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Morphological and agronomic characterisation of climbing bean genotypes

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Abstract

Common bean (*Phaseolus vulgaris*) is an important legume crop grown in Uganda providing a cheap source of protein and income to the resource poor farmers. Basing on growth habit two types of beans occur namely; bush and climbing beans. In Uganda bush beans are generally the most predominant and yet climbing beans have several advantages over bush beans. To exploit such advantages, there is need to avail climbing bean seed to the farming communities. In response, the National Bean Program has bred several varieties of climbing beans but their agronomic traits have not been evaluated. Since release of any new varieties requires characterization and field evaluation for morphology and agronomical traits in order to provide data on genotypes which could be utilized to identify superior characters that will contribute to higher yields as compared to the local varieties. The objective of this study therefore was to characterise and determine the with in genotypes and between genotype phenotypic variation of the 56 climbing bean genotype introductions, and group them in defined groups based on there similarities. Data was collected for the vegetative, inflorescence, fruit, and seed characters of each of the genotypes. Ninety one percent of the total materials in study displayed a narrow genetic diversity, and this reveals the need to collect germplasm to widen the genetic base of climbing bean genotypes. Genotypes, MAC 50, MAC 12-2, DB200-15 and BRC 19 displayed a wider genetic diversity. Genotypes MAC 12-2, LAS 400A and DB 200-15 were identified as large seeded which makes them acceptable for most consumers in Uganda. Promising genotypes with yields greater than the local checks used in the study were MAC 19-1, MAC 35 and MAC 70-2 and are recommended for advanced testing trials.

Key words: Advanced trials, germplasm, introductions, *Phaseaolus vulgaris*, Uganda

Introduction

In Uganda common beans (*Phaseolus vulgaris* L.) is the most important legume crop grown. It is a cheap source of protein and hence an important component in the diet of many Ugandans. Beans provide the bulk of protein to most families who may not afford animal protein (Ugen and Tukamuhabwa, 2000). Besides dietary importance, the bean crop is increasingly becoming an important source of income with a high demand both on the local and international markets. It was identified by Uganda government as a potential non-traditional export crop (Opio *et al.*, 2001). Basing on growth habit, two types of beans are grown, namely bush and climbing bean types.

Climbing beans have several advantages over bush beans including the following; higher yield potential of about 2-3 times higher than bush beans (Niringiye *et al.*, 1994), tolerance to major bean diseases, prolonged harvests, short cooking time and suitability for cultivation in urban areas where arable land is limited. In order to enable farmers exploit these advantages, the Uganda National beans programe has initiated projects to popularise cultivation of climbing beans, and has so far bred and released four varieties (Opio *et al.*, 2001). Further research efforts geared towards development of

other varieties with a view to provide a wide germplasm base are being undertaken. However, before release of any varieties, there is need for assessment and documentation of observed varietal attributes such as agronomic and morphological characters. The objective of this study was to evaluate the morphological and agronomic attributes of candidate climbing bean genotypes and identify varieties that have superior characteristics such as high yielding potential as compared to the other commercial varieties.

Materials and methods

Study area

The study was carried out at Kachwekono Agricultural Research Development Center (ARDC) Kabale district. Kabale receives bimodal rainfall of > 1200 mm yr^{-1} with a distinct dry season during June – July and average temperature of $\leq 20^0$ C (Wortmann and Eledu, 1999).

Planting material

A total of 56 climbing bean genotypes were used in the study. These included five varieties as local checks. The materials were obtained from the International Centre for Tropical Agriculture (CIAT), Rwanda. The genotypes were planted at spacing of 50 cm between rows and 20 cm within rows in a plot size of 1 row x 3 meters. The experiment was arranged in a complete randomized block design with each genotype, treatment, replicated twice.

Data collection

Data taken on various agronomic traits. Three randomly selected plants were used for data collection per plot and data were measured and recorded following established procedures outlined by the International Board for Plant Genetic Resources (IBPGR, 1982). Data were analysed using SPSS computer program version 10.0 (Sokal and Rohlf, 1997; Steel *et al.*, 1997).

The bean germplasm was placed into groups using cluster analysis in which genotypes with relatively uniform traits were assigned to a same score (number) and different if the score was significantly different. Additionally, data were subjected to a hierarchical cluster analysis using the rescaled distance cluster method. The genotypes were scored according to closeness and relative differences based on their genetic constitution, which was reflected in the different characters following procedures described by Andreas and Quellette (2000). Where there was relative uniformity, the same score or number was given and if significantly different the score was different. Qualitative and quantitative analyses were analysed separately (Chahal and Gosal, 2002). Results of qualitative analysis were presented as percentages of genotypes that exhibited a particular trait, while for the quantitative trait results presented are traits specific to a genotype.

Results

Classification of 56 climbing bean genotypes

Fifty-six genotypes were classified basing on the attributes evaluated and were grouped into 5 different clusters. The following genotypes exhibited similar morphological and agronomic attributes and were observed to belong to the same cluster: MAC28, MAC16, MAC33, MAC29, MAC70-1, MAC35, MAC70-3, MAC61-2, MAC13, MAC28-1, MAC61-1, MAC12, MAC20, MAC70-2, MAC76-2, MAC34, MAC36-1, MAC19-1, MAC36-2, MAC19-2, MAC26, MAC63, MAC64, MAC17, MAC60, MAC56, MAC12-1, MAC55, MAC76-1, MAC46, RWV1140, RWV524B, RWV1103, RWV1128-

1, RWV1128-2, RWV524A, RWV1139-1, RWV1129, RWV1105, RWV1128-2, RWV1139-2, G2331, LAS400A, LAS405, Melzwelre, RWR1134, NABE7C, NABE8C, NABE9C, NABE10C and SUG31. This implies that they have relatively close or uniform characteristics. The other genotypes MAC50, MAC12-2, DB200-15 and BRC19 were observed as different from each other with regard to morphological and agronomic attributes and each were thus grouped into a separate cluster.

