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MORPHOLOGICAL AND AGRONOMIC TRAITS VARIATIONS FOR MUNGBEAN VARIETY SELECTION AND IMPROVEMENT IN UGANDA

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ABSTRACT

Mungbean (*Vigna radiata* L. Wilczek), is a pulse species that is widely cultivated in sub-tropical and tropical regions of the world. Unfortunately, the yield of mungbean in Uganda is very low mainly due to inherent genotype failures and losses due to pests and diseases. To achieve a gain in yield through breeding requires collection, characterisation, and evaluation of germplasm, as the first step in identifying genotypes with the desired characteristics. The objective of this study was to describe the nature and extent of genotypic variation among mungbean collections for a range of traits of potential agronomic and adaptive interests in Uganda. A total of 35 mungbean accessions acquired mainly from the World Vegetable Centre (AVRDC) in Taiwan, two local ricebean (*Vigna umbellata* (Thunb.) Ohwi and Ohashi) and one local blackgram genotype (*Vigna mungo*) were evaluated for several diverse traits for two cropping seasons at two different locations in Uganda. Genotype by environment interaction (GEI) was significant ($P < 0.001$) for all the traits, indicating inconsistent performance by some genotypes across two locations and two seasons. However, AMMI bi-plot identified stable genotypes for grain yield, while GGE bi-plot identified the best genotypes in a hypothetical environment. The magnitudes of estimated broad sense heritability (H) for the traits used were generally high. However, single link dendogram and Principal Component Analysis (PCA) revealed narrow diversity in the mungbean collection. The positive relationship between seed size and yield in this sub-set of mungbean germplasm can be used in a breeding programme for a potential gain in selecting large seeded and high yielding genotypes.

Key Words: *Vigna mungo, Vigna radiata*, *Vigna umbellata*

RÉSUMÉ

Le haricot mungo (*Vigna radiata* L. Wilczek), est une espèce de plante qui est largement cultivée en régions tropicales et subtropicales. Le rendement actuel du haricot mungo en Ouganda est comparativement bas par suite d'échecs liés au génotype et pertes dues aux maladies et pestes. Afin de réaliser un gain de rendement à travers l'amélioration, il s'avère nécessaire de faire la collection, la caractérisation, et l'évaluation du germplasme, comme première étape dans l'identification des génotypes avec des caractéristiques désirées. La variation parmi 38 accessions de haricot mungo obtenues du World Végétale Centre (AVRDC), une variété locale de haricot riz (*Vigna umbellata* (Thunb.) Ohwi et d' Ohashi) et un génotype de blackgram (*Vigna mungo*) local, était évaluée pour plusieurs traits directs pendant deux saisons culturales dans des lieux différents en Ouganda. Une variation substantielle était observée dans différent traits de potentiel agronomique et performance adaptive. L'interaction génotype par environnement (GEI) était significatif ($P < 0.001$) pour tous les traits, indiquant une performance inconsistante de quelques génotypes à travers deux milieux et deux saisons. Par ailleurs, un AMMI bi-plot a identifié des génotypes stables en termes de rendement en grain, alors que le GGE bi-plot a identifié les meilleurs génotypes dans un environnement hypothétique. Les niveaux de l'héritabilité estimée (H) pour les traits utilisees étaient généralement élevés. Par ailleurs, le lien simple du dendogramme et l'analyse par composantes Principales

(PCA) ont révélé une petite diversité dans la collection du haricot mungo. Une corrélation positive entre la taille du grain et le rendement dans ce sous groupe du germoplasme du haricot mungo peut être utilisée dans le programme d'amélioration pour un gain potentiel dans la sélection des génotypes à grains larges et rendement élevés.

Mots Clés: *Vigna mungo, Vigna radiata*, *Vigna umbellata*

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is a pulse species of the pan-tropical genus *Vigna* (Saravanakumar *et al.,* 2004) that is native to Asia but widely cultivated in Africa, Asia and Latin America (Tomooka *et al.,* 1992). Its short growth duration allows adaptation to many cropping systems and rotations, hence, diversifying cropping systems (Shanmugasundaram *et al.,* 2009). Meanwhile, its remarkable quality of fixing atmospheric nitrogen enriches soils (Sharma *et al.,* 1996) and its low soil water and fertility requirements (Sangakkara *et al.,* 2001) increases cropping systems productivity and resilience (Ahmad *et al.,* 2001; Keatinge *et al.,* 2011).

Mungbean can provide significant amounts of protein (240 g kg^{-1}), carbohydrate (630 g kg^{-1}) and a range of micronutrients in diets (Anwar *et al.,* 2007). Mungbean protein and carbohydrates are easily digested and create less flatulence than those derived from other legumes (Fleming, 1981). The mungbean lysine content of 504 mg g^{-1} (Saini *et al.,* 2010) makes it a good supplement for most cereal based diets which lack this essential amino acid (Baskaran, *et al.,* 2009). In addition, mungbean is lower in phytic acid, which is commonly high in cereal and other legume crops, and has a negative impact on iron and zinc bioavailability in plant-based diets (Kataria *et al.,* 1989). Thus, mungbean as a major protein supplement in cereal-based diets (Thirumaran and Seralathan, 1988). It is eaten as boiled beans (Abbas, *et al.,* 2010), soup or mungbean pancake (Gwag, *et al.,* 2006). Owing to its palatable taste and nutritional quality, mungbean has been used as an iron-rich whole food source for baby food (Sosulski *et al.,* 1976; Del Rosario *et al.,* 1987).

