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Variability of Common Bean (*Phaseolus vulgaris* L.) in Tanzania as Evidenced by Morphological Assessment

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ABSTRACT

A total of 84 common bean (*Phaseolus vulgaris* L.) accessions were collected from different areas of Tanzania serving as source of germplasm. Nineteen agro-morphological traits of 84 common bean accessions were assessed to analyze the variability as a core objective for this study. Among all the accessions, 40.48% were characterized by indeterminate bush with moderate climbing ability and pods distributed evenly up to the plant habitus followed by 36.9%. Similarly, 14.29% were the genotypes with indeterminate bush with semi-climbing main stem and branches habitus genotypes. Also, 14.29% were the genotypes with the indeterminate bush with prostrate, and 7.14% were the genotypes with indeterminate bush with erect branches habitus while 1.19% were the genotypes with determinate bush least. Phonological, quantitative and qualitative traits were evaluated and their scores were subjected to principal component analysis and cluster analysis. The phylogenetic tree demonstrated 2 major clusters which were further divided into sub-clusters. Principal component analysis accounted for the accumulative variance of 35.78% revealing morphological variation highly attributed with variables which had greater than 0.2 *Eigen values*. The study demonstrated low morphological variation among the genotypes and emphasized the need to broaden genetic variability of the common bean in Tanzania. The results of this study can be used to select the valuable breeding material for use. Besides, molecular markers can be deployed to assess further the variability and diversity of these genotypes.

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.; 2*n* = 2*x* = 22) is a self-pollinated crop and the most widely grown pulse food crop of a high nutritive value for people worldwide including Eastern and Southern Africa (CIAT, 2005). Based on archaeological observations from Peru and South-Western United States in the late 19th century, it was concluded that the common bean was originated from the two centers identified viz. the Andean and the Mesoamerican. The former common bean is characterized by large seeded kidney, cranberry, and many snap beans among others. The latter one is represented by medium and small seeded pinto, pink, black, white, and some snap beans (Beebe et al., 2001). Domestication and subsequent evolution of the common bean affected the reduction of variability in morphological, physiological and other traits, compared with wild bean (Gepts and Debouck, 1991). Thus, diverse common bean accessions represent valuable resources for the improvement of common bean, since co-adapted genes of different accessions can convey similar response to natural and artificial selection pressure if selected for a specific trait.

In Tanzania, the utilization of common bean accessions by plant breeders in their breeding programs is restricted due to lack of official reports or publications about these genetic resources (CIAT, 2008). More than 150 landraces are cultivated by small scale farmers but their data base is not yet officially reported. There is a considerable number of common beans conserved at the NPGRC in Tanzania involving many newly released varieties but both of them face several emerging threats including new persistent diseases, pests, environmental stresses and commercialization as well as socio-economic and political factors. Knowledge about the extent of genetic diversity, identification, differentiation, and characterization of genotypes and populations provides information tool for detection of duplicates in the collection, their effective extension, a characterization and utilization in breeding programs (Beebe et al., 2000). Further, exploration of promising lines is important for genetic improvement of particular traits.) Therefore, this study focuses on the assessment of common bean accessions to detect desirable genotypes for breeding program. This allows the breeder to identify valuable traits or potentially valuable genotypes more efficiently and faster.

MATERIALS AND METHODS

Location of the study

The study was conducted at Sokoine University of Agriculture (SUA)-Morogoro, Tanzania at screen housed behind African Seed building located at latitude 6^{0}84'795'' S and 37^{0}65'904'' E at 543 m above the sea level. The study was for the period of December 2017 to October 2018.

Genotypes collection

A total of eighty-four common bean genotypes were collected from National Plant Genetic Resource Center (NPGRC) at Arusha, Uyole National Research Institute (UNRI) at Mbeya and SUA at Morogoro. They were then stored in a cold room before planting at Sokoine University of Agriculture, Department of Crop Science and Horticulture. The genotypes collected were diverse, representing a range of seed types involving seed coat color, size and shape. The accessions are indicated in Table 1.

Table 1: Common bean (*Phaseolus vulgarism* L.) accessions collected from various locations in Tanzania

S/N	Given accession numbers	Local name	Classification	Collection place
1	SUA10	Jesca	Improved	Morogoro
2	SUA11	Selian 94	Improved	Morogoro
3	SUA16	Msolin	Improved	Morogoro
4	NPGRC 69	Kasukanywele	Landrace	Rukwa
5	NPGRC 70	Kablanketi	Landrace	Rukwa
6	SUA111	Soya Nano	Improved	Morogoro
7	NPGRC 133	Chilemba 3	Landrace	Rukwa
8	NPGRC 134	Chilemba4	Landrace	Rukwa
9	NPGRC 135	Chilemba5	Landrace	Rukwa
10	NPGRC 147	Ilanda / Kalinso	Landrace	Rukwa
11	SUA180	Canadian Wonder	Improved	Morogoro
12	NPGRC 188	Imponzo8	Landrace	Mbeya
13	NPGRC 198	Imponzo9	Landrace	Mbeya
14	SUA200	Roba	Improved	Morogoro
15	NPGRC 218	Malima / Ndondo	Landrace	Mbeya
16	SUA222	Beti 10	Improved	Morogoro
17	NPGRC 286	Chilanda 6	Landrace	Rukwa
18	NPGRC 287	Chilanda 7	Landrace	Rukwa
19	NPGRC 306	Chilemba 6	Landrace	Rukwa
20	NPGRC 307	Chilemba 7	Landrace	Rukwa
21	NPGRC 331	Imponzo 1	Landrace	Mbeya
22	SUA333	Lyamungu 85	Improved	Morogoro
23	NPGRC 334	Imponzo 4	Landrace	Mbeya
24	NPGRC 335	Imponzo 5	Landrace	Mbeya
25	NPGRC 337	Imponzo 7	Landrace	Mbeya
26	SUA401	Fibea	Improved	Morogoro
27	SUA444	Lyamungo 90	Improved	Morogoro
28	SAU500	Selian 05	Improved	Morogoro
29	SUA501	Cal 143	Improved	Morogoro
30	SUA601	Msafiri	Improved	Morogoro
31	SUA777	Selian 06	Improved	Morogoro
32	SUA800	Nanka	Improved	Morogoro
33	SUA808	Mkanamna	Improved	Morogoro
34	SUA909	Nanavala	Improved	Morogoro
35	SUA1001	Zawadi	Improved	Morogoro
36	SUA1003	Mshindi	Improved	Morogoro
37	SAU1007	Pesa	Improved	Morogoro
38	SUA1009	Rojo	Improved	Morogoro
39	SUA1010	Sua 90	Improved	Morogoro
40	SAU1300	Maini	Improved	Morogoro
41	SUA1400	Kigoma	Improved	Morogoro
42	NPGRC1604	Tichakuronza	Landrace	Kagera
43	NPGRC 2154	Biliomunyungu	Landrace	Kagera
44	NPGRC 2158	Kanyamunywa	Landrace	Kagera
45	NPGRC 2178	Mwanamwana	Landrace	Kagera
46	NPGRC 2190	Kibeho	Landrace	Kagera

