

Genetic Inconsistency Assessment and Selection Criteria of Bambara groundnut (*Vigna subterranea* L. Verdc.) Landraces for High Yield Revealed by Qualitative and Quantitative traits

Md Mahmudul Hasan Khan

Laboratory of Climate-Smart Food Crop Production, Institute of Tropical Agriculture and Food Security (ITAFoS), Universiti Putra Malaysia (UPM), 43400, Malaysia.

Mohd Y. Rafii (✉ mrafi@upm.edu.my)

Laboratory of Climate-Smart Food Crop Production, Institute of Tropical Agriculture and Food Security (ITAFoS), Universiti Putra Malaysia (UPM), 43400, Malaysia.

Shairul Izan Ramlee

Department of Crop Science, Faculty of Agriculture, Universiti Putra Malaysia (UPM), 43400, Malaysia.

Mashitah Jusoh

Department of Crop Science, Faculty of Agriculture, Universiti Putra Malaysia (UPM), 43400, Malaysia.

Md Al-Mamun

Laboratory of Climate-Smart Food Crop Production, Institute of Tropical Agriculture and Food Security (ITAFoS), Universiti Putra Malaysia (UPM), 43400, Malaysia.

Research Article

Keywords: *Vigna subterranea* L. Verdc., Genetic inconsistency, Genetic component, Selection 37 criteria; H₂-index, Qualitative and Quantitative traits.

Posted Date: December 21st, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-127584/v1>

License: © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Version of Record: A version of this preprint was published at Scientific Reports on April 7th, 2021. See the published version at <https://doi.org/10.1038/s41598-021-87039-8>.

Genetic Inconsistency Assessment and Selection Criteria of Bambara groundnut (*Vigna subterranea* L. Verdc.) Landraces for High Yield Revealed by Qualitative and Quantitative traits

Md Mahmudul Hasan Khan^{1, 3*}, Mohd Y. Rafii^{1, 2*}, Shairul Izan Ramlee², Mashitah Jusoh² and Md Al Mamun^{1, 4}

¹Laboratory of Climate-Smart Food Crop Production, Institute of Tropical Agriculture and Food Security (ITAFoS), Universiti Putra Malaysia (UPM), 43400, UPM Serdang, Selangor, Malaysia.

²Department of Crop Science, Faculty of Agriculture, Universiti Putra Malaysia (UPM), 43400, UPM Serdang, Selangor, Malaysia.

³Bangladesh Agricultural Research Institute (BARI), Gazipur-1701, Bangladesh.

⁴Bangladesh Jute Research Institute (BJRI), Dhaka, Bangladesh.

*Correspondence: mrafii@upm.edu.my; Tel.: +60-3-8947-1042 and mhasan.bari12@gmail.com

Abstract

As a crop for the new millennium Bambara groundnut (*Vigna subterranea* L. Verdc.) considered as leading legumes in the tropical regions due to its versatile advantages. The main intent of this study was to find out the high yielding potential genotypes and considering these genotypes to develop pure lines for commercial cultivation in Malaysia. Considering the 14 qualitative and 27 quantitative traits of fifteen landraces the variation and genetic parameters namely, variability, heritability, genetic advance, characters association, and cluster matrix were determined. ANOVA revealed significant variation for all the agronomic traits (except plant height). Among the accessions, highly significant differences ($P \leq 0.01$) were found for almost all the traits excluding fifty percent flowering date, seed length, seed width. The 16 traits out of the 27 quantitative traits had a coefficient of variation (CV) $\geq 20\%$. A positive and intermediate to perfect highly significant association ($r = 0.23$ to 1.00 ; $P < 0.00$) was found between yield and its related traits. The trait dry seed weight per plant (g) had the highest GCV = 59.91% and PCV = 59.57% whereas the trait fresh pod weight (99.55%), dry seed weight (98.86%), and yield (98.10%) were highly heritable. The genetic advance recorded the highest for dry seed weight (122.01%) and lowest (3.97%) for plant height. To validate the genetic disparity, an unweighted pair-group produce with arithmetic mean (UPGMA), principal component analysis (PCA), and H'-index was performed considering 27 quantitative traits. The constructed dendrogram showed five distinct groups of accessions. Genotypes G2, G3, and G9 from Group IV consider as promising lines which gave 70.05% higher mean yield compared to grand mean yield (1180 kg ha⁻¹) with desirable traits. Group II had a maximum number of accessions while group III and group V had one of each. However, findings declared that the availability of genetic variance will be beneficial for this crop improvement and plant breeders to prefer desirable traits in *V. subterranea* L. Verdc. for further breeding purposes.

Keywords: *Vigna subterranea* L. Verdc.; Genetic inconsistency; Genetic component; Selection criteria; H'-index; Qualitative and Quantitative traits.

1. Introduction

Bambara groundnut is a future emerging legume grown in Africa and Asia, is usually known as a poor man's crop or as "Women's Crop" [1] and newly noted as Crop for New Millennium [2]. The present binomial name *Vigna subterranea* (L.) Verdc was suggested by Verdcourt, 1980 [3] and chromosome number is $2n=2x=22$ [4]. This crop occupied 3rd position after *Arachis hypogea* and *Vigna unguiculate* in African continent [5] though it is used as food supplement instead of profitable crops due to its low ranked [6]. The word "Bambara" comes from a place name near Timbuktu in central Mali, West Africa and the word "groundnut" is the causes of it pods setting occur under the ground soil, hence jointly its common name is 'Bambara groundnut' [7]. Due to rich in carbohydrate (63-65%), protein (18-20%) and oil (17-18%), Bambara groundnut has been defined as a fully well-adjusted food for human feeding [8]. According to [9] it contains 32.72% essential amino acids and 66.10% non-essential amino acids. The seed is regarded as a balanced food because when compared to other food legumes, it is rich in iron and its protein contains high level of lysine and methionine [10]. Lysine is the major essential amino acid and represents 10.3% of the total essential amino acid [10]. Bambara groundnut can fulfill the regular demand of protein for the marginal users where the animal protein is badly available due to its high cost [11]. The undeveloped fresh seeds of Bambara groundnut can be boiled to make pudding (Moi-Moi or Okpa) [12]; fodders to feed animals [13] and extract of leaves has medicinal values as anti-vomiting agent [14]. In many developing countries where cultivation of other major crops is difficult, but Bambara groundnut can be accommodated nicely due to its drought tolerant and low diseases-insects infestation nature [15] and as legume it can fix atmospheric nitrogen via nodulation [16]. This crop has the capacity to give high yield with low input and mostly grown by female in sole culture without any modern techniques [17] and 10-40 % of their total yield they sold in market rest is used by themselves [18]. According to FAOSTAT [19], the annual production is about 42023 kg/ha, of which Africa produces half, with Burkina Faso occupied the major producing country. Bambara groundnut can well adapt to the tropical area like Malaysia, where cultivation of major crops (Rice, Wheat, Maize, etc.) are increasingly challenging due to drought and unpredictable rainfall patterns [20]. The production of Bambara groundnut is mainly limited due to lack of improved cultural techniques [21] and improvement of Bambara groundnut was neglected for many years by researchers because of the lack of available fund and unprivileged effort on its improvement [22]. On the aspect of Malaysia, the breeding approach of Bambara groundnut is undetermined, and no commercial high yielding variety is available, so the requirement is to discover commercially high yielding cultivar for certain rising areas [23]. Germplasm screening considering the agronomic variables is the initial attempt to identify the targeted characters of interest [24]. This current research reveals the genetic divergence of fifteen Bambara groundnut accessions to discover the existing variation and the selection to develop high yielding pure lines for this crop improvement.