World production statistics for mungbean are difficult to obtain; for example, FAOSTAT includes mungbean together with species from the genus *Phaseolus* under dry beans. Annual world mungbean production is estimated at 3 million metric tons harvested from about 5.5 million hectares (Poehlman, 1991; Weinberger, 2003), of which 90% is in South Asia, especially in Bangladesh, Burma, India, Indonesia, Pakistan, Philippines, Sri Lanka and Thailand (Shanmugasundaram, 2001). The holistic mungbean improvement program of the World Vegetable Centre (AVRDC) in the region is largely credited for this improvement (Shanmugasundaram *et al.,* 2009).

In sub-Saharan Africa, mungbean production still depends on the small-seeded traditional varieties, which reach maturity in 90 -110 days. The varieties are indeterminate in growth and have to be harvested multiple times; yet they are susceptible to diseases and insect pests, and pod shattering (Shanmugasundaram, 1988). Worse still, these varieties are low yielding, producing only about 200 - 500 kg ha^{-1} (Agugo and Chukwu, 2010). Fortunately, they are fairly adapted to the local environmental conditions (Mbowe, *et al.,* 1987). The desired characteristics and performance of the imagined ideal variety needed to transform mungbean from a marginal to a major crop in sub-Saharan Africa include synchronous maturity, larger seeds, higher seed quality and yield, and resistant to diseases and insect pests. The objective of this study was to describe the nature and extent of genotypic variation among mungbean collections for a range of traits of potential agronomic and adaptive interests in Uganda.

MATERIALS AND METHODS

A total of 35 mungbean accessions (Table 1) were evaluated in contrasting environments to document the expression of 14 quantitative and 28 qualitative mungbean plant traits during plant growth (Bisht *et al*., 2005). The accessions consisted of 25 lines introduced from AVRDC in 2010; 7 lines earlier introduced from AVRDC by the Small grain Legumes Research Programme of

TABLE 1. List of mungbean and other genotypes used in the study and their origins

No.	Accession number	Country of origin
Mungbean lines newly (2010) acquired from AVRDC		
1.	V01128 A-G	India
2.	V01128 B-G	India
3.	V02366 A-G	India
4.	V02500 A-G	India
5.	V02551 A-G	India
6.	V02551 B-G	India
7.	V02757 A-G	India
8.	V02817 B-G	Nigeria
9.	V04679 B-BR	India
10.	V04717 B-G	India
11.	V05000 B-G	India
12.	V06094 A-Y	Philippines
13.	V06321 B-G	Taiwan
14.	V06322 A-G	Taiwan
15.	V06323 A-G	Taiwan
16.	V06327 A-G	Taiwan
17.	V06327 A-BR	Taiwan
18.	V06332 A-BR	Taiwan
19.	V06332 A-G	Taiwan
20.	V06342 A-G	Taiwan
21.	V06347 B-G	Taiwan
22.	TV01251 A-G	Indonesia
23.	TV03718 A-G	India
24.	TV03719 A-G	India
25.	TV03720 A-G	India
Mungbean lines acquired earlier (2008) from AVRDC		
26.	VC6153 (B-20)	
27.	VC6173 (B-10)	
28.	VC6148 (50-12)	
29.	VC6137 (B-14)	
30.	VC6372 (45-60)	
31.	KPSI	
32.	Mauritius	
33.	Black gram	
Mung and rice bean lines collected from farmers in Uganda		
34.	Sor I (Mungbean)	
35.	Sor II (Mungbean)	
36.	Pallisa (Mungbean)	
37.	Sor III Red (Ricebean)	
38.	Sor III Green (Ricebean)	

AVRDC = World Vegetable Centre

the National Semi-Arid Resources Research Institute (NaSARRI) Uganda and 3 local varieties collected from farmers in eastern Uganda. Additionally, 2 local ricebean lines collected from farmers in north western (West Nile region) Uganda and 1 blackgram line from AVRDC were included in the evaluation.

Four contrasting experimental environments were obtained by growing the accessions in 2 different growing seasons: September - December 2011 and April - August 2012; in 2 different sites: Makerere University Agricultural Research Institute Kabanyolo (MUARIK) and National Semi-Arid Resources Research Institute (NaSARRI) Serere, with the purpose of eliciting differential responses among the mungbean accessions to climatic conditions experienced during the two cropping seasons at the two sites.

