

# Diversity Among Yellow Seeded Common Beans in Tanzania

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**Abstract:** Common bean is globally the most important leguminous crop for direct human consumption. In Tanzania, it is the most inter-cropped leguminous crop especially with maize. Characterization of common beans is important for genetic improvement and ex-situ germplasm conservation since it allows identification and awareness of key features of the genotypes. The common beans grown in Tanzania are of different seed colours such as red, red mottled, grey, white, yellow, brown etc. Yellow bean is one of the most traded bean types in Tanzania but there is limited information on diversity of the varieties cultivated across the country. Therefore, the objective of this study was to assess the diversity of yellow seeded common beans found in Tanzania. The study was carried out at Sokoine University of Agriculture, Morogoro, Tanzania in 2022. Thirty-two yellow bean genotypes collected from different regions of Tanzania were assessed for diversity using quantitative and qualitative traits. The trials were carried out in the screen house and on the open field. The data collected were subjected to analysis of variance, cluster, principal component, and correlation analyses. Sixteen genotypes were characterized as determinate plant type while the remaining sixteen were classified as indeterminate. About 75% of the genotypes had cuboid shape while 12.5% had kidney and oval shapes. About 78% of the genotypes were dominated by green cotyledon colour while 90% had white hypocotyls colour. The cluster analysis grouped the genotypes into five groups in both field and screen house. The first four principal components accounted for 51.8% of the variation observed on the field and 61.9% in the screen house. There were strong correlations among many important traits which will allow indirect selection for some complex traits. The positive correlation observed between number of locules and number of seed per pod ( $r = 0.87$ ) indicates that number of locules can be used to determine the density and seed yield. There was high level of diversity among the yellow bean genotypes evaluated in this study for quantitative and qualitative traits. The scientific information obtained from this study will be useful in breeding programmes for improvement of yellow seeded beans in Tanzania for the traits.

**Keywords:** Yellow Beans, Qualitative and Quantitative Traits, Principal Component Analysis, Cluster Analysis

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## 1. Introduction

Common bean is the most important leguminous crop globally for direct human consumption. In Tanzania, it is the most inter-cropped leguminous crop especially with maize [10]. Common beans are grown in cold climates, particularly in the Northern and Southern highlands, as well as in the Eastern and Western lowlands [6]. About 80% of the rural population and urban poor in Tanzania use common beans on

a daily basis, hence, its importance as a food crop in the country cannot be overstated. Tanzanians grow common bean mostly for its green shells and dry seeds, but the young tender leaves are frequently consumed as fresh vegetables. For people of all ages, common beans have a significant nutritious content with carbohydrates accounting for 60% of its dry weight providing calories. The calories in 100 g (dry weight basis) of beans are 120 kca [4].

Characterization of common beans is important for genetic

improvement and ex-situ germplasm conservation since it allows identification and awareness of key features of the genotypes. Level of diversity of common beans can be assessed using data acquired from germplasm characterization [3]. The common beans grown in Tanzania are of different seed colours such as red, red mottled, grey, white, yellow, brown etc. However, the yellow beans are one of the most traded bean types in the country [1]. Yellow bean varieties are diverse and vary across the production areas of the country with highest diversity in the Western region of the country [1]. Farmers choose to grow yellow beans because it has greater market opportunities and people consume more of this type of beans than other types. For future use, conservation, improvement, collection, and characterisation, documentation of diversity of yellow seeded common bean landraces and improved cultivars is essential. It's also important to know the distribution of the yellow seeded common bean in bean growing areas of Tanzania. Therefore, the objective of this study was to investigate the diversity of yellow seeded common bean in Tanzania in order to enhance its improvement.

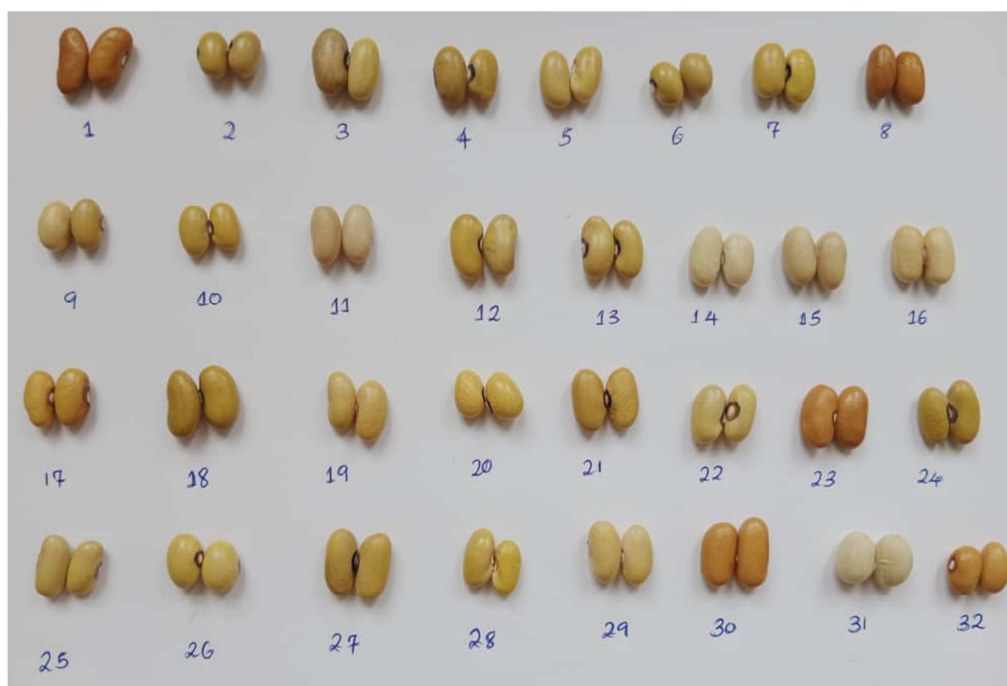
## 2. Materials and Methods

The experiment was conducted in the research fields of the Department of Crop Science and Horticulture (DCSH) of the Sokoine University of Agriculture (SUA) in Morogoro, Tanzania between February and September 2022. A total of 32 diverse yellow seeded common beans (Figure 1) were collected from four zones namely Northern zone (Arusha and Kilimanjaro), Southern Highland zone (Mbeya), Eastern zone (Morogoro) and Lake zone (Kagera and Kigoma) in Tanzania (Figure 2). The samples were collected from the Agricultural research centres and the markets within production areas

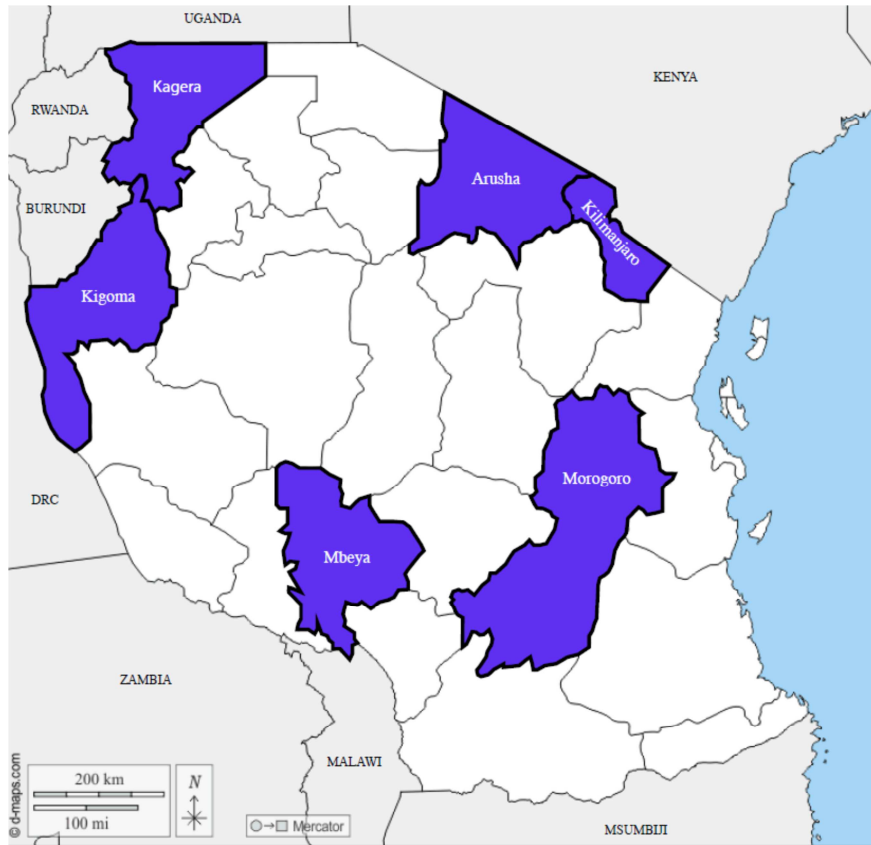
(Table 1).

