



HERITABILITY, VARIABILITY AND CHARACTER ASSOCIATION OF THIRTY MUNG BEAN (*Vigna radiata* L.) GENOTYPES ASSESSED IN OWERRI SOUTHEASTERN NIGERIA

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Abstract

Thirty mungbean (*Vigna radiata* L. Wilczek) genotypes were collected from IITA and evaluated at the Center for Agricultural Research and Extension of the Federal University of Technology, Owerri. The experiment was laid out in a Randomized complete Block Design with three replications. A spacing of 0.4 m × 0.15 m inter row and between plants was utilized. Data were recorded on various morphological and agronomic characters. Data collected were subjected to Analysis of variance, inter-character association among the plant characters evaluated was determined using Pearson coefficient correlation analysis, while relatedness was done using dendrogram. Analysis of variance revealed significant differences ($p < 0.05$) among all the genotypes for the characters studied indicating that there is possibility for selection. There was positive correlation for the morphological and yield traits assessed. Narrow differences between phenotypic and genotypic coefficients of variation for the characters revealed minimal environmental influence on their expression. High heritability values for the traits indicates that there would be high gain from phenotypic selection. Results from cluster analysis resulted in the grouping of the 30 genotypes into 5 clusters, with the two genotypes (Tvr-3 and Tvr-109) in cluster III having the best performance in terms of the agronomic and morphological traits assessed. These genotypes may be further used for parental selection in breeding programmes for improvement of various qualitative and quantitative characteristics in mung bean.

Key words: Heritability. Selection. Improvement.

Introduction

The mung bean (*Vigna radiata* (L.) R. Wilczek) is a legume cultivated for its edible seeds and sprouts. Mung bean grows in a wide range of climatic conditions and has shown to be a fast-growing legume. It grows greatly under most adverse arid and semi-arid conditions (Mogotsi, 2006). It is a highly nutritious crop and contains sufficient amounts of protein, dietary fiber, minerals, vitamins and significant amounts of bioactive compounds capable of meeting basic human nutritive requirements. It offers a vast array of health benefits such as its hypoglycemic, hypolipidemic and

antihypertensive effects, in addition to its anticancer and immune boosting abilities. (Liyanage *et al.*, 2018, Ali *et al.*, 2014, Gupta *et al.*, 2018, Chai *et al.*, 2019). Mung bean production is mainly (90 %) situated in Asia: India is the largest producer with more than 50 % of world production but consumes almost its entire production.

Germplasm evaluation plays a vital role in identification of superior genotypes for different qualitative and quantitative characters in crop breeding programmes which may be further used to create variability by hybridization. The information as well as assessment of genetic

variability in the existing germplasm of a particular crop is sought as prerequisite (Appalaswamy and Reddy, 2004). Plant genetic resources are the most valuable and essential basic raw materials to meet the current and future needs of crop improvement programmes (Paroda *et al.*, 1991). In addition, heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into next generations (Surek and Beser, 2003).

Increased seed yield is the ultimate goal of the breeders. But seed yield itself is a product of interaction of many component traits which influence yield directly or indirectly. So, it is important to see the contribution of each of the traits in order to give more attention to those having the highest influence on yield (Malek *et al.*, 2014). Moreover, understanding the relationship between yield and its component traits is of great importance to a breeder for making the best use of these relationships in selecting desirable genotypes for yield improvement programs (Ismail *et al.*, 2001, Kumar and Shukla, 2002).

For an effective breeding program for crop variety development through hybridization, the analysis of genetic diversity is one of the useful tools and plays a fundamental role in identification of parents (Kwon *et al.*, 2002, Mazid *et al.*, 2013). Moreover, better knowledge on genetic diversity could help to achieve long-term selection gain (Chowdhury, 2002). As a traditional method, morphological traits are used to assess genetic divergence and classify existing germplasm materials. However, this technique, a low level but powerful taxonomic tool, has been utilized for the preliminary grouping of germplasm prior to their characterization using more precise marker technologies. Hence, the objective of this study was to assess the amount of variability in the mung bean genotypes collected, determine the heritability of the traits and group the

genotypes based on their performances using cluster analysis.