Accordingly, this study provides an evidence on Bambara groundnut diversity among the landraces that introduced from Africa (Nigeria) to Asia (Malaysia). All the modern applicable techniques may be applied for the betterment of this ongoing cultivated crops, but the dual approaches like conventional breeding linked with molecular breeding is highly successive over the solely use of one approach. However, traits improvement can be possible through direct selection with valuation of different genetic parameter analysis. The extent of selection approach exceedingly inspire by heritability and genetic gain estimation is the commanding tools for the enhancement of a certain traits [25]. Hence, the core intent of this study was to determine the inherent variation of Bamabara groundnut landraces using both qualitative and quantitative traits via valuation of characters association, variance component and different genetic parameters, resulting the identification of high yielding potentials from which purelines will be developed for commercial cultivation.

2. Materials and Methods

2.1. Experimental site

The research work has experimented under the Institute of Tropical Agriculture and Food Security (ITAFoS), University Agricultural Park, University Putra Malaysia (UPM), Malaysia. Based on the Global Positioning System (GPS) the research location was 2°58'54.0"N latitude and 101°42'53.8"E longitude. The seeds of accessions were sown in open field conditions during the 2018-2019 cropping season. The soil P^H is 6.6 to 7.5 with sandy loam to clay loam type (Dept. of land management, UPM). Fifteen accessions of Bambara groundnut were selected for this current research work, all representing the African accessions collected from the local market of Nigeria. Land races of Bambara groundnut used in this research was listed in Table 1. Randomly five plants were taken into consideration to evaluate genetic variability based on the agronomic traits [26].

Table 1: The line-up of Bambara groundnut accessions evaluated in this research.

Genetic Materials		
G1=Duna	G6=Bidiyashi	G11=Bidibaki
G2=Maikai	G7=Karu	G12=Jatau
G3=Cancaraki	G8=Katawa	G13=Maibargo
G4=Roko	G9=Giina	G14=Bidilalle
G5=Hawayenzaki	G10=Olel	G15=Dai

4.3. Experimental design

The experiment was conducted in a randomized complete block design (RCBD) with three replications. The experimental plot comprised of two rows measuring 1.6m × 0.80m. The distance between plant to the plant was 50cm and row to row distance was 1m and the distance between replication was 2.0m according to [26]. During the growing season the recommended intercultural practices like land preparation, land clearing, weeding, irrigation and fertilizer were approved. The recommended fertilizer rates (100% N= 45kg N/ha, 100% P= 54kg P₂O₅/ha, 100% K= 45kg

K₂O /ha) and all portion of Phosphorus and Potassium were applied during field preparation hence, 70% N was applied at 5 weeks after sowing [27].

2.2. Parameters recorded for data analysis

Twenty-seven quantitative and 14 qualitative characters (Table 2) were considered during the morphological characterization. For comfort description, quantitative traits were categorized as **1) Phenological traits**; **2) Growth and vegetative traits**; **3) Yield traits**. Following the Bambara groundnut description and descriptors states by IPGRI, IITA, BAMNET [28] data were recorded at several growth stages in the field and post-harvest data in the physiology lab.

Table 2: Twenty-seven quantitative and 14 qualitative traits measured according to IPGRI, IITA, BAMNET [28].

Sl.No	Quantitative Traits	Code	SL.No	Qualitative Traits	Code
1) Phenological traits (3)			1	Growth habit	(GH)
1	Days to emergence	DTE (d)	2	Stem hairiness	(SH)
2	Days to fifty % flowering	D50%F (d)	3	First stem Color	(FSC)
3	Days to maturity	DTM (d)	4	Terminal leaflet Shape	(TLS)
2) Growth and Vegetative traits (9)			5	Terminal leaflet colour	(TLC)
4	Plant height	PH(cm)	6	Petiole pigmentation	(PP)
5	Number of branches per stem	NB	7	Shape of Pods	(PS)
6	Number of stems per plant	NS	8	Colour of Pods	(PC)
7	Number of petioles per plant	NP	9	Pods texture	(PT)
8	Number of leaves per plant	NL	10	Seeds shape	(SS)
9	Number of nodes per stem	NNS	11	Seeds colour	(SC)
10	Internode length	IL(cm)	12	Eyes color	(EC)
11	Biomass fresh weight per plant	BFW(g)	13	Testa pattern	(TP)
12	Biomass dry weight per plant	BDW(g)	14	Testa color with eye pattern around hilum.	(TCEP)
3) Yield traits (15)					
13	Total no. of pod per plant	TNP			
14	Mature pods number per plant	NMP			
15	Immature pods number per plant	NIP			
16	Fresh pod weight	FPW (g)			
17	Dry pod weight	DPW(g)			
18	Length of pod	PL (mm)			
19	Width of pod	PW (mm)			
20	Number of seed per	NSP			
21	Dry seed weight per plant	DSW(g)			
22	Length of seed	SL (mm)			
23	Width of seed	SW (mm)			
24	Hundred seed weight	HSW (g)			
25	Shelling percentage (%)	Shell%			
26	Harvest Index	HI (%)			
27	Yield Kg per hectare	Yld(Kg/ha)			

2.3. Statistical analysis

The SAS (statistical analysis software) version 9.3 was followed to test the significant differences using the analysis of variance (ANOVA) procedure at the level of LSD; $P \leq 0.05$ and to compare among the mean of significant of traits. The correlations between the quantitative variables were determined using Pearson [29] correlation coefficient formula. The genotypic and phenotypic variation were calculated as per following the formula given by Singh and Choudhary [30]. The coefficient variation of phenotypic (PCV) and genotypic (GCV): were estimated as per formula given by Shabanimofrad *et al.* [31] also relative differences was estimated using the formula (RD) =

Relative difference between PCV and GCV. The estimated values of PCV and GCV were categorized by Shabanimofrad *et al.* [31], Sohrabi, *et al.* [32] and Robinson *et al.* [33] like as between 0% - 10% for low, 10% - 20% for intermediate and greater than ($\geq 20\%$) for high. Broad sense heritability (h_b^2) was estimated using the formula given by Oladosu *et al.* [34], Usman *et al.* [35] and Falconer [36]. In accordance with Johnson *et al.* [37] and Assefa *et al.* [38], the heritability grade was ordered between 0% - 30% for low, 30% - 60% for intermediate and greater than 60% as high. Genetic Advance (GA) (as a percentage of mean): was calculated with 5% selection intensity (K) following the method of [37]. Genetic advance is categorized as between 0% to 10% for low, 10% to 20% for intermediate and more ($>20\%$) than for high, following the formula given by Juangsamoot *et al.* [39]. K for constant also indicates the intensity of selection. According to Adewale *et al.* [40] the rate is 2.06 at the point when the K is at 5%. Genetic Gain (%) = Estimated as genetic advance (GA) $\times$ 100; it is also categorized [37] [41] as between (0 to 10% for low, (10 to 20%) for intermediate and ($\geq 20\%$) for high GA. Based on the Euclidian Distance Method also Dices's and Jaccard's similarity of coefficient data was analysed for investigation of genetic diversity. In addition to this, based on the Unweighted Pair Group Method using Arithmetic Average (UPGMA) and following the algorithm & sequential, agglomerative, hierarchic and non-overlapping (SAHN) method the genetic inter-relationship (showing dendrogram) among the Bambara groundnut were estimated. For this analysis NTSYS version 2.1 (Numerical Taxonomy Multivariate Analysis System), Exeter Software, Setauket, NY, USA software [42] were used. Using similar software, the principal component analysis (PCA) was done to produce two dimensional (2D) plots. However, the Shannon diversity index is a synonym for the Shannon equitability index and evenness was calculated using the formula given by Weaver & Shannon [43], Shannon [44] and Hennink & Zeven [45].

