the genotypes from the other. Some of the agro-morphological traits may be used as morphological marker in crop improvement and the grouping of genotypes based on these traits can be easily detected by the visual observation and used in mung bean breeding program for improving the seed physical quality. Faruque, et al., (2003) in his research stated that the plant characteristics of mung bean such as plant height, leaf size and leaf inclination angle are also important factors for intercropping with cereals.

In Southeast Nigeria, mung bean is newly introduced to meet up protein requirements in people's diets. Besides, there is limited information on the genetic diversity of mung bean germplasm due to limited genomic research done as compared to other Fabaceae family species. Studies and breeding are still carried on to ascertain the best mung bean varieties for consumption and market value. This led to the broad objective of this study; the characterization of twenty mung bean genotypes in Southeast Nigeria. As the key objectives of this study were to**;** determine the nature of phenotypic characters among twenty mung bean genotypes, evaluate yields and cluster these genotypes for easy selection of parents for future mung bean breeding.

MATERIALS AND METHODS

The experiment was conducted at the Teaching and Research Farm of the Imo State University, Owerri, Nigeria. The mung bean seeds sourced from International Institute of Tropical Agriculture (IITA) Ibadan were planted in an open field measuring 25m x 18m. The soil was Sandy loam with 80.80% sand, 11.20% clay and 8.00% silt. The pH was moderately acidic (5.67). The hydrogen content of the site was 0.60cmol/kg while the available phosphorus content was 6.16ppm. The contents of calcium, aluminium, sodium, potassium and magnesium were 2.45cmol/kg, 0.20cmol/kg, 0.18cmol/kg, 0.20cmol/kg and 2.36cmol/kg respectively. The Organic matter was 1.14%, organic carbon 0.66% and the total nitrogen of the site 0.06%. Total exchangeable acidity in the soil was 0.80cmol/kg and the CEC 5.49cmol/kg. The soil had the optimum pH for mung bean cultivation as stated by Mogotsi (2006) to be 5 to 8. The seeds were sown with 30cm x 50cm spacing on ridges measuring 5m long with 0.5m space between ridges and 1m gap between blocks and the experiment laid out in Randomized Complete Block Design (RCBD) with three replications. Each replication consisted of twenty-five ridges with each having an area of 125m^2 (i.e. 25m x 5m). Poultry manure was applied (10tons/hectare) at 2weeks after planting. Table 1 shows the data collected on 10 randomly selected plants based on forty-four parameters and mode of collection as sourced from the National Plant Genetic Resources Laboratory (NPGRL) descriptors (2018).

Statistical Analysis

The data obtained was subjected to Analysis of Variance (ANOVA) and the significant means were separated using the Duncan's Multiple Range Test (DMRT) at $p<0.05$. The genotypes were further grouped using Euclidean Distance Cluster Analysis to identify groups of morphologically similar and dissimilar accessions for selection as parents in breeding programs.

RESULTS AND DISCUSSION

Classification and Grouping Based on Phenotypic Characters.

Agro-morphological characteristics provide the primary information needed about the genetic differences existing among genotypes. Thirty morphological descriptors were observed and recorded on 20 mung bean genotypes and variations were noticed in twenty-one descriptors. This depicts the relevance of descriptors in identifying the distinctive between genotypes.

Purple pigmentation on the hypocotyl as a result of anthocyanin (Plate I) was present in 10 genotypes with purple coloration and absent on other 10 genotypes with green coloration; this corresponds with Mounika et al., (2020), and Mukherjee and Pradhan (2002) who had found similar reports. Dhruv et al., (2022) stated that anthocyanin colouration of hypocotyl is the useful trait for differentiation and Intellectual property protection of genotypes. The leaf colour of the genotypes were grouped into different categories as light green (four genotypes), intermediate green (fifteen genotypes) and dark green (one genotype) (Table 2). The flower colour (Table 2) was taken on the keel; where two varieties showed white and eighteen varieties greenish-yellow, the calyx; where seventeen genotypes showed greenish purple and three genotypes depicted green colour, the corolla; where fifteen genotypes showed greenish purplish yellow, two showed yellowish green and greenish yellow and only one showed yellow, the flower wing and flower standard colour; where eleven genotypes showed yellowish green, seven showed greenish yellow and two showed yellow. Jain et al., (2002) explained the importance of flower characteristics in characterization of Mung bean genotypes. With regards to petiole colour, green petiole colour was observed in three genotypes (Table 2), green and purple spots on fourteen genotypes and greenish-purple on three genotypes, similar results were observed by Patel et al., (2019) in their research; "Characterization of Mung Bean Genotypes Based on Morphology".

Primary and terminal leaf shapes observed for all genotypes were ovate-lanceolate and deltoid respectively. Leaf pubescence and senescence were present in all the genotypes evaluated. All genotypes showed asynchronous flowering period i.e., period greater than 30 days.