Materials and Methods

Experimental Site and Location

The experiment was carried out at the Center for Agricultural Research and Extension, School of Agriculture and Agricultural Technology, Federal University of Technology Owerri, Imo State. Owerri lies at latitude 05° 27'N and longitude 07° 02'E at an elevation of 55 meters above sea level and is in the tropical rainforest region of southeastern Nigeria. The area has a bimodal pattern of rainfall with peaks in July and September. It has a minimum and maximum annual temperature of 20°C and 32 °C respectively and mean annual rainfall of 2500 mm and relative humidity of 85-89 % (Nwosu and Adeniyi, 1980).

Experimental Design and Experiment

The experiment was laid out in a Randomized Complete Block Design (RCBD) with thirty mung bean varieties which was replicated three times. An experimental field measuring 12.8 m x 5.6 m (71.68 m²) was mapped out. The field was then subdivided into three blocks 1 m apart. Each block measured 12.8 m x 1.2 m and contained 30 mung bean genotypes arranged in single row plots with 8 plants per genotype. The plants had an inter row and intra row spacing of 0.4m and 0.15m respectively. The genotypes were completely randomized within each block. The mung bean genotypes assessed include Tvr-1, Tvr-2, Tvr-3, Tvr-4, Tvr-6, Tvr-7, Tvr-9, Tvr-10, Tvr-11, Tvr-12, Tvr-13, Tvr-17, Tvr-54, Tvr-55, Tvr-56, Tvr-61a, Tvr-63, Tvr-64, Tvr-65, Tvr-67, Tvr-68, Tvr-69, Tvr-61b, Tvr-72, Tvr-109, Tvr-110, Tvr-111, Tvr-117, Tvr-123 and Tvr-124.

Data collected include plant girth, height, number of leaves, number of pods per plant, pod length, pod girth, pod weight, number of seeds per pod, 100-seed weight and yield/ha.

All the data were subjected to Analysis of Variance (ANOVA) test using Genstat software while the mean separation was done using Least Significant Difference at 5% level of probability using the procedure described by Obi (2002). Pearson's correlation and cluster analysis were done using SPSS.

Genetic parameters were estimated by the formula given by Werf, (2009) and Malek *et al.*, (2014). These parameters include the following:

- i. σ^2_G (or V_A which is an estimate of genotypic variance) = $(MS_G - MS_E) / r$, where MS_G is an estimate of mean square of tested accession, MS_E is an estimate of mean square of error and r refers to the number of replications;
- ii. σ^2_P (or V_P which is an estimate of phenotypic variance) = $\sigma^2_G + (MS_E / r)$
- iii. h^2 (an estimate of narrow sense heritability) = V_A / V_P
- iv. GCV (Genotypic coefficient of variation) = $\sqrt{\sigma^2_G / \bar{X}} \times 100$, where σ^2_G is the genotypic component of variance and \bar{X} is the mean of the trait.
- v. PCV (phenotypic coefficient of variation) = $\sqrt{\sigma^2_P / \bar{X}} \times 100$, where σ^2_P is the phenotypic component of variance and \bar{X} is the mean of the trait.
- vi. GA (Genetic advance, which is taken as percent of the mean assuming selection of the superior 5% of the varieties) = $K \times \sqrt{\sigma^2_P / \bar{X}} \times h^2 \times 100$, where K (the standard selection intensity) = 2.06 (at 5% selection intensity), σ^2_P is the phenotypic component of variance, h^2 is the heritability in narrow sense and \bar{X} refers to the mean of the trait being evaluated.