MUARIK (0°28'N, 32°37'E; altitude 1285 m above sea level) is located in central Uganda, a region characterised by high rainfall (about 1300 mm) distributed in a bimodal pattern with an annual mean daily temperature of 24° C (Wortmann and Eledu, 1999). The soils are deep, highly weathered and classified as Latosols and Ferrallitic, with a pH of 5.0 - 6.0.

On the other hand, NaSARRI (0°32'N, 35°27'E; altitude 1140 m) is located in northeastern Uganda, a zone that has an average annual rainfall of 1100 mm also divided into two peaks. The annual mean daily temperature is about 26 ° C. The soils are sandy loams of medium to low fertility and soil pH 5.2 to 6.0 (Tumwegamire *et al.,* 2011).

Mungbean seeds were hand planted in 1.5 m^2 plots at a spacing of 10 cm within rows and 50 cm between rows. The plots were arranged in 8 blocks (5 plots within each block) within an alpha lattice design and replicated 3 times. Borders comprising of the local farmers' line were planted around the perimeter of each block.

Data collection. Twenty eight distinct qualitative and 14 quantitative descriptors of phenology, pod and seed traits and seed yield based on the Bisht *et al*. (2005) descriptor list (Table 2) were assessed. Plots were monitored regularly and data on dates for flowering (the appearance of the first

TABLE 2. List of mungbean genotypes descriptors studied/measured in Uganda

Serial number		Qualitative descriptors and their scores					
1.	Seed germination habit	1. Epigeal	2. Hypogeal				
2.	Attachment of primary leaves (at two leaf stage)	1. Sessile	2. Sub-sessile	3. Petiolate			
3.	Growth habit (recorded at first pod maturity)	1. Erect 2	Semi-erect	3. Spreading	4. Semi-prostrate	5. Prostrate	6. Climbing
4.	Stem colour	1– light green	2– dark green	3– light purple	4– dark purple	5– others	
5.	Leafiness (at 50% flowering)	1. Sparse	2. Intermediate	3. Abundant			
6.	Leaf pubescence	1. Glabrous	2. Very sparsely pubescent	3. Sparsely pubescent	4. Moderately pubescent	5. Densely pubescent	
7.	Petiole pubescence	1. Glabrous	2. Pubescent	3. Moderately pubescent	4. Densely pubescent		
8.	Lobbing of terminal leaflet (at first pod maturity)	1. Unlobbed	2. Shallow	3. Intermediate	4. Deep	5. Very deep	
9.	Terminal leaflet lobe shape	1. Lanceolate	2. Broadly ovate	3. Ovate	4. Rhombic	5. Others	
10.	Stipule size	1. Small	2. Medium	3. Large			
11.	Stipule shape	1. Ovate	2. Lanceolate	3. Others			
12.	Stem pubescence	1. Glabrous	2. Sparsely pubescent	3. Moderately pubescent	4. Highly pubescent		
13.	Raceme position (at first pod maturity)	1. Mostly above canopy	2. In upper canopy	3. Throughout canopy			
14.	Calyx colour	1. Green	2. Purplish green	3. Greenish purple	4. Others		
15.	Corolla colour	1. Yellow	2. Greenish yellow	3. Yellowish green	4. Green-purplish yellow	5. Others	
16.	Bracteole size	1. Small	2. Intermediate	3. Large			
17.	Bracteole shape	1. Linear	2. Lanceolate	3. Others			
18.	Flowering period	1. Asynchronous	2. Intermediate	3. Synchronous			
19.	Pod attachment to peduncle	1. Erect	2. Horizontal	3. Horizontal-pendent	4. Pendent	5. Others	
20.	Pod pubescence	1. Glabrous	2. Sparsely pubescent	3. Moderately pubescent	4. Densely pubescent		
21.	Pod curvature	1. Straight	2. Slightly curved	3. Curved (sickle shaped)			
22.	Pod beak shape	1. Pointed	2. Blunt	3. Others			
23.	Constriction of pod between seeds	1. Absent	2. Slight	3. Pronounced			

TABLE 2. Contd.

Serial number		Qualitative descriptors and their scores						
24.	Pod cross section	1. Semi flat	2. Round	3. Others				
25.	Seed shape	1. Globose	2. Ovoid	3. Narrowly ellipsoid	4. Cubical to oblong	5. Kidney shaped	6. Drum shaped	7. Others
26.	Seed colour	1. White	2. Cream	3. Light brown	4. Intermediate brown	5. Dark brown	6. Grey	7. Mottled grey 8. Mottled brown 9. Mottled cream 10. Light cream 11. Green brown 12. Chocolate 13. Black
27.	Lusture on seed surface	1. Absent	2. Present					
28.	Mottling on seed surface	1. Absent	2. Slight	3. Intermediate	4. Heavy			
29.	Hilum shape	1. Concave	2. Plain	3. Convex	4. Others			