Two experiments were established under different environmental conditions, one in the open field and the second one in the screen house using Randomized Complete Block Design (RCBD) with three replications. The seeds were planted at a spacing of 0.20 m within row and 0.50 m between rows with one row as an experimental unit. In the screen house, three seeds of each genotype were planted per pot which was 20 cm in diameter and 19 cm in depth. Forest soil was used as the medium for planting.

Data were collected using the standard *Phaseolus vulgaris* descriptors by International Board for Plant Genetic Resources IBPGR, 1982. Data were recorded at different stages from plant emergence to pod harvesting on five plants per plot on the field and three plants in each pot in the screenhouse. The morphological characters recorded are: Days to emergency (DE), Days to 50% flowering (DTFLO), Hypocotyls colour (HYPCLR), Emerging cotyledon colour (COTYCLR), Days to 85% seed maturity (DSM), Nodules colour (NC), Colour of standard petal (CLRSTD), Colour of wing petals (CLRWG), Plant type (PTP), Flower colour (FC), Leaflet length (LF in cm), Number of nodes on main stem from base to first inflorescence (Nodeno), Plant height (PH in cm), Flower buds per inflorescence (FLB/INFLO), Pod length (PDLG in cm), Number of locules per pod (NLP), Number of nodules (NoN), Number of pod per plant (NPPP), Number of seeds per pod (NSPP), Weight of seeds per pod (WSP) (g). Pod traits observed in this study are: Pod cross section (PDXSC), Pod curvature (PDCUV), Pod colour at physiological maturity (PDCLRPM), Pod beak orientation (PDBO), Pod beak position (PDBP). Seed traits recorded are: Seed coat patterns (SDCTPTN), Brilliance of seed (BRLSD), Seed shape (SDSHP), 100 seeds weight (100Ws) (g), and Seed yield per plot (SY) (kg).



**Figure 1.** Yellow seeded common beans collected from different regions of Tanzania.



**Figure 2.** Map of Tanzania showing the regions where the yellow bean samples were collected.

**Table 1.** Yellow common bean samples collected from various locations in Tanzania.

S/N	Name of genotypes	Given name	Classification	Collection Place
1	P-IT Selian	Arusha 1	Breeder line	Arusha
2	123-45	Arusha 2	Breeder line	Arusha
3	134-52	Arusha 3	Breeder line	Arusha
4	259-9	Arusha 4	Breeder line	Arusha
5	144-25	Arusha 5	Breeder line	Arusha
6	118-4	Arusha 6	Breeder line	Arusha
7	116-4	Arusha 7	Breeder line	Arusha
8	311-12	Arusha 8	Breeder line	Arusha
9	216-34	Arusha 9	Breeder line	Arusha
10	Njanofupi	Arusha 10	Landrace	Kilimanjaro
11	Njanondefu	Arusha 11	Landrace	Kilimanjaro
12	Gololi	Arusha 12	Landrace	Kilimanjaro
13	Yellow chato	Bukoba 1	Landrace	Kagera
14	Masindi yellow	Bukoba 2	Landrace	Kagera
15	Njanondefu	Bukoba 3	Landrace	Kagera
16	Rushara	Bukoba 4	Landrace	Kagera
17	A	Bukoba 5	Breeder line	Kagera
18	B	Bukoba 6	Breeder line	Kagera
19	C	Bukoba 7	Breeder line	Kagera
20	D	Bukoba 8	Breeder line	Kagera
21	E	Bukoba 9	Breeder line	Kagera
22	F	Bukoba 10	Breeder line	Kagera
23	G	Bukoba 11	Breeder line	Kagera
24	Kigoma	Morogoro 1	Landrace	Morogoro
25	Mgeta	Morogoro 2	Landrace	Morogoro
26	Bukoba	Morogoro 3	Landrace	Morogoro
27	Selian 13	Selian 13	Improved	Mbeya
28	Uyole 16	Uyole 16	Improved	Mbeya
29	Maini	Maini	Landrace	Mbeya
30	Fibea	Fibea	Improved	Mbeya
31	Kigoma	Kigoma	Improved	Mbeya
32	NjanoUyole	NjanoUyole	Improved	Mbeya

The distances between pair of genotypes using the mixture of variables (continuous, ordinal and binary) were calculated and a cluster analysis of the genotypes using the Ward minimum variance method, Ward, 1963 was applied on the distances matrix. Cluster analysis and analysis of variance (ANOVA) were computed using the Statistical Analysis System, SAS V9.3 (SAS/STAT, 2010). Principal Component Analysis (PCA) was used to observe the interrelationship among the set of variables. This was carried out using the PRINCOMP procedure SAS-V9.3 (SAS/STAT, 2010). The principal components with Eigen values > 0.2 were selected. Pearson correlation coefficients were calculated to understand the relationship between pairs of morphological traits.

### 3. Results

Analysis of variance revealed highly significant differences among the 32 common bean genotypes evaluated in this study for phenological traits. For Days to Emergency (DE), it ranged from 7 to 10 days in field while in the screen house, it ranged from 3 to 8 days. The mean, minimum, maximum and the percent of coefficient of variation (CV%)

of the traits evaluated are shown in Tables 2 and 3. For days to flowering (DTFLO), it ranged from 31 to 68 days on the field and 25 to 35 days in the screen house. Days to seed maturity (DSM) ranged from 63 to 78 in both field and screen house.

#### 3.1. Quantitative Traits

Highly significant differences of the quantitative traits were obtained among the genotypes evaluated. Number of Nodules (NoN) produced by the genotypes ranged from 0 to 38 in both field and screen house. Number of flower bud per inflorescence (FLB) ranged from 3 to 5 in field while in the screen house it ranged from 3 to 6. For the pod length (PDLG), it ranged from 4.4 to 29.5 cm in field while in the screen house it ranged from 3 to 15 cm. Number of pods per plant (NPPP) ranged from 3 to 12 in the field and 4 to 5 in the screen house. Plant height (PH) ranged from 72.5 to 234.2 cm in the field 71 to 238 cm in the screenhouse. Number of nodes from the base to first inflorescence (Nodeno) ranged from 7 to 14 among the genotypes evaluated in both field and screen house (Tables 2 and 3).

**Table 2.** Mean, minimum, maximum and CV values for the 32 morphological traits of the yellow beans evaluated in field in Tanzania 2022.