Variation spotted for several pods characters (Plate I and II) such as colours of mature and immature pods, where eighteen genotypes showed light green and two genotypes dark green for immature pod colour. Tvr133 was distinct for brown mature pod colour, seven genotypes were both brown and black and twelve genotypes showed black colour only, similar results were recorded on mature pod colour by Dhruv et al., (2022). Tvr10 was distinct in pubescence on pods where it showed a glabrous pod surface (i.e., absence of pubescence) while others showed variable amount of pubescence on pod. All the twenty mung bean genotypes evaluated exhibited no variation for colour of ventral suture on immature pods, pod cross section, pod beak shape as well as on pod constriction between seeds. Two genotypes recorded medium pod curvature as the other eighteen where least curved. All twenty mung bean genotypes can be differentiated based on their pod attachment to peduncle as twelve genotypes showed pendant attachment, seven genotypes showed sub-erect attachment and only Tvr181 showed erect attachment. Singh et al. (2014) and Kaur et al. (2017) made corresponding categorization in mung bean; likewise, Bayahi and Rezgui (2015) in chickpea. Also, Das et al. (2014) in french bean, then, Kumar and Shrikant (2016) in cowpea and finally, Kanaka et al., (2015) in horse gram.

Nine genotypes displayed shiny type on seed lustre (Plate I) while the rest showed dull seeds. Mottling on seeds was noticed on Tvr156 only and other 19 genotypes (Table 2) showed no mottling. Seed colour (Plate I) was grouped into light green (fifteen genotypes), dark green (two genotypes) and yellow (three genotypes). Relatable reports of exploring the differences in seed characters in green gram was presented by Khajudparn and Tantasawat (2011).

The 20 genotypes all exhibited an erect plant growth habit, Rupinder et al., (2017) showed similar results in his experiment on characterization of mung bean varieties using morphological and molecular descriptors. None of the 20 mung bean genotypes evaluated showed any variation for branching pattern and growth pattern as all possessed determinant growth pattern and branched all over the main stem (Plate II); this indicates these morphological characters are not useful in the differentiating these genotypes. While Tvr112 showed minimum twining (Plate II), it was prominent in Tvr181. Other genotypes showed no twining; this presents an easiest way to distinguish Tvr181 and Tvr112 from other genotypes by mere visual observation. Genotypes Tvr10 and Tvr118 were distinct amongst the 20 genotypes with intermediate raceme position (Plate II) while others where above the canopy.

Tvr139 had the highest yield with 824kg/ha, followed by Tvr1166 while Tvr111 had the lowest yield. There was clear variation for the yield in kg/ha for the mung beans studied (Table 5)

Mean Values of Morphological and Agronomic Characters of Genotypes.

Table 3, table 4 and table 5 depict the mean values of the agronomic characters evaluated on 20 mung bean genotypes. There were significant differences ($p<0.05$) observed among the mung bean genotypes.With respect to days to 50% seedling emergence. All varieties had means of 4.00 except Tvr105 and Tvr1172 with means of 5.00, showing emergence of their seedlings after five days of planting. Notable differences ($p<0.05$) prevailed in the means of all twenty genotypes with respect to seedling vigour. The means ranged between 4.33-7.00 with two varieties (Tvr111 and Tvr161) having the smallest mean while nine varieties (Tvr10, Tvr156, Tvr52, Tvr177, Tvr105, Tvr100, Tvr125, Tvr152 and Tvr1172) with highest mean 7.00.

The results pertaining to the terminal leaflet length showed considerable significant difference ($p>0.05$) among the means of the genotypes. The means ranged between 3.00-5.00 with Tvr133, Tvr118 and Tvr181 had the least mean (3.00) and the rest of other genotypes had means of 5.00. However, terminal leaflet width showed no significance difference ($p>0.05$) among the genotypes. Results showed significant differences ($p<0.05$) among the genotypes on number of clusters as Tvr111 with the lowest mean of 3.33 which was significantly different from Tvr139 and Tvr1166 containing highest number of pod cluster (5.67). Tvr161 had the smallest mean of 4.00, followed by Tvr52 (4.33) and Tvr10 with the highest mean of 8.00 on number of primary branches.

Results pertaining to plant height varied among the genotypes as the mean ranged between 38.00-85.00. Tvr161 had the smallest mean of 38.00 while Tvr10 with the highest mean of 85.00. With respect to days to 50% flowering, ANOVA results showed significant differences ($p<0.05$) on days to 50% flowering among the genotypes. Their means ranged between 36.67-55.00 with Tvr100 having the lowest mean (36.67) which was significantly different from Tvr181 with the highest mean (55.00). In days to first pod maturity, quick maturity was in Tvr118 with lowest mean of 53.00 is significantly different from Tvr166 with the highest mean (79.67).

Furthermore, results on pod different pod characters showed significant differences in Pod length, mean ranged between 7.00-9.33. Five genotypes (Tvr166, Tvr100, Tvr158, Tvr125 and Tvr139) had the lowest mean value (7.00) and is significantly different from Tvr10 and Tvr1172 which had the highest mean value (9.33). Also, number of seeds per pod showed that there was significant difference ($p<0.05$) in the 20 mung bean genotypes evaluated. Tvr118 with lowest mean (8.67) is significantly different from Tvr10, Tvr125 and Tvr1166 with the highest mean value (14.00). Variabilities were evident on 10 pod weight with mean range of 4.67-8.67 and Tvr100 showed the highest mean value (8.67). Consistent results were observed in seed characters recorded (100 seed weight and seed yield per plant) as they displayed considerable differences (Table 5). Results obtained with respect to yield per plant showed significant differences ($p<0.05$) between the genotypes evaluated, while Tvr111 had the lowest mean value, Tvr139 showed the highest mean value. Consequently, in exploring yield in kg/ha, significant differences among the genotypes evaluated. The mean range recorded was 380-824.33 and Tvr111 had lowest mean value while Tvr139 with the highest mean value.