Hierarchical character cluster analysis of 56 genotypes

Figure 1 illustrates the genetic distances among the 56 climbing bean genotypes based on relative closeness or difference from one genotype to another. Four clusters were reflected in the dendrogram. Highest significant difference was found for genotype MAC 12-2 which was grouped separately, this was followed by genotypes DB200-15, MAC50 and BRC19 grouped into one cluster each. Climbing bean genotypes MAC13, MAC36-2, MAC28-1, MAC29, MAC34, MAC12, MAC56, RWV524B, RWV524A, MAC20, MAC70-2, MAC76-1, MAC76-2, NABE9C, RWV1103, SUG31, RWV1140, MAC61-2, MAC63, LAS405, MAC55, MAC46, MAC61-1, RWV1132, MAC35, RWR1134, Melzwelre, MAC36-1, MAC70-3, MAC64, NABE8C, LAS400A, MAC12-1, MAC70-1, RWV1139-2, MAC28, RWV1128-1, MAC19-2 and MAC33 were all scaled in one cluster, reflecting relatively low significant differences among them. The following genotypes, RWR1129, MAC60, NABE10C, MAC16, MAC17, MAC26, RWV1105, RWV1128-2, G2331, RWV1139-1, NABE7C, MAC19-1, and RWV1138 were according to the scale grouped in one cluster with relatively slight differences within the group (Fig. 1).

Qualitative traits of the 56 climbing bean genotypes

Hypoctyl pigmentation

The study demonstrated a predominance of green hypoctyl pigmentation of the genotypes by 96.4%, followed by genotypes with occurrence of a mixture of light green and pinkish pigmentation and others with a purplish pigmentation expressed by 1.8 % of the genotypes.

Leaf shapes and persistence

Two different leaf shapes (triangular and round) and three levels of leaf rentation (when 90% of pods in a plot are dry), were observed among the 56 genotypes (Table 1). The majority of the genotypes (98.2%) had a triangular leaf shape. Types of leaf persistence observed included; all leaves dropped, intermediate and all leaves persisted. The intermediate kind leaf persistence was the most predominant type with 43 out of 56 genotypes in study (76.8%). Twelve genotypes had all leaves persisted (Table 1).

Growth habit

Climbing bean genotypes studied were grouped according to two different classes of growth habit; type IV (intermediate climbing type) and type III b (climbing ability though not well developed). The majority of the genotypes 95% possessed the indeterminate growth habit, type IV.

Colour of flower wings, standard and pods

Data on different types of flower colour (standard and wing) and pod colouration, which were observed among the genotypes are presented in Table 2. The highest frequency of genotypes (34) demonstrated a light green colour of standard. This was followed by two different colours of standard (in freshly

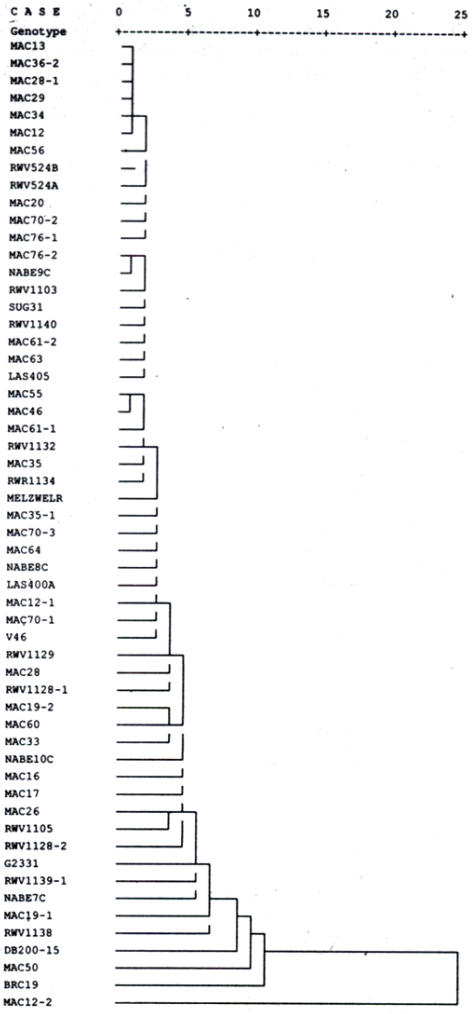

Figure 1. Hierarchical character cluster of 56 genotypes.

opened flower), purple (7 genotypes) and purplish colour expressed by 5 out of 56 genotypes. Six other colours of standard were observed; green, dark green, pink, yellowish, white and pinkish. A total of 42 genotypes had white flower colour of wing. Four other colours of flower wings observed were; purple, dark green and pinkish. Purple and purplish colour of wing among the different genotypes did not have a significant difference of occurrence (6 out 56 genotypes). Of the 56 genotypes 49 possessed light green colour of fully expanded immature pod, and 1 genotype with green pod colour. In addition, three genotypes were variable (Table 2) and exhibited a mixture of either; light green with purple red stripes (7.1%), green with pink (1.8%) or yellow with red stripes (1.8%). Genotypes with pods at

Table 1. The frequency of leaf traits of 56 climbing bean genotypes tested.