S/N	Given accession numbers	Local name	Classification	Collection place
47	NPGRC 2213	Ndimila Enkobe	Landrace	Kagera
48	NPGRC 2220	Rukurulana	Landrace	Kagera
49	NPGRC 3005	Njano Ndefu	Landrace	Kigoma
50	NPGRC 3119	Mwolo -Yellow	Landrace	Kigoma
51	NPGRC 3120	Mulembegwa	Landrace	Kigoma
52	NPGRC 3141	Mbuvamutwe	Landrace	Kigoma
53	NPGRC 3150	Mutsinga	Landrace	Kigoma
54	NPGRC 3153	Gwezamenyo	Landrace	Kigoma
55	NPGRC 3154	Nyamanza	Landrace	Kigoma
56	NPGRC 3155	Mwanja	Landrace	Kigoma
57	NPGRC 3156	Seredi	Landrace	Kigoma
58	NPGRC 3157	Kalambi	Landrace	Kigoma
59	NPGRC 3164	Mamesa	Landrace	Kigoma
60	NPGRC 3175	Kashiransoni	Landrace	Kigoma
61	NPGRC 3182	Ugweza	Landrace	Kigoma
62	NPGRC 3511	Maharage - Kienyeji	Landrace	Kigoma
63	NPGRC 3816	Maharage Karanga	Landrace	Kigoma
64	NPGRC 4221	Shona	Landrace	Kagera
65	NPGRC 4248	Ruhondela	Landrace	Kagera
66	NPGRC 4258	Inula	Landrace	Kagera
67	NPGRC 4259	Kya Karagwe	Landrace	Kagera
68	NPGRC 4265	Kisapuli	Landrace	Kagera
69	NPGRC 4269	Maliwalinda	Landrace	Kagera
70	NPGRC 4312	Fukama Okole	Landrace	Kagera
71	NPGRC 4322	Shona Egunia	Landrace	Kagera
72	NPGRC 4336	Kiisiki	Landrace	Kagera
73	NPGRC 4352	Ruvunja	Landrace	Kagera
74	UYL5009	Uyole84	Improved	Mbeya
75	UYL5010	Njano Uyole	Improved	Mbeya
76	UYL5011	Calima Uyole	Improved	Mbeya
77	UYL5012	Uyole 16	Improved	Mbeya
78	UYL5013	Uyole 96	Improved	Mbeya
79	UYL5015	Nyeupe Uyole	Improved	Mbeya
80	UYL5016	Uyole 04	Improved	Mbeya
81	UYL5017	Uyole 03	Improved	Mbeya
82	UYL5018	Pasi	Improved	Mbeya
83	UYL5020	Uyole 94	Improved	Mbeya
84	SUA6301	Cheupe	Improved	Morogoro

Key: UYL- Uyole, SUA-Sokoine University of Agriculture.

Soil sampling and chemical analysis

Composite soil samples obtained were analyzed as described by (Carter, 1993). Bulk soil samples were taken at a depth of 0 - 20 cm on an area of 2 × 2 m^2. Composite soil constituted nine sub-samples randomly collected from forestry area covering 1.0 ha. Sub-samples were thoroughly mixed, sterilized, air dried and ground to pass through an 8.0 mm mesh. The 2.0 mm sieved composite soil samples were used for physical and chemical analyses in the laboratory. Composite soil samples were analyzed for pH, cation exchange capacity, exchangeable bases (Ca, K, Mg and Na), micronutrients (Fe, Zn, Mn and Cu), nitrogen, available P, particle size distribution and organic carbon (OC) as described by (Carter, 1993). The soil pH was determined in water at a soil: water ratio of 1:2.5 suspension using pH meter (Thomas,

1996). Electrical conductivity was measured in 1: 2.5 soil: water using the electric conductivity meter (Thomas, 1996). Cation exchange capacity (CEC) was determined by the ammonium-acetate saturation method and quantification of exchangeable bases: K, Ca, Na and Mg were determined from the ammonium-acetate filtrates following the Lindsay and Norvel (1978) methods. Exchangeable calcium (Ca) and magnesium (Mg) were determined by atomic absorption spectrophotometry whereas K and Na were extracted using ammonium acetate and analyzed by flame spectrophotometry.

The DTPA extractable Cu, Fe, Mn and Zn were determined by atomic absorption spectrophotometry (Lindsay and Norvel, 1998). Total nitrogen was determined by the micro-Kjeldahl digestion distillation method (Bremner and Mulvaney, 1982). Soil extractable P was determined by using the Bray-1-P method (Kuo, 1996) and colour was developed by the ascorbic acid-molybdate blue method Organic carbon was determined by the Walkley-Black wet combustion method. Particle size analysis was determined by the hydrometer method after dispersing the soil samples with sodium hexametaphosphate solution (Gee and Baunder, 1986). Soil textural classes were determined using the USDA textural class triangle (USDA, 1975).

Screen house experimentation and agronomical practices

Eighty-four genotypes were arranged in a completely randomized design (CRD) and replicated three times. Before sowing, the 4 kg potted soil was watered and allowed to stay for one day. Four seeds were sown; thinning was done at age of 10 days after emergence. Irrigation by re-introducing trapped water (infiltrates) on bottomed trays was carried out regularly to maintain the moisture content.