S/N	Morphological traits	Mean	Min	Max	CV
1	ED	8.26	7.00	10.00	5.11
2	DTFLO	38.51	31.00	68.00	4.86
3	NoN	14.73	0.00	38.00	26.64
4	FLB	4.39	3.40	5.60	6.42
5	PDLG	10.58	4.40	29.50	20.13
6	NPPP	6.82	3.40	12.80	10.95
7	DSM	67.77	63.00	78.00	2.14
8	PH	140.47	71.00	238.00	4.81
9	Nodeno	9.91	7.00	14.00	4.63
10	NLP	3.95	3.00	5.20	8.66
11	NSPP	3.95	3.00	5.00	8.89
12	LFL	12.93	9.20	15.00	8.52
13	HSW	36.55	30.50	44.80	4.80
14	WSP	42.11	30.80	108.50	12.83
15	SY	418.82	308.00	1085.00	12.89
16	COTYCLR	1.37	1.00	4.00	0.00
17	HYPCLR	1.09	1.00	2.00	0.00
18	FC	1.09	1.00	2.00	20.59
19	CLRSTD	1.09	1.00	2.00	20.59
20	CLRWG	1.09	1.00	2.00	20.59
21	NC	1.84	1.00	3.00	0.00
21	PTP	1.50	1.00	2.00	0.00
23	PDCUV	1.13	1.00	2.00	15.48
24	PDXSC	1.44	1.00	2.00	0.00
25	PDCLRPM	1.19	1.00	2.00	0.00
26	PDBP	1.75	1.00	2.00	0.00
27	SDSHP	2.63	1.00	3.00	3.87
28	BRLSD	1.76	1.00	3.00	16.88
29	SDCPTN	1.09	1.00	2.00	0.00
30	PDBO	1.79	1.00	3.00	5.74

DE- Days to Emergency, DTFLO- Days to Flowering, NoN- Number of Nodules, FLB- Flower buds, PDLG- Pod Length, NPPP- Number of Plant Per Pod, DSM- Days to Seed Maturity, PH- Plant Height, Nodeno- Number of internodes from the base to the main inflorescence, NLP- Number of Locules Per Pod, NSPP- Number of Seeds Per Pod, LFL- Leaflet Length, HSW- Hunderd Seeds Weight, WSP-Weight of Seed per Plot, SY- Seed Yield, COTYCLR- Cotyledon Colour, HYPCLR- Hypocotyl Colour, FC- Flower colour, CLRSTD- Colour of Standard Petal, CLRWG- Colour of Winged Petal, NC- Nodules Colour, PTP- Plant Type, PDCUV- Pod Curvature, PDXSC- Pod Cross Section, PDBO- Pod Beak Orientation, PDBP- Pod Beak Position, PDCLRPM- Pod Colour at Physiological Maturity, SDSHP- Seed Shape, BRLSD- Brilliance of Seed, SDCPTN- Seed Coat Pattern.

**Table 3.** Mean, minimum, maximum and CV values for the 32 morphological traits of the yellow beans evaluated in screen house in Tanzania 2022.

Variables	Mean	Min	Max	CV (%)
DE	4.14	3	8	8.87
DTFLO	29.81	25	35	1.3
NoN	14.73	0	38	26.8
FLB	4.45	3	6	8.87
PDLG	10.41	3	15	14.72
NPPP	2.36	4	5	18.54
DSM	67.59	63	78	0
PH	139.5	71	238	4.81
Nodeno	9.89	7	14	4.16
NLP	5.86	0	11	38.45
NSPP	5.58	0	10	38.61
LFL	13.11	9	15	3.66

DE- Days to Emergency, DTFLO- Days to Flowering, NoN- Number of Nodules, FLB- Flower buds, PDLG- Pod Length, NPPP- Number of Plant Per Pod, DSM- Days to Seed Maturity, PH- Plant Height, Nodeno- Number of internodes from the base to the main inflorescence, NLP- Number of Locules Per Pod, NSPP- Number of Seeds Per Pod, LFL- Leaflet Length.

S/N	GENOTYPE	COTY CLR	HYP CLR	FC	CLR STD	CLR WG	NC	PTP	PDCUV	PDXSC	PDBO	PDBP	PDCLR PM	SDSHP	BRLSD	SDCPTN
1	Bukoba 1	G	W	P	P	P	P	dt	SC	PS	D	NM	G	kidney	medium	RS
2	Bukoba 2	G	W	P	P	P	P	dt	SC	RE	S	NM	M	cuboid	matt	RS
3	Bukoba 3	G	W	P	P	P	none	dt	SC	PS	S	NM	G	cuboid	medium	RS
4	Bukoba 4	G	W	P	P	P	none	indt	SC	PS	S	M	G	cuboid	medium	RS
5	Bukoba 5	G	W	P	P	P	P	indt	SC	RE	D	M	G	cuboid	shinny	ST
6	Bukoba 6	G	W	P	P	P	P	dt	SC	RE	S	M	G	cuboid	medium	RS
7	Bukoba 7	PG	W	P	P	P	P	dt	S	PS	S	NM	G	cuboid	matt	RS
8	Bukoba 8	G	W	P	P	P	W	dt	SC	RE	S	NM	G	cuboid	matt	RS
9	Bukoba 9	PG	P	P	P	P	P	dt	SC	PS	S	M	G	cuboid	matt	RS
10	Bukoba 10	G	P	P	P	P	none	dt	SC	PS	D	M	M	cuboid	medium	RS
11	Bukoba 11	PG	W	P	P	P	P	indt	SC	PS	S	M	G	cuboid	shinny	RS
12	Arusha 1	G	W	P	P	P	W	indt	SC	RE	D	M	G	cuboid	medium	RS
13	Arusha 2	red	W	P	P	P	W	indt	SC	PS	S	M	G	cuboid	matt	RS
14	Arusha 3	G	W	P	P	P	P	dt	SC	PS	D	M	M	kidney	medium	RS
15	Arusha 4	G	W	P	P	P	none	indt	S	PS	S	M	G	oval	medium	RS
16	Arusha 5	G	W	P	P	P	none	dt	SC	RE	S	M	G	oval	medium	RS
17	Arusha 6	G	W	P	P	P	W	dt	SC	PS	S	NM	G	cuboid	medium	RS
18	Arusha 7	red	W	P	P	P	W	indt	SC	RE	S	M	G	cuboid	matt	RS
19	Arusha 8	G	W	W	W	W	none	dt	S	PS	S	M	G	cuboid	shinny	RS
20	Arusha 9	G	W	W	W	W	P	dt	SC	PS	D	NM	M	cuboid	shinny	RS
21	Arusha 10	G	W	P	P	P	W	indt	SC	PS	S	M	G	cuboid	medium	RS
22	Arusha 11	G	W	P	P	P	P	indt	SC	RE	S	M	G	cuboid	shinny	RS
23	Arusha 12	G	W	P	P	P	P	indt	SC	PS	S	M	G	cuboid	shinny	RS
24	Morogoro 1	P	W	P	P	P	none	dt	SC	PS	S	M	M	kidney	medium	RS
25	Morogoro 2	PG	W	P	P	P	none	indt	SC	PS	S	M	G	cuboid	medium	RS
26	Morogoro 3	G	P	P	P	P	P	indt	SC	RE	D	M	M	oval	medium	RS
27	Selian 13	PG	W	P	P	P	P	dt	SC	RE	S	NM	G	oval	shinny	RS
28	Maini	G	W	P	P	P	none	indt	S	RE	S	M	G	cuboid	medium	RS
29	Fibea	G	W	W	W	W	W	indt	S	PS	S	M	G	cuboid	matt	RS
30	Njano uyole	G	W	P	P	P	W	indt	SC	RE	D	M	G	kidney	shinny	ST
31	Uyole 16	G	W	P	P	P	W	indt	SC	RE	U	M	G	cuboid	matt	ST
32	Kigoma	G	W	P	P	P	P	dt	SC	RE	U	M	G	cuboid	shinny	RS

**Figure 3.** Qualitative traits observed among 32 genotypes of yellow seeded common beans collected in Tanzania.

P-purple, W-white, G-green, PG-pale green, dt-determinate, indt-indeterminate, S-straight, SC- slightly curved, PS-pear shaped, RE- round elliptic, D- downward, U-upward, M-marginal, NM-non marginal, M-mottled, ST-stripped, RS- rhomboid spotted.

### 3.2. Qualitative Traits

There was highly significant variation among the genotypes evaluated in both field and screen house for all the qualitative variables (Figure 3). Predominantly emerging cotyledon colour (COTYCLR) among the genotypes was green (78.13%), while 15.63% and 6.25% of the genotypes had pale green and reddish COTYCLR, respectively. Most genotypes (90.63%) had white coloured hypocotyl (HYPCLR) while 9.37% of genotypes had purple colour. The plant type (PTP) was equally distributed with an average of 50% being determinate (dt) the remaining and indeterminate (indt). The commonest colour of freshly opened flower (FC) was purple (P) (90.63%) followed by white (W) which was observed only on three genotypes

(9.37%). In terms of colour of standard (CLRSTD) and colour of wing (CLRWG), half of the genotypes were purple (P) while the remaining half were white (W).