Leaf shape	Frequency	Leaf Persistence	Frequency
Triangular	55	All leaves dropped	1
Round	1	Intermediate	43
Others	0	All leaves persisted	12

Table 2. Frequency distribution of flower wing, standard and pods coloration.

Trait	Description	Frequency
Color of standard	Dark green	1
	Purple	7
	Purplish	5
	White	3
	Pinkish	3
	Green	1
	Light green	34
	Pink	1
	Yellowish	1
Color of wing	Dark green	1
	Purple	6
	Purplish	6
	White	42
	Pinkish	1
Color ofimmature pod	Yellow with red strips	1
	Light green with purple strips	4
	Green with pink strips	1
	Green	4
	Light green	49
Pod colour at physiological maturity		
	Yellow	16
	Yellow with red stripes	31
	Yellow with purple stripes	8
	Red	1
Dry pod color	Yellow	1
	Cream	24
	Cream with purple stripes	29
	Yellow with red stripes	1
	Maroon	1

physiological maturity observed having yellow with red strips were the most predominant (55.4%). This was followed by yellow colour at physiological maturity with comparatively a large number of genotypes (28.6%). Unlike yellow with purple stripes that was observed with 8 genotypes, there was only a small number (1 out of 56), which showed red pods at physiological maturity. The cream colour with purple stripes of the dry pod was the most predominant (29 out of 56 genotypes), followed by cream colour possessed by 24 genotypes. Yellow with red stripes, maroon and yellow colour were exhibited by only one genotype each.

Pod characteristics

The proportion of pod cross-section, curveture, and shape of apex, wall fiber, beak orientation and position among the genotypes tested are presented in Table 3. Two types of pod cross sections were observed; the very flat type which was the most frequently encountered (80.4%) and the pear shaped pod cross-section (19.6%). Out of the 56 genotypes 36 (64.3%) were observed with straight pods, 17 genotypes exhibited pods that were slightly curved and 3 genotypes had pods that were curved. Three shapes of the pod apex were observed; slightly curved pod apex and the curved shape were the most predominant shapes possessed by 29 and 25 genotypes, respectively. The straight pod apex shape was represented by two (2) genotypes. Pod wall fiber was expressed at three levels which included strongly contradicting, leathery pods and strong twisting dry pods (Table 4). Two pod beak positions were expressed, marginal and non-marginal and were exhibited by 46 genotypes and 10 genotypes, respectively. The genotypes were divided into two classes of pod beak orientation; up- wards (beak curving to the dorsal side) were 48 (85.7%) and 8 genotypes with straight beak orientation. Three classes of position of pods were observed. Twenty-two genotypes, had pods positioned at the base; other 22 were observed at the center and 12 genotypes (21.4%) had pods evenly distributed, from the base to the top of the plant.

Table 3. Frequency of qualitative traits on pods of climbing bean genotypes.

Trait	Description	Frequency
Shape of apex	Straight	2
	Slightly curved	25
	Curved	29
Pod curveture	Straight	36
	Slightly curved	17
	Curved	3
Pod position	Base	22
	Center	22
	Evenly distributed	12
Pod wall fiber	strongly contracting	5
	Leatherly podded	50
	Strong twisting dry pods	1
Pod beak orientation	Up- wards	48
	Straight	8
Pod beak position	Marginal	46
	Non-marginal	10
Pod cross section	Very flat	45
	Pear shaped	11

Seed characteristics

The frequency and proportion of shape and brilliance of bean genotypes is given in Table 4. Cuboid seed shape was the largest class represented by 23 genotypes. This was followed by an oval shape 35.7% and kidney shape 16.1%. Other shapes observed were truncate-fastigate (3.6%) and round seed shape. Three classes of seed brilliance were recognised; medium brilliance was shown by 39 genotypes, shiny 9 genotypes while the least was observed with matt kind of seed brilliance. There was no apparent seed veining for most of the genotypes studied (98%).

Seed colours of brown, maroon, cream and purple were common in all the seed colouration parameters (Table 5). Eight darker colours were observed on the seed coats of the 56 genotypes. The most predominant was maroon 41.1%, followed by cream, purple and pink. The other seed colours displayed 1.8% of the genotypes studied for each colour; whitish, bluish, brown and pinkish. Twelve genotypes (21.4%) were observed lacking a darker colour in the colour pattern on the seed coat. Cream was the most predominant lighter colour observed on the seed coat 51.8%, followed by maroon colour (21.4%). Others colours observed were, purple, yellow, brown whitish, pink and red. Two genotypes (3.6%) did not display lighter colour in the colour pattern of the seed coat. The majority of the genotypes (51.8%) possessed a maroon colour of ring around the helium. This was followed by brown (16.1%) and black (10.7%). The other colours observed were purple, cream and yellow. Of the 56 genotypes 1.8% had no primary colour on the seed coat. A comparatively large number of the genotype (46.4%) showed a maroon colour followed by cream colour (25), yellow and purple each represented by four genotypes. Other colours observed were; whitish and pink (3.6% each), brown, grey and red (1.8%). The largest number of genotypes (42.9%) was observed with cream, as a secondary colour on the seed coat. Only 14.3% were recorded with maroon and 10.7% with a purple colour. Other colours include; brown and bluish. Among the different colours on the seed coat and or colour pattern of the genotypes in study, 16 genotypes did not display a secondary colour on the seed coat.