Quantitative descriptors

1. Days to first flowering – Number of days from planting to appearance of first flower.
2. Days to maturity – Number of days from planting to 80% dry pods.
3. Terminal leaflet length (cm) – Length from base to the tip of expanded terminal leaflet.
4. Terminal leaflet width (cm) – Length of the widest part of an expanded terminal leaflet.
5. Petiole length (cm) – Length from point of attachment to point of attachment of trifoliate leaflets.
6. Peduncle length (cm) – Length from point of attachment to cluster of flowers.
7. Number of primary branches – counted at 80% maturity.
8. Plant height (cm) – Measured with a meter rule at harvest maturity, plants were stretched out to the tip.
9. Number of pods per plant – Counted at harvest maturity.
10. Number of pods per cluster – Counted at harvest maturity.
11. Pod length (cm)– Length from point of pod attachment to the tip of the pod taken after harvest.
12. Number of seeds per pod – Counted after harvest.
13. 100-seed weight (g) – Dried seeds were counted and weighed using a digital electric weighing scale.
14. Yield per plant (g) – Weight of dried seed from 3-5 well bordered plants was taken using a digital electric weighing scale and averaged to get seed yield per plant.

Source: Bisht *et al*. (2005)

flowers on 50% of plants), and the physiological maturity (85% of pods ripened) recorded. Data on phenology descriptors including terminal leaflet length (cm), terminal leaflet width (cm), petiole length (cm), plant height (cm), peduncle length (cm), number of primary branches; pod traits including number of pods per plant, number of pods per cluster, pod length (cm); and seed traits including number of seeds per pod, 100 - seed weight (g) and yield per plant (cm), were collected from a random sample of five well-bordered plants of each accession.

Data on 28 qualitative descriptors was used to draw a single link dendrogram, while data on the 14 quantitative descriptors were subjected to analysis of variance (ANOVA) using Genstat (4th Edition). Individual replication data were used for Additive Main Effects and Multiplicative Interactions (AMMI) analysis. Broad Sense Heritability (H) was estimated using variance components. An AMMI plot of the interactive principal component analysis (IPCA) scores and genotype-environment means, as well as a genotype plus genotype-by-environment variation (GGE) scatter bi-plot were drawn. Principal component scores and correlations were calculated using environmental means and overall means, respectively. All analyses were done using the 14th edition Genstat Statistical computer software.

RESULTS AND DISCUSSION

Ricebean genotypes had exceedingly high variable means, especially yield, compared to the mungbean genotypes in the sub-set evaluated (Table 3) and, thus, were excluded from further analysis. The mungbean genotypes were compared as groups according to where/when collected (Table 1), and there were significant differences in all quantitative traits across the two locations and the two seasons within and between these mungbean groups (Table 4). This suggests presence of a substantial amount of variability among the genotypes studied. However, since the grouping was based on geographic origin/distribution of genotypes, the observed genetic diversity may be misleading (Das *et al.,* (2010).

The coefficient of variation was highest for grain yield per plant across the four environments but error mean square for grain yield per plant was fairly low (Table 4). This indicates the highly variable but low yield of the evaluated genotypes.

TABLE 3. Four environment means (± se), range and standard deviations of farmer lines, AVRDC lines, NaSARRI mungbean collections, Black Gram and Rice Bean for 14 Quantitative Traits

Quantitative trait	Mungbean lines collected from farmer	Mungbean lines newly (2010) acquired from AVRDC	Mungbean lines acquired earlier (2008) from AVRDC	Black gram	Rice bean
Days to first flowering	48.3 ± 2.6	39.1 ± 1.5	38.2 ± 1.4	44.0 ± 1.2	53.2 ± 2.1
Days to 80 maturity	91.9 ± 7.0	71.1 ± 2.6	70.7 ± 2.0	92.9 ± 2.4	104.1 ± 1.4
Terminal leaflet length (cm)	9.7 ± 0.7	8.8 ± 0.9	8.7 ± 1.1	10.2 ± 1.1	10.6 ± 1.1
Terminal leaflet width (cm)	8.6 ± 0.8	6.9 ± 0.9	7.2 ± 1.1	6.1 ± 1.0	6.7 ± 0.8
Petiole length (cm)	13.1 ± 1.2	10.2 ± 1.4	9.8 ± 1.2	13.0 ± 1.9	17.1 ± 3.3
Peduncle length (cm)	4.8 ± 1.4	5.4 ± 1.4	6.1 ± 1.8	3.0 ± 1.0	10.5 ± 1.2
Number of primary branches	2.9 ± 0.6	1.8 ± 0.4	1.5 ± 0.3	2.9 ± 0.4	4.3 ± 0.8
Pods per plant	26.3 ± 7.5	15.0 ± 3.5	13.8 ± 3.0	44.6 ± 9.5	75.5 ± 14.9
Pods per cluster	3.6 ± 0.7	3.7 ± 0.5	3.6 ± 0.5	3.6 ± 0.3	4.9 ± 0.5
Plant height (cm)	41.8 ± 6.5	26.4 ± 4.5	28.5 ± 3.9	28.8 ± 9.1	101.4 ± 13.1
Pod length (cm)	7.4 ± 0.4	7.0 ± 0.5	8.4 ± 0.6	4.9 ± 0.3	9.1 ± 0.7
Seeds per pod	11.4 ± 1.1	10.0 ± 1.1	9.4 ± 1.0	6.7 ± 0.7	6.5 ± 0.8
100 seed weight (g)	3.5 ± 0.4	3.8 ± 0.4	5.3 ± 0.4	3.9 ± 0.4	6.7 ± 0.4
Grain yield per plant (g)	6.6 ± 2.1	3.9 ± 1.2	4.9 ± 1.5	8.6 ± 1.4	22.1 ± 6.0