The predominantly observed nodule colour (NC) among the genotypes was purple (P) found in 43.75% of the genotypes followed by 28.13% having white (W), 28.12% of the genotypes had no colour on their nodules. About 84% of the genotypes had slightly curved pods (PDCUV) while 15.63% had straight pods. For pod cross section (PDXSC), 56.25% of the genotypes had pear shape (PS) pod cross section while the remaining 43.75% had round elliptic (RE). Also, 25% of the genotypes had non marginal (NM) pod beak position while the remaining 75% had marginal ones (M). In respect to pod beak orientation, three forms were

observed whereby 68.75% of the genotypes had straight (S) pod beak orientation, 25% had downward (D) orientation and only two genotypes (6.25%) had upward (U) orientation.

Variation was also observed for pod colour at physiological maturity (PDCLRPM) with most of the genotypes (81.25%) having green colour (G) while 18.75% of the genotypes had green colour with red mottles (M) on it. For seed coat pattern (SDCPTN), only two patterns were observed: rhomboid spotted (RS) found in about 90.63% of the genotypes while stripped (ST) pattern was found in about 9.37% of the genotypes. In terms of Brilliance of seed (BRLSD), 46.87% had medium, 28.13% were shinny and 25% were matt. For seed shape (SDSHP), cuboid was dominant (75% of the genotypes) followed by oval and kidney shapes each observed in 12.5% of the genotypes.

The first three principal components explained 42.2% of the total variation (Table 4) Observed on the field. The first principal component (PC1) mostly correlated with Plant type (PTP) (0.358), Days to seed maturity (DSM) (0.324), Plant

height (PH) (0.349), Number of nodes from the base to first inflorescence (NODENO) (0.342), Days to emergency (DE) (0.265) and Pod Beak Position (PDBP) (0.231) which positively contributed to the total variation with higher loadings on the PC1 axes while flower buds per inflorescence (FLB) (-0.231) loaded negatively on PC1.

In the screen house experiment, the principal component analysis and percentage contribution of each component to the total variation showed that the first three principal components explained 45.0% of the total variation (Table 5). The first principal component was mostly correlated with DTFLO (0.215), DSM (0.262), PH (0.360), NODENO (0.374), NSPP (0.202), PTP (0.389) and DSM (0.262) which positively contributed to the total variation with higher loadings on the PC1 axes while FLB (-0.271) and HSW (-0.254) loaded negatively on the PC1. Seed traits NPPP (0.298), LP (0.254) and NSPP (0.247) contributed positively to the PC2 axis. Yield parameters such as HSW (0.249), WSP (0.253) and SY (0.253) also contributed positively to the PC 2 axis.

**Table 4.** Eigen values and contribution of the first three principal component axes to variation in yellow bean genotypes evaluated on morphological traits in field.

Variables	Eigenvectors		
	PC1	PC2	PC3
DE	0.265	0.152	0.006
DTFLO	0.295	0.02	0.056
NoN	-0.038	-0.154	-0.318
FLB	-0.231	0.1	0.132
PDLG	0.06	0.164	-0.078
NPPP	0.083	-0.209	-0.061
DSM	0.324	-0.027	0.019
PH	0.349	-0.142	0.027
Nodeno	0.342	-0.098	0.027
NLP	0.072	0.274	0.302
NSPP	0.061	0.291	0.263
LFL	0.048	-0.056	-0.105
HSW	-0.112	-0.032	0.24
WTP	-0.125	-0.126	0.267
SY	-0.125	-0.126	0.267
COTYCLR	0.029	-0.117	0.054
HYPCLR	-0.119	-0.011	0.075
FC	0.035	0.364	-0.262
CLRSTD	0.035	0.364	-0.262
CLRWG	0.035	0.364	-0.262
NC	0.149	0.15	0.209
PTP	0.358	-0.166	-0.075
PDCUV	0.168	0.206	0.219
PDXSC	-0.007	-0.179	-0.197
PDBO	0.068	-0.069	0.218
PDBP	0.231	-0.098	0.08
PDCLRPM	-0.164	0.097	-0.062
SDSHP	0.136	0.058	-0.063
BRLSD	-0.039	-0.084	-0.236
SDCPTN	0.031	-0.197	-0.167
EIGEN VALUES	5.447	4.373	3.678
PERCENT VARIATION	0.17	0.137	0.115
CUMULATIVE PROPORTION	0.17	0.307	0.422

PC- Principal Component, DE-Days to Emergency, DTFLO- Days to Flowering, NoN- Number of Nodules, FLB- Flower buds, PDLG- Pod Length, NPPP- Number of Plant Per Pod, DSM- Days to Seed Maturity, PH- Plant Height, Nodeno- Number of internodes from the base to the main inflorescence, NLP- Number of Locules Per Pod, NSPP- Number of Seeds Per Pod, LFL- Leaflet Length, HSW- Hunderd Seeds Weight, WSP-Weight of Seed per Plot, SY- Seed Yield, COTYCLR- Cotyledon Colour, HYPCLR- Hypocotyl Colour, FC- Flower colour, CLRSTD- Colour of Standard Petal, CLRWG- Colour of Winged Petal, NC- Nodules Colour, PTP- Plant Type, PDCUV- Pod Curvature, PDXSC- Pod Cross Section, PDBO- Pod Beak Orientation, PDBP- Pod Beak Position, PDCLRPM- Pod Colour at Physiological Maturity, SDSHP- Seed Shape, BRLSD- Brilliance of Seed, SDCPTN- Seed Coat Pattern.

**Table 5.** Eigen values and contribution to the first three principal component axes to variation of yellow bean genotypes evaluated on morphological traits in screen house.

Variables	Eigen Vectors		
	PC 1	PC 2	PC 3
DE	0.14	-0.261	-0.14
DTFLO	0.215	0.077	-0.036
NoN	0.059	0.111	0.26
FLB	-0.271	-0.003	-0.072
PDLG	-0.049	-0.107	0.209
NPPP	0.117	0.298	0.278
DSM	0.262	-0.054	-0.097
PH	0.36	0.013	-0.183
Nodeno	0.374	0.034	-0.118
LP	0.19	0.254	0.304
NSPP	0.202	0.247	0.287
LFL	-0.029	-0.031	-0.04
HSW	-0.254	0.249	-0.063
WTP	-0.189	0.253	-0.102
SY	-0.189	0.253	-0.102
COTYCLR	-0.015	0.02	-0.174
HYPCLR	-0.12	0.004	-0.1
FC	0.008	-0.335	0.289
CLRSTD	0.008	-0.335	0.289
CLRWG	0.008	-0.335	0.289
NC	0.071	-0.208	-0.259
PTP	0.389	0.039	-0.089
PDCUV	0.117	-0.135	-0.115
PDXSC	0.054	0.157	0.131
PDBO	0.032	0.142	-0.135
PDBP	0.229	0.068	-0.161
PDCLRPM	-0.164	-0.111	0.04
SDSHP	0.114	-0.053	0.059
BRLSD	0.017	0.115	0.271
SDCPTN	0.088	0.116	0.091
EIGEN VALUES	5.229	4.409	3.857
PERCENT VARIATION	0.174	0.147	0.129
COMMULATIVE PROPORTION	0.174	0.321	0.45

PC- Principal Component, ED- Emergency Day, DTFLO- Days to Flowering, NoN- Number of Nodules, FLB- Flower buds, PDLG- Pod Length, NPPP- Number of Plant Per Pod, DSM- Days to Seed Maturity, PH- Plant Height, Nodeno- Number of internodes from the base to the main inflorescence, NLP- Number of Locules Per Pod, NSPP- Number of Seeds Per Pod, LFL- Leaflet Length, HSW- Hunderd Seeds Weight, WSP-Weight of Seed per Plot, SY- Seed Yield, COTYCLR- Cotyledon Colour, HYPCLR- Hypocotyl Colour, FC- Flower colour, CLRSTD- Colour of Standard Petal, CLRWG- Colour of Winged Petal, NC- Nodules Colour, PTP- Plant Type, PDCUV- Pod Curvature, PDXSC- Pod Cross Section, PDBO- Pod Beak Orientation, PDBP- Pod Beak Position, PDCLRPM- Pod Colour at Physiological Maturity, SDSHP- Seed Shape, BRLSD- Brilliance of Seed, SDCPTN- Seed Coat Pattern.