Six seed coat patterns were recorded among the 56 genotypes, the most predominant were rhomboid spotted (42.9 %) and the speckled with 14.3% genotypes. These were followed by stripped, constant mottled and marginal colour pattern, respectively. Some genotypes (26.8%) were observed with a plain seed coat (i.e., no pattern observed) (Table 5).

Table 4. Frequency distribution of seed characteristics of 56 climbing bean.

Trait	Description	Frequency
Seed brilliance	Matt	8
	Medium	39
	Shiny	9
Seed shape	Round	1
	Oval	21
	Cuboid	23
	Kidney	9
	Truncate	2
	Fastigate	0
Seed coat pattern	Constant mottled	3
	Stripped	5
	Rhomboid spotted	24
	Speckled	8
	Marginal color pattern	1
	Absent	15

Analysis of quantitative traits

Table 6, shows means of quantitative traits of plant, pod and dry seed of 56 climbing bean genotypes, for all the characters evaluated. The longest hypoctyl length was observed with genotypes MAC 28-1 and SUG 31, which was 4.4 cm long, followed by lines MAC 76-2 and MAC 29 which had hypoctyl length of 4.3 and 4.1 cm, respectively. The shortest hypoctyl length of 2 cm was recorded on genotype NABE 7C which was used as the local check.

Results of days to flowering showed that the earliest genotype to flower was MAC55, which flowered within 51 days. This was followed by MAC 61-2, MAC 61-1 and BRC 19, which flowered within 52 (for both MAC 61-2 and MAC61-1) and 53 days, respectively. The five genotypes that followed flowered within 55 days (Table 6).

Period to maturity for early maturing genotypes ranged from 97 – 99 days. These included genotypes RWV 1140; RWV1139-1, RWV 1128-2, BRC19 and RWR 1134.4. The late maturing genotype MAC 36-1, took 117 days to mature. In general most genotypes (47 in number) reached physiological maturity at 100 - 109 days. Among the local checks only NABE 10C was among the early maturing genotypes.

Table 5. Frequency distribution of seed coat color and color pattern in the 56. genotypes of beans.

Trait	Description	Frequency
Seed coat primary color	Brown	1
	Marron	26
	Cream	14
	Purple	4
	Whitish	2
	Pink	2
	Red	1
	Absent	1
	Yellow	4
	Grey	1
Seed coat lighter colour	Brown	1
	Marron	12
	Cream	29
	Purple	5
	Whitish	1
	Pink	1
	Red	1
	Absent	2
	Yellow	4
Secondary seed coat colour	Brown	1
	Marron	8
	Cream	24
	Purple	6
	Blueish	1
	Absent	16
Color of ring around the hilium	Brown	9
	Marron	29
	Cream	4
	Purple	5
	Yellow	3
	Black	6
Seed coat darker color	Brown	1
	Marron	23
	Cream	9
	Purple	5
	Whitish	1
	Pink	3
	Absent	12
	Blueish	1

Table 6. Shows means for qualitative traits of the 56 climbing bean genotypes.

Genotype	*HL	DF	DOF	DM	PL	LPP	PW	PPP	SPP	NSPP	SL	SH	SW100	PSW	SYLD
MAC28-2	4.0	59	78	113	17.0	6	10.3	21	6	82	2.0	2.4	40.0	32.0	99
MAC16	4.0	62	74	104	15.0	5	5.0	14	4	31	2.0	3.0	45.0	28.0	40
MAC 33	3.0	67	79	108	14.0	5	4.1	4	5	14	2.0	3.0	52.0	4.0	19
MAC29	3.4	65	79	106	17.0	6	4.2	11	6	51	2.0	2.4	46.0	21.0	75
MAC70-1	4.0	63	82	101	14.0	6	4.4	6	6	31	2.0	3.0	55.1	16.3	51
MAC35	3.3	65	79	103	24.0	7	4.3	14	7	62	2.0	3.0	51.5	34.0	104
MAC70-3	3.2	64	79	103	18.0	6	4.0	12	6	39	2.0	2.2	44.4	18.4	58
MAC61-2	2.4	52	77	103	14.0	7	4.0	14	6	75	1.4	2.1	32.3	26.0	75
MAC13	2.4	66	80	104	15.0	7	4.2	12	6	61	2.0	3.0	51.0	33.0	96
MAC28-1	4.4	66	79	106	16.0	6	4.2	13	6	53	2.0	3.0	45.4	25.4	79
MAC61-1	3.1	52	74	102	16.0	5	4.1	18	5	51	2.0	3.0	56.0	31.2	95
MAC12	3.1	59	75	107	14.0	6	4.0	19	5	69	2.0	2.4	46.1	27.0	88
MAC20	3.0	64	75	105	14.1	6	4.0	12	6	44	2.0	3.0	41.0	20.4	55
MAC70-2	3.4	64	74	101	18.0	7	4.0	14	6	59	2.0	2.4	52.4	37.0	101
MAC76-2	4.3	64	79	111	14.0	8	4.0	15	8	69	1.4	2.4	39.1	27.0	83
MAC34	4.0	59	74	100	15.0	6	4.0	14	5	58	2.0	3.0	46.2	26.3	81
MAC36-1	3.6	65	80	114	15.0	7	4.2	21	7	63	2.0	2.3	53.0	23.0	73
MAC19-1	4.0	63	76	105	15.0	6	4.4	21	5	91	2.0	3.0	51.2	48.3	147
MAC36-2	4.0	62	79	109	14.2	6	4.5	11	6	52	2.0	3.0	51.0	29.0	89
MAC19-2	4.0	59	77	106	15.0	6	5.0	10	5	25	2.0	2.4	34.0	11.0	35
MAC26	4.0	60	80	106	30.2	7	4.1	15	7	63	2.1	3.0	51.4	31.0	95
MAC63	3.0	63	78	108	16.1	6	4.3	13	6	49	2.0	2.5	49.4	23.4	73
MAC64	3.0	59	80	108	17.0	5	4.0	17	5	55	2.0	3.0	57.1	28.0	92
MAC17	4.0	65	79	105	12.5	7	4.2	21	7	233	2.0	3.0	47.1	49.0	98
MAC60	3.1	59	77	103	12.3	6	4.2	11	5	41	1.4	2.5	27.0	12.0	39
MAC56	3.3	64	78	103	14.4	6	4.4	11	6	50	2.0	3.0	53.0	25.4	63
MAC12-1	4.0	66	79	107	15.3	6	4.2	11	6	31	2.0	2.5	49.3	22.0	62
MAC50	4.0	64	77	104	14.0	5	4.0	9	6	28	2.0	3.0	52.0	66.0	100
MAC55	4.0	51	71	105	18.0	6	4.0	10	6	46	2.0	2.5	66.0	30.1	93
MAC76-1	3.0	62	78	104	13.0	5	4.0	11	5	52	2.0	3.0	49.0	17.3	55
MAC12-2	4.0	62	74	105	15.0	6	4.3	18	6	51	1.4	2.1	63.0	34.2	77
MAC46	4.0	62	79	106	17.0	6	4.5	11	6	46	2.0	3.0	63.0	30.0	93
RWV1138	3.0	59	75	100	15.1	6	3.4	17	5	58	3.3	2.3	41.0	23.1	72
RWV1140	3.2	55	74	97	13.2	5	3.5	19	5	62	1.5	2.2	35.0	22.0	67
RWV524B	3.1	56	75	102	14.1	6	4.3	13	6	39	2.0	3.0	47.0	24.2	76