Data collection

With the guide according to the International Board for Plant Genetic Resources (IBPGR) descriptors for *Phaseolus vulgaris* L. documentation (CIAT, 1987), a total of twenty traits were scored. Three (4) phenological traits were recorded viz. days to emergence (ED), days to flowering, days to 50% flowering days (DTFLO) and days to 90% maturity. Twelve qualitative traits including hypocotyl color (HYP.CLR), emerging cotyledon color (COT.CLR), growth habit (Gr.H), color of standard (CLRSTD), color of wings (CLRWNG), pod color (PDCLR) was also recorded. Other recorded traits included seed coat patterns (SCt.P), seed coat color (SCt.CLR), pod curvature (PDCUV), seed shape (SDSHP), brilliance of the seed (SD.BR) and seed size (SSize). Four (5) traits were quantitative which included; number of pods per plant (No. PDpP), pod length (PDL), locules per pod (LOC/PD), seeds per pod (SD/PD) and 100 seeds weight (100Ws).

Data analysis

Distribution analysis

Numerical values for the categorical traits from the 84 common bean genotypes were coded according to descriptor list (CIAT, 1987)]. Frequency distributions, minimum, maximum, standard deviation and correlations among traits were analyzed using the XLSTAT program, 2018.

Cluster analysis

Numerical values for the categorical traits from the 84 common bean genotypes were coded according to I descriptor list (CIAT, 1987). Data were analyzed by numerical taxonomy techniques, using XLSTAT 2018. Unweighted pair-group average (UPGA) of Hierarchical was used for cluster analysis and development of the dendrogram of the common bean genotypes based on 21 agro-morphological traits.

Principal component analysis

The phenotypic diversity of the traits was analyzed with the Pearson correlation aided with Principal component analysis (PCA) on ranged data with linear dimensionality reduction using XLSTAT (2018) to project the data into lower dimensions and to display genetically related genotypes in clusters (Mohammadi and Prasanna, 2003). The PCA was also used to show the traits which accounted for significant variation in the common bean germplasm.

RESULTS

Soil chemical analysis

The experimental forestry soils had medium to high chemical and sandy clay loam textural class as physical characteristics (Table 2). The analyzed composite forestry soil based on the selected soil parameters showed optimal condition that favors growth of common bean as described (Landon, 1991). Therefore, the forestry soils were suitable for production of common beans and other field crops like cereals.

Table 2: Physical-chemical properties of the experimental forestry soil

Soil parameter	**Values**	**Remark** (Landon, 1991)
pH in water	6.79	Neutral
Electrical Conductivity (EC) (µS/cm)	451	Medium
Cationic Exchange Capacity (CEC)	32.6	High
Organic Carbon (% OC)	2.62	High
Organic matter (% OM)	4.52	High
Nitrogen (%)	0.50	Medium
C:N	9.04	Good quality of the Organic Matter
Phosphorous ($mgkg^{-1}$)	9.33	Medium
Extractable K ($Cmol(+)\ kg^{-1}$)	1.90	High
Extractable Na ($Cmol(+)\ kg^{-1}$)	0.14	Low
Extractable Mg ($Cmol(+)\ kg^{-1}$)	0.41	Low
Extractable Ca ($Cmol(+)\ kg^{-1}$)	16.85	High
DTPA Extractable micronutrients ($mg\ kg^{-1}$)		
Fe	34.96	High
Zn	4.08	High
Mn	237.49	High
Particle size analysis (PSA)		
%Clay	33.56	
%Silt	9.64	
%Sand	56.8	
Textural class	Sandy clay loam (USDA, 1975)	

Distribution of characters

Phenological traits

After planting, a total of 34 (40.48%) and 32 (39.29%) common bean genotypes took five and six days respectively to emerge while 12 genotypes (14.29%) emerged early (4 days) and 5 genotypes (5.95%) emerged late (7 days). The maximum, minimum, mean and standard deviation values for the 21 agro-morphological traits among the genotypes are shown in Table 3. The traits were significantly ($P<0.01$) different among the genotypes. Mean early flowering days among genotypes was 22 days for 3 (3.57%) genotypes, mean late flowering days among genotypes was 30 days for 1 (1.19%) genotype and majority had mean flowering days of 25 days for 19 (22.62%) genotypes. Among the genotypes, the 90% maturity day ranged from 65 to 73 days whereby 3 (3.57%) genotypes matured early when it was 65 days, high number of genotypes (19) 22.62% matured full after 68 days and the late maturing genotype (1)1.19% was observed at 73 days averagely (Table 4).

Table 3: The maximum, minimum, mean and standard deviation values for the 21 agro-morphological traits.

S/N	Variables	Minimum	Maximum	Mean	SD
1	Days to emergence	4	7	5.369	0.803
2	Cotyledon color	1	6	3.012	0.898
3	Hypocotyl color	1	3	1.976	0.346
4	Flowering days	22	29.667	24.988	1.744
5	Days to 50% flowering	27	34.667	29.988	1.744
6	Days to 90% maturity	64	71.667	66.988	1.744
7	Color of wings	1	9	2.702	2.368
8	Color of standard petals	1	9	2.702	2.368
9	Color of immature pod	3	9	6.476	1.177
10	Pod length (cm)	4.58	13	8.112	1.362
11	Brilliance of the seed	2	3	2.119	0.326
12	Seed shape	1	5	3.643	1.411
13	Seed coat color	2	16	6.321	3.777
14	Seed coat patterns	0	9	2.798	3.474
15	Number of locules per pod	2	5	3.242	0.598
16	Pod curvature	1	3	1.690	0.620
17	Growth habit	1	5	4.083	0.972
18	Number of pods per plant	1.833	15.333	6.893	2.448
18	Number of seeds per pod	1.350	6.859	2.504	0.743
20	100 seeds weight (g)	15.404	)59.977	31.974	8.337
21	Seed size	1	3	1.964	0.610

Quantitative traits

Number of pods per plant ranged from 1.83 to 15.33. A range of pod length was 4.6 to 13.0 cm and number of locules per pod was 2 to 5. The number of seeds per pod ranged from 1.35 to 6.86 and the 100 seeds weight ranged from 15.4 g to 60.0 g (Table 3).