Euclidean Distances and Dendrogram Representation for all 20 Genotypes.

Cluster analysis grouped the 20 genotypes in clusters and sub-clusters of closely related morphological and genetically similar accessions and also in closely linked genotypes (Fig.1). In the quest to choose for parents for a breeding program, genotypes will be chosen based on how close they are linked or how dissimilar they are in morphology and genes depending on the aim of the breeder. From the dendrogram (Fig 1) Tvr1172 and Tvr125 showed the closest linkage. Followed by Tvr125 and Tvr152. However, the farthest linkage existed between Tvr10 and Tvr161, followed by Tvr10 and Tvr139.

CONCLUSION

Statistical information from this research pointed that yield and its related characters like number of pod clusters, number of primary branches, plant height, number of seeds per pod, pod length, 10 pod weight, 100 seed weight, seed yield/plant, yield/plant and yield in kg/ha, represented as the important characters for classification of significant diversity among the tested germplasm. Win et al (2020) also showed relatable investigations. The highest coefficient variation was observed in yield per plant (33.50%) followed by seed yield per plant (30.66%), 100 seed weight (24.21%). Moderate coefficient variation was found in 10 pod weight (20.70%), Yield in kg/ha (20.74%), Seedling vigour (20.42%), Number of pod clusters (18.87%), Plant height at maturity (14.58%), Number of primary branches (13.59%), pod length (12.53%), Number of seeds per pod (11.84%). Days to 50% flowering and Days to first mature pod which are represented as low variability among tested mung bean germplasm with the coefficient of variation of 2.12% and 1.18% respectively. Many research findings were similar with this finding including: Singh et al., 2014, Shyamalee et al., 2016, Hapsari et al., 2018, and Win et al., 2020. It should not be neglected that environmental factors both soil and climatic environments have influence on the outcome of some morphological characters and we recommend that more research should be carried out on the genotypes in different seasons or in a controlled environment to compare the outcome of characters.

Table 2 including data on the phenotypes serves as a knowledge repository for plant breeders to derive information from on characters pertaining any genotype recorded that have interest in for subsequent future breeding programs. For the best yield and profit maximization, which is the primary aim of commercial farmers, characters of genotypes with maximum yields, number of seeds per pod and number of pod cluster should be put into consideration during selection.

We recommended that more research should be carried out in many other agricultural areas including other universities in Owerri and surroundings, also in different local governments in Imo state and within other states in the Southeastern Nigeria so as to give these findings on mung bean introduction to the Southeast wider or more universal acceptance. Research on pests and diseases of mung bean and their effects is highly recommended to be carried out due its high negative impact on the yield of the genotypes explored in this study and genotypes with higher pod and leaf pubescence be put into consideration as they possess high tendencies to repel pests attack.

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Table 1: Parameters, Period and Mode of Data Collection

Parameter	Period recorded	Code/Mode of Record
Days to 50% seedling emergence	From sowing to 50% emergence	Visual observation. Data recorded in days
Hypocotyl colour	10 days after emergence	Visual observation. **Code**: 1.Green 2.Green-purple 3.Purple 4.Dark Purple 5.Mixed
Seedling vigour	15 days after emergence	Visual observation. **Code**: 3.Poor 5.Intermediate 7.Vigorous
Primary leaf shape	3 weeks after planting	Visual observation. **Code:** 1.Ovate-lanceolate 2.Lanceolate 3.Ovate 4.Lineate. (fig 3.2)
Primary leaf length and width	3 weeks after planting	Measured in cm **Code for length;** 3.Short(<2.0cm)5.Intermediate(2.0-3.0cm) 7.Long(>3.0cm) **For width;** 3.Narrow(<0.4cm) 5.Intermediate(0.4-1.0cm) 7.Broad(>1.0cm)
Growth habit	When 1st pod changes colour	**Code:** 1.Erect (straight with prominent main stem with few branches ascend. 2.Semi-erect main stem less prominent; branches do not touch ground.
Growth pattern	When 1st pod changes colour	**Code:**1.Determinate apical bud of main stem reproductive 2.Indeterminate
Twining tendency	When 1st pod changes colour	**Code:** 0.None 3.Slight 5.Intermediate 7.Pronounced
Leaf Colour	Intensity of green color of trifoliate leaves at50% flowering	**Code:** 3.Lightgreen 5.Intermediate green 7.Darkgreen 9.Other
Leafiness	At 50% flowering	**Code:** 3.Sparse main stem easily 5.Intermediate 7.Abundant very leafy
Terminal leaflet length and width	Recorded for the leaf on the 4th node	**Code for length:** 3.Short(<10cm)5.Intermediate(10-13cm)7.Long(>13cm) **For width:** 3.Narrow(<2.6cm) 5.Intermediate(2.6-5.5cm)7.Broad(>5.5cm)
Terminal leaflet shape	Recorded for the leaf on the 4th nod	**Code:** 1.Deltoid 2.Ovate 3.Ovate-lanceolate 4.Lanceolate 5.Rhombic 6.Obovate 7. Others, specify.