Results and Discussion

Results

Information regarding the mean performances of 30 mung bean genotypes based on morphological and yield attributes is shown in Table 1. The tallest plants were observed in Tvr-109 with mean height value

of 29.27 cm while Tvr-61a was the shortest with a mean height value of 7.87 cm. The highest mean number of leaves of 6.83 was obtained in Tvr-3, while the lowest mean number of leaves was obtained in Tvr-61a with a value of 2.33. Tvr-109 were observed to have the largest leaf area possessing a mean leaf area of 1805.66 cm² and closely followed by Tvr-3 with a mean leaf area of 1560.15 cm². The smallest mean leaf area was observed in Tvr-54 with a mean leaf area of 57.75 cm². Tvr-61a produced the fewest number of pods per plant with an average of 1.67 pods per plant. On the other hand, Tvr-124 produced the highest number of pods, with an average of 18.33 pods per plant. This was closely followed by Tvr-3 which produced an average of 16.00 pods per plant. For pod length, Tvr-109 on average produced the longest pods with a mean pod length of 9.15 cm, followed by Tvr-72 with a mean pod length of 8.21 cm. Tvr-54 produced the shortest pods on average with a mean pod length of 3.24 cm. Tvr-109 produced the highest number of seeds per pod with a mean number of 11 seeds. This was closely followed by Tvr-124 and Tvr-55 with mean values of 10.67 and 10 seeds per pod respectively. Tvr-6, Tvr-7, Tvr-65 and Tvr-69 produced no pod and as such there were no seeds. The 100 seed weight ranged from 5.08g to 104.17g with the highest value obtained from Tvr-110 and the lowest from Tvr-17. Tvr-109 had the highest mean yield with 1300.74 kg/ha which was closely followed by Tvr-3 with 1200.99kg/ha. The lowest mean yield was 38.52kg/ha obtained from Tvr-54.

The result from correlation analysis of the various mung bean characters evaluated is presented in Table 2. From the table, it can be observed that 100 seed weight as well as the yield per hectare were positively correlated to the growth parameters recorded which includes girth, height, number of leaves and leaf area. 100 seed weight and yield per hectare were also positively correlated to pod length, pod

girth, pod weight as well as number of seeds per pod.

Information regarding the details of clustering are shown in table 3 and table 4. Table 3 shows the Mean distribution of 30 Mung bean varieties in clusters evaluated in Owerri. Thirty genotypes of mungbean were grouped into 5 clusters based on various agro morphological traits. Cluster I comprised of 21 varieties, cluster II had only one variety, cluster III, IV and V comprised of 2, 4 and 2 varieties respectively.

Table 4 shows the cluster means for the different traits of mung bean genotypes evaluated. From the table it can be observed that cluster 3 had the highest mean values for girth (2.06 cm), height (27.67 cm), number of leaves (6.58), leaf area (1682.91 cm²), number of pods (14.50), pod length (8.13 cm), pod girth (1.91cm), pod weight (7.64 g), number of seeds (10), 100 seed weight (88.60 g) as well as yield per hectare (1250.87 kg). On the other hand, cluster 5 had the lowest values for girth (1.37 cm), height (12.23 cm), Number of leaves (3.83), leaf area (149.83 cm²), number of pods (1.98), pod length (4.27 cm), pod girth (1.13 cm), pod weight (0.66 g), number of seeds

(4.69), 100 seed weight (8.75 g) and yield per hectare (83.92 kg). The shortest number of days to 50 % anthesis was also observed in cluster 5 (39 days) while the longest number of days to 50 % anthesis was seen in cluster 2 (58 days).

Narrow sense heritability, phenotypic variance, genotypic variance, phenotypic and genotypic coefficient of variation (PCV and GCV) as well as genetic advance were calculated and the results are presented in table 5. The results showed narrow differences between phenotypic variance and genotypic variance for most of the traits. All the characters exhibited high heritability which ranged from 74.00 % in 100-seed weight to 99.50 % in pod girth. The highest PCV and GCV were observed for pod weight (94.56% and 88.78% respectively) and the lowest PCV and GCV were recorded for leaf area (6.77% and 6.51% respectively). Narrow differences between PCV and GCV were also observed for most of the traits. The genetic advance as percent of the mean (GA%) ranged from 44.81% in plant girth to 97.44% in plant height.