Qualitative traits

Predominantly emerging cotyledon color of most genotypes (82.14%) was green (COT.CLR), 8.33% was purple, 5.95% was very pale green, 2.38% was pinkish and 1.19% was reddish. Most genotypes (86.9%) had green colored hypocotyl (HYP.CLR), 7.14% of genotypes had purple color; while 4.76% were pale green colored hypocotyl. The predominant growth habit (Gr.H) was indeterminate bush with moderate climbing ability and pods distributed evenly up to the plant (40.48%), followed by indeterminate bush with semi-climbing main stem and branches (36.9%), then indeterminate bush with prostrate (14.29%), indeterminate bush with erect branches (7.14%) and determinate bush least (1.19%).

In freshly opened flowers, 48 genotypes (57.14%) had white predominant color of standard petals (CLRSTD). Others were white with lilac edges (34.52%) for 29 genotypes and purple (8.33%) for 7 genotypes. Most accessions (57.14%) had white colour of flower wings (CLRWG), while 34.52% were white with carmine strips, and 8.33% purple. The predominant fully expanded immature pod color among 84 genotypes, 69 genotypes had green pod (82.14%). Others were carmine stripe on green (7.14%) for 6 genotypes, pale red stripe on green (5.95%) for 5 genotypes, and purple stripe on green (4.76%) for 4 genotypes as shown in Table 4. Forty-four (44) common bean genotypes (52.4%) had slightly curved pods (PDCUV), 33 genotypes (39.3%) had straight pods and 7 genotypes (8.3%) were curved pods.

The dominant seed coat colour was maroon (26.2%) for 22 genotypes. Others were brown yellow 25% for 21 genotypes followed with, whitish seed coat color 13.1% for 11 genotypes, yellow to greenish yellow 9.5% for 8 genotypes, purplish seed coat color 7.1% for 6 genotypes, both brown and grey, brown to greenish seed coat colors 6% for 5 genotypes respectively, both brown, pale to black and pale cream to buff seed color 2.4% for 2 genotypes and were both green to olive and pinkish seed color least (1.2%) for 1 genotype. Thirty-six genotypes (42.9%) had no seed coat patterns. Also, 22 genotypes (26.2%) had stripped seeds, 18 genotypes (21.4%) had spotted bicolor seeds, 8 genotypes (8.3%) had speckled seeds and 1 genotype (1.2%) had constantly mottled seeds. The dominant seed shape was truncate fastigiated in 31 genotypes (36.9%) followed by the kidney shaped seed in 22 genotypes (26.2%), cuboid in 13 genotypes (15.6%), round

shaped seed in 12 genotypes (14.3%) and oval shaped seeds in 6 genotypes (7.1%). The predominantly seed size was medium in 53 genotypes which accounted of 63.10%, small seeded genotypes were 17 (20.24%) and larger seeded genotypes were 14 (16.67%) (Table 4).

Table 4: The frequency and percentage distribution of common bean accessions based on the agro-morphological traits and their score based on descriptor developed by CIAT

Scores	Morphological trait	Frequency	Percentage
	Days to emergence		
	4	12	14.29
	5	34	40.48
	6	33	39.29
	7	5	5.95
	Cotyledon color		
1	Purple	7	8.333
2	Red	1	1.190
3	Green	69	82.14
4	White	0	0.00
5	Very pale green	5	5.95
6	Pinkish	2	2.38
7	Others (Specify)	0	0.00
	Hypocotyl color		
1	Purple	6	7.14
2	Green	73	86.91
3	Pale green	4	4.76
4	Others (specify)	0	0.00
	Growth habit		
1	Determinate bush	1	1.19
2	Indeterminate bush with erect branches	6	7.14
3	Indeterminate bush with prostrate branches	12	14.29
4	Indeterminate with semi-climbing main stem and branches	31	36.91
5	Indeterminate with moderate climbing ability and pods distributed evenly up to the plant	34	40.48
6	Indeterminate with aggressive climbing ability and pods mainly on the upper nodes of the plant	0	0.00
7	Others (Specify)	0	0
	Color of standard		
1	White	48	57.14
2	Green	0	0
3	Lilac	0	0
4	White with lilac edge	29	34.53
5	White with red strips	0	0
6	Dark lilac purple outer edge	0	0
7	Dark lilac with purplish spots	0	0
8	Carmine red	0	0
9	Purple	7	8.33
10	Others (specify)	0	0
11	Pink	0	0
	Color of wings		
1	White	48	57.14
2	Green	0	0
3	Lilac	0	0
4	White with carmine strips	29	34.52
5	Strongly veined in red to dark lilac	0	0
6	Plain red to dark lilac	0	0
7	Lilac with dark lilac veins	0	0
8	Others (specify)	0	0
9	Purple	7	8.33
	Pod color		
1	Dark purple	0	0
2	Carmine red	0	0

Scores	Morphological trait	Frequency	Percentage
3	Purple stripe on green	4	4.76
4	Carmine stripe on green	6	7.14
5	Pale reed stripe on green	5	5.95
6	Dark pink (rose)	0	0
7	Normal green	69	82.14
8	Shiny green	0	0
9	Dull green to deep yellow	0	0
10	Golden or deep yellow	0	0
11	Pale yellow to white	0	0
12	Others (specify)	0	0
	Pod curvature		
1	Straight	33	39.29
2	Slightly curved	44	52.38
3	Curved	7	8.33
4	Recurving	0	0
	Seed coat color		
1	Black	0	0
2	Brown, pale to black	2	2.38
3	Maroon	22	26.19
4	Brown	5	5.95
5	Brown yellow	21	25
6	Grey, brownish to greenish	5	5.95
7	Yellow to greenish yellow	8	9.52
8	Pale-cream to buff	2	2.381
9	Pure white	0	0
10	10. Whitish	11	13.10
11	White, purple tinged	0	0
12	Tan green	0	0
13	Green to olive	1	1.19
14	Reddish	0	0
15	Pinkish	1	1.19
16	Purplish	6	7.14
17	Others (specify)	0	0
	Seed coat patterns		
0	Absent	36	42.86
1	Constant mottled	1	1.19
2	Stripped	22	26.19
3	Rhomboid spotted	0	0
4	Speckled	7	8.33
5	Circular mottling-	0	0
6	Marginal color patterns	0	0
7	Broad stripped	0	0
8	Bicolor	0	0
9	Spotted bicolor	18	21.43
10	Patterns around	0	0
11	Others (specify)	0	0
	Seed shape		
1	Round	12	14.29
2	Oval	6	7.14
3	Cuboid	13	15.48
4	Kidney shaped	22	26.19
5	Truncate fastigiated	31	36.90
	Seed Size		
1	Small (when 100Ws is less than 25 g)	17	20.24
2	Medium (when 100Ws ranges from 25 to 40 g)	53	63.10
3	Large (when 100Ws is above 40 g) [16]	14	16.67