Leaf pubescence		Observed by feeling with fingers. **Code:** 1.Glabrous 3.Verysparsely pubescent 5.Puberulent sparsely pubescent7.Moderately pubescent 9.Densely pubescent
Petiole colour		**Code:** 1.Green 2.Green with purple spots 3.Greenish purple 4.Purple 5.Dark purple 6.Other specify
Number of primary branches	When first pod changes colour.	An Only pod-bearing branch whose origin is in the leaf axils on the main stem is counted.
Branch length	When 1st pod changes colour	The longest branch is measured in cm
Branching pattern	When 50% pod have dried	**Code:** 1.Basal 3.Central 5.Top 7.Allover
Leaf senescence	When 50% pods have dried	Visual observation. 0.No visible senescence 3.Slight visible senescence 5.Moderate senescence 7.Conspicuous current senescence
Plant height	When 50% pods have dried	Mean height of 10 randomly selected plants are taken in cm
Days to 50% flowering	From sowing to stage when 50% of plants have begun to flower	Visual observation and data recorded in days
Flower colour	During flowering the calyx, corolla, wing, keel and standard colours of freshly opened flowers are taken	**Code for calyx:**1.Green 2.Purplish green 3.Greenish purple 4.Yellow green 5.Purple **For corolla:** 1.Yellow 2.Greenishyellow 3.Yellowish green 4.Greenish-purplish yellow 5. Other specify **For wing:** 1.Yellow 2.Greenish yellow 3.Yellowish green 4.Greenish-purplish yellow 5. Other specify **For keel:** 1.Yellow3.Greenish yellow5.Greenish-purplish yellow 7.Other specify **For standard colour:** 1.Yellow 2.Greenish yellow 3.Yellowish green 4.Greenish-purplish yellow 5. Other specify
Flowering period	From beginning to the end of flowering	**Code:** 1.Asynchronous(>30days) 3.Intermediate(15-30days) 5.Synchronous(<15days)
Raceme position	When 1st pod changes colour	**Code:** 1.Mostly above canopy 2.Intermediate 3.No pods visible above canopy
Pod attachment to peduncle	When pods are full grown	**Code:** 3.Pendant 5.Sub-erect 7.Erect

Immature pod colour		**Code;** 1.Light green 3.Darkgreen 5.Other(specify)
Colour of ventral suture on immature pod		**Code:** 1.Lightgreen 3.Darkgreen 5.Purple 7.Other specify
Days to first mature pod	From sowing to days when 50% of plants have mature pods	Counted and recorded in days
Mature pod colour		**Code:** 1.Straw 2.Tan 3.Brown 4.Brown and black 5.Black 6.Other specify
Pod pubescence	When 1st pod changes colour	Observed by feeling with finger. **Code:** 0.Glabrous3.Puberulent sparsely pubescent 5.Moderately pubescent 7.Densely pubescent
Pod length	After harvest	Mean length of 10 randomly selected mature pods measured in cm
Number of cluster	During harvest	Mean number of clusters having at least one fully grown pod at harvest including both main stem and branches
Pod cross section:	When pods are fully grown	**Code:** 1.Semi-flat 2.Round
Pod beak shape	When pods are dried	**Code:** 1.Hook 2.Knob3.Pointed
Constriction of pods between seeds	Between seeds of mature pods	**Code:** 0.Absent 1.Present
Pod curvature	When pods are fully grown	**Code:** 1.Least curved 3.Medium 5.Most curved
Number of seeds per pod	After harvest when mature pods are opened	Mean number of seeds for 10 randomly selected pods are recorded
Seed shape	After harvest	**Code:** 1.Globose 2.Ovoid 3.Drum-shaped 4.Other (fig 3.3)
Seed colour	After harvest	**Code:** 1.Lightgreen 2.Darkgreen 3.Green-yellow4.Yellow 5.Brown 6.Black 7.Grayishgreen 8.Mottled light brown
Mottling on seed	After harvest	**Code:** 1.Absent 2.Light 3.Medium 4.Heavy.
Lustre on seed surface	After harvest	**Code:** 0.Absent(dull) 1.Present(shiny)
10 pod weight	After harvest	Weight of 10 randomly selected pods recorded in grams
100 seed weight	After harvest	Weight of 100 randomly selected seeds recorded in grams
Yield per plant:	After harvest	Mean weight to fall harvested pods of 10 plants after being dried to appropriate moisture content
Yield per hectare	After harvest	Yield in gram converted to kg/ha

Table 2 Classification and grouping of 20 mung bean genotypes based on morphological characters using descriptors.