3. Result

3.1. Assessment of Qualitative variation

The frequency of distribution of some qualitative variables are summarized in Table 3 and Figure 1. After two weeks later, we observed 46.67% of the accessions had greenish stems, 20% had stripped stems and 33.33% were reddish stems. The terminal leaflets had two different colours: 73.33% accession had a greenish leaflet while the purple was 26.67 % accessions. The 53.33% of the total accessions had terminal leaflets shaped like lanceolate whereas 26.67% had oval and 20% had elliptic in shape. Among the 15 characterized accession, three growth habits were found: bunch type accessions (13.33%), semi bunch type accessions (53.33%) and the spreading type was (33.33%). Among the landraces, 33.33% had sparse hair on their stems and 20% had dense hair while 46.67% did not have any. Most of the landraces had reddish-brown (46.67%) and brown (33.33%) colour pods some had yellowish-brown (13.33%), and purple (6.67%) colour pods. Maximum accessions were found oval (73.33%) seeds shape and few had round (26.67%).

Seed colour had cream and red (26.67%), black cream and cream purple (20.00%), only 6.67% had black colour. 13.33% of landraces had black eye color and 86.67% had no eye colour (Table 3).

Table 3: The incidence of the qualitative traits' distribution of Bambara groundnut accessions.

Qualitative Traits	Scale	Percentage (%)	Genotypes
Habits of growth (GH)	1. Bunch	13.33	G4, G10
	2. Semi-bunch	53.33	G7, G8, G9, G11, G12, G13, G14, G15
	3. Spreading	33.33	G1, G2, G3, G5, G6
Stem Hairiness (SH)	1. Absent	46.67	G1, G2, G3, G5, G6, G10, G11
	2. Sparse	33.33	G4, G10, G12, G13, G14
	3. Dense	20	G7, G8, G9
First stem Color (FSC)	1. Green	46.67	G8, G9, G10, G11, G12, G13, G14
	2. Reddish	33.33	G1, G2, G3, G4, G7
	3. Striped	20	G5, G6, G15
Terminal Leaflet shape (TLS)	1. Oval	26.67	G13, G14, G15
	2. Lanceolate	53.33	G3, G5, G6, G7, G8, G9, G10, G11
	3. Elliptic	20	G1, G2, G4
Terminal Leaflet Colour (TLC)	1. Green	73.33	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G12
	2. Red	0	-
	3. Purple	26.67	G11, G13, G14, G15
Petiole pigmentation (PP)	1. Green	73.33	G2, G4, G5, G6, G7, G8, G12, G13, G14, G15
	2. Reddish Green	26.67	G1, G10, G11, G9
Pod shape (PS)	1. Hook with ending point on the opposite side.	13.33	G1, G10
	2. Round with ending point on the opposite side.	26.67	G9, G11, G12, G15
	3. Hook with ending point on the both sides.	60	G2, G3, G4, G5, G6, G7, G8, G13, G14
Pod colour (PC)	1. Brown-yellowish	13.33	G8, G13
	2. Brown	33.33	G1, G4, G5, G7, G12
	3. Reddish brown	46.67	G2, G3, G6, G10, G12, G14, G15
	4. Purple	6.67	G9
Pod texture (PT)	1. Smooth few grooves	53.33	G15, G14, G12, G9, G7, G4, G3, G2
	2. Enough grooved	33.33	G13, G11, G8, G6, G5
	3. Enough folded	13.33	G1, G10
Seed shape (SS)	1. Round	26.67	G3, G4, G10, G11
	2. Oval	73.33	G1, G2, G5, G6, G7, G8, G9, G12, G13, G14, G15
Seed colour (SC)	1. Creamy	26.67	G10, G11, G13, G15
	2. Reddish	26.67	G5, G6, G7, G12
	3. Purple creamy	20	G3, G9, G14
	4. Blackish	6.67	G1
	5. Black creamy	20	G2, G4, G8
Eye Colour (EC)	1. Absent	86.67	G1, G3, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15
	2. Black	13.33	G2, G4
Testa pattern (TP)	1. Absent of pattern	33.33	G1, G10, G11, G4, G6
	2. Full line with marbled striped	6.67	G3
	3. Entirely dotted spot	26.67	G5, G13, G14, G15
	4. Few rhomboid spots on one side of hilum	6.67	G2.
	5. Few rhomboid spots on both side of hilum	20	G7, G9, G12
	6. Enough rhomboid spot on both side of hilum	6.67	G8
Testa colour with eye pattern round hilum (TCEP)	1. Black like butterfly eye with cream testa	6.67	G4
	2. Without eye with black testa	6.67	G1
	3. Black like butterfly eye with black strip on creamy background	6.67	G2
	4. Without eye with black small dotted spots on cream background	13.33	G3, G8
	5. Without eye with light brown testa	6.67	G6
	6. Without eye with dark brown marbled spots	20	G5, G12, G13
	7. No eye with light brownish red testa	6.67	G7
	8. No eye with brown stripes on cream background.	20	G9, G14, G15
	9. Cream testa without eye.	13.33	G10, G11

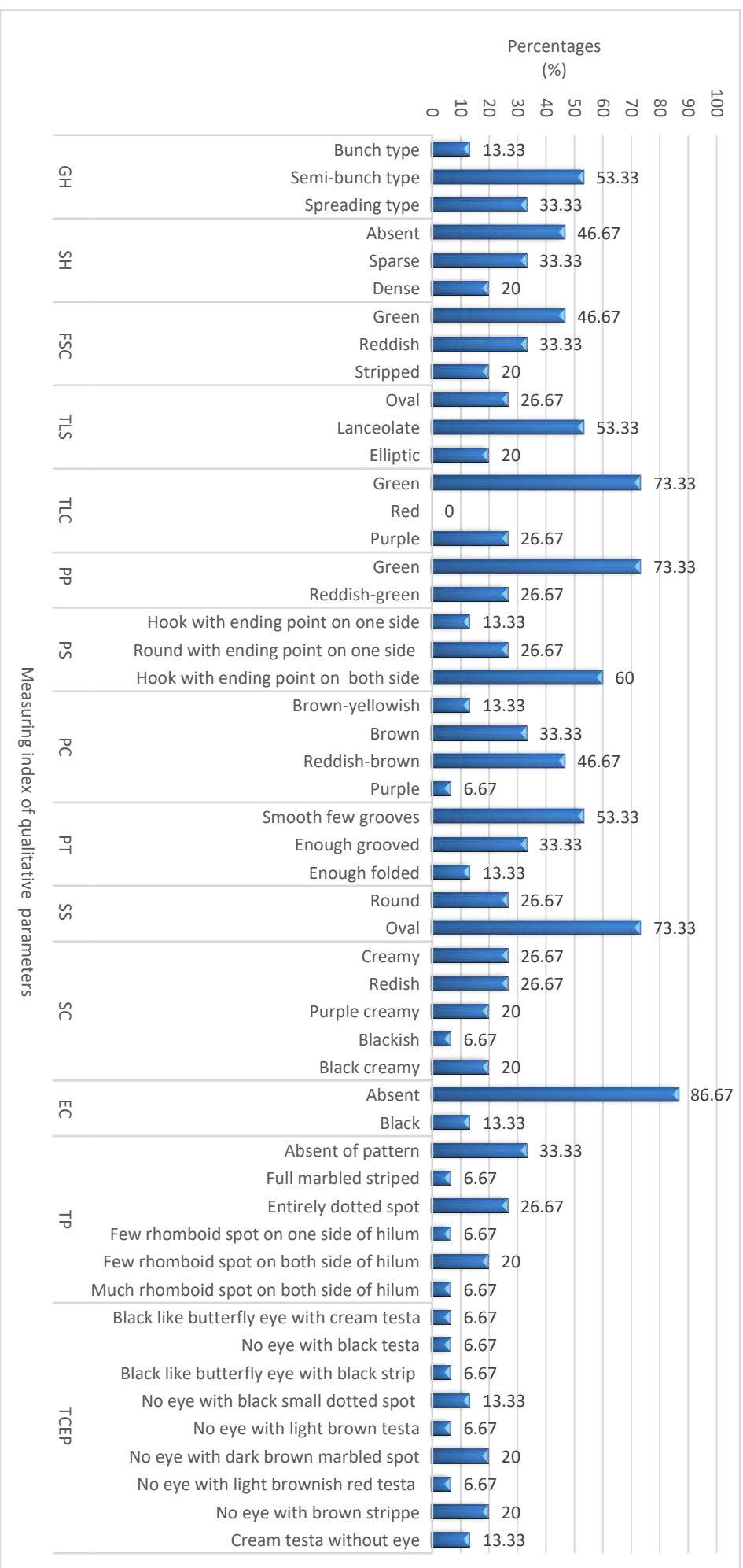


Figure 1: Graphical display of qualitative traits' frequency distribution of Bambara groundnut accessions