Phenotypic correlations among traits

Pair wise correlations among traits are shown in Table 5. The most strongly correlated traits were flowering days (FD) (r = 1) with 50% flowering days (50%FLWD), color of wings (W.CLR) (r = 1) with the color of standard (CLR.STD) and 100 seeds weight (r = 0.848, $p<0.05$) with seed size. Medium positive correlation was observed between cotyledon color trait (CCL) (r = 0.659, $p<0.05$) and the hypocotyl color (HYP.CRL), but lowest positive correlation was between days of emergence (ED) (r = 0.007) and number of seeds per pod (SDPD). The medium negative correlation (r = -0.494) between color of wings (W.CLR) and hypocotyl color was significant ($p<0.05$) similar to correlation between color of standard petals (STD.CLR) (r = -0.494) and hypocotyl color (H.CLR). The lowest negatively correlation was between 100 seeds weight and hypocotyl color (r = -0.004).

Table 5: Correlation coefficients among 21 morphological traits of common bean accessions from regions of Tanzania

Variables		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
ED	1																					
CCLR	0.011ns	1																				
HCLR	-0.055ns	0.659***	1																			
FD	-0.048ns	0.041ns	-0.087ns	1																		
50% FD	-0.048ns	0.041ns	-0.087ns	1	1																	
90% MD	-0.048ns	0.041ns	-0.087ns	1	1	1																
CLRW	0.039ns	-0.412***	-0.494***	-0.006ns	-0.006ns	-0.006ns	1															
STDCLR	0.039ns	-0.412***	-0.494***	-0.006ns	-0.006ns	-0.006ns	1	1														
PCLR	-0.022ns	0.211ns	0.235*	-0.099ns	-0.099ns	-0.099ns	-0.333**	-0.333**	1													
PL	0.299**	-0.063ns	-0.047ns	0.127ns	0.127ns	0.127ns	0.141ns	0.141ns	-0.126ns	1												
BR.SD	0.244*	0.119ns	0.025ns	-0.316**	-0.316**	-0.316**	0.015ns	0.015ns	0.165ns	-0.183ns	1											
SD.SH	-0.074ns	0.041ns	0.056ns	0.259**	0.259**	0.259**	-0.047ns	-0.047ns	-0.143ns	0.038ns	-0.116ns	1										
SDC.CLR	-0.143ns	0.049ns	0.19ns	0.077ns	0.077ns	0.077ns	-0.153ns	-0.153ns	0.233*	-0.034ns	-0.139ns	-0.069ns	1									
SDC.P	0.372***	-0.053ns	-0.124ns	0.019ns	0.019ns	0.019ns	0.111ns	0.111ns	-0.256**	0.202ns	-0.127ns	-0.032ns	-0.135ns	1								
LOC/PD	-0.038ns	-0.178ns	-0.146ns	0.336**	0.336**	0.336**	0.182ns	0.182ns	-0.114ns	0.456***	-0.17ns	0.17ns	-0.058ns	-0.03ns	1							
PD.CUR	0.159ns	-0.058ns	-0.035ns	0.067ns	0.067ns	0.067ns	0.092ns	0.092ns	-0.159ns	0.261**	0.065ns	0.079ns	-0.296**	-0.035ns	0.172ns	1						
GH	-0.318**	-0.043ns	-0.066ns	0.297**	0.297**	0.297**	-0.026ns	-0.026ns	-0.088ns	0.035ns	-0.26*	0.189ns	0.078ns	-0.22ns	0.062ns	0.103ns	1					
PD/P	-0.069ns	-0.041ns	0.011ns	-0.064ns	-0.064ns	-0.064ns	0.094ns	0.094ns	-0.119	0.062ns	0.024ns	0.115ns	0.026**	-0.196ns	0.345**	0.088ns	0.052ns	1				
SD/PD	0.007ns	-0.061ns	0.019ns	0.094ns	0.094ns	0.094ns	0.058ns	0.058ns	-0.104ns	0.259**	-0.131ns	-0.041ns	-0.038ns	0.061ns	0.422***	0.098ns	-0.078ns	0.105ns	1			
100Ws	0.291**	0.029ns	0.015ns	-0.332**	-0.332**	-0.332**	0.162ns	0.162ns	-0.044ns	0.095ns	0.214ns	-0.378***	0.051ns	0.208ns	-0.35**	-0.098ns	-0.305**	-0.238*	-0.228ns	1		
SDSZ	0.322**	0.023ns	-0.004ns	-0.261**	-0.261**	-0.261**	0.109ns	0.109ns	-0.127ns	0.103ns	0.204ns	-0.351***	-0.115ns	0.156ns	-0.351**	-0.093ns	-0.3**	-0.265**	-0.214ns	0.848***	1	

KEY: ED- Emergency days, CCLR-Cotyledon colour, HCLR-hypocotyl color, FD- Flowering days, MD- Maturity days, CLRW- Colour of wings, STDCLR-Standard colour of petal, PCLR-Pod colour, PL-Pod length, BR.SD-Brilliance of the seeds, SDSH-Seed shape, SDC.CLR- Seed coat colour, SDC.P-seed coat patterns, LOC/PD-Locules per pod, PD.CUR-pod curvature, GH-Growth habit, PD/p-pod per plant, SD/PD-Seeds per pod, 100Ws- 100 Seed Weigh and SDSZ- Seed size.

ns-No significant differences. *- Significant differences, ** Highly significant differences, ***-Very highly significant differences

