ADAPTATION OF INTRODUCED MUNGBEAN GENOTYPES IN UGANDA

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ABSTRACT

Mungbean (*Vigna radiata* (L.) Wilczek) is an important source of nutrients and income for smallholder farmers in East Africa. Mungbean production in countries like Uganda largely depends on landraces, in the absence of improved varieties. In order to enhance productivity, efforts have been underway to develop and evaluate mungbean varieties that meet farmers' needs in various parts of the country. This study was conducted at six locations in Uganda, to determine the adaptability of introduced mungbean genotypes, and identify mungbean production mega-environments in Uganda. Eleven genotypes (Filsan, Sunshine, Blackgram, Mauritius1, VC6148 (50-12), VC6173 (B-10),Yellowmungo, KPS1, VC6137(B-14),VC6372(45-60),VC6153(B-20P) and one local check were evaluated in six locations during 2013 and 2014. The locations were; National Semi Arid Resources Research Institute (NaSARRI), Abi Zonal Agricultural Research and Development Institute (AbiZARDI),Kaberamaido variety trial center, Kumi variety trial center, Nabuin Zonal Agricultural Research and Development Institute (NabuinZARDI), and Ngetta Zonal Agricultural Research and Development Institute (NgettaZARDI). G × E interactions were significant for grain yield. Through GGEBiplot analysis, three introduced genotypes (Filsan, Blackgram and Sunshine) were found to be stable and high yielding, and therefore, were recommended for release. The six test multi-locations were grouped into two candidate mega-environments for mungbean production (one comprising of AbiZARDI and Kaberamaido and the other comprising of NaSARRI, NabuinZARDI, Kumi, and NgettaZARDI). National Semi Arid Resources Research Institute (NaSARRI) was the most suitable environment in terms of both discriminative ability and representativeness and therefore can be used for selection of widely adaptable genotypes.

Key Words: Biplot, mega-environment, *Vigna radiata*

RÉSUMÉ

La fève (*Vigna radiata* (L.) Wilczek) est une importante source de nutriments et de revenu pour les paysans en Afrique de l'Est. La production de la fève dans des pays comme Ouganda dépend largement des variétés locales, à défaut des variétés améliorées. Dans le but d'accroitre la productivité, des efforts ont été fournis pour développer et évaluer les variétés de fèves pouvant satisfaire les besoins des producteurs dans différents coins du pays. La présente étude a été conduite dans six emplacements en Ouganda, en vue de déterminer l'adaptabilité de variétés introduites de fèves et identifier les zones majeures de production de fèves. Onze variétés introduites (Filsan, Sunshine, Blackgram, Mauritius1, VC6148 (50-12), VC6173 (B-10),Yellowmungo, KPS1, VC6137(B-14),VC6372(45-60),VC6153(B-20P) et une variété locale utilisée ici comme témoin, ont été évaluées dans six emplacements au cours des années 2013 et 2014. Les emplacements étaient : l'Institut Nationale de Recherche sur les Ressources Semi-Aride (NaSARRI), l'Institut Zonale de Recherche Agricole et Développement de Abi (AbiZARDI), le centre d'expérimentation des variétés de Kaberamaido, le centre d'expérimentation des variétés

de Kumi, l'Institut Zonale de Recherche Agricole et Développement de Nabuin (NabuinZARDI) et l'Institut Zonale de Recherche Agricole et Développement de Ngetta (NgettaZARDI). L'interaction génotypes et environement G × E était significatif pour le rendement en grain. Une analyse se servant de biplot, a révélé trois stables variétées introduites (Filsan, Blackgram and Sunshine), ayant des rendements élevés. Ces trois variétées sont donc recommendées pour être lancées. Les six emplacements utilizes dans cette étude peuvent être groupés en deux grandes zones proprices à la production de la fève (la première zone est constituée de AbiZARDI et Kaberamaido, tandis que la seconde est faite de NaSARRI, NabuinZARDI, Kumi et NgettaZARDI). NaSARRI s'est révélé l'emplacement le plus propice, en ce sens que cet emplacement était le plus discriminant et le plus représentatif, et de ce fait peut être utilisé pour sélectionner des variétées à large adaptation.

