Research Application Summary

Agro-morphological characterisation of exotic and local green gram (Mung bean) (*Vigna radiata*) for breeding purposes in Uganda

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Abstract

In order to start a good breeding programme that will potentially develop high yielding and disease resistant varieties, germplasm collection and characterisation is a prerequisite. The objectives of this study were to characterise 38 local and exotic mung bean genotypes with potential of being released as varieties or being used for breeding purposes. The study also aimed at determining the general and specific combining abilities for crosses between local and exotic materials. This study was done at Makerere University Agricultural Research Institute Kabanyolo (MUARIK) and the National Semi-Arid Resources Research Institute (NaSARRI). Results indicated significant differences ($P < 0.001$) for nearly all traits in the two experimental sites, indicating a high genetic diversity in the genotypes studied. Genotype by environment interactions was significant ($P < 0.001$) for all the traits indicating inconsistent performance by some genotypes across the two locations. The magnitudes of estimated broad sense heritability for the traits used were generally high as the error and G x E variance components were lower compared to genetic variance component.

Key words: Combining ability, germplasm characterisation, green gram, *Vigna radiata*

Résumé

Afin de commencer un programme de reproduction de qualité qui permettra de développer potentiellement des variétés de haut rendement et résistantes aux maladies, la collecte du matériel génétique et sa caractérisation constituent une condition préalable. Les objectifs de cette étude étaient de caractériser 38 génotypes locaux et exotiques de haricot mungo à fort potentiel d'être libérés comme variétés ou utilisés à des fins de reproduction. L'étude a visé également à déterminer les aptitudes générales et spécifiques de combinaison pour les croix entre des matériaux locaux et exotiques. Cette étude a été réalisée à l'Institut de Recherche en Agriculture de l'Université de

Makerere, à Kabanyolo (MUARIK) et à l'Institut National de Recherche en Ressources Semi-Arides (NaSARRI). Les résultats ont indiqué des différences significatives (P <0,001) pour presque tous les traits dans les deux sites expérimentaux, ce qui indique une grande diversité génétique pour les génotypes étudiés. Le génotype par interactions avec l'environnement était significatif (P <0,001) pour tous les traits indiquant les performances incompatibles par certains génotypes dans les deux endroits. Les ampleurs de l'héritabilité estimée au sens large pour les traits utilisés étaient généralement si élevées que l'erreur et les composantes de la variance G x E étaient inférieures comparativement à la composante de la variance génétique.

Mots clés: Caractérisation, aptitude de combinaison, haricot mungo, *Vigna radiate*

Background

Green gram (*Vigna radiata*) is a species native to Asia of the pan-tropical genus *Vigna* and is an important food crop in developing countries of Africa, Latin America as well as Asia (Raturi *et al.,* 2011). It has extensive importance as it is a widely cultivated pulse crop because of its adaptation to short growth duration, low water requirement, low soil fertility requirement and can be used in crop rotations (Lavanya *et al.,* 2008). Other good attributes of the crop include easy digestibility and low proportions of flatulence (Lavanya *et al.,* 2008), and for these reasons, it is used for human consumption and for animal feeds (Karuppanapandian *et al.,* 2006). It can be consumed as boiled beans (Abbas *et al.,* 2010), or like in Korea, the bean seed flour can be used for making soup and pizza-like 'Bindaeddeog' (Gwag *et al.,* 2006). On average, the seed contains 24% protein (Das *et al.,* 2010) which is rich in lysine that lacks in cereals (Shil, 2007).

Literature Summary

Despite the importance of mung bean, the average yield of 384 kg ha^{-1} worldwide is very low. World green gram production is estimated to be on an area of 5.5 million hectares (Weinberger, 2003). Yield is hindered by both abiotic and biotic stresses including diseases, insect pests, drought, high temperature, salinity as well as heavy metals (Karuppanapandian *et al.,* 2006).Compared to cereals in the past few decades, breeders have not substantially increased yield of green gram due to lack of sufficient genetic diversity for desirable traits (Skrotch and Neinhuis, 1995; Das *et al.,* 2010; Raturi *et al.,* 2011). Thus, the

mung bean improvement programme at the Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan has attempted to solve narrow diversity limitation through use of induced mutation in addition to conventional breeding techniques since 1974. This effort has resulted into development of 10 varieties through use of local and exotic germplasm majorly from the Asian Vegetable Research and Development Centre (AVRDC), Thailand (Abbas *et al.*, 2010). The way forward is to continuously explore the genetic diversity available and use it effectively to improve crop yield (Karuppanapandian *et al.*, 2006). But to effectively utilise a green gram gene pool for development of promising varieties, it is paramount to sufficiently characterise various germplasm both local and exotic (Lavanya *et al.*, 2008). This is due to the fact that crosses between parents with maximum genetic divergence are most responsive for genetic improvement (Arunachalam, 1981). A number of markers (morphological and molecular marker) can successfully be used to identify and assess genetic diversity and phylogenetic relationships in plant genetic resources (Karuppanapandian *et al.*, 2006). Conventionally, morphological traits have been easily and cheaply used to assess genetic diversity. However, it is worth noting that morphological markers are not clear-cut as they can be affected by the environment (Wrigley *et al.*, 1987).