3.2. Estimation of quantitative parameters

3.2.1 Morphological diversity

For crop upgrading plant breeders considered yield and its related traits as a controlling parameter. In current research, to select the best performing accessions for next breeding program a total number of 27 numerical traits of 15 Bambara groundnut landraces were analysed. The analysis of variance revealed the significant variation, mean, standard error of mean (SEm), standard deviation (St.Dev), and coefficient of variation (CV%) displayed in Table 4. Except the traits (fifty percent flowering day, seed length, seed width) all other quantitative traits showed highly significant ($P \leq 0.01$) difference. No significant difference was found for the trait plant height ($24.36\text{cm} \pm 0.39$). Within replication no significant variation was observed. The highest and lowest values for the respective traits across all plants were presented in Table 4. We found 16 out of the 27 quantitative traits had coefficient of variation (CV) $\geq 20\%$ which ranged from 5.96% (Shelling%) to 58.55% (dry seed weight per plant (g)). The average days to maturity was found (131.56 ± 1.18) days which is statistically significant ($p \leq 0.01$). The highest value of standard deviation (SD) was found for yield kg/ha (650.98) with standard error (SEm ± 97.04) while the lowest was for internode length (SD = 0.49; SEm ± 0.07) (Table 4). Standard error (SE) is the indication of consistency of the average values, lowest SE values indicate the sample mean is more precise reflection of the real population mean.

The maximum and minimum values for overall accessions and mean comparison with least significant difference (LSD = 0.05) were shown in the Table 5 & 6. Figure 2 showing the graphical relationship of DSW(g) and HSW(g) with yield (kg ha^{-1}). The days to 50% flowering varied from 31 to 49 days after sowing (DAS) while 66.67% of the accessions gave 50% flower before 40 days after sowing. Most of the landraces (80%) took more than 120 days to maturity which varied from 122 DAS to 141 DAS. The genotype G1 marked as short duration line with a total day to maturity of 119 DAS (Table 4). The genotype G2 recorded highest values for the traits like - BFW (614.67g); BDW(361.57g) (Table 5); TNP (93.67); NMP (74.33); FPW (568.56g); DPW (359.01g); NSP (92.17); DSW (274.96g); SW(10.74mm); HSW(360.15g); Sell% (76.68%) and yield ($2991.77 \text{ kg ha}^{-1}$) while the accession G13 had lowest values. The next maximum yield (kg ha^{-1}) was recorded for the genotype G9 ($2226.30 \text{ kg ha}^{-1}$) followed by G3 ($1557.61 \text{ kg ha}^{-1}$), G6 ($1414.67 \text{ kg ha}^{-1}$) and G10 ($1250.73 \text{ kg ha}^{-1}$) (Table 5 & 6).

Table 4. Summary of the signification variation revealed by Analysis of Variance (ANOVA).

Traits	Replication (df=2)	Genotype (df=14)	Mean $\pm$ SEm	Max	Min	St. Dev	CV (%)
Phenological traits							
DTE	0.42	7.85**	7.96 $\pm$ 0.27	13.00	5.00	1.81	22.73
D50%F	6.20	41.24*	39.27 $\pm$ 0.74	49.00	31.00	4.98	12.68
DTM	6.16	172.46**	131.56 $\pm$ 1.18	144.00	118.00	7.93	6.03
Vegetative traits							
PH	7.69	9.18ns	24.36 $\pm$ 0.39	29.46	16.21	2.60	10.69
NB	0.82	295.08**	34.82 $\pm$ 1.47	59.00	12.00	9.86	28.32
NS	6.02	21.68**	13.36 $\pm$ 0.51	25.00	7.00	3.39	25.40
NP	451.47	17849**	298 $\pm$ 11.68	410.00	150.00	78.34	26.29
NL	4063.2	160641**	894 $\pm$ 35.07	1230.00	450.00	235.01	26.29
NNS	5.40	6.91**	11.6 $\pm$ 0.28	16.00	8.00	1.92	16.58
IL	0.25	0.46**	3.15 $\pm$ 0.07	4.60	2.40	0.49	15.66
BFW	473.98	57774.96**	316.85 $\pm$ 20.38	621.00	92.70	136.72	43.15
BDW	1396.43	18453.82**	141.012 $\pm$ 11.88	373.64	43.41	79.74	56.55
Yield traits							
TNP	25.27	488.09**	67.67 $\pm$ 1.97	96.00	48.00	12.92	19.10
NMP	7.22	403.40**	51.69 $\pm$ 1.76	78.00	33.00	11.79	22.80
NIP	5.49	45.83**	15.98 $\pm$ 0.66	26.00	8.00	4.45	27.85
FPW	66.84	49298.44**	281.46 $\pm$ 18.70	589.00	145.50	125.44	44.57
DPW	328.36	18889.72**	141.64 $\pm$ 11.65	375.13	64.72	78.12	55.15
PL	1.32	125.31**	27.48 $\pm$ 0.96	44.47	17.96	6.45	23.49
PW	0.86	7.82**	13.17 $\pm$ 0.28	18.59	9.42	1.88	14.29
NSP	33.01	488.09**	66.17 $\pm$ 1.93	95.00	46.00	12.94	19.55
DSW	30.27	11220.87**	102.47 $\pm$ 8.94	277.71	46.88	59.99	58.55
SL	0.83	7.76*	13.27 $\pm$ 0.32	20.45	9.33	2.13	16.06
SW	0.22	2.39*	9.07 $\pm$ 0.18	11.57	6.42	1.21	13.34
HSW	1.09	11.49**	228.02 $\pm$ 7.71	389.32	160.98	51.73	22.69
Shel%	6.94	39.71**	71.79 $\pm$ 0.64	79.97	59.29	4.28	5.96
HI	57.44	433.91**	50.46 $\pm$ 1.87	83.88	33.82	12.54	24.85
Yld	22803.08	1311786.57**	1180.34 $\pm$ 97.04	3126.00	539.33	650.98	55.15

Legend: df= degree of freedom; ns= non-significant; SEm = standard error of the mean; St. Dev = standard deviation; Max= maximum; Min= minimum; $P \leq 0.05$ = significant (*); $P \leq 0.01$ = highly significant (**), CV= Coefficient of variation for error. Days to emergence = DTE (d), Days to 50% flowering = D50%F (d), Days to maturity = DTM (d), Plant height (cm) = PH, Number of branches per plant = NB, Number of stems per plant = NS, Number of petioles per plant = NP, Number of leaves per plant = NL, No. of nodes per stem=NNS, Inter nodes length = IL (cm), Biomass fresh weight per plant = BFW(g), Biomass dry weight per plant = BDW(g), Total no. of pods per plant = TNP, Number of mature pods per plant = NMP, Number of Immature pods per plant = NIP, Fresh pods weight = FPW(g), Dry pods weight = DPW(g), Pod length = PL(mm), PW = PW (mm), Number of seeds per plant = NSP, Dry seed weight per plant = DSW(g), Seed length = SL(mm), Seed width =SW (mm), Hundred seed weight = HSW(g), Shelling percent = Shel%, Harvest index =HI (%) and Yield = Yld (Kgha⁻¹).