Mots Clés: Biplot, zones majeures, *Vigna radiata*

INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek), also known as greengram, is an important pulse crop not only in the Indian sub-continent where it has been cultivated for centuries, but also globally, where it serves both as a food crop and source of income (Mogotsi, 2006). The crop is rich in nutrients, especially proteins (23-25%) and micronutrients (iron and zinc), and is associated with low ant-nutritional factors such as those which cause flatulence, making it a suitable food for weaning babies (Paul *et al*., 2011; Puranik *et al*., 2011). Mungbean is considered a wonder crop due to its ability to tolerate or escape drought conditions, yet has short maturity periods and improves soil fertility through biological nitrogen fixation (Swaminathan *et al*., 2012).

In Uganda, mungbean is widely grown by smallholder farmers in the eastern and northern regions of the country (Ibedo, 2014). However, these regions are characterised by variable climatic, edaphic, biotic and land use patterns, which influence productivity of the crop (Wortmann and Eledu, 1999). Therefore, new adaptable varieties are needed to ensure profitable and sustainable production of mungbean in these areas. The new varieties must show high performance in terms of yield and other important agronomic traits. Moreover, the good performance must be reliable over a wide range of environmental conditions (Annicchiarico, 2002).

A difference in yield stability among genotypes where the performance of any one of the genotypes relative to the remaining genotypes grown in the same environment is inconsistent, is due to the wide occurrence of genotype x environment interactions (G x E). Growing awareness of the importance of G x E interactions has led crop genotypes to be assessed in multi-environment/ regional trials before variety recommendation or for the final stages of elite breeding material selection. This is because in this *era* of niche-specific variety development, G x E effects should not be ignored, rather analysed using appropriate techniques in order to explore their potential opportunities and disadvantages (Annicchiarico, 2002).

Information from multi-environment trials can help breeding programmes to understand the type and size of the G x E interactions expected in a given region, and reasons for their occurrence as well as defining a strategy to successfully cope up with the effects of interactions (Annicchiarico, 2002). Presence of G x E effects of a crossover nature results in change of variety ranking from one environment to another and this has strong implications for breeding for specification adaptation. This is important to a plant breeding programme in allocation of resources, increasing the efficiency of testing and breeding programmes, and targeting of genotypes to appropriate production areas (Yan and Tinker, 2006). Under Ugandan regulations, imported/ introduced varieties can only be recommended for release after evaluation in variety performance trials for at least two growing seasons (Seeds and Plant Act, 2006).

The objective of this study was to determine the adaptability and stability of introduced mungbean varieties in different environments of Uganda, and identify mungbean production mega environments in Uganda.

MATERIALS AND METHODS

Field trials of introduced mungbean genotypes (Table 1) were conducted at five locations (Table 2) during 2013 - 2014 cropping seasons. Each location and season constituted an environment, giving a total of eleven evaluation environments. The trial sites represented diverse environments in terms of climate, edaphic, biotic and land use patterns (Wortmann and Eledu, 1999).

In all trial sites for the entire study period, genotypes were planted in 2.4 m × 3 m plots at a spacing of 60 cm × 30 cm. A randomised complete block design (RCBD), with three replicates for each genotype, was used across seasons and sites. Plots within each replicate/block were separated from each with a space of two metres. In each season, experimental plots were kept free of weed by hand-hoeing. Pre-flowering pests, especially aphids were controlled by 1-2 sprays (depending on pest pressure) using Dimethoate 40%EC. Post-flowering pests such as flower thrips (*Megalurothrips sjostedti* Trybom), pod borers (*Maruca vitrata* Fabricius) and pod sucking bugs were controlled by 2-3 insecticide sprays using Profenofos 40% + Cypermethrin 4% starting from the budding stage.

At physiological maturity, all pods from all plants within each plot (7.2 m^2) were handpicked (two pickings), sun-dried for three to four days before threshing and winnowing. The threshed grain was weighed on a plot basis and later extrapolated to yield per hectare. A combined analysis of variance (ANOVA) across trial sites was conducted to assess the significance of genotype × environment interactions, using R Software, Version 3.2.1 (R Core Team, 2015). The following ANOVA model was adopted:

$$Y_{ij} = w + G_i + E_j + GE_{ij} + e_{ij} \dots\dots\dots\dots\dots (1)$$

Where:

Y_{ij} is the yield response of genotype i in environment j, w is the grand mean, G, E and GE indicate the effects of genotype, environment and genotype by environment interactions respectively and e is random error. GGE biplots were generated using the GGEBiplotGUI-package (Frutos *et al*., 2014) implemented in R Software. GGE biplot analysis was based on model 13 (Yan and Tinker, 2006), since it simultaneously considers genotypic main effects and genotype x environment interactions. Model 13 (environment centered) is expressed as follows:

$$P_{ij} = Y_{ij} - \mu - \beta_j = \alpha_i + \phi_{ij} \dots\dots\dots\dots (2)$$