Characters	Descriptors	Number of Genotypes	Name of genotypes
Hypocotyl colour	Green	10	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112.
	Purple	10	Tvr10, Tvr118, Tvr181, Tvr166, Tvr100, Tvr125,Tvr133,Tvr139,Tvr1166,Tvr1172.
Growth habit	Erect	20	All genotypes.
Growth pattern	Determinant	20	All genotypes.
Twining tendency	None	18	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr10, Tvr118, Tvr166, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166,Tvr1172.
	Intermediate	1	Tvr112.
	Pronounced	1	Tvr181.
Primary leaf shape	Ovate-lanceolate	20	All genotypes
Terminal Leaflet shape	Deltoid	20	All genotypes
Leaf colour	Light green	4	Tvr10, Tvr156, Tvr105, Tvr111
	Intermediate green	15	Tvr52, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr112,Tvr118,Tvr166, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172
	Dark green	1	Tvr181
Leafiness	Sparse main stem	1	Tvr111
	Abundant; very leafy	19	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr112, Tvr10, Tvr118, Tvr181, Tvr166, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172
Leaf pubescence	Very sparsely pubescent	10	Tvr156, Tvr181, Tvr166, Tvr100, Tvr152, Tvr133, Tvr149, Tvr111, Tvr112, Tvr1172
	Sparsely pubescent	6	Tvr118, Tvr177, Tvr105, Tvr125, Tvr161, Tvr139

	Moderately pubescent	4	Tvr1166, Tvr10, Tvr52, Tvr158
Branching pattern	All over	20	All genotypes
Petiole colour	Green	3	Tvr161, Tvr156, Tvr100
	Green with purple spots	14	Tvr105, Tvr52, Tvr177, Tvr158, Tvr149, Tvr111, Tvr112, Tvr118, Tvr166, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172
	Greenish purple	3	Tvr152, Tvr181, Tvr10
Leaf senescence	Slight visible senescence	9	Tvr52, Tvr156, Tvr166, Tvr100, Tvr158, Tvr125, Tvr161, Tvr152, Tvr149
	Moderate senescence	8	Tvr10, Tvr118, Tvr105, Tvr133, Tvr111, Tvr112, Tvr139, Tvr1166
	Conspicuous senescence	3	Tvr181, Tvr177, Tvr1172
Calyx colour	Green	3	Tvr100, Tvr181, Tvr156
	Greenish Purple	17	Tvr105, Tvr52, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112, Tvr10, Tvr118, Tvr166, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172
Corolla colour	Yellow	1	Tvr181
	Greenish yellow	3	Tvr100, Tvr111, Tvr112
	Yellowish green	2	Tvr166, Tvr133
	Greenish purplish yellow	14	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr10, Tvr118, Tvr125, Tvr139, Tvr1166, Tvr1172
Flower standard colour and flower wing colour	Yellow	2	Tvr166, Tvr181
	Greenish yellow	7	Tvr177, Tvr105, Tvr158, Tvr161, Tvr111, Tvr112, Tvr1172.

	Yellowish green	11	Tvr52, Tvr156, Tvr152, Tvr149, Tvr10, Tvr118, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166,
Flower keel colour	White	2	Tvr166, Tvr133
	Greenish yellow	18	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112, Tvr10, Tvr118, Tvr181, Tvr100, Tvr125, Tvr139, Tvr1166, Tvr1172
Flowering period	Asynchronous (>30 days)	20	All genotypes
Raceme position	Mostly above canopy	18	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112, Tvr181, Tvr166, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172
	Intermediate	2	Tvr10, Tvr118
Pod attachment to peduncle	Pendant	12	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr149, Tvr111, Tvr10, Tvr118,Tvr100, Tvr133, Tvr139,
	Sub-erect	7	Tvr166, Tvr125, Tvr161, Tvr152, Tvr112, Tvr1172, Tvr1166
	Erect	1	Tvr181
Colour of ventral suture of immature pod	Dark green	20	All genotypes
Immature pod colour	Light green	18	Tvr105, Tvr52, Tvr156, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112, Tvr10, Tvr118, Tvr181, Tvr100, Tvr133, Tvr139, Tvr1166, Tvr1172.
	Dark green	2	Tvr125, Tvr166
Mature pod colour	Brown	1	Tvr133
	Brown and black	7	Tvr10, Tvr118, Tvr156, Tvr158, Tvr161, Tvr111, Tvr112
	Black	12	Tvr105, Tvr52, Tvr177, Tvr152, Tvr149, Tvr181, Tvr166, Tvr100, Tvr125, Tvr139, Tvr1166, Tvr1172.
Pod pubescence	Glabrous	1	Tvr10