Table 1: Mean performances of 30 mung bean genotypes based on morphological and yield attributes

Genotypes	Height	NLvs	LA(cm ²)	NumPod	PodL	NumSeed	100seedwgt(g)	Yield/ha(Kg)
Tvr-1	12.10	4.00	224.04	2.33	6.17	7.33	17.10	183.70
Tvr-2	26.22	6.33	1270.23	13.33	8.10	8.67	53.02	697.78
Tvr-3	26.07	6.83	1560.15	16.00	7.10	9.00	97.39	1200.99
Tvr-4	16.08	4.33	369.07	6.33	5.49	6.67	46.86	483.95
Tvr-6	11.28	5.67	193.70	0.00	0.00	0.00	0.00	0.00
Tvr-7	13.00	3.33	111.68	0.00	0.00	0.00	0.00	0.00
Tvr-9	11.37	4.00	131.09	5.33	7.20	9.00	26.52	353.58
Tvr-10	18.78	6.17	674.15	11.00	7.96	5.00	87.20	645.93
Tvr-11	20.18	6.00	714.15	9.00	8.01	8.33	34.47	430.62
Tvr-12	12.17	4.17	155.13	5.33	7.41	8.00	15.50	183.70
Tvr-13	12.98	4.33	188.82	2.00	6.12	6.33	13.61	134.32
Tvr-17	13.07	3.83	139.44	2.00	5.33	5.67	5.08	42.96
Tvr-54	10.10	3.00	57.75	2.00	3.24	3.33	8.00	38.52
Tvr-55	14.08	3.67	121.18	2.00	6.62	10.00	6.67	112.59
Tvr-56	14.40	3.83	158.70	3.00	6.37	7.00	13.71	153.58
Tvr-61a	7.87	2.33	63.04	1.67	4.88	5.00	6.80	50.37
Tvr-63	10.90	3.83	201.95	3.00	5.90	4.33	22.85	150.12
Tvr-64	12.00	3.83	127.21	4.33	5.90	6.33	15.56	145.19
Tvr-65	12.93	3.83	121.03	0.00	0.00	0.00	0.00	0.00
Tvr-67	14.78	4.00	147.06	2.00	6.18	7.00	6.35	63.70
Tvr-68	16.15	4.67	265.49	4.67	7.70	9.00	19.57	255.31
Tvr-69	11.72	3.83	236.78	0.00	0.00	0.00	0.00	0.00
Tvr-61b	25.18	6.50	955.62	7.33	7.72	8.67	47.84	627.16
Tvr-72	27.20	5.67	1133.05	10.00	8.21	9.67	68.17	959.01
Tvr-109	29.27	6.33	1805.66	13.00	9.15	11.00	79.82	1300.74
Tvr-110	15.63	6.33	543.35	13.67	3.92	6.00	104.17	925.93
Tvr-111	11.93	4.17	139.42	5.67	7.63	9.67	28.38	414.32
Tvr-117	14.70	4.17	257.41	5.67	6.52	5.33	51.09	454.32
Tvr-123	22.47	5.17	581.70	10.00	7.11	5.67	68.96	603.95
Tvr-124	25.75	6.33	1004.30	18.33	8.07	10.67	62.35	998.02
LSD(0.05)	5.04	1.30	408.84	5.16	1.02	2.00	45.64	521.34
Key:	NLvs - Number of Leaves, LA - Leaf Area, NumPod - Number of Pod, PodL - Pod Length							

Table 2. Pearson Correlation matrix for mungbean plant characteristics in Owerri West Southeast Nigeria