Where:

i is the value of genotype in environment j, Y_{ij} is the genotype by environment two way table, μ is

TABLE 1. List of mungbean varieties evaluated in an adaptation study in Uganda

Genotype code	Genotype name	Parentage	Species	Source
G1	Blackgram	Unknown	*Vigna mungo*	AVDRC
G2	Filsan	CES 59/ML-5	*Vigna radiata*	AVDRC
G3	KPS1	CES ID-21/EG-MG-16	*Vigna radiata*	AVDRC
G4	Localgram (check)	Local germplasm	*Vigna radiata*	NaSARRI
G5	Mauritius1	Unknown	*Vigna radiata*	AVDRC
G6	Sunshine	Unknown	*Vigna radiata*	AVDRC
G7	VC6137(B-14)	Unknown	*Vigna radiata*	AVDRC
G8	VC6148(50-12)	Unknown	*Vigna radiata*	AVDRC
G9	VC6153(B-20P)	VC 1560A/VC 6370-92	*Vigna radiata*	AVDRC
G10	VC6173(B-10)	VC 1560A / VC 6370-92	*Vigna radiata*	AVDRC
G11	VC6372(45-60)	VC 6370-92/VC 6371-93	*Vigna radiata*	AVDRC
G12	Yellowmungo	Unknown	*Vigna radiata*	AVDRC

AVDRC = Asian Vegetable Development and Research Centre (The World Vegetable Centre), NaSARRI= National Semi Arid Resources Research Institute

TABLE 2. Description of six experimental sites used to evaluate mungbean genotypes in an adaptation study in Uganda

Geographical variable	Locations					
	AbiZARDI	Kaberamaido	Kumi	Nabuin	Ngetta	NaSARRI
Coordinates	3°4.58'N/	1°41'46.80N/	1°29'02.39N/	2°29'30.00N/	2°18'27.44N/	01°32'229N/
	30°56.74'E	33°12'49.86E	33°56'28.90E	34°35'49.68E	32°55'44.45E	033°26'86E
Altitude (m)	1206	1048.5	1150.32	1282.3	1125	1131
Soil type	Sandy	Sandy	Sandy loam	Sandy loam	Sandy	Loam
[1]AEZ	NWFWS	NMF	SELKB	NESGPS	NMF	SELKB
Season A Temp in °C (min)	19.5	18.1	17.8	17.6	17.3	18.3
Season A Temp in °C (max)	31.7	29.8	29.4	29.6	29.6	29.7
Season A rainfall (mm)	391	547	573	359	540	598
Season B Temp in °C (min)	17.9	17.4	16.9	16.8	162.2	17.6
Season B Temp in °C (max)	29.8	29.7	29.2	29.6	29	29.9
Season B rainfall (mm)	545	543	415	292	581	504

Source: Wortmann and Eledu, (1999): [1]AEZ = agro-ecological zone: NWFWS = North Western Farmland- Wooded Savanna, NMF = Northern Moist Farmlands, SELKB = Southern and Eastern Lake Kyoga Basin, NESGPS = North-eastern Short Grass Plains with Sandy Soils. Season A = first planting season and season B = second planting season

the grand mean, α_i is the genotype (row) main effect, β_j is the environment (column) main effect, ϕ_{ij} is the specific genotype by environment interaction, P_{ij} is the matrix that is subjected to singular value decomposition (SVD).

RESULTS AND DISCUSSION

There were significant (P<0.05) genotype (variety) x environment interactions (G x E) (Table 3). The genotypic and environmental main effects were, however, highly significant (P<0.001). For genotypes grown in a wide range of environments, G x E interactions especially of a cross-over type (qualitative) are common (Ceccarelli, 2012) and these pose a serious problem to breeders in choosing the best variety,

as this decision depends considerably on where the comparison is conducted. Eisemann *et al*. (1990) proposes that when G × E interactions are present, they should either be avoided by selecting material that is broadly adapted to the entire range of target environments, or exploited by selecting a range of material, each adapted to a specific environment (Ceccarelli, 1989).