Morphological diversity

Principal component analysis

The morphological characterization was required to describe the phenotypic variability in common bean genotypes collected from different regions of Tanzania. The PCA reduced the data to a few dimensions and explained 35.723% of total phenotypic variation in the germplasm as presented in Table 6. Eigen-values for these traits show that for the first component the highest absolute values corresponded to both flowering days, 50% flowering days and the 90% maturity days, as well as number of locules per pod, 100 seeds weight (g), brilliance of seeds, seed size and growth habit. For the second component the highest values were for colour of standard petals and the wings, as well as the hypocotyl colour, the cotyledon colour and the colour of the pods. The spatial distribution of the common bean genotypes with the 90% maturity days, flowering days and low 100 seeds weight are in the I and II quadrant as reading clockwise in Figure 1. The genotypes *Belta 10, Nanka,* and *Mwolo-yellow* are exemplified for such dispersion. In quadrant III and IV clockwise, there are genotypes that are characterized by great 100 seeds weight, attaining early 90% maturity and early emergence and these genotypes include *Canadian wonder, Soya, Rukululana, Shona Egunia* and *Malima/Ndondo.*

Table 6: Eigen-values of the first two principal component axes (PC) for the 18 agro-morphological traits used to classify the common bean genotypes

S/N	Variables	Principal Component Axes	
		PC1	PC2
1	Emergency days	-0.117	0.151
2	Cotyledon color	-0.042	**-0.335**
3	Hypocotyl color	-0.065	**-0.374**
4	Flowering days	**0.415**	-0.014
5	50% Flowering days	**0.415**	-0.014
6	90% Maturity	**0.415**	-0.014
7	Color of wings	0.017	**0.469**
8	Color of standard	0.017	**0.469**
9	Color of pod	-0.079	**-0.286**
10	Pod length	0.098	0.195
11	Brilliance of the seed	**-0.224**	-0.004
12	Seed shape	**0.213**	-0.056
13	Seed coat color	0.027	-0.183
14	Seed coat patterns	-0.040	0.185
15	Locules per pod	**0.278**	0.154
16	Pod curvature	0.079	0.125
17	Growth habit	**0.228**	-0.065
18	Pods/plant	0.080	0.038
19	Seeds/pod	0.130	0.083
20	100 seed weight (g)	**-0.321**	0.143
21	Seed size	**-0.297**	0.145
Eigen-value/latent roots for each PC		4.241	3.261
Variation in Percentage (%) for each PC		20.194	15.529

Principal component axes 1 and 2 and traits with Eigen-values set arbitrarily above 0.2 (highlighted), explained 35.78% of total variation in the bean germplasm.

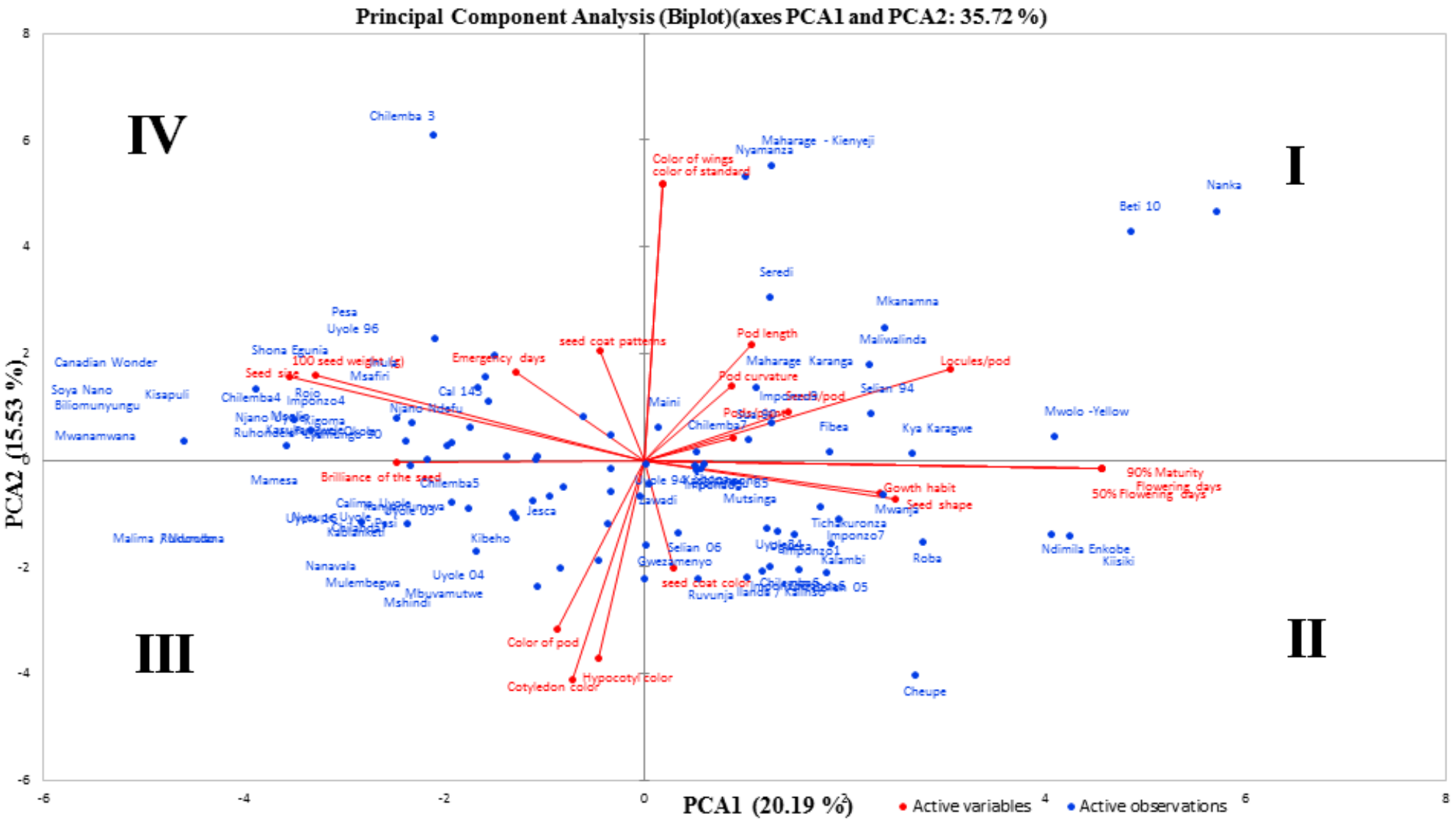

Figure 1: Dispersion of populations of common bean genotypes distributed across the regions of Tanzania based on two principal components (PC 1 and PC 2) of agro-morphological trait