From the field experiment, cluster analysis grouped the genotypes into five clusters with 7, 3, 13, 7 and 2 genotypes in Clusters I, II, III, IV and V, respectively (Figure 4). Cluster I contains 21.87% of genotypes namely Arusha 10, Arusha 2, Arusha 7, Arusha 4, Bukoba 4, Morogoro 2 and Maini. Phenotypically, Bukoba 4 and Morogoro 2 were the most closely related genotypes with the closest distance of 0.0048 in cluster I. Cluster II has only 9.38% of the genotypes; Bukoba 5, NjanoUyole and Uyole 16. Cluster III contains the highest number of genotypes (40.63%) with up to 7 genotypes coming from Bukoba (Bukoba 1, Bukoba 2, Bukoba 3, Bukoba 7, Bukoba 8, Bukoba 9, and Bukoba 10) followed by Morogoro 1, Arusha 3, Arusha 5, Arusha 6 and Kigoma. Arusha 12, Bukoba 11, Arusha 1, Bukoba 6, Fibeaa, Morogoro 3 and Arusha 11 were grouped in Cluster IV while only Arusha 8 and Arusha 9 representing 6.25% of the genotypes were placed in cluster V. Using the data collected in the screen house, the genotypes were also grouped into

five clusters with 12, 14, 3, 2 and 1 genotypes in Clusters I, II, III, IV and V, respectively (Figure 5). Cluster I contains 37.5% of genotypes namely Arusha 11, Arusha 12, Arusha 2, Arusha 7, Bukoba 5, Bukoba 5, NjanoUyole, Bukoba 4, Morogoro 2, Bukoba 11, Uyole 16, Arusha 1 and Fibeaa. Phenotypically, Arusha 11 and Arusha 12, Arusha 2 and Arusha 7 were the most closely related genotypes with the closest distance of 0.0071 and 0.0083 respectively in cluster I. Cluster II contains the highest number of genotypes which constitutes 43.75% of all the genotypes namely; Bukoba 2, Bukoba 8, Bukoba 3, Bukoba 7, Bukoba 6, Bukoba 1, Bukoba 10 and Bukoba 9, Selian 13, Arusha 5, Arusha 3 and Arusha 6. Also Bukoba 2 and Selian 13 phenotypically were the most closely related genotypes with the closet distance of 0.0093 in this cluster. Cluster III has 9.375% of the genotypes namely Arusha 4, Maini and Arusha 10. Arusha 8 and Arusha 9 were grouped in Cluster IV (6.25%) while only one (3.125%) genotype Kigoma was placed in Cluster V.

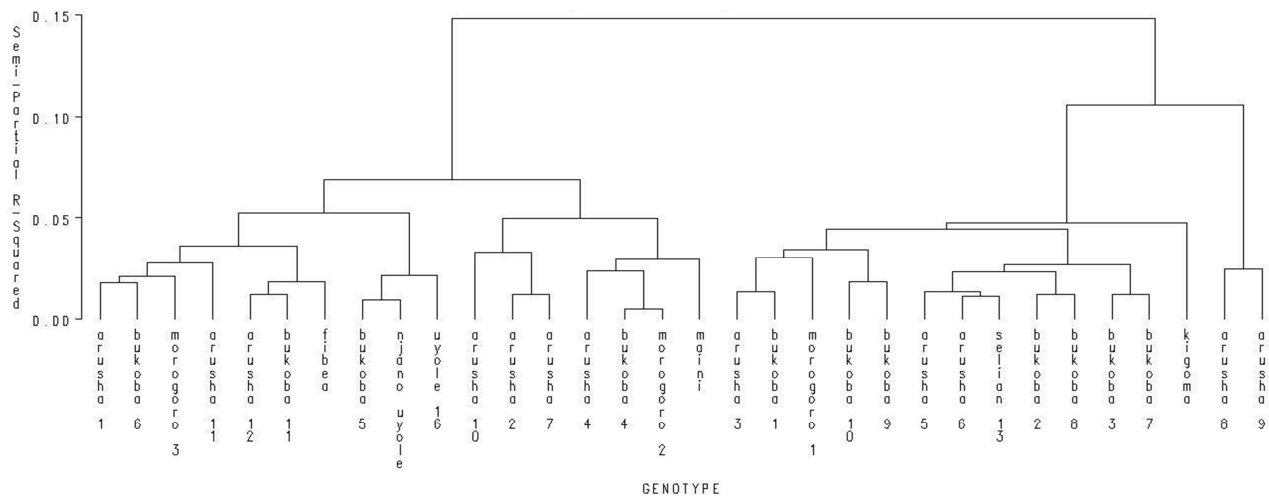


Figure 4. Dendrogram showing genetic relationship among 32 common bean genotypes based on 32 morphological traits from the field experiment.