Across the test environments, the highest yielding greengram genotype was Filsan, with a mean yield of 491 kg ha⁻¹; while the poorest was VC6153 (B-20P), with a mean yield of 360.1 kg ha⁻¹ (Table 4). The highest yielder in the highest yielding site (Kumi), was the local check (732.4 kg ha⁻¹); while the lowest yielder in Kumi was KPS1 (521.1 kg ha⁻¹). AbiZARDI was the lowest yielding site with Sunshine and Yellowmungo

TABLE 3. Analysis of variance for grain yield among 12 mungbean genotypes grown in 11 environments in Uganda

Source of variation	Df	Sum sq	Mean sq	F value	P value
Environment	10	9884566.85	988456.68	63.33	<0.001
Genotype	11	846853.32	76986.67	4.93	<0.001
Replicate	2	3584.79	1792.39	0.115	0.891
Environment x replicate	19	337343.79	17754.94	1.14	0.315
Environment x genotype	110	2476306.96	22511.88	1.44	0.011
Residuals	229	3574318.63	15608.38		

TABLE 4. Yield (kg ha⁻¹) of 12 mungbean genotypes evaluated at six sites in Uganda

Genotype code	Genotype name	Experimental sites						Genotype mean
		Abi	Kaberamaido	Kumi	Nabuin	Ngetta	NaSARRI	
G1	Blackgram	351.9	525.5	675.0	379.6	386.1	526.5	486.9
G2	Filsan	389.4	532.4	627.8	347.2	435.5	532.1	491.0
G3	KPS1	258.6	497.7	521.1	335.6	387.0	269.0	364.5
G4	Check	299.4	544.0	732.4	381.9	415.0	412.3	464.7
G5	Mauritius1	328.3	625.0	593.1	324.1	320.3	320.6	401.7
G6	Sunshine	396.9	625.0	632.2	439.8	413.3	347.9	455.7
G7	Vc6137(B-14)	254.2	472.2	606.5	319.4	239.0	339.6	368.0
G8	Vc6148(50-12)	240.0	555.6	580.6	379.6	459.3	319.2	409.9
G9	Vc6153(B-20P)	245.3	544.0	578.7	358.8	244.8	294.0	360.1
G10	Vc6173(B-10)	266.7	509.3	633.1	347.2	285.0	335.9	388.6
G11	Vc6372(45-60)	276.7	497.7	578.2	358.8	268.9	283.0	364.5
G12	Yellowmungo	135.3	506.9	668.1	356.5	415.0	371.9	409.8
Site mean		286.9	536.3	618.9	360.7	355.8	361.8	413.7

having the highest and lowest yield values, respectively. The yield of genotypes obtained was generally lower than in previous studies (Asfaw *et al*., 2011; Pratap *et al.*, 2013) and this may partly be attributed to low plant density (60 cm x 30 cm) used in this study compared to 30 cm x 10 cm in previous studies conducted at Awassa, Gofa and Inseno in southern Ethiopia and Kanpur in India respectively. This relatively low plant density allowed the genotypes to express more vegetative growth (more branches and leaves, broader leaf surface area) than reproductive growth (grain yield). Similar observations were made while evaluating effect of plant density on vegetative growth and yield performance of French bean (Pawar *et al.* 2007) and peanut (Giayetto *et al.,* 1998).