Cluster analysis

Cluster analysis based on morphological and agronomical traits grouped genotypes into 2 main clusters (I and II) at 0.98 coefficient of similarity for 21 morphological and agronomical traits. The traits are days to emergence, cotyledon color, hypocotyl color, days to flowering, days to 50% flowering days to 90% maturity, color of wings, color of standard, color of pod, pod length (cm), brilliance of the seed, seed size, seed shape, seed coat color, seed coat patterns, number of locules per pod, pod curvature, growth habit, number of pods per plant, number of seeds per pod and 100 seeds weight (g). The main cluster I comprised three (3) sub clusters namely sub-cluster A, B, and C makes a total of 82 common bean genotypes as they can be identified by reading the dendrogram ascending from the genotype named *Uyolee 04* to *Mkanamna*. The main cluster II comprises 2 genotypes as they can be identified by reading the dendrogram descending from the genotype named *Biliomunyungu* to *Kablanketi.* No sub cluster formed.

Table 7: Characteristics genotypes being group together using Agglomeration method: Unweighted pair-group average (UPGA) of Hierarchical Cluster analysis. Scored traits are described in the descriptor by CIAT (1987).

CLUSTERS	ED	CCLR	HCLR	FLWD	50% FLWD	90% MD	CLRW	STDCLR	PCLR	PL	BR.SD	SDH	SDC.CLR	SDC.P	LOC/PD	PD.CUR	GH	PD/P	SD/PD	100WS	SDSZ
IA	5	3	2	23	28	65	1	1	7	8	2	4	5	2	3	2	4	5	2	36	2
IB	7	3	2	27	32	69	9	9	3	13	2	3	5	9	4	3	4	8	2	42	3
IC	5	3	2	27	32	69	1	1	7	8	2	5	5	2	3	2	5	5	3	26	2
II	5	3	2	24	29	66	4	4	7	7	2	1	16	4	3	1	2	6	2	60	3

Key C.CLR-3-Green colour, H.CLR-2-Green, CLRW-1-White, 9-purple, 4-white with carmine strips, STDCLR-1-white, 9-purple, 4-white with lilac edge, P.CLR-3-Purple strips on green, 7-Green, BRSD-2-Medium, SDSHP-1-Round, 3-Cuboidal, 4-Kidney, 5-Truncate fastigiated, SDC.CLR-5-Brown yellow, 16-Purplish, SDCP-2-stripped, 4-Speckled, 9-Spotted bicolor, PD.CURV-1-straight, 2-straight curved, 3-Curved, Gr.H-2-Indeterminate bush with erect branches, 4-Indeterminate with semi-climbing main stem and branches, 5-Indeterminate with moderate climbing ability and pods distributed evenly up to the plant, SDSZ-2-Medium, 3-Large.`