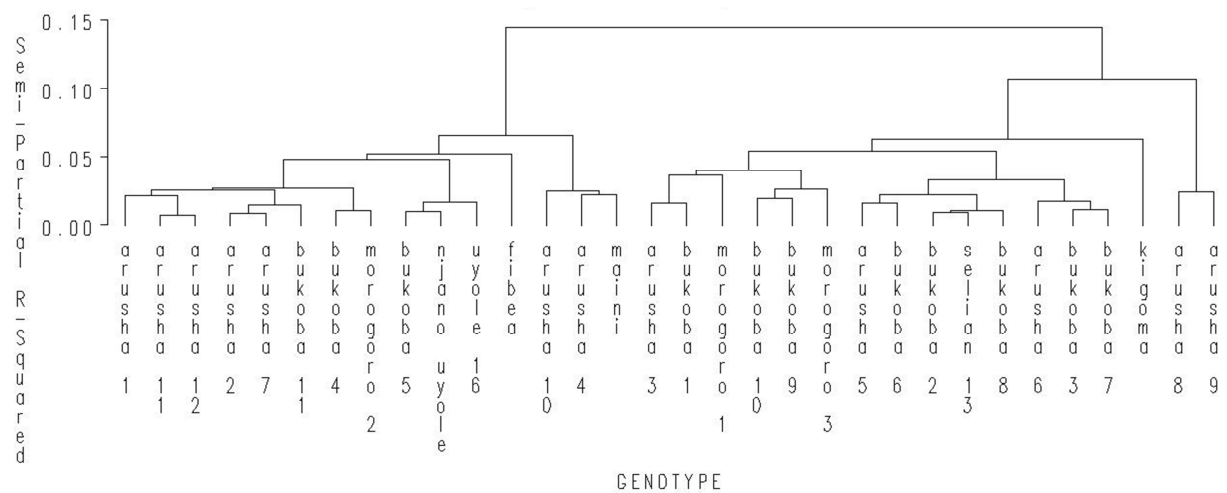


Figure 5. Dendrogram showing genetic relationship among 32 Common bean genotypes based on 32 morphological traits from the screen house experiment.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
DTFLO	0.42	1																														
NoN	-0.20	-0.06	1																													
FLB	-0.22	-0.12	-0.16	1																												
PDLG	0.18	-0.04	0.00	0.07	1																											
NPPP	0.07	0.07	0.11	-0.05	0.09	1																										
DSM	0.40	<b>0.60</b>	0.05	-0.36	0.13	0.25	1																									
PH	0.34	0.39	0.07	<b>-0.40</b>	-0.07	0.09	<b>0.50</b>	1																								
Nodeno	0.22	0.26	0.08	<b>-0.46</b>	0.00	0.01	<b>0.44</b>	<b>0.87</b>	1																							
NLP	0.16	0.06	-0.36	0.03	0.13	0.01	0.13	-0.07	0.05	1																						
NSPP	0.16	-0.02	-0.34	0.07	0.19	-0.05	0.06	-0.08	0.05	<b>0.87</b>	1																					
LFL	0.26	0.05	-0.04	-0.08	0.15	0.01	-0.09	0.06	-0.03	-0.19	-0.12	1																				
HSW	-0.14	0.09	-0.05	0.15	-0.07	0.05	0.04	-0.01	-0.10	-0.01	-0.04	-0.20	1																			
WTP	-0.11	-0.02	-0.03	0.11	0.06	0.38	0.02	-0.11	-0.12	0.17	0.14	-0.12	<b>0.53</b>	-0.06	0.11	1																
SY	-0.11	-0.02	-0.03	0.11	0.06	0.38	0.02	-0.11	-0.12	0.17	0.14	-0.12	<b>0.53</b>	-0.06	0.11	1	1															
COTYCLR	0.16	0.00	-0.07	-0.26	-0.09	0.02	0.11	0.08	0.00	-0.23	-0.18	0.16	0.00	0.03	-0.12	0.06	0.06	1														
HYPCLR	-0.11	-0.09	0.00	0.34	-0.02	-0.14	-0.10	-0.12	-0.11	-0.07	-0.10	-0.15	0.18	0.16	0.05	0.07	0.07	-0.02	1													
FC	0.15	0.00	0.10	-0.01	0.17	-0.03	0.03	-0.14	-0.12	0.08	0.10	0.03	0.00	0.01	-0.10	-0.12	-0.12	-0.16	-0.10	1												
CLRSTD	0.15	0.00	0.10	-0.01	0.17	-0.03	0.03	-0.14	-0.12	0.08	0.10	0.03	0.00	0.01	-0.10	-0.12	-0.12	-0.16	-0.10	1	1											
CLRWG	0.15	0.00	0.10	-0.01	0.17	-0.03	0.03	-0.14	-0.12	0.08	0.10	0.03	0.00	0.01	-0.10	-0.12	-0.12	-0.16	-0.10	1	1	1										
NC	0.34	0.19	-0.70	0.02	-0.10	-0.13	0.14	0.17	0.08	0.18	0.19	0.17	0.00	0.10	-0.12	-0.16	-0.16	0.10	-0.07	0.02	0.02	0.02	1									
PTP	0.36	0.35	0.18	<b>-0.48</b>	0.03	0.20	0.55	<b>0.85</b>	<b>0.76</b>	-0.08	-0.10	0.06	-0.19	-0.13	-0.24	-0.15	-0.15	0.00	-0.11	-0.11	-0.11	-0.11	0.11	1								
PDCUV	0.26	0.16	-0.29	0.07	0.03	-0.07	0.21	0.16	0.22	<b>0.43</b>	<b>0.43</b>	-0.12	0.02	0.04	-0.17	0.00	0.00	-0.16	-0.13	0.19	0.19	0.19	0.37	0.15	1							
PDXSC	-0.11	-0.03	0.22	-0.14	-0.05	0.11	0.00	-0.12	-0.09	-0.24	-0.26	0.14	-0.30	-0.01	0.02	-0.07	-0.19	-0.19	-0.14	-0.14	-0.14	-0.14	-0.21	0.13	-0.16	1						
PDBO	-0.01	0.15	-0.28	0.09	-0.05	0.04	0.25	0.10	0.01	0.10	0.10	0.15	0.12	-0.09	0.04	0.20	0.20	0.20	-0.27	-0.14	-0.14	-0.14	0.18	0.04	0.15	0.02	1					
PDBP	0.20	0.17	-0.10	-0.25	0.05	0.12	0.36	<b>0.44</b>	0.49	0.08	0.12	-0.01	-0.18	0.00	-0.21	0.00	0.00	0.10	0.19	-0.14	-0.14	-0.14	0.24	<b>0.58</b>	0.09	0.07	0.04	1				
PDCLRPM	-0.04	-0.15	0.13	0.02	-0.05	-0.18	-0.15	-0.28	-0.34	-0.06	0.00	-0.04	0.07	0.11	0.05	0.01	0.01	0.08	0.39	0.12	0.12	0.12	-0.10	-0.32	-0.19	-0.10	<b>-0.41</b>	-0.09	1			
SDSHP	0.19	0.14	0.00	0.07	0.12	0.06	0.32	0.14	0.17	0.00	-0.02	-0.05	-0.09	-0.13	-0.14	-0.04	-0.04	-0.14	0.01	0.17	0.17	0.17	-0.01	0.17	0.08	0.04	0.39	-0.03	-0.32	1		
BRLSD	-0.13	-0.11	0.29	0.02	0.14	0.31	-0.01	-0.13	-0.14	-0.13	-0.07	0.03	-0.16	-0.08	0.15	0.09	0.09	0.03	-0.16	0.22	0.22	0.22	<b>-0.49</b>	0.09	-0.07	0.20	0.15	-0.05	-0.15	0.19	1	
SDCPTN	-0.17	0.06	0.12	-0.16	-0.09	0.22	0.09	0.04	0.01	-0.21	-0.23	0.20	-0.05	-0.02	0.15	-0.08	-0.08	-0.16	-0.10	-0.10	-0.10	-0.10	-0.07	0.32	-0.13	0.36	-0.07	0.19	-0.15	-0.14	0.35	1

Figure 6. Correlation coefficient among 32 morphological traits of yellow seeded common bean evaluated in field.

DTFLO- Days to Flowering, NoN- Number of Nodules, FLB- Flower buds, PDLG- Pod Length, NPPP- Number of Plant Per Pod, DSM- Days to Seed Maturity, PH- Plant Height, Nodeno- Number of internodes from the base to the main inflorescence, NLP- Number of Locules Per Pod, NSPP- Number of Seeds Per Pod, LFL- Leaflet Length, HSW- Hunderd Seeds Weight, WSP-Weight of Seed per Plot, SY- Seed Yield, COTYCLR- Cotyledon Colour, HYPCLR- Hypocotyl Colour, FC- Flower colour, CLRSTD- Colour of Standard Petal, CLRWG- Colour of Winged Petal, NC- Nodules Colour, PTP- Plant Type, PDCUV- Pod Curvature, PDXSC- Pod Cross Section, PDBO- Pod Beak Orientation, PDBP- Pod Beak Position, PDCLRPM- Pod Colour at Physiological Maturity, SDSHP- Seed Shape, BRLSD- Brilliance of Seed, SDCPTN- Seed Coat Pattern.

Significant correlation at \*P<0.05, \*\*P<0.01, \*\*\*P<0.001.



The results from the pair wise correlation among traits are shown in Figures 6 and 7. In the field experiment, the results showed that most strongly correlated traits were number of locules per pod (NLP) with number of seed per pod (NSPP) ( $r = 0.87$ ), plant type (PTP) with plant height (PH) ( $r = 0.85$ ), plant type with node number from the base to the first inflorescence (Nodeno) ( $r = 0.76$ ) and Nodeno with PH ( $r = 0.87$ ). Days to flowering (DTFLO) had moderate positive correlation with days to seed maturity (DSM) ( $r = 0.50$ ). Also, correlation was moderate between PH and DSM ( $r = 0.50$ ), seed yield (SY) and hundred seed weight (HSW) ( $r =$

0.53), weight of seed per plot (WSP) and HSW ( $r = 0.58$ ) (Figure 6).

In screen house, the results showed that the most strongly correlated traits were NSSP with LP ( $r = 0.99$ ), WSP with HSW ( $r = 0.9$ ), SY with HSW ( $r = 0.9$ ). Also, Nodeno with PH ( $r = 0.87$ ), PTP with PH ( $r = 0.84$ ), LP with NPPP ( $r = 0.81$ ), NSPP with NPPP ( $r = 0.80$ ) Nodeno with PH ( $r = 0.87$ ) and PTP and Nodeno ( $r = 0.77$ ) were strongly correlated traits. Moderate correlation was observed between PDBP and PTP ( $r=0.58$ ), PDBP and Nodeno ( $r=0.50$ ), and between DSM and DTFLO ( $r = 0.49$ ) (Figure 7).