Traits	1	2	3	4	5	6	7	8	9	10	11
1). Girth	-										
2). Height	0.880**	-									
3). No of leaves	0.823**	0.835**	-								
4). Leaf Area	0.887**	0.940**	0.836**	-							
5). Days to 50% Anthesis	0.284	0.266	0.2	0.171	-						
6). No of Pods	0.747**	0.817**	0.823**	0.829**	0.436*	-					
7). Pod Length	0.585**	0.556**	0.418*	0.497**	0.880**	0.615**	-				
8). Pod Girth	0.390*	0.366*	0.242	0.369*	0.828**	0.511**	0.853**	-			
9). Pod Weight	0.844**	0.874**	0.838**	0.922**	0.365*	0.952**	0.627**	0.515**	-		
10). No of Seeds	0.513**	0.550**	0.407*	0.504**	0.822**	0.609**	0.916**	0.788**	0.613**	-	
11). 100 Seed weight(g)	0.704**	0.736**	0.790**	0.771**	0.347	0.904**	0.516**	0.497**	0.918**	0.456*	-
12). Yield/ha(Kg)	0.793**	0.864**	0.820**	0.905**	0.333	0.936**	0.582**	0.504**	0.981**	0.604**	0.931**

* Correlation is significant at the 0.05 level (2-tailed), ** Correlation is significant at the 0.01 level (2-tailed).