3.3. Analysis of correlation

The phenotypic correlation among the 27 numerical traits of fifteen Bambara groundnut accessions is given in Table 7. Days to 50% flowering showed negative and intermediate ($0.25 \leq r < 0.75$) significant association with NB ($r = -0.29$; $P = 0.04$), NNS($r=0.33$; $P= 0.02$), TNP ($r = -0.38$; $P = 0.00$), NMP ($r = -0.35$; $P = 0.01$) and NSP ($r = -0.38$; $P = 0.00$). A positive and highly strong ($0.75 \leq r < 1$) significant association was found for the traits like NMP ($r = 0.93$; $P \leq 0.00$), DPW ($r = 0.76$; $P \leq 0.00$), NSP ($r = 0.99$; $P \leq 0.00$), DSW ($r= 0.77$; $P \leq 0.00$) and yield ($r = 0.76$; $P \leq 0.00$) with the total number of pods. The trait yield (kgha⁻¹) revealed positive and perfect ($r = 1.00$) highly significant association with DPW ($r = 1.00$; $P \leq 0.00$) while positive and highly strong ($0.75 \leq r < 1$) significant association was found with DSW ($r =0.99$; $P \leq 0.00$), NSP ($r = 0.76$; $P \leq 0.00$) and HSW ($r =0.76$; $P \leq 0.00$) per plant (Table 7).

Table 5: The mean and mean comparison of 3 phenological and 9 vegetative traits of 15 Bambara groundnut accession

Genotypes	DTE	D50%F	DTM	PH	NB	NS	NP	NL	NNS	IL	BFW	BDW
G1	5.33d	39.33bcd	119.67f	25.56a-d	44.67b	11cde	349.33b-e	1048b-e	13ab	3.53ab	364.24c	150.57d
G2	7.33bc	37.33bcd	121f	23.87a-e	34de	16.67a	279.33g	838g	12abcd	2.97bcd	614.67a	361.57a
G3	7.33bc	35d	132.33bcd	26.72ab	32ef	11.67b-e	179.33i	538i	12.33abc	3bcd	296.8de	140.39d
G4	6.67cd	43.67abc	139.67a	22.31cde	13h	9.67de	304.33fg	913fg	9.33ef	2.7d	188.04hg	62.39f
G5	8.33bc	38.67bcd	138.33a	24.08a-e	35de	12.67a-d	316.67efg	950efg	10.33c-f	3.83a	329.83cd	146.77d
G6	6.67cd	44.33ab	129d	25.87abc	40.33c	15abc	369.67abc	1109abc	13ab	3.83a	485.57b	218.55b
G7	11a	37.33bcd	138.33a	23.11b-e	36.67cd	16ab	328.67c-f	986c-f	11b-f	2.93bcd	344.84c	160.81cd
G8	9b	34.33d	122.33ef	25.23a-e	56.67a	16.67a	165i	495i	12.33abc	3.3a-d	511b	197.68cb
G9	8bc	37.33bcd	121.67f	27.14a	45b	16.33a	361.67a-d	1085a-d	11.67b-e	3.2bcd	155.98h	62.84f
G10	7.67bc	37.67bcd	136abc	23.65a-e	31.33ef	12.67a-d	226.66h	680h	12.67abc	3.4abc	275.66e	78.56f
G11	7cd	37cd	130.33cd	23.8a-e	35de	16ab	310efg	930efg	11b-f	2.8cd	195.55g	87.19ef
G12	7.33bc	47.67a	138ab	21.92de	34.33de	13.33a-d	177.33i	532i	9.67def	2.73d	359.38c	122.04de
G13	8bc	42.33abc	128de	21.57e	23.67g	12.33a-e	402a	1206a	9f	2.77d	109.97i	50.22f
G14	8bc	40bcd	141.33a	26.45ab	31.67ef	8e	381.67ab	1145ab	12.33abc	3.5ab	286.51e	141.03d
G15	11.67a	37cd	137.33ab	24.13a-e	29f	12.33a-e	318.33d-g	955d-g	14.33a	2.77d	234.68	134.63d
Mean	7.96	39.27	131.56	24.36	34.82	13.36	298.00	894.00	11.60	3.15	316.85	141.02
LSD	1.82	7.07	5.83	ns	3.82	4.36	43.83	131.50	2.35	0.60	35.65	43.15
Min	5.33	34.33	119.67	21.57	13.00	8.00	165.00	495.00	9.00	2.70	109.97	50.22
Max	11.67	47.67	141.33	27.14	56.67	16.67	402.00	1206.00	14.33	3.83	614.67	361.57

Legend: Max=maximum, Min= minimum, C.V = coefficient of variation; LSD = Least significant difference at 5% level, Days to emergence = DTE (d), Days to 50% flowering (d), Days to maturity= DTM (d), Plant height (cm) = PH, Number of branches per plant = NB, Number of stems per plant = NS, Number of petioles per plant = NP, Number of leaves per plant = NL, No. of nodes per stem=NNS, Inter nodes length = IL (cm), Biomass fresh weight per plant = BFW(g), Biomass dry weight per plant = BDW(g),

Table 6: The mean and mean comparison of 15 yield related traits of 15 Bambara groundnut accession

Genotypes	TNP	NMP	NIP	FPW	DPW	PL	W	NSP	DSW	SL	SW	HSW	Shel%	HI	Yld
G1	71.67de	53.33c	18.33abc	188.59g	132.21de	24.79d	12.24cd	70.17de	95.68d	12.91bc	9.76abc	225.96de	72.35a-d	46.92def	1101.72de
G2	93.67a	74.33a	19.33ab	568.55a	359.01a	38.68b	15.48ab	92.17a	274.96a	16.29a	10.74a	360.15a	76.68a	49.82cd	2991.77a
G3	78.67cb	57c	21.67a	325.06d	186.91c	25.34d	13.19c	77.17cb	134.47c	13.71abc	9.19abc	224.43def	71.93a-d	57.13cb	1557.61c
G4	50.67j	40.33efg	10.33e	186.22g	88.68fg	20.95ef	12.25cd	49.17j	61.36fg	11.48c	8.90bc	201.15e-i	69.11cde	58.69b	739.05fg
G5	59.67fgh	41efg	18.67ab	157.17i	92.02f	24.51d	12.75cd	58.17fgh	65.26fg	12.43bc	8.64bc	208.67efg	70.96b-e	38.56fg	766.81f
G6	65.33ef	54.67c	10.67e	332.97d	169.76c	24.15d	14.05bc	63.83ef	124.72c	13.75abc	9.18abc	188.33ghi	73.54abc	44.34d-g	1414.67c
G7	57.67ghi	45.33de	12.33de	180.95gh	93.53f	30.27c	13.51bc	56.17ghi	71.71f	12.95bc	9.5abc	244.46d	76.67a	36.86g	779.47
G8	81.33b	67.67ab	13.67cde	391.64c	123.25e	31.56c	14.09bc	79.83b	92.05de	13.75abc	9.32abc	278.25c	74.66ab	39.07fg	1027.09e
G9	83.67b	66.67b	17a-d	469.11b	267.16b	32.39c	16.63a	82.17b	197.12b	16.62a	9.94ab	309.73b	73.84abc	81.10a	2226.3b
G10	72cde	56c	16bcd	281.08e	150.09d	42.70a	13.27c	70.5cde	98.56d	12.71bc	8.19cd	204.63e-h	66.49ef	65.60b	1250.73d
G11	60fgh	51cd	9e	174.75gf	83.22fg	19.56f	9.89e	58.5fgh	62.61fg	11.43c	9.09abc	177.52i	75.22ab	48.87cde	693.54fg
G12	61.67gf	42.66ef	19ab	167.14hi	83.12fg	24.69d	13.22c	60.17gf	57.09gh	13.21bc	8.98bc	212.91efg	68.62def	40.56efg	692.74fg
G13	51.67ij	35g	16.67bcd	155.5i	70.67g	24.11d	11.03de	50.17ij	50.15h	11.03c	6.65d	198.35f-i	71.00b-e	58.58b	588.97g
G14	54.67hij	38fg	16.67bcd	388.44c	130.56e	23.31de	12.64cd	53.17hij	83.35e	12.32bc	9.03abc	181.48hi	63.83f	48.58de	1088.15e
G15	72.67cd	52.33c	20.33ab	254.63f	94.38f	25.14d	13.26c	71.17cd	67.93fg	14.49ab	8.88bc	204.23e-i	71.99a-d	42.22d-g	786.47f
Mean	67.67	51.69	15.98	281.46	141.64	27.48	13.17	66.17	102.47	13.27	9.07	228.02	71.80	50.46	1180.34
LSD	6.82	6.70	4.67	14.37	18.41	2.75	2.11	6.82	10.98	2.99	1.74	26.75	4.86	8.53	153.39
Min	50.67	35.00	9.00	155.50	70.68	19.56	9.90	49.17	50.15	11.03	6.65	177.52	63.83	36.86	588.98
Max	93.67	74.33	21.67	568.56	359.01	42.70	16.63	92.17	274.96	16.62	10.74	360.15	76.68	81.10	2991.77