Variables	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	
ED	1																														
DTFLO	-0.13	1																													
NoN	-0.02	0.06	1																												
FLB	-0.18	-0.21	-0.17	1																											
PDLG	-0.02	-0.05	0	-0.11	1																										
NPPP	-0.36	0.08	0.14	-0.11	0.23	1																									
DSM	0.25	<b>0.49***</b>	0.1	-0.34	-0.1	-0.09	1																								
PH	0.28	0.38	0.05	-0.35	-0.3	0.03	0.51	1																							
Nodeno	0.19	<b>0.49***</b>	0.09	-0.46	-0.1	0.09	<b>0.47***</b>	<b>0.87***</b>	1																						
LP	-0.36	0.21	0.16	-0.17	0.23	<b>0.81***</b>	0.03	0.09	0.16	1																					
NSPP	-0.36	0.23	0.14	-0.17	0.22	<b>0.80***</b>	0.05	0.1	0.17	<b>0.99***</b>	1																				
LFL	-0.01	-0.11	-0.02	-0.1	-0.2	-0.08	-0.2	-0.04	-0.11	-0.09	-0.1	1																			
HSW	-0.21	0.03	0.02	0.25	-0	0.04	-0.09	-0.17	-0.21	0.09	0.08	-0.1	1																		
WTP	-0.19	0.1	-0.02	0.18	0.02	0.08	0.02	-0.11	-0.13	0.12	0.11	-0.2	<b>0.90*</b>	1																	
SY	-0.19	0.1	-0.02	0.18	0.02	0.08	0.02	-0.11	-0.13	0.12	0.11	-0.2	<b>0.90*</b>	1	1																
COTYCLR	0.13	0.05	-0.07	-0.17	-0	-0.11	0.12	0.04	-0.02	-0.11	-0.11	0.28	0.05	0.05	0.05	1															
HYPCLR	-0.04	-0.03	0	0.31	0	-0.14	-0.1	-0.11	-0.11	-0.13	-0.12	-0.2	0.11	0.07	0.07	-0.02	1														
FC	0.06	-0.03	0.1	-0.05	0.28	-0.01	0.13	-0.13	-0.12	0.15	0.14	-0.1	-0.1	-0.12	-0.12	-0.16	-0.1	1													
CLRSTD	0.06	-0.03	0.1	-0.05	0.28	-0.01	0.13	-0.13	-0.12	0.15	0.14	-0.1	-0.1	-0.12	-0.12	-0.16	-0.1	1	1												
CLRWG	0.06	-0.03	0.1	-0.05	0.28	-0.01	0.13	-0.13	-0.12	0.15	0.14	-0.1	-0.1	-0.12	-0.12	-0.16	-0.1	1	0.02	1											
NC	0.17	-0.03	<b>-0.70***</b>	0.04	-0	-0.21	0.14	0.18	0.09	-0.17	-0.15	0.15	-0.21	-0.16	-0.16	0.1	-0.07	0.02	0.02	0.02	1										
PTP	0.34	0.3	0.18	<b>-0.48***</b>	-0.2	0.09	0.55	<b>0.84***</b>	<b>0.77***</b>	0.16	0.18	-0	-0.26	-0.16	-0.16	0	-0.11	-0.11	-0.11	-0.11	0.11	1									
PDCUV	0.1	0.31	-0.29	-0.01	0.09	-0.13	0.31	0.17	0.22	-0.03	-0.01	-0.3	-0.1	0	0	-0.16	-0.13	0.19	0.19	0.19	0.37	0.15	1								
PDXSC	-0.16	-0.16	0.22	-0.15	-0.2	0.17	-0.03	-0.13	-0.08	0.17	0.17	0.26	-0.1	-0.07	-0.07	-0.19	-0.07	-0.14	-0.14	-0.14	-0.21	0.13	-0.16	1							
PDBO	-0.08	0.15	-0.28	0.11	-0.2	0.02	0.28	0.09	-0.01	0.06	0.07	0.01	0.17	0.2	0.2	0.2	-0.27	-0.14	-0.14	-0.14	0.18	0.04	0.15	0.02	1						
PDBP	0.17	0.31	-0.1	-0.25	-0	0.04	0.36	<b>0.45***</b>	<b>0.50***</b>	0.08	0.09	-0.2	-0.05	0.01	0.01	0.1	0.19	-0.14	-0.14	-0.14	0.24	<b>0.58***</b>	0.09	0.07	0.04	1					
PDCLRPM	-0.01	0.02	0.13	0.02	0.11	-0.17	-0.14	-0.27	-0.34	-0.13	-0.12	0.08	0.05	0	0	0.08	0.39	0.12	0.12	0.12	-0.1	-0.32	-0.19	-0.1	<b>-0.41</b>	-0.09	1				
SDSHP	0.19	0.09	0	0.03	-0	0.01	0.31	0.13	0.15	0.09	0.12	-0.2	-0.07	-0.04	-0.04	-0.14	0.01	0.17	0.17	0.17	-0.01	0.17	0.08	0.04	0.39	-0.03	-0.32	1			
BRLSD	-0.02	0.04	0.29	0	0.05	0.2	-0.03	-0.13	-0.14	0.19	0.18	-0	0.07	0.09	0.09	0.03	-0.16	0.22	0.22	0.22	<b>-0.49***</b>	0.09	-0.07	0.2	0.15	-0.05	-0.15	0.19	1		
SDCPTN	-0.15	-0.1	0.12	-0.15	-0.1	0.1	0.01	0.04	0.01	0.1	0.11	0.25	-0.08	-0.08	-0.08	-0.16	-0.1	-0.1	-0.1	-0.1	-0.07	0.32	-0.13	0.36	-0.07	0.19	-0.15	-0.14	0.35	1	

Figure 7. Correlation coefficient among 32 morphological traits of yellow seeded common bean.

ED-Emergency Day, DTFLO- Days to Flowering, NoN- Number of Nodules, FLB- Flower buds, PDLG- Pod Length, NPPP- Number of Plant Per Pod, DSM- Days to Seed Maturity, PH- Plant Height, Nodeno- Number of internodes from the base to the main inflorescence, NLP- Number of Locules Per Pod, NSPP- Number of Seeds Per Pod, LFL- Leaflet Length, HSW- Hunderd Seeds Weight, WSP-Weight of Seed per Plot, SY- Seed Yield, COTYCLR- Cotyledon Colour, HYPCLR- Hypocotyl Colour, FC- Flower colour, CLRSTD- Colour of Standard Petal, CLRWG- Colour of Winged Petal, NC- Nodules Colour, PTP- Plant Type, PDCUV- Pod Curvature, PDXSC- Pod Cross Section, PDBO- Pod Beak Orientation, PDBP- Pod Beak Position, PDCLRPM- Pod Colour at Physiological Maturity, SDSHP- Seed Shape, BRLSD- Brilliance of Seed, SDCPTN- Seed Coat Pattern. Significant correlation at \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .

## 4. Discussion

Assessment of diversity in plants involves evaluation of phenotypic and genotypic characteristics. Common bean is one of the leguminous crops with large diversity as it has great variation in traits such as flower pigmentation, growth habit, pod colour, seed traits and many other characters [8] and [12]. In this study, the results showed that the yellow seeded bean collections in Tanzania have wide range of diversity for the traits evaluated. This is due to genetic differences among the genotypes and variation in light, temperature and moisture regimes resulting in variation observed among the yellow bean genotypes.

Among the genotypes, cuboid was the most common seed shape followed by oval and kidney shape. The variation observed for the trait among the yellow seeded common beans collected in Tanzania will enable breeders select appropriate genotypes for different end-users. [14] reported the three types of seed shape in Bulgaria and Portugal among existing common bean accessions but kidney shape was the dominant one in those countries. In Tanzania, seeds with cuboid shape referred to as 'Gololi' is the mostly consumed and marketable one in almost every region [1]. Seed colour and shape of common bean are the most considered traits by the consumers and farmers [14], hence, breeders should lay emphasis on them in breeding programmes to ensure high adoption by farmers and consumers.

In common beans, yield and its components are strongly

influenced by genetic make-up of the bean genotypes, environmental conditions and their interactions [11], hence, the need to understand the variability existing in common bean germplasm from different parts of the country. The observed influence of some parameters on others, for example, days to emergence (ED) which had influence on days to flowering and days to seed maturity; number of seeds per pod (NSPP) and the number of pods per plant (NPPP) which had influence on yield indicates that the more complex traits can be indirectly selected for using the other traits that can be easily measured. These traits are of major importance to bean yield and selection [13].