Table 6. Contd.

Genotype	*HL	DF	DOF	DM	PL	LPP	PW	PPP	SPP	NSPP	SL	SH	SW100	PSW	SYLD
RWV1103	3.2	60	75	101	15.0	6	4.0	17	4	56	2.0	2.3	45.0	24.3	76
RWV1128-1	3.1	71	73	101	14.5	6	4.5	13	5	44	2.0	3.0	50.0	21.1	69
RWV524A	3.1	60	79	100	15.5	6	4.1	13	5	49	2.0	3.0	48.0	23.0	72
RWV1139-1	3.1	60	74	98	14.0	6	4.4	16	5	61	2.0	3.0	41.0	28.4	88
RWV1132	2.3	55	74	100	17.0	6	4.0	14	5	49	3.4	2.3	53.4	31.0	95
RWV1129	4.1	57	74	100	14.1	5	4.0	14	5	41	2.0	3.0	44.3	21.0	64
RWV1105	3.1	57	75	103	17.0	6	4.0	19	4	62	2.0	2.4	45.0	30.0	92
RWV1128-2	4.0	55	74	99	13.0	6	11.0	11	5	37	2.0	2.3	45.3	15.0	34
RWV11 39-2	3.0	74	77	101	16.0	7	4.1	17	6	56	2.0	2.4	44.1	29.4	77
G2331	3.0	58	74	103	12.0	7	3.4	18	6	67	1.4	2.3	27.0	17.4	55
LAS400A	3.0	64	79	107	16.0	6	4.3	12	7	36	2.0	3.0	57.0	25.0	74
LAS405	3.5	63	78	106	15.0	6	3.8	12	6	55	2.0	3.0	54.2	28.0	87
DB200-15	3.0	58	71	103	15.0	6	4.0	12	6	55	2.0	2.3	56.0	36.0	51
DRC19	3.1	53	77	99	14.3	5	4.0	17	5	54	2.0	3.0	48.1	58.3	51
MELZWLRE	3.0	55	75	101	16.0	5	4.2	17	5	54	2.0	3.0	45.0	23.0	79
RWR1134	2.5	56	72	99	11.2	7	3.3	16	6	72	1.2	2.1	28.0	22.1	69
NABE7C	2.0	64	74	103	16.0	9	3.1	15	9	75	1.3	2.0	32.0	17.4	55
NABE8C	3.0	55	80	103	15.4	6	4.0	16	5	43	2.0	3.0	40.0	21.0	56
NABE9C	3.0	58	78	104	16.0	6	4.0	17	5	70	2.0	2.3	41.0	26.0	80
NABE10C	3.0	58	74	100	12.3	7	3.4	18	7	88	1.1	3.0	23.2	21.3	63
SUG31	4.4	63	79	105	12.3	6	6.0	12	6	49	1. 5	3.0	45.0	23.1	72
LSD (0.05)	1.0	9	7	5	7.3	1	3.4	9	2	71	0.9	0.4	10.2	23.1	49
Grand mean	3.2	60	76	104	15.2	6	4.3	14	6	56	1.7	2.5	46.2	26.6	74
Standard error	0.5	5	3	2	3.6	1	1.7	5	1	35	0.5	0.2	5.1	11.5	24
CV%	14.9	8	4	2	24.0	13	40.1	32	1	63	27:8	7.4	11.0	43.3	33

*HL = Hypoctyl length, DF =days to flowering, DOF = duration of flowering, DM =days to maturity, PL =pod length, LPP =locules per pod, PW= pod width, PPP = pods per plant, SPP =seeds per pod, NSPP = number of seeds per plant, SL =seed length, SH =seed height, 100 SW =seed weight for 100 seeds, PSW =plant seed weight and SYLD =Seed yield.