Study Description

Genetic materials used included 25 lines from the World Vegetable Centre, and 13 lines from the NaSARRI gene bank. Of the 13 lines from NaSARRI, five were locally adapted while eight lines were obtained from the World Vegetable Centre and had undergone some testing at NaSARRI. The exotic lines were generally early maturing, potentially high yielding but some showed susceptibility to diseases. The experiments were set up in three replications with plots of size 1.5 m x 1 m in an alpha lattice design with eight blocks and five plots within each block. Two plots in each replicate were repeated with exotic lines which were used in inheritance studies. Two rows of 1.5m at spacing of 50 cm x 10 cm were planted in each plot and optimum agronomic practices were followed. Using different randomisations, the experiments were set up at Makerere University Agricultural Research Institute, Kabanyolo (MUARIK) and at NaSARRI for two cropping seasons. The first season was in 2011 between September and December while the second season was in 2012 between April and July.

MUARIK lies 0° 28 N and 32° 37 E at an average elevation of 1200m above sea level. The institute is about 20km north of

Kampala. It has wet and dry climatic conditions of the tropical regions. It receives mean annual rainfall of 1160mm distributed in a bimodal pattern. The first and second rains are received from March – June and September to November respectively, monthly temperatures average 24°C (Yost andand Eswaran, 1990). On the other hand, NaSARRI characterised by Grass-Bush Farmlands (Ramathani, 2010) is located 0° 32' N and 35° 27 E at an elevation of 1128m above sea level. The research station has sandy soils which have low organic content. It receives an annual mean rainfall of 1427mm but it is potentially a drier area of Uganda as it has larger variation in rainfall between years. The rainfall pattern is bimodal with peaks in April/May and August/September in the first and second cropping seasons respectively – first rains are more reliable. Mean annual temperature is 24°C with maximum and minimum annual temperatures of 29.4°C and 17.9°C respectively, relative humidity of 72% to 84% has been recorded (Mulindwa *et al.*, 2006).

Qualitative data at appropriate stages were collected from the MUARIK site only in the second season of experimentation (April to July) by observing and scoring descriptors for each genotype. Quantitative data were collected from a random sample of five well bordered plants by measuring the different descriptors using standard procedures. The various quantitative descriptors were subjected to analysis of variance (ANOVA) using Genestat 14th edition statistical computer software.

Research Application

Analysis of variance revealed high level of significant differences ($P < 0.001$) for all the quantitative traits studied in the two locations (Tables 1 and 2). Only pods per cluster and seeds per pod were not significantly different ($P > 0.05$) among genotypes at MUARIK. This suggests a substantial amount of variability among the genotypes in the study thus these genotypes can start a potentially good breeding programme. The coefficients of variation for yield per plant were generally high especially for the MUARIK location.

Though there was a low error mean square for yield per plant at NaSARRI, the yields were low as indicated by the grand mean (Table 2). This can be attributed to the high disease pressure that was observed at NaSARRI with anthracnose being the most pronounced.

Table 1. Analysis of variance for various agronomic and morphological traits at MUARIK.

Source	Df	DTFF	DTM 80%	PPPlt	PPClu	Plt Ht (cm)	Pod Length	Seeds per pod	100 seed wt	YPPlt (g)
Rep	2	11.18	48.11	1.60	1.98	167.85	1.86	5.33	0.82	3.62
Blocks/Rep	21	5.37	8.21	74.07		47.46				11.95
Genotype	37	79.529***	209.376***	1074.06***	0.4275ns	1886.15***	5.1293***	2.812ns	6.2447***	167.404***
Error	74				0.34		0.44	1.85	0.15	
L.E.E		4.15	5.88	53.73		37.31				9.84
L.d.d.f		61	60	62		60				61
s.e		2.04	2.43	7.33	0.58	6.11	0.67	1.36	0.39	3.14
s.e.m		1.13	1.33	4.06	0.33	3.40	0.38	0.78	0.23	1.76
s.e.d		1.66	1.98	5.98	0.47	4.99	0.54	1.11	0.32	2.56
l.s.d		3.33	3.96	11.96	0.94	9.98	1.08	2.21	0.64	5.12
G M		44.87	84.59	21.37	3.86	34.29	7.29	9.88	4.32	7.05
c.v%		5	3	34	15	18	9	14	9	45

DTFF – Days to first flower, DTM 80% - Days to 80% maturity, PPPlt – Pods per plant, PPClu – Pods per cluster, Plt Ht (cm) – Plant height (cm), YPPlt (g) – Yield per plant (g).