Analysis of G x E using GGEBiplot gave a good visual assessment with PCA1 (Axis 1) and PCA2 (Axis 2), explaining 70.47% of the total G x E sums of squares. GGEBiplot allows for effective evaluation of genotype stability (G x E) and mean performance (genotypic main effects) (Blanche *et al*., 2007) and was, therefore, used to determine stability among the mungbean genotypes. Mungbean genotypes further along the average tester axis (ATA), away from the biplot origin and in direction of the arrow (to the left), exhibited higher mean performance (Fig. 1). Therefore, the genotypes that gave higher yield values were in the order of Filsan (G2) >Blackgram (G1) >Sunshine (G6) > local check (G4); while the lowest yielding genotype was VC6153(B-20P) (G9).
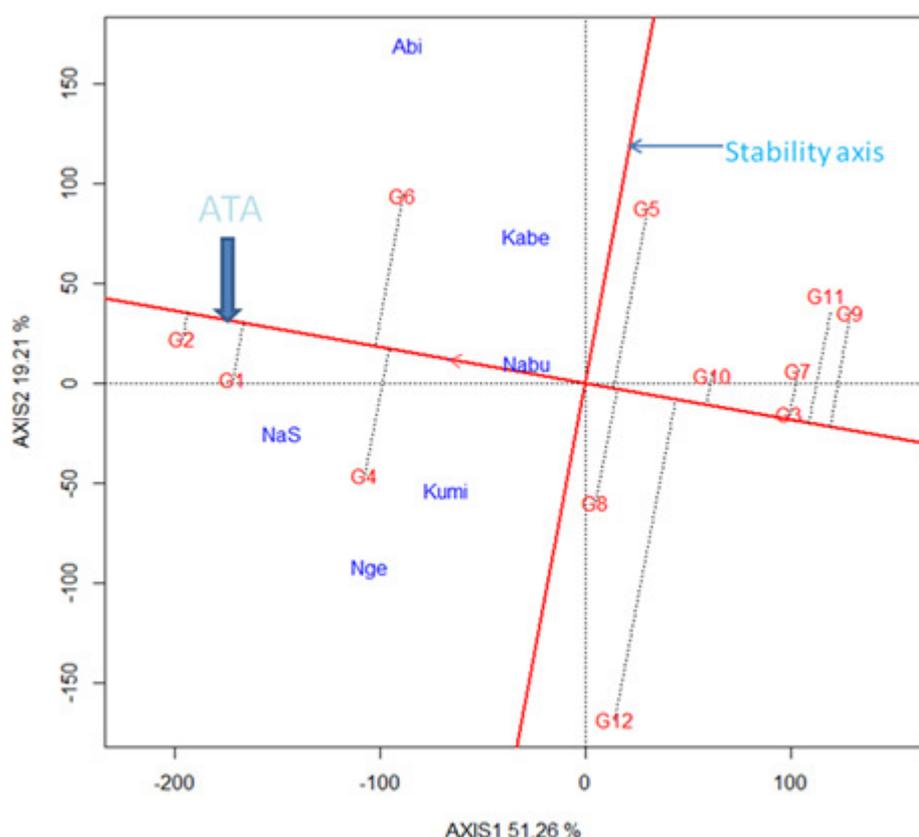

Figure 1. Biplot showing mean grain yield and yield stability of mungbean genotypes. The biplot was tester-centered; SVP = row-metric preserving; data not scaled. Kabe =Kaberamaido TVC, Nabu =NabuinZARDI, NaS =NaSARRI, Kumi =Kumi TVC, Nge = NgettaZARDI, Abi = AbiZARDI. Genotype names are as in Table 1.
[1]Genotypes further to the left along the ATA in the direction of the single arrow yield more
[2]Genotypes further away from the ATA in either direction of the stability axis are less stable

The stability of the genotypes was graphically represented by the projection from the genotype to the stability axis (Fig. 1). The longer the projection away from the average tester axis (ATA), regardless of direction, the greater was the G x E interaction and, therefore, the lower was, the stability of the genotype across test locations (Ceccarelli, 2012). In this case, the most stable genotypes were G3> G2 >G10 > G7 > G1, while the most unstable genotype was G12.

Simultaneous selection for ideal genotypes (those with high mean performance and high stability), was carried out with the aid of concentric circle biplot (Blanche *et al.*, 2007) (Fig. 2). Genotypes at/or closer to centre of the concentric circles were referred to as ideal genotypes (Yan, 2001) and on this basis, the most desirable genotypes were G2, G1,G4 and G6 being greater than the grand mean. These four genotypes gave the best combination of yield and stability (Ceccarelli, 2012).

The remaining eight genotypes were undesirable, since they were unstable and also low yielding (lower than the genotype grand mean of 413.7 kg ha^{-1}) (Table 4). This is in agreement with a recent study by Mbeyagala *et al.* (2015) in which a yield stability statistic (YS_i) proposed by Kang (1993) identified the same genotypes (G2, G1, G4 and G6) as being high yielding and stable.

The six test sites used in this study, could only be grouped into two mega-environments (Fig. 3), the first mega-environment comprising of two sites (AbiZARDI and Kaberamaido TVC) with only a single winning genotype (G6).