	Sparsely pubescent	5	Tvr181, Tvr166, Tvr139, Tvr1166, Tvr1172
	Moderately pubescent	9	Tvr52, Tvr177, Tvr105, Tvr125, Tvr125, Tvr133, Tvr149, Tvr111, Tvr112
	Densely pubescent	5	Tvr118, Tvr156, Tvr100, Tvr158, Tvr161
Pod cross section	Round	20	All genotypes.
Pod beak shape	Pointed	20	All genotypes.
Constriction of pod between seeds	Present	20	All genotypes
Pod curvature	Least curved	18	Tvr52, Tvr156, Tvr177, Tvr158, Tvr152, Tvr149, Tvr111, Tvr112, Tvr10, Tvr118, Tvr181, Tvr166, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172.
	Medium	2	Tvr105, Tvr161
Seed shape	Globose	20	All genotypes
Seed colour	Light green	15	Tvr52,Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112, Tvr10, Tvr118, Tvr166, Tvr125, Tvr133, Tvr139, Tvr1172, Tvr181
	Dark green	2	Tvr100, Tvr156
	Yellow	3	Tvr105, Tvr177, Tvr1166
Mottling on seed	Present	1	Tvr156
	Absent	19	Tvr105, Tvr52, Tvr177, Tvr158, Tvr161, Tvr152, Tvr149, Tvr111, Tvr112, Tvr10, Tvr118, Tvr181, Tvr166, Tvr100, Tvr125, Tvr133, Tvr139, Tvr1166, Tvr1172.
Lustre on seed surface	Shiny	9	Tvr10, Tvr118, Tvr156, Tvr181, Tvr158, Tvr100, Tvr161, Tvr111, Tvr1166
	Dull	11	Tvr105, Tvr52, Tvr177, Tvr152, Tvr149, Tvr112, Tvr166, Tvr125, Tvr133, Tvr139, Tvr1172.

Table 3 Mean recorded for some agronomic characters among 20 accessions of mung bean germplasm.

Genotypes	Days to 50% emergence	Seedling vigour	Primary leaf length (cm)	Primary leaf width (cm)	Terminal leaflet length (cm)	Terminal leaflet width (cm)	Number of cluster
Tvr10	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	5.33a
Tvr118	4.00b	5.67ab	7.00a	7.00a	3.00b	7.00a	5.00a
Tvr52	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	5.00a
Tvr156	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	4.67ab
Tvr181	4.00b	6.33ab	7.00a	7.00a	3.00b	7.00a	4.67ab
Tvr177	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	5.00a
Tvr105	5.00a	7.00a	7.00a	7.00a	5.00a	7.00a	5.33a
Tvr166	4.00b	6.33ab	7.00a	7.00a	5.00a	7.00a	5.00a
Tvr100	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	4.67ab
Tvr158	4.00b	5.00ab	7.00a	7.00a	5.00a	7.00a	4.33ab
Tvr125	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	5.33a
Tvr161	4.00b	4.33b	7.00a	7.00a	5.00a	7.00a	4.67ab
Tvr152	4.00b	7.00a	7.00a	7.00a	5.00a	7.00a	5.00a
Tvr133	4.00b	5.67ab	7.00a	7.00a	3.00b	7.00a	5.00a
Tvr149	4.00b	5.00ab	7.00a	7.00a	5.00a	7.00a	5.00a
Tvr111	4.00b	4.33b	7.00a	7.00a	5.00a	7.00a	3.33b
Tvr112	4.00b	5.67ab	7.00a	7.00a	5.00a	7.00a	4.67ab
Tvr139	4.00b	6.33ab	7.00a	7.00a	5.00a	7.00a	5.67a
Tvr1166	4.00b	5.67ab	7.00a	7.00a	5.00a	7.00a	5.67a
Tvr1172	5.00a	7.00a	7.00a	7.00a	5.00a	7.00a	5.33a
Mean	4.10	6.17	7.00	7.00	4.70	7.00	4.92
CV%	0%	20.42%	0%	0%	0%	0%	18.97
Root SME	0.00	1.26	0.00	0.00	0.00	0.00	0.79

Means in the same column bearing the same letter(s) are not significantly different at 5% level based on Duncan's Multiple Range Test (DMRT)

Table 4 Mean recorded for some agronomic characters among 20 accessions of mung bean germplasm continued.

Genotypes	**Number of primary branches**	**Plant height (cm)**	**Days to 50% flowering**	**Days to first mature pod**	**Pod length (cm)**	**Number of seeds per pod**
Tvr10	8.00a	85.00a	42.00de	68.67e	9.33a	14.00a
Tvr118	5.33efg	47.00ghi	37.00g	53.00l	7.33cd	8.67d
Tvr52	4.33gh	51.67fghi	46.00c	57.00j	8.00abc	13.33ab
Tvr156	6.67bcd	60.67defg	38.67f	54.33k	7.33cd	11.67abc
Tvr181	6.33bcde	55.00efgh	55.00a	72.67bc	8.00abc	12.33abc
Tvr177	7.00abc	62.00def	44.67c	73.33b	7.67bcd	12.67abc
Tvr105	5.67def	76.33abc	46.00c	65.00g	8.00abc	12.33abc
Tvr166	5.67def	56.67efgh	54.33a	79.67a	7.00cd	13.67ab
Tvr100	4.67fgh	47.33ghi	36.67g	59.67i	7.00cd	11.33bc
Tvr158	4.67fgh	55.33efgh	45.00e	59.00i	7.00cd	12.33abc
Tvr125	5.33efg	63.33bcde	54.00a	71.00d	7.00cd	14.00a
Tvr161	4.00h	38.00i	41.00e	59.33i	8.00abc	11.66abc
Tvr152	4.33gh	71.00bcd	51.33b	67.00f	7.67bcd	13.33ab
Tvr133	5.33efg	55.00efgh	43.00d	71.33d	6.33d	12.67abc
Tvr149	6.00cde	51.00fghi	51.00b	62.33h	6.67cd	12.33abc
Tvr111	6.00cde	46.67hi	45.00c	69.33e	6.33d	10.33cd
Tvr112	6.00cde	46.00hi	45.00c	71.33d	7.33cd	12.00abc
Tvr139	6.67bcd	38.33i	51.33b	67.00f	7.00cd	12.69abc
Tvr1166	7.00abc	81.67ab	51.33b	72.00cd	9.00ab	14.00a
Tvr1172	7.33ab	67.00cde	54.00a	69.33e	9.33a	12.67abc
Mean	5.82	58.00	46.65	66.12	7.57	12.40
CV%	13.59	14.58	2.12	1.19	12.53	11.84
Root SME	8.46	0.99	0.78	0.95	1.47	0.93