VRDC = World Vegetable Centre

TABLE 4. Relative magnitudes of mungbean accessions (G) and accessions x environment (G x E) effects and broad sense heritability for selected traits of local and imported Mungbean lines when grown in 4 contrasting environments in Uganda

Source	Genotype	GXE	Error'	BSCGD	%CV
Degrees of freedom	35	105	256		
Days to first flowering	34.4***	2.9***	0.9	0.87	2
Days to 80 maturity	189.1***	12.3***	4.1	0.90	3
Terminal leaflet length (cm)	1.2***	0.5***	0.3	0.39	6
Terminal leaflet width (cm)	2.5***	0.5***	0.3	0.65	7
Petiole length (cm)	5.7***	1.7***	0.5	0.60	7
Peduncle length (cm)	2.1ns	2.0***	0.7	0.03	15
Number of primary branches	0.9***	0.2***	0.1	0.72	13
Pods per plant	158.9***	14.3***	5.7	0.85	14
Pods per cluster	0.1ns	0.2***	0.1	0.00	8
Plant height (cm)	116.8***	15.8***	7.0	0.77	9
Pod length (cm)	4.3***	0.2***	0.1	0.91	4
Seeds per pod	2.9***	0.8***	0.4	0.59	6
100 seed weight (g)	5.8***	0.2***	0.1	0.95	6
Grain yield per plant (cm)	7.4***	2.4***	0.7	0.57	19

BSCGD – Broad Sense Coefficient of Genetic Determination calculated on genotype means basis across environments. Trait level of significant difference: *: P<0.05; **: P<0.01; ***: P<0.001; ns = not significant

The low yield obtained can be attributed to high incidence and severity of Anthracnose (data not reported) among the genotypes. Broad Sense Coefficient of Genetic Determination (BSCGD) estimating Broad Sense Heritability (H), was fairly high for the majority of the measured traits (Table 4). This suggests that genetic variance was far more important than variability due to environment as asserted by Bernardo, 2002, further implying that the mungbean traits studied can be selected with fewer challenges.

From AMMI ANOVA, environments were significantly different for all the measured traits (Table 5). Additionally, both Generalised Linear and AMMI ANOVA showed significant (P<0.001) genotype-environment interactions (GEI) for all measured traits. This implies that the assembled lines did not perform consistently across the environments and, therefore, it would be beneficial to evaluate the genotypes in more than one environment (Yan and Kang, 2003). An AMMI biplot using grain yield per plant showed genotypes 13 (V06321 B-G) and 18 (V06332 A-BR) as the most stable; while genotype 34 (Sor I) as the most unstable across the environments (Fig. 1). The unstable genotypes 1 (V01128 A-G), 23 (TV03718 A-G), 34 (Sor 1) and 36 (Pallisa) were responsible for the significant GEI observed in the Generalised Linear ANOVA and AMMI ANOVA. A symmetric scaling of genotype plus genotype-by-environment variation (GGE) scatter plot showed that the four environments were in different sectors of the plot (Fig. 2). This is a case of crossover G - E interaction, implying that the target environment may be divided into different sub-environments (Yan *et al.,* 2007). Subsequently, NaSARRI and MUARIK 2011B were grouped together as mega environments; while NaSARRI and MUARIK 2012A were unique environments, when the criteria of Yan and Rajcan (2002) was used. The winning genotypes in the experimental environments as illustrated in Figure 2 are the local genotype SOR II (35) in MUARIK 2012A environment, Blackgram (33) and MUARIK 2011B and NaSARRI 2011B (32) in environments NaSARRI 2012A.

There were positive and significant linear correlations between yield and early maturity, as well as leaf size and petiole length (Table 6). Whereas the common concept is that there is a trade-off of reduced yield in selecting early maturity (Gambin and Borrás, 2010), there was an increase in yield in early maturing mungbean lines, possibly due to a large photosynthetic area/leaf size (Borrel *et al*., 2000). This is further affirmed by the relation between yield traits, traits related

TABLE 5. AMMI ANOVA for 14 mungbean quantitative traits from 4 environments in Uganda