Table 2. Analysis of variance for various agronomic and morphological traits at NaSARRI.

Source	Df	DTFF	DTM 80%	PPPlt	PPClu	Plt Ht (cm)	Pod length (cm) pod	Seeds per pod	100 seed weight (g)	YPPlt
Rep	2	2.90	31.62	0.58	0.48	39.67	0.48	3.92	0.34	2.37
Blocks/Rep	21		3.21		0.16	25.59	0.16	1.48	0.20	3.05
Genotype	37	53.02***	169.69***	247.23***	0.66***	305.78***	2.21***	7.51***	4.68***	28.07***
Error	74	3.56		8.93						
L.E.E			3.11		0.15	19.53	0.16	1.16	0.14	1.52
L.d.d.f			60		59	61	58	61	60	60
s.e		1.89	1.76	2.99	0.39	4.42	0.40	1.08	0.37	1.23
s.e.m		1.09	0.59	1.72	0.13	1.47	0.13	0.36	0.12	0.41
s.e.d		1.54	0.83	2.44	0.18	2.08	0.19	0.51	0.18	0.58
l.s.d		3.07	1.66	4.86	0.36	4.15	0.37	1.01	0.35	1.16
G M		38.01	70.08	19.47	3.75	23.04	6.69	8.83	3.54	3.94
c.v%		5	3	15	10	19	6	12	11	31

Table 3. Analysis of variance for entry means and broad sense coefficient of genetic determination (BSCGD).

Source	Df	DTFF	DTM 80%	PPPlt	PPClu	Plt Ht (cm)	Pod length (cm)	Seeds PP	100 seed wt	YPPlt (g)
Total	75	34.43	114.40	211.99	0.18	383.50	1.30	1.96	1.96	1.00
Location	1	895.54***	4001.96***	68.69**	0.26ns	2404.40**	6.82ns	20.93ns	11.69*	183.85**
Reps/Loc	4	7.04	39.87	1.09	1.23	103.76	1.17	4.62	0.58	3.00
Entry	37	39.80***	120.90***	369.92***	0.21ns	577.3***	2.19***	2.43**	3.42***	52.01***
Genotype X Location	37	5.78***	2.83*	57.92***	0.15*	135.10***	0.25**	0.99**	0.24***	11.80***
Pooled error		3.83	4.49	29.35	0.25	28.34	0.32	1.54	0.15	5.72
Pooled error -entry means basis		1.28	1.50	9.78	0.08	9.45	0.11	0.51	0.05	1.91
Pooled df		67.5	60	68	66.5	60.5	66	67.5	67	60.5
Variance Components	δ^2_e	1.28	1.50	9.78	0.08	9.45	0.11	0.51	0.05	1.91
	δ^2_{GXE}	4.51	1.34	48.14	0.07	125.65	0.15	0.47	0.20	9.89
	δ^2_G	17.01	59.03	156.00	0.03	221.10	0.97	0.72	1.59	20.11
BS CGD – Within environment basis		0.75	0.95	0.73	0.16	0.08	0.79	0.42	0.87	0.63
BS CGD – Across environment basis		0.85	0.98	0.84	0.27	0.77	0.88	0.59	0.93	0.77

There were significant differences ($P < 0.05$) in the performance of the genotypes across the two experimental sites (Table 3). There were also significant ($P = 0.05$) genotype by environment interactions for all the traits measured (Table 3) implying that the genotypes tested did not perform consistently across the two experimental sites.

Broad sense coefficient of genetic determination (BSCGD), which estimates broad sense heritability (H), was generally high for the traits measured. This indicates that the variability due to genetic factors was higher than random error and genotype by environmental interactions (Table 3). Significant G x E interactions was likely brought about by the high error degrees of freedom otherwise the magnitudes of the G x E variance components were far lower than the genotype variance components. BSCGD was highest for days to 80% maturity at 0.98 while the lowest recorded was for pods per cluster at 0.27 on across environment basis. The low BSCGD for pods per cluster was brought about by the high error variance component of 0.08 which was nearly three times larger than the genotype variance component 0.03.

Conclusion

It is beyond doubt that there is genetic diversity in the genotypes that were included in the study. The question whether these traits are the desirable traits to make real crop improvements may be answered when a breeding programme commences. Nonetheless, the genotypes tested can start a potentially successful breeding programme in the country.

Recommendation

Based on preliminary results of germplasm characterisation, some genotypes performed well and can farther be tested as potential varieties. Better still, these genotypes can be used as parents to introgress some traits in the already adapted local materials.

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