Genotypes observed with the highest pod load per plant were MAC 28-2, MAC 36-1, MAC 19-1 and MAC17 with an average number of 21 pods per plant. The lowest pod load per plant was observed with MAC 33 with an average pod load of 3 pods. This was followed with genotypes recorded with eight pods per plant. The highest average number of seeds was observed with genotype MAC17 which had 233 seeds. Genotypes MAC 19-1 and NABE 10C followed with 91 seeds and 88 seeds per plant respectively. The lowest average number of seeds per plant was observed with genotypes MAC 33, MAC 19-2, and MAC 50 (14, 25, and 28 seeds per plant, respectively).

The highest average plant seed weight (66) per plant among the 56 genotypes was exhibited by MAC 50. It was followed by genotype BRC 19 weighing 58.3 seed weight per plant. The least average plant seed weight was observed with genotype MAC 33 (4). There was significant difference among genotypes in terms of seed yield (Table 7). The seed yield was highest for genotype MAC 19-1 (0.147 kg ha^{-1}). Other high yielding genotypes identified were MAC 35 (0.104 kg ha^{-1}), MAC 70-2 (0.101 kg ha^{-1}) and MAC 50 (0.100 kg ha^{-1}). The least seed yield was observed with genotype MAC 33, RWV 1128-2 and MAC 19-2 (0.019 kg ha^{-1}, 0.343 kg ha^{-1} and 0.035 kg ha^{-1}, respectively).

The longest pod length was observed with genotype MAC 26 (30.2 cm) followed by MAC 35 (24 cm) and NABE 9C (20 cm). The lowest pod length 11.2 cm was observed with genotype RWV 1134 followed by G2331. The highest pod width was 11 cm observed in genotype RWV 1128-2, while the genotypes that followed, MAC 28-2, SUG 31 and genotypes MAC 16 and MAC 19-2 exhibited average pod width of 10.3cm, 6 cm and 5 cm, respectively. The least pod width was observed with genotype NABE 7C measuring 3.1 cm. Genotype NABE 7C was identified as having the highest number of locules per pod (9 locules), followed by, MAC 76-2 having 8 locules per pod. The least number of locules observed per pod was 5. Most of the genotypes (60.7%) were observed with six locules per pod. The highest number of seeds per pod was observed with genotype NABE 7C and three genotypes MAC 16, RWV 1103 and RWV 1105 were not significantly different with regard to an average number of seeds per pod. Twenty-two genotypes were observed with an average score of 5 seeds per pod (Table 6). Local varieties NABE 7C and NABE 10C are among the genotypes with a high number of seeds per pod.

Genotype NABE 10C was observed having the lowest seed length of 1.1 cm followed by genotypes RWV 1134 and NABE 7C with a seed length of 1.2 cm and 1.3 cm, respectively. The highest seed length was observed with genotype RWV 1132 (3.4 cm), while genotypes (RWV 1138 and MAC 26) that followed were observed with an average seed length of 3.3 cm and 2.1 cm. Forty-three genotypes were noted to have similar seed length (seed length of 2 cm). Among these were the local checks NABE 8C and NABE 9C. Thirty genotypes were observed with a highest average seed height of 3 cm. Amongst the genotypes that have 3 cm average seed height, are local checks, NABE 10C, NABE 8C and SUG 31. These were followed by MAC 19-1 with an average seed height of 2.7 cm. Local check NABE 7C was observed having the lowest average seed height of 2 cm.

Only one genotype had a weight of 100 seeds less than 25 gm (small seeded), ten genotypes had 100 seed weight of 25 gm to 40 gm (medium seed size) and the largest number of the genotypes (80%) weighed 41 and above. The weights were highest for genotype MAC 55, weighing 66 gm for 100 seed weight. The least average weight for 100 seeds was observed with genotype NABE 10C weighing 23.2 gm. Only one genotype had a weight of 100 seeds less than 25 gm (small seeded), ten genotypes had 100 seed weight of 25 gm to 40 gm (medium seed size).

Correlation between quantitative traits of climbing bean genotypes

The correlations among traits of climbing beans studied are presented in Table 7. Days to maturity were negatively associated with days to flowering and seed yield. Other negative correlations observed were between duration of flowering and days to maturity, pods per plant and number of seeds per pod. 100 seed- weight was positively correlated with number of locules per pod and seed yield was constantly correlated with all the traits in study.

Table 7. Correlation coefficients among qualitative traits measured from 56 climbing bean genotypes.