Source	Total	Trts	Gen	Envt	R/Envt	GXE	IPCA	IPCA	Res	Errors
Degrees of freedom	431	143	35	3	8	105	37	35	33	280
Days to first flowering	21.8	60.1***	102.2***	1367***	4.7ns	8.7***	17.1***	6.4***	1.7***	2.8
Days to 80 maturity	113	313.1***	567.8***	7018***	33.1*	366.6***	85.0***	13.0ns	7.5ns	13.1
Terminal leaflet length (cm)	2.8	6.3***	3.5***	202***	8.1***	1.6***	2.4***	1.3*	1.1ns	0.9
Terminal leaflet width (cm)	3.3	7.3***	7.3***	212***	19.5***	1.5***	2.4***	1.0ns	1.0ns	0.8
Petiole length (cm)	7.2	17.5***	17.5***	449***	8.5***	5.2***	9.0***	4.1***	2.1ns	1.8
Peduncle length (cm)	13.4	34.9***	6.6***	1361***	23.2***	6.4***	12.9***	4.9***	0.6ns	2.2
Number of primary branches	0.8	1.9***	2.8***	40***	1.2***	0.5***	1.0***	0.4***	0.2ns	0.2
Pods per plant	71.8	178.9***	479.5***	1434***	62.0***	42.8***	74.0***	31.3**	20.1ns	17.4
Pods per cluster	0.5	0.9***	0.4ns	20***	0.6*	0.5***	0.7***	0.5**	0.4*	0.3
Plant height (cm)	115.3	289.1***	375.4***	7644***	209.7***	50.1***	88.8***	37.1*	20.7ns	23.9
Pod length (cm)	1.6	4.3***	13.0***	28***	0.6*	0.7***	1.1***	0.6***	0.3ns	0.2
Seeds per pod	2.4	4.9***	8.8***	48***	2.4*	2.3***	3.3***	2.4***	1.1ns	1.1
100 seed weight (g)	1.8	5.2***	17.4***	27***	0.5**	0.5***	0.7***	0.4***	0.2ns	0.2
Grain yield per plant (cm)	7.9	19.3***	22.3***	410***	11.8***	7.2***	14.8***	4.3***	1.8ns	2

Trait level of significant difference; * at P<0.05, ** at P<0.01, *** at P<0.001 and ns = none significant

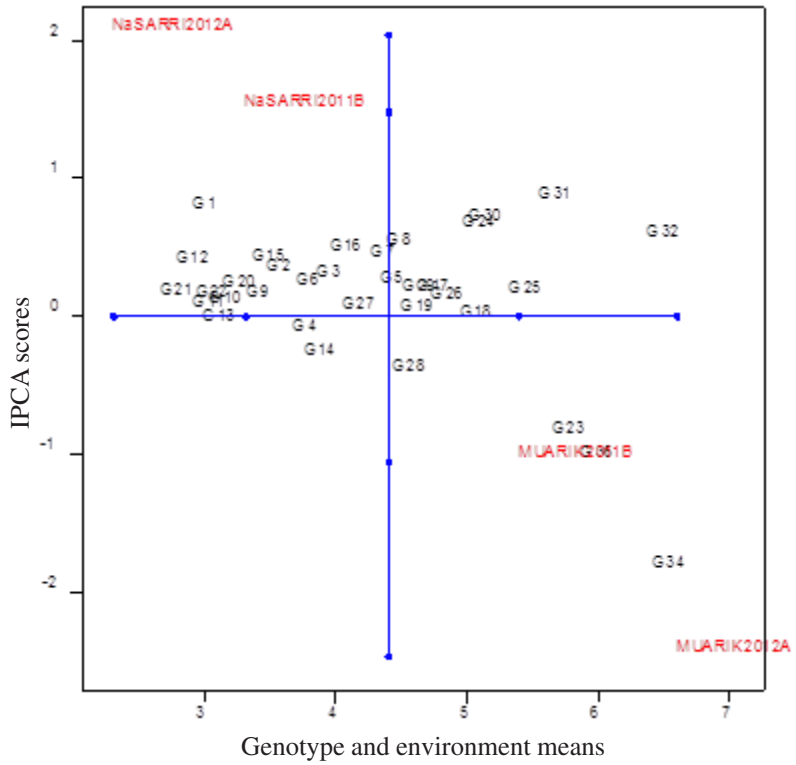

Figure 1. An AMMI biplot using mean yield per plant (Seasons: 2011B = September – December 2011; 2012 = April – August 2012) in Uganda.