Means in the same column bearing the same letter(s) are not significantly different at 5% level based on Duncan's Multiple Range Test (DMRT)

Table 5 Mean recorded for some agronomic characters among 20 accessions of mung bean germplasm continued.

Genotypes	10 pod weight (g)	100 seed weight (g)	Seed yield per plant (g)	Yield per plant (g)	Yield (kg/ha)
Tvr10	6.67abcd	4.00abc	12.67abcd	17.80abc	593.33abc
Tvr118	7.00abc	4.00abc	9.07cd	12.63c	421c
Tvr52	7.00abc	5.00a	14.13abcd	20.47abc	682.33abc
Tvr156	6.00bcd	3.33bc	10.00abcd	14.93abc	497.67abc
Tvr181	5.00cd	4.00abc	9.67cd	13.80bc	460bc
Tvr177	7.67ab	5.00a	12.40abcd	19.47abc	649abc
Tvr105	7.00abc	4.67ab	15.13abc	19.20abc	640abc
Tvr166	6.33bcd	3.83abc	15.13abc	20.73abc	691abc
Tvr100	8.67a	5.00a	14.13abcd	23.07ab	769ab
Tvr158	5.67bcd	3.33bc	9.80bcd	14.93abc	497.67abc
Tvr125	5.67bcd	3.33bc	12.87abcd	18.87abc	629abc
Tvr161	7.00abc	5.00a	12.80abcd	18.40abc	613.33abc
Tvr152	7.00abc	4.00abc	12.40abcd	17.80abc	593.33abc
Tvr133	5.33cd	3.33bc	13.80abcd	20.33abc	677.67abc
Tvr149	5.67bcd	3.67abc	15.13abc	22.53ab	751ab
Tvr111	4.67d	3.00c	7.80d	11.40c	380c
Tvr112	5.00cd	3.00c	9.67cd	13.87bc	462.33bc
Tvr139	6.33bcd	4.33abc	16.13ab	24.73a	824.33a
Tvr1166	5.67bcd	3.33bc	16.33a	23.80ab	793.33ab
Tvr1172	6.33bcd	4.00abc	12.00abcd	17.20abc	573.33abc
Mean	6.28	3.96	12.55	18.27	609.93
CV%	20.70	24.21	30.66	30.66	20.73
Root SME	1.30	0.96	3.85	6.12	126.48

Means in the same column bearing the same letter(s) are not significantly different at 5% level based on Duncan's Multiple Range Test (DMRT)