The second mega-environment comprised of NabuinZARDI, NaSARRI, Kumi TVC and NgettaZARDI with winning genotypes (G1, G4 and G2). G2 was the highest yielding genotype in
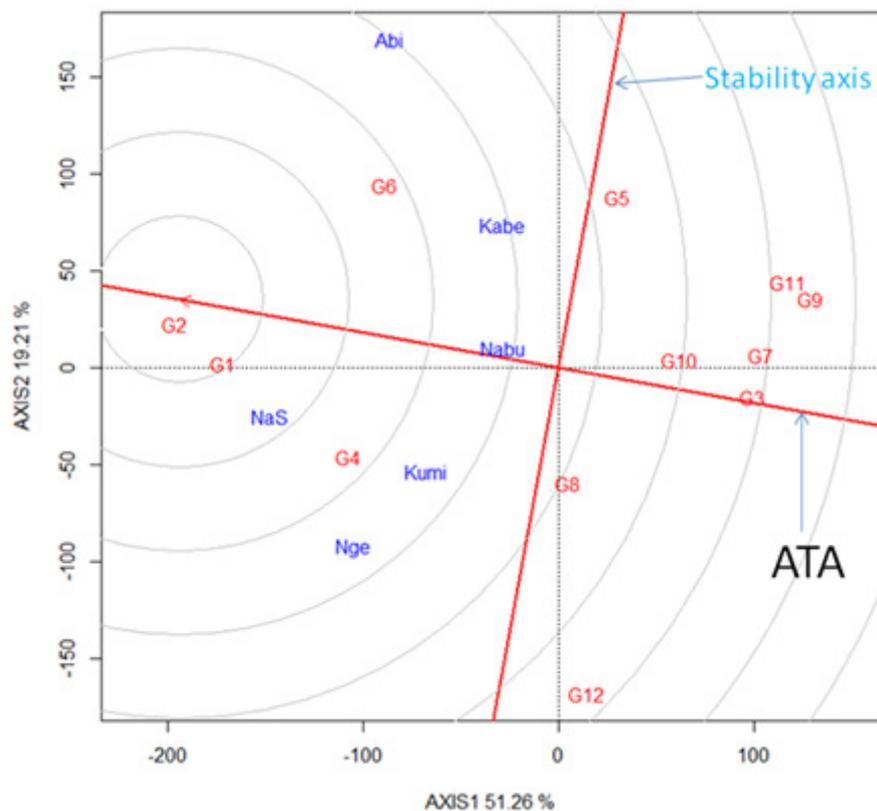

Figure 2. Biplot of concentric circles ranking mungbean genotypes for yield and yield stability. The biplot was tester-centered; SVP = row-metric preserving; data not scaled. Names of sites are as in Figure 1. Genotype names are as in Table 1.
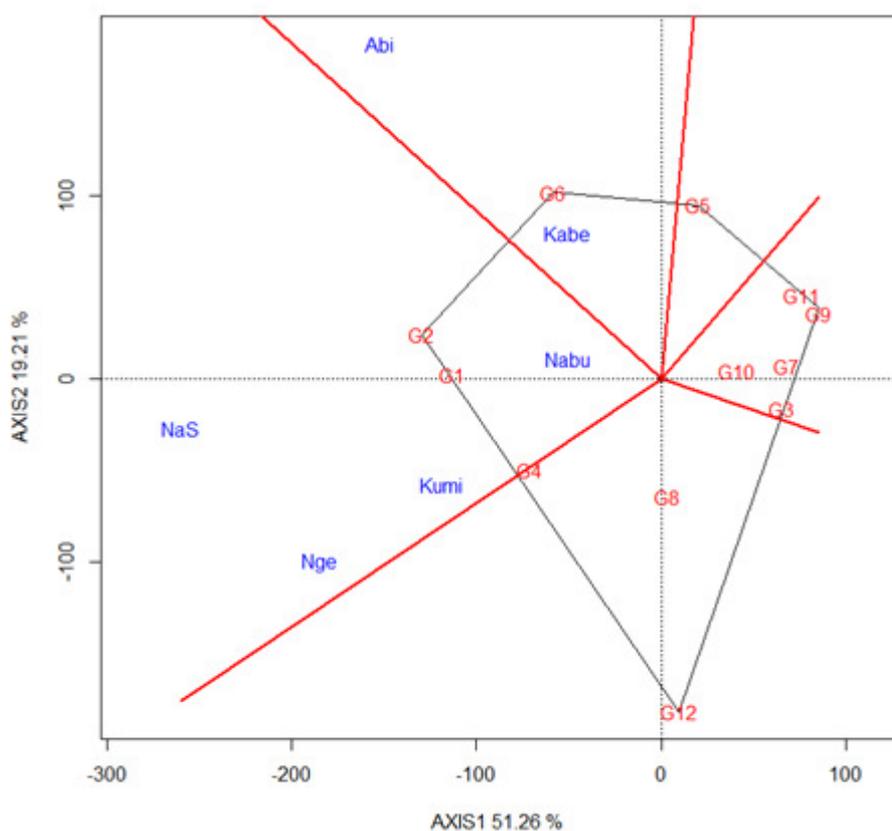
Figure 3. Biplot showing mega-environments and "winning" genotypes. The biplot was tester-centered; SVP = column-metric preserving; data not scaled. Names of sites are as in Figure 1. Genotype names are as in Table 1.