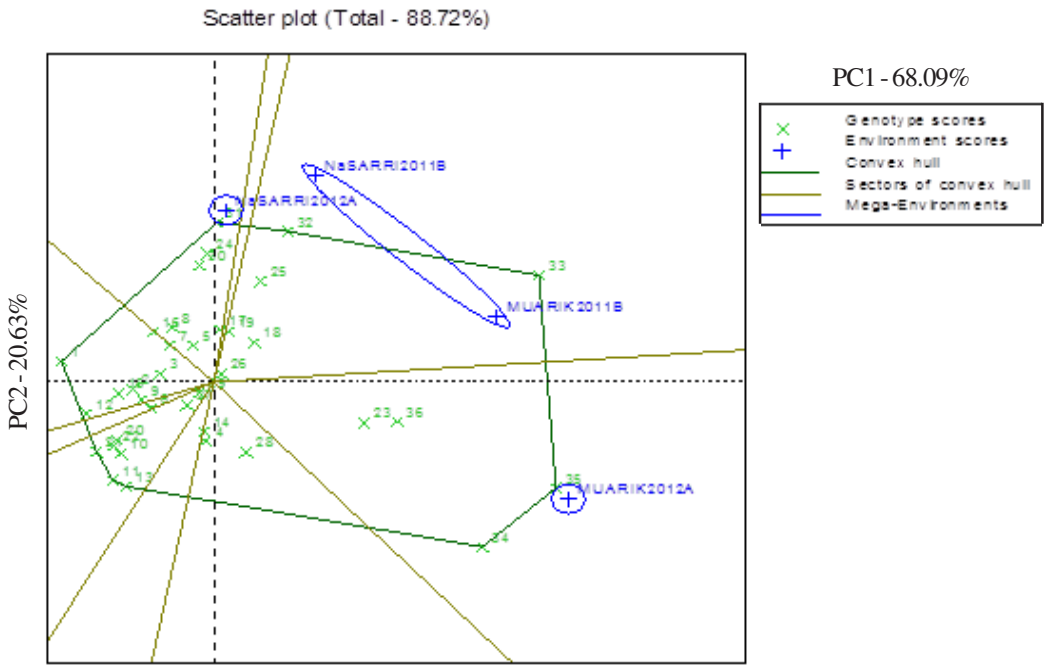

Figure 2. A symmetric scaling GGE scatter plot showing genotype scores, winning genotypes and mega environments seasons: 2011B = September – December 2011, 2012A = April – August 2012.

TABLE 6. Correlation coefficients between measured traits for mungbean genotypes evaluated in Uganda

	DTFF	DTM	TLL	TLW	PetL	PedL	Prim Br	PPPlt	PPClu	Plt Ht	PodL	SPP	100SW
DTM	0.92***	-											
TLL	0.58***	0.72***	-										
TLW	0.45**	0.44**	0.68***	-									
PetL	0.81***	0.84***	0.79***	0.64***	-								
PedL	-0.39*	-0.54***	-0.36*	0.14	-0.34*	-							
Prim Br	0.84***	0.82***	0.60***	0.28	0.74***	-0.58***	-						
PPPlt	0.68***	0.85***	0.61***	0.07	0.67***	-0.65***	0.75***	-					
PPClu	-0.15	-0.19	-0.29	-0.23	-0.15	-0.15	-0.02	-0.09	-				
Plt Ht	0.79**	0.76***	0.66***	0.69***	0.79***	-0.07	0.60***	0.49**	-0.19	-			
PodL	-0.14	-0.20	-0.01	0.46**	-0.10	0.58***	-0.39*	-0.52**	-0.40*	0.06	-		
SPP	0.36*	0.09	-0.05	0.36*	0.15	0.18	0.22	-0.26	0.16	0.31	0.11	-	
100SW	-0.27	-0.20	0.03	0.32	-0.13	0.43**	-0.45**	-0.35*	-0.35*	-0.14	0.84***	-0.22	-
YPPlt	0.57***	0.69***	0.66***	0.52**	0.63***	-0.14	0.44**	0.58***	-0.41*	0.51**	0.31	-0.11	0.48**

Level of correlation coefficient significant difference from zero: * at P<0.05, ** at P<0.01, *** at P<0.001. DTFF = Days to First flowering, DTM 80% = Days to 80% Maturity, TLL = Terminal Leaflet Length, TLW = Terminal Leaflet Width, PetL = Petiole Length, PedL = Peduncle Length, Prim Br = Number of Primary Branches, PPPlt = Pods Per Plant, PPClu = Pods Per Cluster, Plt Ht = Plant Height, PodL = Pod Length, SPP = Seeds Per Pod, 100 SW = 100 Seed Weight, YPPlt = Yield Per Plant

TABLE 7. First 4 of 14 Principal Components using 14 mungbean traits averaged across four environments in Uganda

	1	2	3	4
Days to first flowering	0.26	0.14	0.28	-0.42
Days to 80 maturity	0.66	0.01	0.54	-0.10
Terminal leaflet length (cm)	0.04	0.01	0.00	0.10
Terminal leaflet width (cm)	0.03	0.12	0.06	0.13
Petiole length (cm)	0.10	0.06	0.02	0.04
Peduncle length (cm)	-0.04	0.09	-0.04	0.12
Number of primary branches	0.04	-0.01	0.01	-0.08
Pods per plant	0.55	-0.64	-0.41	0.18
Pods per cluster	0.00	-0.01	-0.02	-0.04
Plant height (cm)	0.42	0.71	-0.52	0.13
Pod length (cm)	-0.03	0.14	0.22	0.33
Seeds per pod	0.00	0.12	0.09	-0.28
100 seed weight (g)	-0.03	0.06	0.28	0.55
Grain yield per plant (cm)	0.09	0.01	0.22	0.47
Latent roots	105.46	18.44	4.32	2.96
Variation (%)	79.28	13.86	3.25	2.22
Trace	133			