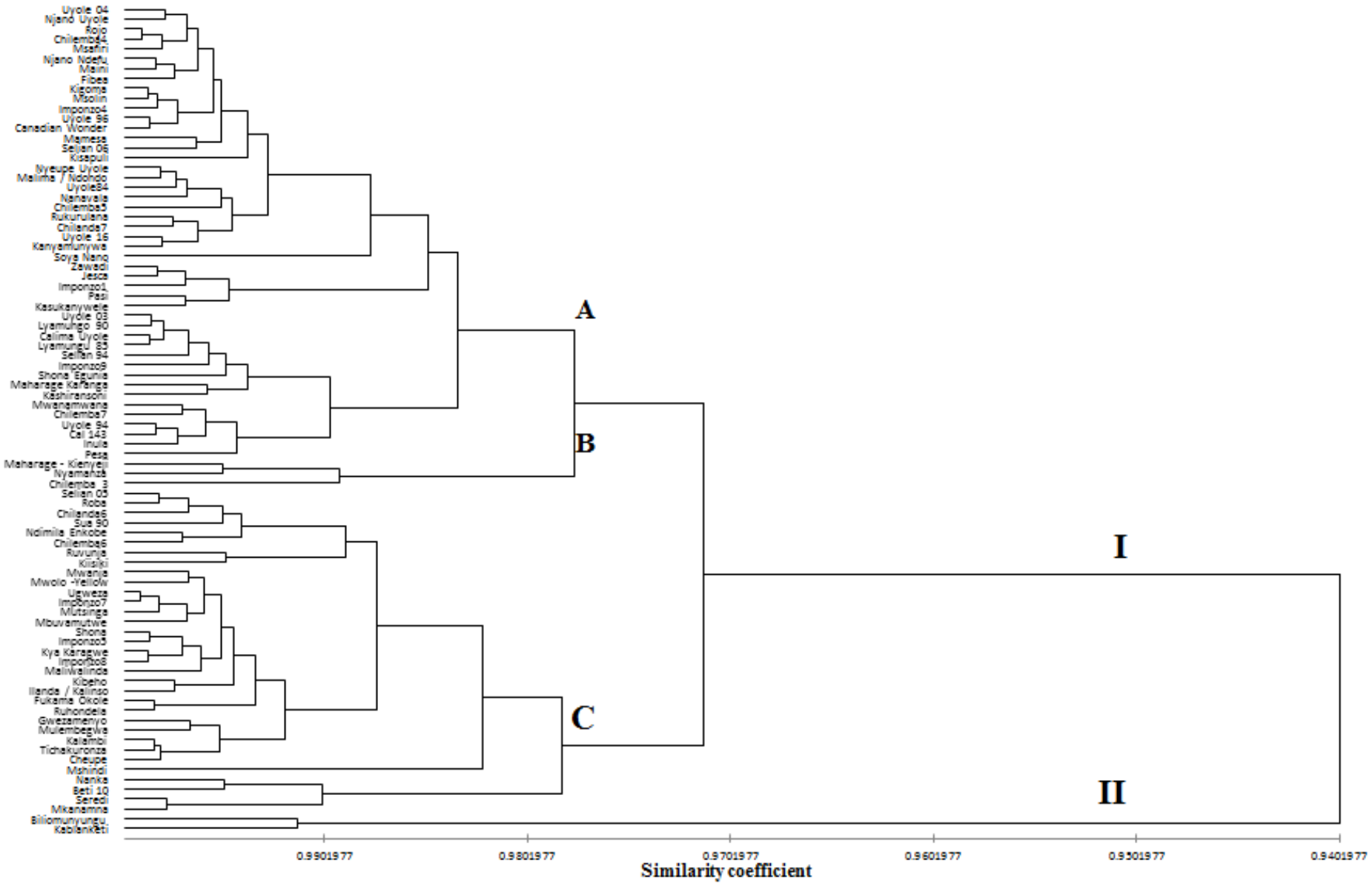

Figure 2: Dendrogram representing genetic similarities based on the Pearson correlation similarity coefficient using Agglomeration method: Unweighted pair-group average (UPGA) of Hierarchical Cluster analysis for the genotypes of the common bean, based on 21 agro-morphological traits.

DISCUSSION

Genetic diversity of any food crop is an essential component in germplasm evaluation and as a pre-requisite in conservation prospects. Common bean has an important role in dry land farming systems and provides high amount of crude protein used for human consumption and animal feed. The rational use of genotype collections requires a good knowledge about their characteristics. Well characterized and documented ex-situ genotype collections can consequently provide useful information to plant breeders. This aids researchers in identification of potential parents with desirable genes for incorporation into local cultivars for improved crop productivity. Morphological traits have long been the means of studying taxonomy and variability among common bean genotypes.

Phenotypic trait correlations.

Correlation matrix helps to determine pairs of characters that vary in the same or opposite direction and useful guide; especially for the plant breeders who may wish to associate a set of their desired traits in their breeding programs. The strongly correlated traits are possibly under the influence of the same genes or pleiotropic effects (Miko, 2008). There were strong correlations between some traits (Table 5), which allows for simultaneous selections and use of the related traits interchangeably. Practically, during bean improvement, if two or more strongly correlated traits are desired, they can both be selected simultaneously basing on one of the influential traits. For example, the positive correlations between seed size ($r = 0.848$, $p<0.05$) and 100 seed weight, indicates that the seed size can be used to determine grain weight and consequently yield. On the other hand, selection for relative 100 seed weight would lead to late flowering ($r = -0.332$, $p<0.05$), low locules per pod ($r = -0.350$, $p<0.05$) and number of seeds per pod ($r = -0.228$) since these traits were negatively correlated. The near to unit correlations ($r = 1.00$) of wing and standard petal colours suggests that these traits are controlled by one gene (pleiotropy) or are very closely linked (Miko, 2008).

Morphological diversity

Principal component analysis

PCA is the method of data reduction to clarify the relationships between two or more traits and to divide the total variance of original traits into a limited number of uncorrelated new variables (Wiley, 1980). Based on morphology, the PCA results (Table 6 and Figure 1) illustrated the overall picture of the pattern of genetic diversity of the common bean genotypes. The *Eigen value* formed the basis for identifying component axes (PCA1 and PCA 2) (Panthee et al., 2006) with scores, cut off level arbitrarily set above 0.2 to show traits, which explained most variations in the common bean accessions. The first PC summarizes most of the variability present in the collected data relative to the remaining PCs, hence recorded the highest Eigen value 0.415 (Table 6) and accounted for 20.194 % of the total variation. For instance, considering only PCA *Eigen values* in PC1 for both quadrants I and II clockwise, most genotypes had late flowering days, 50% flowering days and 90% maturity days. This axis indicates that most accessions were attributed to the positive phenological traits complemented with the number of locules per pod and the growth habit. This suggests that the traits above are the most important for future common bean characterization and conservation studies. In other studies, in common bean, Okii et al. (2014) characterized 284 landraces from Uganda, using the IPBRI descriptor for *P. vulgaris* and identified suitable traits for breeding purposes.

Cluster analysis

The cluster analysis for the morphological traits included in this study placed common bean genotypes into two main clusters with sub clusters for main cluster I (Figure 2). These results agreed with Blair et al. (2010) who also reported that in cluster analysis cultivars are grouped together with the greater morphological similarities. Clusters were also grouped together for the improved and landraces signifying that they are less variable in their morphological traits.

For instance, in the main cluster I sub-cluster A, the improved variety of *Zawadi, Mshindi, Pasi* and *Jesca* were placed together with the landraces of *Kanyamunywa*, *Rukurulana* and *Kashiransoni*. This indicates that they consisted of the heterogeneous group of accessions with same origin. The diversity of the common bean genotypes observed in this study could be in part due to farmers' customary seed exchanges as it was reported by CIAT (2005) since the exchange of seed materials is not unique to farmers. Further, Blair et al (2010) reported farmers' preference for many landraces and diversified bean types are used for various agronomic and cultural reasons. In addition, varieties preferred for home cooking with unique seed colours are selected for sale in the local markets, hence, increasing bean diversity across regions of Tanzania. Frequent mutations and genetic recombination are the other possible causes of high diversity of the common bean genotypes studied.

CONCLUSION

Common bean accessed displayed a considerable range of morphological diversity for most of the agro-morphological traits studied. Phenological traits of days to emergence, days to flowering, days to 50% flowering and days to 90% flowering exhibited a strong positive correlation as those of qualitative traits

like color of standard petal and color of wings. Seed size strongly positive correlated with 100 weight traits which determine the yield potential of a variety. A significant variation accounted in the principal component analysis on the collected common bean genotypes was contributed by phenological traits (days to emergence, days to flowering, days to 50% flowering and days to 90% flowering) for the PCA1 and qualitative traits (colour of standard petal and colour of wings) for the PCA2. Further, both improved and landrace genotypes were clustered in the same group hence clarifying that they're heterogeneous but with the same origin. Therefore, we recommend that morphological traits were useful for the preliminary evaluation and can be used as a general approach of assessing variability or variation among morphologically distinct common bean genotypes; molecular analysis of the collected common bean genotypes is recommended to be carried out in order to detect possible genetic relationships of this material, as a further step.

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