Traits	*DF	DM	DOF	HL	LPP	NSPP	PL	PPP	PSW	PW	SH	SL	SSP	SW	
1. Conastant	1.000														
2. DF	-0.184	1.000													
3. DM	-0.547	-0.040	1.000												
4. DOF	-0.197	-0.116	-0.492	1.000											
5. HL	0.035	0.021	-0.152	-0.063	1.000										
6. LPP	-0.127	-0.182	-0.071	0.027	-0.043	1.000									
7. NSPP	0.065	-0.019	0.120	-0.137	-0.100	-0.090	1.000								
8. PL	0.024	-0.052	0.113	-0.163	-0.016	-0.105	0.093	1.000							
9. PPP	-0.021	0.028	-0.253	0.105	0.162	-0.065	-0.325	-0.130	1.000						
10. PSW	0.007	0.051	0.060	0.089	-0.033	-0.018	-0.303	-0.074	-0.373	1.000					
11. PW	0.085	0.028	-0.134	0.032	-0.205	-0.014	-0.018	-0.047	-0.035	0.027	1.000				
12. SH	-0.218	-0.042	0.126	-0.333	-0.080	0.126	0.007	0.064	0.022	-0.175	-0.048	1.000			
13. SL	-0.172	0.126	0.009	0.016	0.086	-0.106	-0.006	-0.098	-0.077	-0.013	0.027	-0.030	1.000		
14. SSP	0.130	0.031	-0.163	0.002	0.194	-0.662	-0.138	-0.084	0.222	-0.045	0.002	-0.110	0.229	1.000	
15. SW 100	0.13	-0.147	-0.268	0.061	-0.077	0.345*	0.092	-0.250	0.282	-0.380	0.0461	-0.109	-0.222	-0.135	1.000
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15

*HL = Hypoctyl length, DF =days to flowering, DOF = duration of flowering, DM =days to maturity, PL =pod length, LPP =locules per pod, PW= pod width, PPP = pods per plant, SPP =seeds per pod, NSPP = number of seeds per plant, SL =seed length, SH =seed height, 100 SW =seed weight for 100 seeds, PSW =plant seed weight and SYLD =Seed yield.

* Significant at $p < 0.01$.

Discussion

The results of this study reveal a narrow diversity among the population of the genotypes studied. Genotypes, which were grouped in one cluster, were derived from the same parents or related ones, reflecting narrow genetic background. Ninety one percent of the total materials tested therefore, belong to the same group.

It is also deduced that due to breeders' preference of using mostly intraracial populations in the past (Welsh *et al.*, 1995), has resulted in reduced genetic variation. This implies that a wider genetic base of genotypes is highly recommended for the bean-breeding programme (Escribano *et al.*, 1994). Advanced testing could consider genotypes MAC50, MAC 12-2, DB 200-15, BRC19 and MAC 12-2 (Fig. 1) which exhibited significant polymorphic status.

It is most likely that 91% of the climbing bean genotypes studied were hybridized from intraracial population (Welsh *et al.*, 1995). This accounts for the limited variation observed among the genotypes. Thus, growing interest in hybridizing and or combining interracial species to produce heterogenous populations is necessary in order to enlarge the genetic base for more durable and increased levels of resistance to both biotic and abiotic stress factors affecting bean production.

The results of this study suggest that variation of climbing bean genotypes tested is narrow to be used effectively in the breeding programmes. This calls for collection of more germplasm to widen the genetic base of climbing bean germplasm at Namulonge.

Based on results from the study, two types of growth habit were observed. The distinctions among the two growth habits may be explained as a result of differences in internal correlation among the plant parts. It may also be reasoned that the substantial variation in growth habit especially for type IIIb, could be due to environmental effects (soil fertility, plant density, availability of support). Flower colours (standard and wing) produced varied greatly, due to the genetic constitution of the genotype. It was observed that, flower colour (of standard and wing), leaf shape and seed shape could be used to classify beans into Andean versus middle American gene pools and subsequently into races (Allen *et al.*, 1996). Most of the genotypes possessed green colour (58.9%) and dark green colour (39.3%) of leaf chlorophyll. This could be attributed to the ability of the plant to sustain (manufacturing food adequately) the different phases of plant development, which tend to overlap from flowering to maturity. It could be deduced that lack of colour of anthocyanin within leaves, observed in all the genotypes originates from intraracial populations, confirms a narrow genetic constitution for the bean germplasm used.

Climbing bean varieties are reported to having been characterized by having phased flowering and pod formation trait (Debeouck *et al.*, 1986). Due to variation in genetic constitution, some genotypes pod set is concentrated at the base of the plant while in others is at the middle or upper part of the plant. In other genotypes pods are evenly distributed along the plant. It could be deduced that genotypes with evenly distributed pods have high pod load. It was reported that, the presence or absence of fibers in the pod wall and suture is used to identify the French (snap or green) bean from dry bean (Zeven *et al.*, 1999). Pod wall fiber is associated with pod texture. Pod texture would be expected to demonstrate genotypes that will either shatter excessively (with strong twisting dry pods), leatherly podded (dry pod will not spontaneously open) or strongly contracting. Information in this study also explain the fact that bean growers use pod texture to describe the bean varieties using traits such as pod wall fiber, plant growth habit, seed colour pattern and use (Zeven *et al.*, 1999).

The genotypes used in the study were improved climbing bean varieties (indeterminate growth habit), and almost mature uniformly despite phased flowering and pod formation. This explains why the majority of the genotypes (76.8%) were with intermediate of leaf persistence while only 21.4% of the genotypes had all leaves persist up to drying time.

Debeouck *et al.* (1986) reported that Pods can be uniform in colour or streaked and that differences can exist between the immature pod stages and between the mature and completely dry pods. In general

this information agrees with results obtained in the study. Pod colouration could also be attributed to particular genotypes. Colour variation may be related to the different genotypes used in the study.