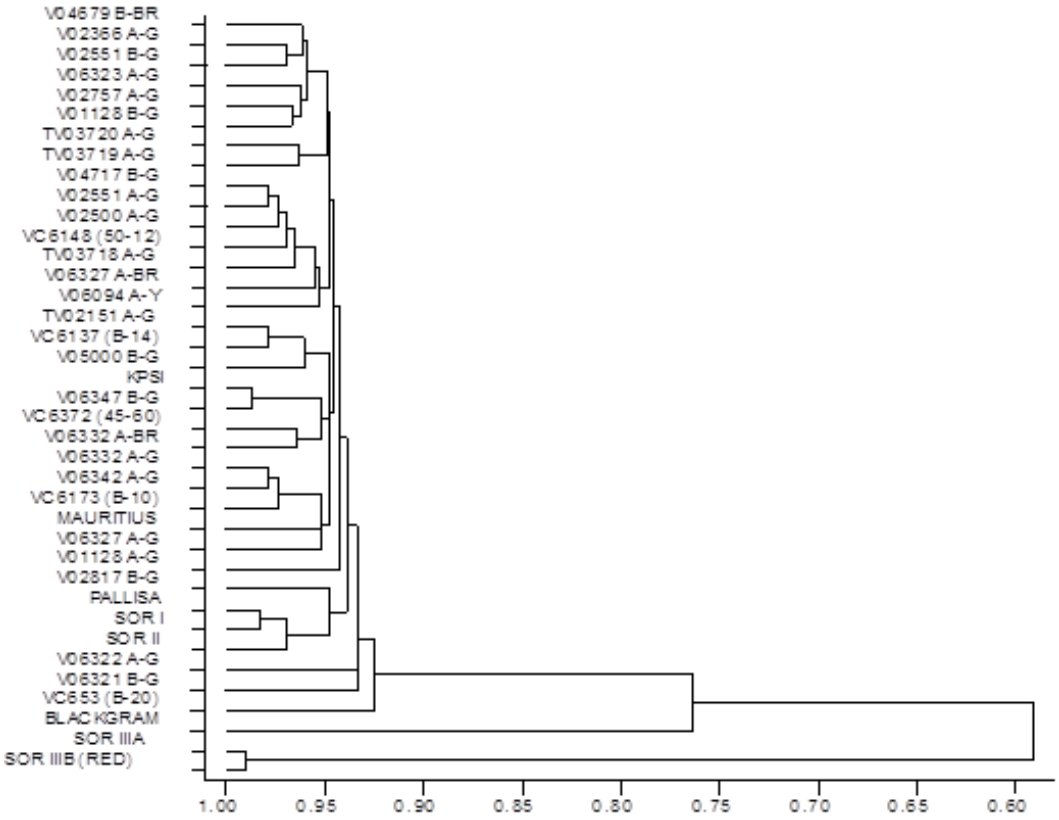

Figure 3. A single link dendrogram using qualitative descriptors of mungbean evaluated in Uganda.

to plant vigour and earliness (Table 6). Seed size, which is a critical mungbean trait, was positively correlated with seed yield, implying that large seeded and high yielding lines can easily be selected together (Mishra and Singh, 2012).

Principal Component Analysis (PCA) using genotype means of 14 quantitative descriptors showed that the first two Principal Components jointly accounted for 93% of the observed variation (Table 7). Days to maturity, pods per plant and plant height were the most important traits. Since a very large amount of variability was explained by the first two Principal Components, it can be inferred that there is narrow diversity in the evaluated genotypes, contrary to the inferance from analysis of variance (Table 4).

A dendrogram constructed using data of 28 qualitative descriptors showed 90-100% similarity among the genotypes (Fig. 3). This implies that, either the morphological markers were not polymorphic enough or there is less genetic distance among the mungbean lines. Genotype V06321 B-G (newly acquired from AVRDC in 2010) and genotype VC6153 (B-20) (earlier acquired by NaSARRI from AVRDC in 2008) were not separated suggesting that they are either duplicates or closely related. Comparing mungbean to its close relatives, namely blackgram (*Vigna mungo*) and ricebean (*Vigna umbellata*), revealed a 75 % and 60 % similarity, respectively. All local farmers' lines were grouped in the same cluster indicating that they may be closely related.

Based on the comparison of a sub-set of the mungbean accessions collected thus far in Uganda, the genetic variability for characters of economic importance that were studied would be sufficiently extensive for progress in a mungbean breeding programme. The close similarity between mungbean and its closest relatives, blackgram and ricebean, may indicate that transfer of genes from these relatives into mungbean would be relatively straightforward. These mungbean relatives have genes for disease resistance and nutritional quality, factors that would be useful in mungbean (Poehlman, 1991) but so far not much success has been accomplished in transferring genes for useful characters from related species to mungbean (James *et al.*, 1999). The GGE was significant for stability and performance of the mungbean subset evaluated, thus necessitating further multi-location and multi-season trials to improve the breeding and selection efficiency.

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