the second mega-environment. This, therefore, means that the country has two broad sub-regions with unique environmental characteristics, with specific high yielding mungbean genotypes. Based on data from introduced materials used in this study, this is the first study to attempt to classify mungbean producing regions in Uganda into meaningful mega-environments. However, data for several years (multi-year data) are needed to confirm this finding, i.e., to ascertain the reproducibility of this pattern across several years (Yan, 2005; Yan and Tinker, 2006). Yan and Tinker (2005) proposed that dividing test locations into meaningful mega-environments, and deploying genotypes in different mega-environments, is the only way of exploiting positive G x E interactions, while avoiding the negative ones. Therefore, for the two mega-environments identified in this study (Fig. 3), different genotypes among the

introduced materials should be selected and deployed.

In terms of discriminating ability of test sites, environment vectors (i.e lines that connect test environments to the biplot origin) were used. The length of the vectors approximated the standard deviation within the respective environments, which is a measure of the discriminating ability of the environments. Environments with longer environment vectors were considered as more discriminative (informative) than environments with shorter vectors (non informative) (Yan, 2005; Yan and Tinker, 2006). Therefore, among the six test sites, NaSARRI and AbiZARDI were the most discriminating (informative) since they had the longest environmental vectors (lines connecting the sites to the biplot origin); while the least discriminating location was NabuinZARDI followed by Kaberamaido TVC as indicated by shorter environmental vectors (Fig. 4). The biplot
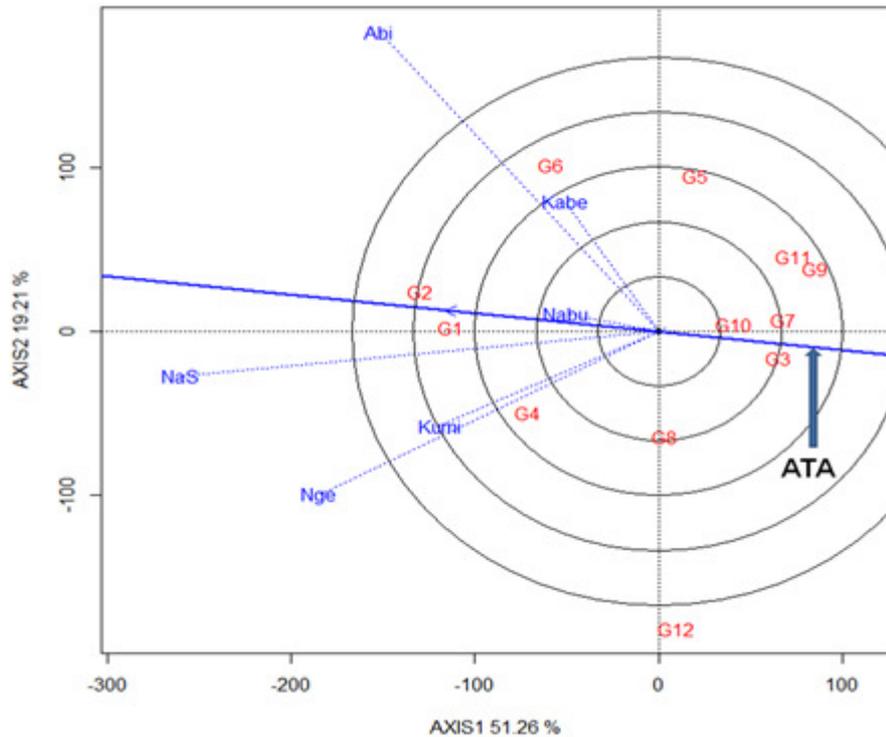
Figure 4. Discriminating ability and representativeness of test locations. The biplot was tester-centered; SVP = column-metric preserving; data not scaled. Names of sites are as in Figure 1.