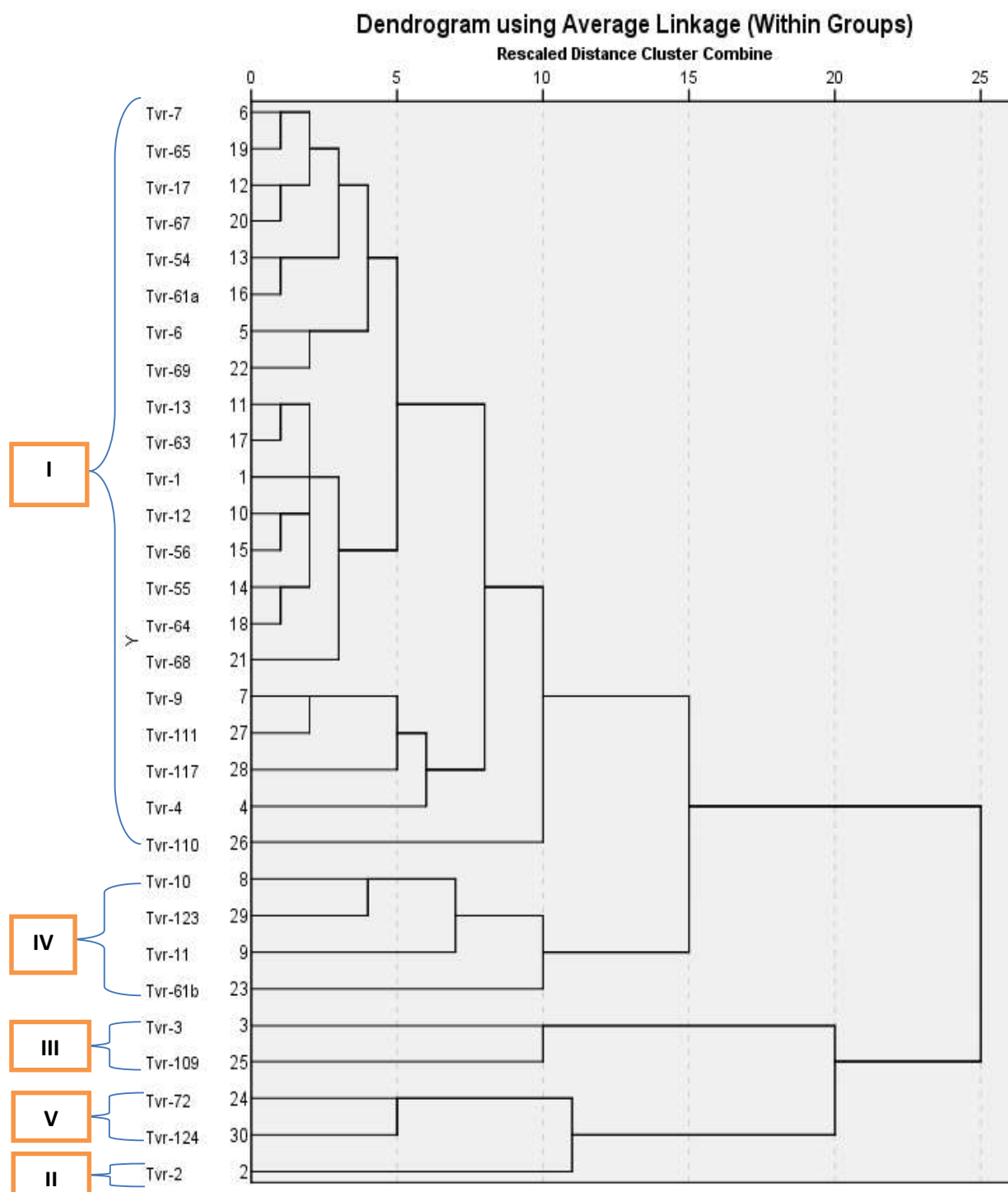


Table 3: Mean distribution of 30 Mungbean genotypes in clusters evaluated in Owerri West Southeast Nigeria

Cluster	No of genotypes	Genotypes
I	21	Tvr-1, Tvr-4, Tvr-6, Tvr-7, Tvr-9, Tvr-12, Tvr-13, Tvr-17 Tvr-54, Tvr-55, Tvr-56, Tvr-61a, Tvr-63, Tvr-64, Tvr-65, Tvr-67, Tvr-68, Tvr-69, Tvr-110, Tvr-111, Tvr-117
II	1	Tvr-2
III	2	Tvr-3, Tvr-109
IV	4	Tvr-10, Tvr-11, Tvr-61b, Tvr-123
V	2	Tvr-72, Tvr-124

Table 4: Cluster means for different traits of 30 Mungbean genotypes evaluated in Owerri

Trait	Cluster				
	I	II	III	IV	V
Girth	1.45	1.83	2.06	1.67	1.37
Height	14.05	26.09	27.67	19.27	12.23
No of leaves	4.27	6.21	6.58	5.92	3.83
Leaf Area	232.50	1090.80	1682.91	628.34	149.83
Days to 50% Anthesis	54.00	58.00	43.00	54.00	39.00
Number of pods	5.53	12.25	14.50	10.92	1.98
Pod Length	6.91	8.03	8.13	6.75	4.27
Pod Girth	1.51	1.58	1.91	1.52	1.13
Pod Weight	2.13	4.87	7.64	4.20	0.66
Number of seeds	7.93	9.42	10.00	6.25	4.69
100 seed weight(g)	34.48	57.85	88.60	73.70	8.75
Yield/ha(Kg)	392.30	820.49	1250.87	651.61	83.92

Table 5: Estimation of genetic parameters of eleven different morphological characters and Yield attributes among 30 Mung bean genotypes

Trait	Genotypic variance	Phenotypic variance	Heritability (%)	GCV (%)	PCV (%)	GA (%)
Plant Girth	0.12	0.13	92.31	22.64	23.57	44.81
Height	65.72	72.22	91.00	49.58	51.98	97.44
Number of Leaves	2.52	2.96	85.14	34.14	37.00	64.89
Leaf area	876.97	948.43	92.47	6.51	6.77	12.89
Pod Weight	4.54	5.15	88.16	88.78	94.56	85.86
Pod Girth	0.32	0.32	99.50	41.59	41.59	85.26
Pod Length	6.88	7.01	98.15	45.22	45.65	92.30
Number of pods per plant	22.93	26.26	87.32	80.20	85.84	77.20
Number of seeds per pod	9.70	10.21	95.00	48.51	49.77	97.40
100-seed weight	728.77	988.70	73.71	80.42	93.67	71.11
Yield	112273.00	146189.33	76.80	64.27	73.34	58.01