Seeds are reported to have either one colour or they may have a predominant primary colour along with a secondary colour (Schoonhoven *et al.*, 1987). This information is in agreement with the results of this study. Colours may also be arranged in different patterns, such as mottled and striped. The variations observed among genotypes about seed colour, colour pattern, brilliance and seed shape could form a basis characterising of bean seed for growers and consumers. The majority of the genotypes possessed seeds with medium brilliance (69.6%) and very few were shiny. It should be noted that this character attracted the special attention of the breeders and or farmers. From the different seed colours and pattern observed, it could be concluded that maroon and cream were the most predominant colours. Debeouck *et al.*, 1986 reported that, seeds vary widely in colour, shape brilliance and also colour combinations. Thus, such variability is important for the classification of the genetic diversity existing among the bean varieties used in the study.

Pod shape and pod cross-section, together with other quantitative traits such as seed size, number of seeds per pod and number of pods per plant, determine the reproductive adaptation of the different genotypes, which is more defined by the pod load (Schoonhoven *et al.*, 1987). Nonetheless, characterising bean genotypes using qualitative traits was possible to identify the percentage of genotypes exhibited by each trait.

Considerable variation among the 56 genotypes was recorded for each of the 15 quantitative traits analysed. Analysis of variance showed that significant differences existed among the genotypes for each trait evaluated. Ranges of variation displayed a wide diversity among the genotypes for all the characters studied. In general, these results are in agreement with those presented by Escribano *et al.* (1994).These results prove that the genotypes used in the study have a wide genetic base in terms of quantitative traits. This variation could be used in a breeding programme to improve yield, considering that the yield of the current cultivated bean populations are usually rather low.

Increase in number of days to maturity resulted in more pods per plant, observed genotypes were MAC 28-2 and MAC 36, appearing as both late maturing and having a high pod load. Genotype MAC 28-2 was also observed among genotypes with high seed yield. It is clear that, different genotypes have either the same or varying maturity period, hence influencing the duration of the stages of development in the bean plant. Fernando *et al.* (1985) reported that maturity period causes important differences in the development of genotypes of same growth had it. In general it could be concluded that there is a close genetic proximity in maturity trait among the released climbing beans, NABE 7C and NABE 12C (released currently), which lies between 95 – 115 days. The remaining genotypes in the study were observed to fall in the same ranges.

The results of analysis of pods length and width reveal that pods increase in size depending on the genotypes. The variation in pod size deferred greatly despite the fact that the genotypes were of the same growth habit, this could be due to genotypic constitution. This was confirmed in the report by Fernando *et al.* (1985) that 15 – 20 days after flowering, valves increase in weight markedly after pods have reached their maximum size and weight. Studies by Escribano *et al.* (1994) reported that large pod and seed size of some population, such as PHA-0124, PHA-0196, PHA-0201, PHA-0255 and PHA0256, make them acceptable to consumer and industry. Results of this study, indicated genotypes MAC 12-2, LAS 400A and DB 200-15 to produce large seeds.

Agronomical traits such as days to maturity, pods per plant, seeds per pod and yield were variable. This implies that they are affected by environmental influences. Welsh *et al.* (1991); reported that variation of agronomical traits for morphological, proteins and isozyme markers were larger in interracial populations than in intraracial populations. Seed weight was not positively associated with many quantitave parameters in the study. This could be explained in relation to the inherent characters of the different genotypes: Locules that had premature dead seeds could have attributed to the negative correlation with number of seeds per plant and positive correlation with 100 seed weight. This should explain for the negative correlation between 100 seed weight and number of seeds per pod. Seed weight

in terms of grams of 100 seeds randomly chosen expresses the seed size (Schoonhoven *et al.*, 1987) and the majority of the lines (43) were expressed as large seeded (> 40 gm per 100 seed weight). Report by Gepts and Bliss 1985, grouped the small seed size (100 – seed weight < 40 gm), and the large seed size (100 – seed weight > 40gm), into two different major forms; the Middle American and Andean South America, respectively. Information from the study reveals the forms, which could be of interest in using them in the crossing programmes to enlarge the genetic base. The variability in seed size is the deduced as extremely important for classification of the genetic diversity existing among the large number of bean varieties within the 56 genotypes used in the study.

Thirty-three genotypes have a yield in range between 71 – 147 g plot^{-1}, some of these genotypes could play part in breeding program with a goal to improve yield but also to maintain good seed quality at the same time. The mean yield of 31 genotypes were higher than that of the local checks. This demonstrated the greater usefulness of new introductions for increasing yield potential in common bean (Welsh *et al.*, 1995). Yield variations among the different genotypes could also be subjected to environmental influences. It could also be deduced that genotypes with low yields originate from intraracial populations than interracial. Welsh *et al.* (1991) revealed that, more high yielding lines were from interracial populations than the intraracial populations. The performance of 9% of the genotypes in study was promising and it was observed that they scored desirably (average means) in a number of different traits, though not consistently. They are thought to be originating from interracial populations basing on the explanation above. In general yields of the promising genotypes were below the recommended yield for climbing beans (2500 - 4000 kg ha^{-1}). It was observed by Escribano *et al.* (1994), that dry bean productivity is poor in general, so it is important to find the genotypes with high yields. Further studies revealed that some of the promising genotypes PHA-0029, PHA-0028, PHA-0315 and PHA0419 (with yields > 70 gm per plant) could be parents in breeding programmes with the goal to improve dry bean yield and also addressing the seed quality. These are in agreement with the results of this study, in that genotypes with promising yields MAC 19-1, MAC 35, MAC 70-2 and MAC 50 could be used in the breeding programmme.

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