Legend: Max=maximum, Min= minimum, C.V = coefficient of variation; LSD = Least significant difference at 5% level, Total no. of pods per plant = TNP, Number of mature pods per plant = NMP, Number of Immature pods per plant = NIP, Fresh pods weight = FPW(g), Dry pods weight = DPW(g), Pod length = PL(mm), PW = PW (mm), Number of seeds per plant = NSP, Dry seed weight per plant = DSW(g), Seed length = SL(mm), Seed width =SW (mm), Hundred seed weight = HSW(g), Shelling percent = Shel%, Harvest index =HI (%) and Yield = Yld (Kg/ha).

16 Table 7: Correlation matrix (r) for 27 quantitative traits of Bambara groundnut accessions

Traits	DTE	D50F	DTM	PH	NB	NS	NP	NL	NNS	IL	BFW	BDW
DTE	1	-0.178	0.258	-0.055	0.017	0.229	-0.017	-0.017	0.086	-0.224	-0.076	-0.008
D50%F		1	0.182	-0.206	-0.293*	-0.057	0.125	0.125	-0.333*	0.042	-0.077	-0.2
DTM			1	-0.233	-0.554**	-0.386**	-0.065	-0.065	-0.152	-0.124	-0.299*	-0.287*
PH				1	0.330*	0.129	0.072	0.072	0.310*	0.352*	0.114	0.135
NB					1	0.423*	-0.187	-0.187	0.365*	0.376*	0.495**	0.333*
NS						1	-0.13	-0.13	-0.047	0.095	0.286	0.249
NP							1	1.00**	-0.007	0.21	-0.347*	-0.16
NL								1	-0.007	0.21	-0.347*	-0.16
NNS									1	0.293*	0.274	0.341*
IL										1	0.281	0.161
BFW											1	0.903**
BDW												1

Traits	TNP	NMP	NIP	FPW	DPW	PL	PW	NSP	DSW	SL	SW	HSW	Shel%	HI	Yld
DTE	0.052	0.013	0.116	-0.016	-0.204	0.121	0.139	0.051	-0.172	0.111	-0.099	0.087	0.231	-0.25	-0.204
D50%F	-0.387**	-0.357*	-0.177	-0.265	-0.205	-0.283	-0.056	-0.389**	-0.212	-0.231	-0.109	-0.245	-0.232	0.049	-0.205
DTM	-0.629**	-0.669**	-0.055	-0.445**	-0.531**	-0.262	-0.268	-0.629**	-0.563**	-0.301*	-0.203	-0.541**	-0.480**	-0.274	-0.531**
PH	0.331*	0.344*	0.049	0.391**	0.304*	0.068	0.344*	0.337*	0.282	0.330*	0.382*	0.141	-0.005	0.163	0.304*
NB	0.514**	0.558**	0.015	0.354*	0.247	0.273	0.311*	0.513**	0.262	0.328*	0.340*	0.393**	0.349*	-0.172	0.247
NS	0.390**	0.481**	-0.143	0.245	0.330*	0.331*	0.403**	0.387**	0.362*	0.214	0.352*	0.465**	0.501**	0.026	0.330*
NP	-0.372*	-0.341*	-0.176	-0.088	-0.034	-0.278	-0.142	-0.369*	-0.036	-0.118	-0.082	-0.195	-0.045	0.166	-0.034
NL	-0.372*	-0.341*	-0.176	-0.088	-0.034	-0.278	-0.142	-0.369*	-0.036	-0.118	-0.082	-0.195	-0.045	0.166	-0.034
NNS	0.428*	0.429*	0.105	0.343*	0.241	0.227	0.141	0.431*	0.233	0.388**	0.291*	0.027	0.08	-0.133	0.241
IL	0.046	0.063	-0.034	0.142	0.139	0.105	0.211	0.053	0.114	-0.058	0.125	-0.08	-0.113	-0.028	0.139
BFW	0.489**	0.517**	0.053	0.481**	0.462**	0.375*	0.354*	0.489**	0.486**	0.306*	0.421**	0.477**	0.320*	-0.497**	0.462**
BDW	0.514**	0.525**	0.102	0.559**	0.570**	0.326*	0.371*	0.515**	0.600**	0.432**	0.467**	0.533**	0.386**	-0.498**	0.570**
TNP	1	0.939**	0.417**	0.741**	0.763**	0.615**	0.582**	0.999**	0.779**	0.649**	0.442**	0.733**	0.382*	0.199	0.763**
NMP		1	0.08	0.746**	0.744**	0.594**	0.583**	0.939**	0.764**	0.615**	0.464**	0.715**	0.455**	0.19	0.744**
NIP			1	0.177	0.246	0.213	0.145	0.417**	0.238	0.255	0.055	0.236	-0.095	0.076	0.246
FPW				1	0.877**	0.546**	0.641**	0.741**	0.869**	0.580**	0.416**	0.700**	0.165	0.306*	0.877**
DPW					1	0.589**	0.647**	0.761**	0.993**	0.583**	0.486**	0.768**	0.238	0.404**	1.000**
PL						1	0.551**	0.615**	0.572**	0.403**	0.235	0.604**	0.062	0.279	0.589**
PW							1	0.578**	0.631**	0.603**	0.429**	0.628**	0.066	0.217	0.647**
NSP								1	0.777**	0.651**	0.443**	0.730**	0.386**	0.197	0.761**
DSW									1	0.589**	0.483**	0.800**	0.338*	0.366*	0.993**
SL										1	0.665**	0.587**	0.253	0.084	0.583**
SW											1	0.490**	0.207	-0.07	0.486**
HSW												1	0.483**	0.181	0.768**
Shel%													1	-0.183	0.238
HI														1	0.404**
Yld															1

Legend: “***” correlation is significant at the 0.01 level; “**” correlation is significant at the 0.05 level, Days to emergence = DTE (d), Days to 50% flowering = D50%F (d), Days to maturity = DTM (d), Plant height (cm) = PH, Number of branches per plant = NB, Number of stems per plant = NS, Number of petioles per plant = NP, Number of leaves per plant = NL, No. of nodes per stem=NNS, Inter nodes length = IL (cm), Biomass fresh weight per plant = BFW(g), Biomass dry weight per plant = BDW(g), Total no. of pods per plant = TNP, Number of mature pods per plant = NMP, Number of Immature pods per plant = NIP, Fresh pods weight = FPW(g), Dry pods weight = DPW(g), Pod length = PL(mm), PW = PW (mm), Number of seeds per plant = NSP, Dry seed weight per plant = DSW(g), Seed length = SL(mm), Seed width =SW (mm), Hundred seed weight = HSW(g), Shelling percent = Shel%, Harvest index =HI (%) and Yield = Yld (Kgha⁻¹).