The observed high level of variation among the 32 yellow beans evaluated in this study for quantitative traits is a reflection of the existing genetic differences that can be exploited in breeding programmes. The average days to emergence (DE) on the field (8 days) and screen house (4 days), days to flowering (DTFLO) in the field (38.51 days) and screen house (29.81 days) and days to seed maturity (DSM) in the field and screen house (67 days) are different from those obtained in other studies [7]. These differences could be due to the fact that these physiological traits are highly influenced by environmental conditions such as temperature and photoperiod length [9].

The results from the PCA illustrated the overall picture of the pattern of genetic diversity of the yellow seeded common beans based on morphology. The Eigen value formed the basis for identifying component axes [11] with scores, cut off level arbitrarily set above 0.2 to show traits, which explained most variations in the collections. For instance, considering eigen values in PC1, the genotypes among other traits had different plant height, early seed maturity, different plant types, variation in the number of nodes from the base to first inflorescence (Nodeno), early emergence and different pod beak position. This implies that these traits are among the most important ones for future common bean characterisation and conservation studies.

The level of diversity as evidenced by the clusters formed in this study further underlies how much variation existing among the genotypes for the characteristics they were evaluated for which could be due to both genetic and environmental factors. Several authors reported different clustering patterns of common beans evaluated for morphological traits. However, the observed clustering in this study is consistent with findings of in some past studies. For example, [2] grouped common beans assessed in Uganda into two major clusters with sub groups within each cluster which. [5] also reported two major groups among the common beans from Caribbean evaluated for morphological traits.

The strong correlations between some traits reported in this study indicate that indirect selection for some complex traits is possible using related traits, most especially those difficult to measure. It is known that two strongly correlated desirable traits can be jointly selected for using one of the traits in a breeding programme. For example the positive correlation between number of

locules and number of seed per pod ( $r = 0.87$ ) indicates that number of locules can be used to determine the density and yield. Also, plant height of common bean can be used to determine the plant type whether it is determinate or indeterminate due to the strong correlation ( $r=0.85$ ) observed between the two traits. [5] reported strong positive correlation between seed yield per plant and each of number of pods per plant ( $r = 0.79$ ) and maturity ( $r = 0.28$ ) of common beans from Caribbean.

The fact that the climbing common bean genotypes had higher number of nodes compared to the bush types shows that plant type is the determinant for the number of nodes in common beans. The variation for plant type also depends on the geographical areas where the yellow beans are cultivated. Most of the yellow beans from Bukoba and Arusha are climbing types with higher number of nodes compared to those from other regions of Tanzania.

## 5. Conclusion

Evaluation of common bean genotypes for quantitative and qualitative traits provides the opportunity to choose and include desirable ones in future plant breeding activities or for conservation purposes. In this study, a wide variability for quantitative and qualitative traits was observed among the yellow beans collected from different areas of Tanzania. Days to emergence (DE) varied among the genotypes and had significant effect on days to flowering and seed maturity of the genotypes. Therefore, DE has influence in determining earliness in yellow seeded common beans. Also the most important traits with high variations among the genotypes are number of seeds per pod (NSPP) and number of pods per plant (NPPP) which determine the grain yield of a particular genotype. From the findings in this study, the highest yield was observed in genotypes Kigoma, Bukoba 9 and Arusha 3. Both landraces and improved genotypes clustered into the same groups in this study indicating that they are probably from the same origin or the landraces are the progenitors of the improved genotypes.

The scientific information obtained from this study is useful for other researchers, breeding programmes and farmers for improvement of production of yellow beans in Tanzania. Therefore, it is recommended that the identified high yielding genotypes be evaluated further in breeding programmes to improve the crop. Also, molecular diversity of the yellow bean genotypes is recommended for more detailed information about genetic relationships among them.

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## References

- [1] Birachi, E. A., Sperling, L., Kadege, E., Mdachi, M., Upendo, T., Radegunda, K., Mutua, M., Mbiu, J., Raya, N., and Ndunguru, A. (2021). *Analysis of the Yellow Bean Corridor in Tanzania*. A Feed the Future Global Supporting Seed Systems for Development activity (S34D) report.
- [2] Kiwuka, C., Bukenya-Ziraba, R., Namaganda, M. and Mulumba, J. W. (2012). Assessment of common bean cultivar diversity in selected communities of central uganda, *African Crop Science Journal*, 20 (4), 239–249.
- [3] Chiorato, A. F., Carbonell, S. A. M., Colombo, C. A., Dias, L. A. S., and Ito, M. F. (2005). Genetic diversity of common bean accessions in the germplasm bank of the Instituto Agronômico - IAC. *Crop Breeding and Applied Biotechnology*, 5 (1), 1–9. <https://doi.org/10.12702/1984-7033.v05n01a01>
- [4] Cichy, K. A., Porch, T. G., Beaver, J. S., Cregan, P., Fourie, D., Glahn, R. P., Grusak, M. A., Kamfwa, K., Katuuramu, D. N., McClean, P., Mndolwa, E., Nchimbi-Msolla, S., Pastor-Corrales, M. A., and Miklas, P. N. (2015). A *Phaseolus vulgaris* diversity panel for Andean bean improvement. *Crop Science*, 55 (5), 2149–2160. <https://doi.org/10.2135/cropsci2014.09.0653>
- [5] Durán, L. A., Blair, M. W., Giraldo, M. C., Macchiavelli, R., Prophete, E., Nin, J. C., and Beaver, J. S. (2005). Morphological and molecular characterization of common bean landraces and cultivars from the Caribbean. *Crop Science*, 45 (4), 1320–1328. <https://doi.org/10.2135/cropsci2004.0501>
- [6] Hillocks, R. J., Madata, C. S., Chirwa, R., Minja, E. M., and Msolla, S. (2006). Phaseolus bean improvement in Tanzania, 1959-2005. *Euphytica*, 150 (1–2), 215–231. <https://doi.org/10.1007/s10681-006-9112-9>
- [7] Laura, E. Y. L., Azize, O., Arlette, A., Joel, A., Joelle, T., Gustave, D., and Alexandre, D. (2018). Morphological characterization of common bean (*Phaseolus vulgaris* L.) landraces of Central region of Benin Republic. *Journal of Plant Breeding and Crop Science*, 10 (11), 304–318. <https://doi.org/10.5897/jpbcs2018.0766>
- [8] Leakey, C. L. A. (1988). Genotypic and Phenotypic markers in Common Bean pp. 245-327 In GEPTS P. Ed. Genetic Resources of Phaseolus beans. 245-327.
- [9] Meza, N., Carlos, J., and Mart, J. P. (2013). Biodiversity of common bean (*Phaseolus vulgaris* L.) in Honduras, evidenced by morphological characterization. 1329–1336. <https://doi.org/10.1007/s10722-012-9922-7>
- [10] Nassary, E. K., Baijukya, F., and Ndakidemi, P. A. (2020). Productivity of intercropping with maize and common bean over five cropping seasons on smallholder farms of Tanzania. *European Journal of Agronomy*, 113 (October 2019), 125964. <https://doi.org/10.1016/j.eja.2019.125964>
- [11] Panthe, D. R., K. C. R. B., Regmi, H. N., Subedi, P. P Bhattari, S. and Dhakal, J. 2006. Diversity analysis of garlic (*Allium sativum* L.) germplasms available in Nepal based on morphological characters. *Genetic Resources and Crop Evolution* 53: 205-212.
- [12] Philipo, M., Ndakidemi, P. A., and Mbega, E. R. (2021). Environmentally stable common bean genotypes for production in different agro-ecological zones of Tanzania. *Heliyon*, 7 (1). <https://doi.org/10.1016/j.heliyon.2021.e05973>
- [13] Stoilova, Tsvetelina, Pereira, G., Traveres de sousa, M. M., and Carnide, V. (2005). Diversity in common bean landraces (*Phaseolus vulgaris* L.) from Bulgaria and Portugal, *Journal of Central European Agriculture*, 6 (4), 443–448.
- [14] Stoilova, T, Pereira, G., and Traves-de-sousa, M. (2013). Morphological characterization of a small common bean (*Phaseolus vulgaris* L.) collection under different environments. *Journal of Central European Agriculture*, 14 (3), 1–11. <https://doi.org/10.5513/JCEA01/14.3.127>