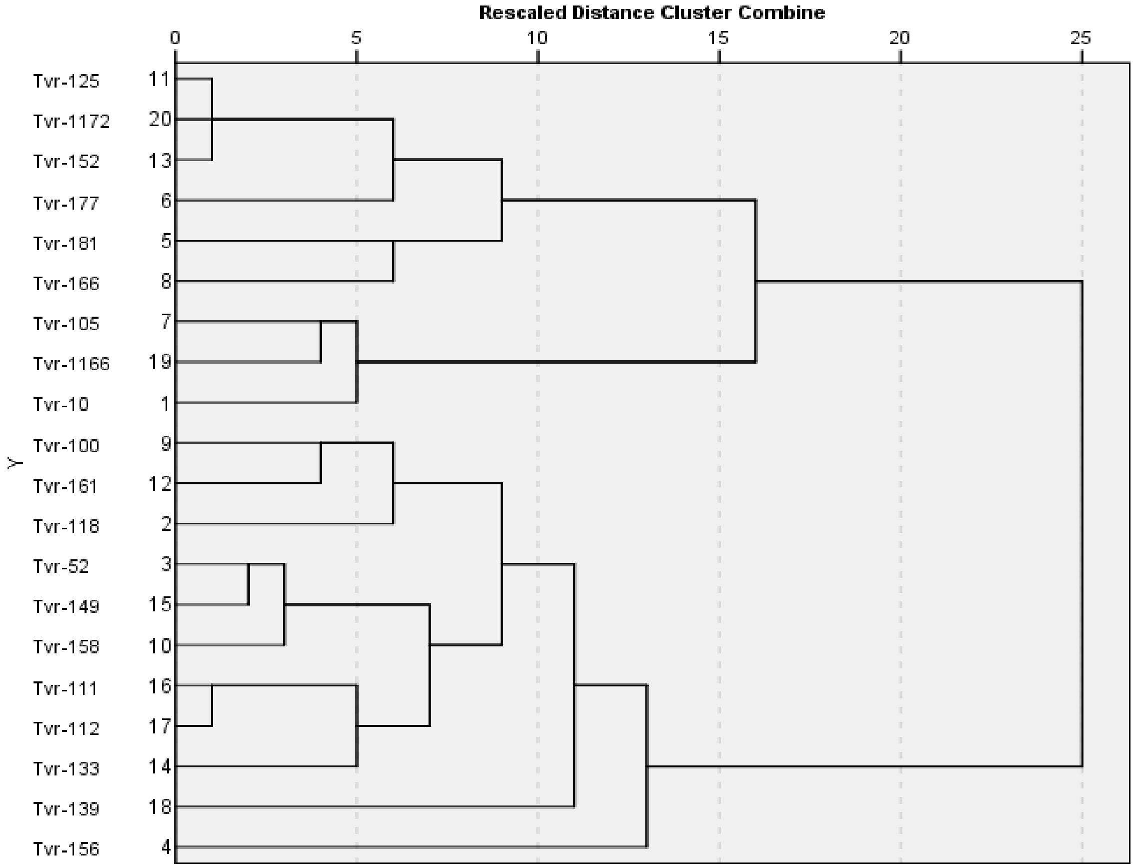

Fig 1: Dendrogram representation of the twenty genotypes clustered using Average Linkage (Between Groups)

Dark and light leaf colour

Intermediate raceme position

Medium curved pod,dark green pod and round cross-section

Pointed beak shape, sub-erect Pod attachment to peduncle

Twining character of genotype

Purple spots on green petiole and leaf pubescence present

Determinate growth pattern And erect growth habit

All over branching pattern and intermediate leaf colour

Pod pubescence present

PLATE II: Pictorial representations of some observed characters on genotypes continued.

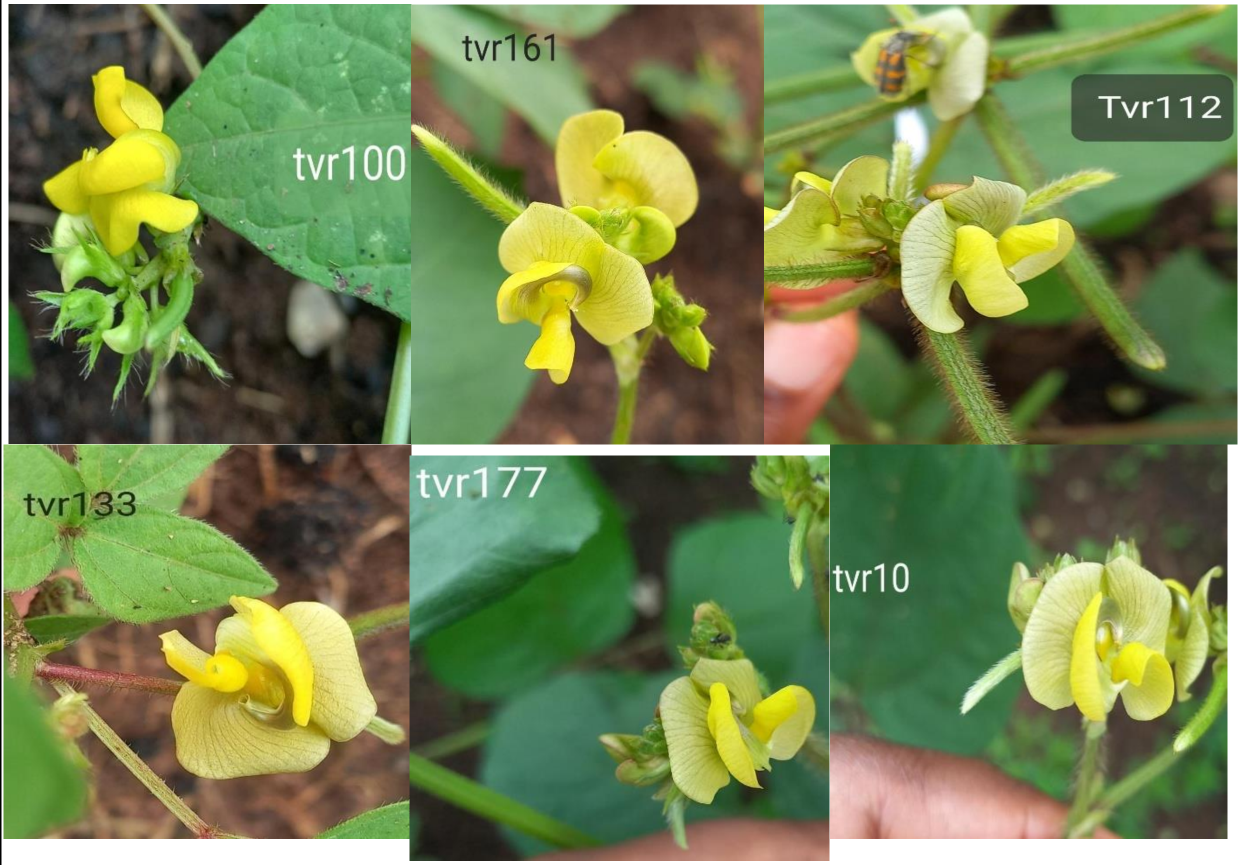

PLATE III: Some genotypes flower colour.