in Figure 4 was also used to assess the representativeness of test environments. According to Yan (2005) and Yan and Tinker (2006), the average environment has the average coordinates of all test environments and ATA/ AEA (the line that passes through the average environment and the biplot origin). Thus, a test environment that has a smaller angle with the AEA or a shorter projection on to the AEA is more representative of the target environment (Yan, 2001; Yan, 2005; Yan and Tinker, 2006). On this basis, NabuinZARDI appeared to be the most representative site (Fig. 4) since its coordinates were closer to that of the average environment. However, selection/identification of high mean performing materials should be done in an ideal test locations/environments (ideal environment should be both most discriminating and most representative) as suggested by Yan (2005). Therefore, NaSARRI was both more discriminative and representative, since it was closer to the ideal test environment (centre of

concentric circles) (Fig. 5). This site, therefore, can provide the necessary information needed for selection by breeders since it can resolve genotype differences, and coupled with representativeness, make it an ideal test location for selecting generally adapted genotypes (Yan and Tinker, 2006). Yan (2005), however, cautions that a test location or environment can only be declared as ideal if it is so across years; therefore, multi-year data are needed to confirm this finding. AbiZARDI and NgettaZARDI were discriminating but not representative sites and these could be useful for selecting specifically adapted genotypes if the target environments can be divided into mega-environments (Yan and Tinker, 2006). Yan and Tinker (2006) also suggested that discriminating, but not representative, sites, can be useful for culling unstable genotypes if the target environment is a single mega-environment. Among all the sites, Kaberamaido TVC and NabuinZARDI were the
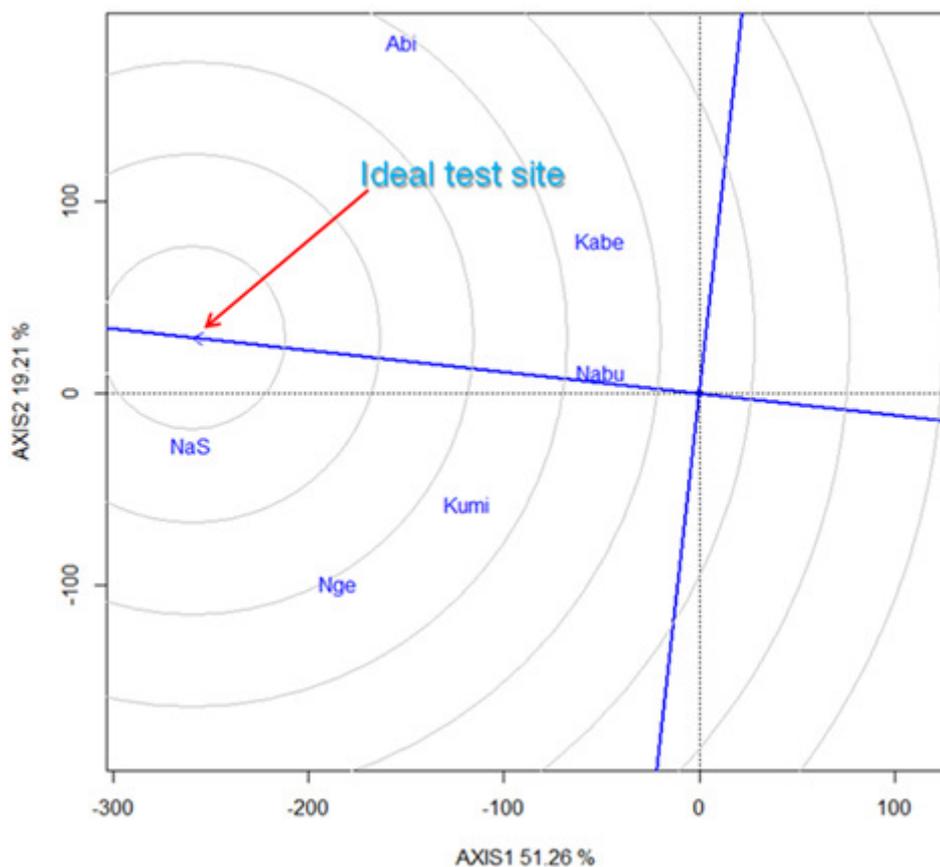
Figure 5. Ranking of environments based on both discriminating ability and representativeness. The biplot was tester-centered; SVP = column-metric preserving; data not scaled. Names of sites are as in Figure 1.

poorest testers, therefore evaluation in these sites may give useless results (Yan, 2001; Yan, 2006).

CONCLUSION

Three introduced genotypes (G1, G2 and G6) exhibit stability and high yield under Uganda conditions, and are therefore, recommended for release to farmers for cultivation. Mungbean growing areas can be divided, at least, into two candidate mega-environments in terms of grain yield; one comprising of AbiZARDI and Kaberamaido and the other comprising of NaSARRI, NabuinZARDI, Kumi, and NgettaZARDI. NaSARRI was the most discriminative and representative site, and therefore, ideal for selection of widely adaptable new mungbean genotypes in the country. Multi-

year trial data are needed to validate the suitability of NaSARRI as the best testing site for wide adaptation.

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