Key: GCV - Genetic coefficient of variation

PCV - Phenotypic coefficient of variation

GA - Genetic Advance

For all the traits assessed, narrow differences between PCV and GCV was observed. This gives an indication of minimal influence of environmental factors on the expression of the traits and a chance of high selection gain. High heritability values for all the traits indicate a high degree of gene influence on the traits which also indicates less influence of environmental factors on the expression of these traits and the chance of high gain from phenotypic selection. The heritability estimates help the breeders in selection on the basis of phenotypic performance. Heritability and GA with GCV values can provide a very good image of the amount of advancement to be expected through phenotypic selection (Malek *et al.*, 2014). Therefore, high values of heritability and GA in conjunction with high GCV for characters like pod weight, number of pods per plant, 100-seed weight and yield can be considered as favorable morphological traits for mung bean improvement through effective phenotypic selection of these traits and high expected genetic gain from selection for these

characters can be achieved. This also indicates that these characters are under the control of additive gene action and would respond very well to continuous selection and is in line with reports by Malek *et al.*, (2014).

Current results also suggest that mung bean yield could be increased through the selection of higher number of pods per plant with higher number of seeds per pod. Therefore, in mung bean, number of pods per plant and number of seeds per pod can be considered as the major and effective characters influencing the seed yield in mung bean. Malek *et al.*, 2014 reported that correlation analyses indicate that pod number per plant and seeds per pod appeared to be the first order yield components and priority should be given during selection due to having strong associations as well as high direct effects on seed yield. Significant positive correlations of plant height, number of leaves, leaf area and pods per plant, seeds per pod, and 100-seed weight with seed yield indicate that in selecting high yielding genotypes these

characters are very important selection criteria. These results also are in agreement with the results reported by others in soybean (Faisal *et al.*, 2007, Machikowa and Laosuwan, 2011). Highly significant and positive correlation between seed yield per plant and yield per ha indicates that in mung bean individual plant yield contributed significantly towards yield per unit area. This is also in agreement with results reported by Malek *et al.*, (2014) in soybean and Kadams and Sajo, (1998) in Bambara groundnut.

The thirty (30) mung bean genotypes were grouped into five clusters based on their agronomic performances and indicates that 30 mung bean genotypes exhibited notable genetic divergence in terms of morphological traits. Ngwuta (2008) reported that clustering helps to reduce the size of the data generated from evaluations into manageable groups based on certain variables which will permit the selection of the best entities within any desired group. The result of the grouping showed that twenty one genotypes fall into cluster I, only one genotype fall into cluster II, two genotypes fall into cluster III, four genotypes fall in cluster IV and two genotypes fall in cluster V. Ojo *et al.*, (2012); Cui *et al.*, (2001) and Iqbal *et al.*, (2008) also reported formation of different number of clusters using morphological characters in diverse legume genotypes. The dendrogram tends to group some of the genotypes with similar morphological traits into the same cluster. Similar results were also reported in soybean and other crops by Cui *et al.*, (2001) Iqbal *et al.*, (2008) and Rafii *et al.*, (2012).

Conclusion

The present study revealed the presence of high levels of variability and heritability for the morphological traits including yield attributes and seed yield among the genotypes. This implies that there will be genetic gain from selection. Positive

correlation between the growth and yield parameters was also observed. Mung bean genotypes with high yield potential can be considered for selection, while characters with high heritability estimate can be used as criteria for selection during breeding programs.

Recommendation

Genotypes Tvr-124, Tvr-109 and Tvr-55 with high number of seed per pod and Tvr-124 and Tvr-3 for pods per plant could be considered during selection and further breeding work.

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