3.4. Analysis of genetic components

3.4.1. Variance and covariance, heritability in broad sense, relative differences and genetic advances

The output of genetic components analysis was compiled in Table 8. Apparently, the phenotypic variance (σ_p^2) is higher than the genotypic variance (σ_g^2) regarding all the traits evaluated. The trait grain yield kg ha^{-1} reported higher genotypic (434458.5) and phenotypic (442869.6) variance while the lower genotypic (0.11) and phenotypic (0.24) value was recorded for the trait internode length. The traits such as TNP (PCV 19.48% & GCV 18.53%), PW (PCV 14.55% & GCV 10.95%), NSP (PCV 19.92% and GCV 18.95%), SL (PCV 16.37% & GCV 9.30%), SW (PCV 13.61% & GCV 7.29%) and shell% (PCV 6.05% & GCV 4.50%) showed below 20% of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). For the improvement of this crop further selection could be done considering the traits having GCV $\geq 20\%$ (BFW, BDW, FPW, DPW, DSW and grain yield) which indicated high degree of variability among these traits although the variation is due to the effect of additive genes. Due to the lower GCV values ($\leq 10\%$) the vegetative traits (PH, D50%F, and DTM) and yield traits (SL, SW, and Shel%) indicated the limited chance of selection based on respective traits due to the effect of environment on their phenotypic expression.

The relative difference (RD) is the ratio of GCV in association with the respective PCV and the estimated RD values varied from 0.22% (fresh pods weight) to 57.46% for plant height (Table 8). Relatively low difference value between GCV and PCV was recorded for the traits like DTM(9.74%), NB(2.59%), BFW(1.17%), BDW(5.18%), TNP(4.91%), FPW(0.22%), DPW(0.95%), PL(3.15%), DSW(0.57%), HSW(4.71%), and yield (0.95%) kg ha^{-1} and noticed that the variation present among the traits due to the effect of gene and have a better response to direct selection. On the other hand, the traits with higher difference in between their PCV and GCV values indicated the wider genetic variability due to environmental effect and not better feedback to direct selection for the improvement of traits.

The values of heritability in broad sense were observed high for most of the traits evaluated (Table 8) which ranged from 18.09% (PH) to 99.55% (FPW). Very high ($\geq 60\%$) heritability was measured for traits like DTM (81.47%), NB (94.89%), BFW (97.68%), BDW(89.91%), TNP(90.42%), PL(93.79%), DPW(98.10%), DSW(98.86%), HSW (90.80%), HI(83.93%) and yield (98.10%) is the indication of limited chance of environmental effect. The heritability value 30% to 60% was marked for the traits like D50%F(30.32%), PW (56.64%), Shel% (55.22%) and SL(32.25%) which indicate the traits are moderately heritable whereas the trait PH (18.09%) and SW (28.71%) showed heritability below 30% i.e. low heritability. The trait dry seed weight (122.01%) had topmost genetic advance (as percentage mean) value ($\geq 20\%$) or genetic gain

while the lowest had (3.97%) for plant height (PH) (Table 8). Moreover, the higher genetic gain was recorded for the traits like grain yield (113.94%), DPW (113.94%), BDW (106.66%), FPW (93.54%) and BFW (88.82%) with high heritability. In our study, most of the yield contributing traits showed moderate to high heritability with genetic advance ($\geq 20\%$) excluding the traits like SW (GA 8.05%) and Shel% (GA 6.88%) which was $\leq 10\%$. Consideration of higher value of genotypic coefficient of variation along with higher heritability and genetic advance is the powerful tools of selection for crop improvement than the consideration of individual genetic matrix or measuring unit. However, these traits were governed by additive genes having limited response to environment and suggestively notable for the selection procedure.

Table 8: Variance components, relative difference, heritability and genetic advance of 27 quantitative traits

Traits	Mean	σ_e^2	σ_g^2	σ_p^2	PCV (%)	GCV (%)	RD (%)	(h_b^2) %	GA (%)
Phenological Traits									
DTE	7.96 $\pm$ 0.27	1.18	2.22	3.41	23.20	18.74	19.23	65.24	31.18
D50%F	39.27 $\pm$ 0.74	17.89	7.79	25.68	12.90	7.11	44.93	30.32	8.06
DTM	131.56 $\pm$ 1.18	12.16	53.43	65.59	6.16	5.56	9.74	81.47	10.33
Vegetative traits									
PH	24.36 $\pm$ 0.39	5.52	1.22	6.74	10.66	4.53	57.46	18.09	3.97
NB	34.82 $\pm$ 1.47	5.20	96.63	101.83	28.98	28.23	2.59	94.89	56.65
NS	13.36 $\pm$ 0.51	6.81	4.96	11.77	25.69	16.68	35.08	42.15	22.30
NP	298 $\pm$ 11.68	686.82	5720.70	6407.52	26.86	25.38	5.51	89.28	49.40
NL	894 $\pm$ 35.07	6181.40	51486.50	57667.90	26.86	25.38	5.51	89.28	49.40
NNS	11.6 $\pm$ 0.28	1.97	1.65	3.62	16.40	11.07	32.53	45.53	15.38
IL	3.15 $\pm$ 0.07	0.13	0.11	0.24	15.65	10.65	31.95	46.31	14.93
BFW	316.85 $\pm$ 20.38	454.27	19106.90	19561.17	44.14	43.63	1.17	97.68	88.82
BDW	141.012 $\pm$ 11.88	665.71	5929.40	6595.11	57.59	54.61	5.18	89.91	106.66
Yield traits									
TNP	67.67 $\pm$ 1.97	16.65	157.15	173.80	19.48	18.53	4.91	90.42	36.29
NMP	51.69 $\pm$ 1.76	16.06	129.12	145.17	23.31	21.98	5.69	88.94	42.71
NIP	15.98 $\pm$ 0.66	7.80	12.68	20.48	28.32	22.28	21.31	61.91	36.12
FPW	281.46 $\pm$ 18.70	73.85	16408.20	16482.05	45.61	45.51	0.22	99.55	93.54
DPW	141.64 $\pm$ 11.65	121.12	6256.20	6377.32	56.38	55.84	0.95	98.10	113.94
PL	27.48 $\pm$ 0.96	2.70	40.87	43.57	24.02	23.26	3.15	93.79	46.41
PW	13.17 $\pm$ 0.28	1.59	2.08	3.67	14.55	10.95	24.74	56.64	16.97
NSP	66.17 $\pm$ 1.93	16.65	157.15	173.80	19.92	18.95	4.91	90.42	37.11
DSW	102.47 $\pm$ 8.94	43.08	3725.90	3768.98	59.91	59.57	0.57	98.86	122.01
SL	13.27 $\pm$ 0.32	3.20	1.52	4.72	16.37	9.30	43.21	32.25	10.88
SW	9.07 $\pm$ 0.18	1.09	0.44	1.52	13.61	7.29	46.42	28.71	8.05
HSW	228.02 $\pm$ 7.71	255.82	2525.90	2781.72	23.13	22.04	4.71	90.80	43.27
Shel%	71.79 $\pm$ 0.64	8.45	10.42	18.87	6.05	4.50	25.69	55.22	6.88
HI	50.46 $\pm$ 1.87	26.04	135.96	162.00	25.22	23.11	8.39	83.93	43.61
Yld	1180.34 $\pm$ 97.04	8411.10	434458.50	442869.60	56.38	55.84	0.95	98.10	113.94

Legend: σ_e^2 = Error variance; σ_g^2 = Genotypic variance; σ_p^2 = Phenotypic variance; h_b^2 = Heritability in broad sense; PCV= Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; RD = Relative difference; GA = Genetic advance, Days to emergence = DTE (d), Days to 50% flowering = D50%F (d), Days to maturity = DTM (d), Plant height (cm) = PH, Number of branches per plant = NB, Number of stems per plant = NS, Number of petioles per plant = NP, Number of leaves per plant = NL, No. of nodes per stem=NNS, Inter nodes length = IL (cm), Biomass fresh weight per plant = BFW(g), Biomass dry weight per plant = BDW(g), Total no. of pods per plant = TNP, Number of mature pods per plant = NMP, Number of Immature pods per plant = NIP, Fresh pods weight = FPW(g), Dry pods weight = DPW(g), Pod length = PL(mm), PW = PW (mm), Number of seeds per plant = NSP, Dry seed weight per plant = DSW(g), Seed length = SL(mm), Seed width =SW (mm), Hundred seed weight = HSW(g), Shelling percent = Shel%, Harvest index =HI (%) and Yield (Kgha⁻¹) = Yld

3.5. Cluster patterns

In this study, the homogenized data was used to calculate the Euclidean distances among the 15 Bambara groundnut accessions and a UPGMA dendrogram was designed (Figure 3). To discriminate against the relations in the population, the dendrograms of the 15 Bambara groundnut accessions were clustered into five major groups based on their twenty-seven measurable traits at 1.16 dissimilarity coefficients. In the dendrogram, there was a cut off at the point of 1.16 coefficient for ease of interpretation. The Table 9 showed the mean performances of the selections according to each class. Group I represented by G1, G6 and G12 are characterized by early germinating (6 days) but need more time to flowering close to 44 days among the group also took medium time to maturity and plant height (24.45cm). Internode length was maximum while hundred seed weight and yield kg/ha showed medium values within the five groups. Group II is formed by maximum number of (G4, G5, G7, G11, G14 and G15) accessions characterized by the following traits: maximum maturation date (137 days) and minimum pod length (3.37mm) with compared to other groups. Group III was illustrated by only one accession (G13). This accession was distinguished by the following traits with minimum values like plant height, branches number, stem number, leaves number, nodes number, internode length, biomass fresh & dry weight, total pod number, no. of mature pod, dry & fresh pod weight, pod width, seed number, dry seed weight, seed length & width, hundred seed weight, shelling percent, yield kg/ha as their most isolated characters. Group IV comprised of four accession G2, G3, G9 and G10 with maximum values of traits like plant height (cm), total pod number, no. of immature pod, dry & fresh pod weight, pod length & width, seed number, dry seed weight, seed length & width, hundred seed weight, harvest index and yield kg/ha as their most special characters. All the accessions under this group had mean yield maximum 2 ton/ha which was due to maximum value of yield contributing traits. The last Group V captured only one accession G8 seemed to have long time to emergence (9 days) but gave early flower with maximum values of traits like branches number, stem number, nodes number, biomass fresh & dry weight, mature pod number, pod length, hundred seed weight and shelling percent as their most distinctive characters. Group IV gave the highest yield (36.48%), while Group III gave the lowest yield (10.71%). Two groups I (19.44%) and group V (18.67%) had accessions near to each other on the aspect of yield traits (Table 9). Moreover, we estimated 70.07% higher (+) mean yield over the average grand mean yield (1180 kg/ha⁻¹) for cluster IV whereas the cluster I (9.34%), cluster II (31.44%), cluster III (50.08%) and cluster V (12.95%) produced lower (-) yield.

Table 9: Mean values of quantitative traits for 5 groups revealed by cluster analysis of Bambara groundnut.

Traits	Cluster or Group				
	Group I	Group II	Group III	Group IV	Group V
	G1, G6, G12	G4, G5, G7, G11, G14, G15	G13	G2, G3, G9, G10	G8
DTE	6.44	8.78	8.00	7.58	9.00
D50%F	43.78	38.94	42.33	36.83	34.33
DTM	128.89	137.56	128.00	127.75	122.33
PH	24.45	23.98	21.57	25.35	25.23
NB	39.78	30.06	23.67	35.58	56.67
NS	13.11	12.44	12.33	14.33	16.67
NP	298.78	326.61	402.00	261.75	165.00
NL	896.33	979.83	1206.00	785.25	495.00
NNS	11.89	11.39	9.00	12.17	12.33
IL	3.37	3.09	2.77	3.14	3.30
BFW	403.06	263.24	109.97	335.78	511.00
BDW	163.72	122.14	50.22	160.84	197.68
TNP	66.22	59.22	51.67	82.00	81.33
NMP	50.22	44.67	35.00	63.50	67.67
NIP	16.00	14.56	16.67	18.50	13.67
FPW	229.57	223.70	155.50	410.95	391.64
DPW	128.37	97.07	70.68	240.79	123.25
PL	24.55	23.96	24.11	34.78	31.56
PW	13.17	12.39	11.03	14.65	14.10
NSP	64.72	57.72	50.17	80.50	79.83
DSW	92.50	68.71	50.15	176.28	92.05
SL	13.29	12.52	11.03	14.83	13.75
SW	9.31	9.01	6.65	9.51	9.32
HSW	209.07	202.92	198.35	274.73	278.26
Shel%	71.50	71.30	71.01	72.24	74.67
HI	43.94	45.63	58.58	63.41	39.07
Yld	1069.71	808.92	588.98	2006.60	1027.09
RPMY (%)	19.44	14.7	10.71	36.48	18.67
RPGY (%)	(-) 9.34	(-) 31.44	(-) 50.08	(+) 70.05	(-) 12.95

Legend: RPMY = Relative proportion (%) of mean yield; Grand average yield = 1180 kg/ha⁻¹; Relative proportion of grand average yield = RPGY (%); '(+)' = yield higher; '(-)' = yield lower. Days to emergence = DTE (d), Days to 50% flowering = D50%F (d), Days to maturity = DTM (d), Plant height (cm) = PH, Number of branches per plant = NB, Number of stems per plant = NS, Number of petioles per plant = NP, Number of leaves per plant = NL, No. of nodes per stem = NNS, Inter nodes length = IL (cm), Biomass fresh weight per plant = BFW(g), Biomass dry weight per plant = BDW(g), Total no. of pods per plant = TNP, Number of mature pods per plant = NMP, Number of Immature pods per plant = NIP, Fresh pods weight = FPW(g), Dry pods weight = DPW(g), Pod length = PL(mm), PW = PW (mm), Number of seeds per plant = NSP, Dry seed weight per plant = DSW(g), Seed length = SL(mm), Seed width = SW (mm), Hundred seed weight = HSW(g), Shelling percent = Shel%, Harvest index = HI (%) and Yield (Kg/ha⁻¹) = Yld

3.6. Valuation of principal component analysis

Based on the results from Table 10 it appeared that the principal component 1 (PC1) accounted for close to 45.88% of the total variation and the characters responsible for genotypes separation along this axis were TNP (highest 0.271), NMP, FPW, DPW, NSP, DSW, SL, HSW and YLD (Kg/ha⁻¹) with high and positive value of coefficient of variation. The second principal component (PC2) associated with the traits D50%F, PH, NP, NL, FPW, DPW, DSW, HI (maximum 0.447) and YLD (Kg/ha⁻¹) accounted for 10.64% of the total variation. About 8.78% of the total variation was detected for Principal Component 3 (PC3) and displayed differences based on PH, NB, NS, NP, NL, NNS, IL (largest 0.472), BFW and BDW. The principal

component 4 (PC4) accounted for 8.19% of the total variation and consisted mostly of the traits of D50%F, NS, NP, NL, HSW, and Shell% (maximum 0.444). The variation (6.75%) was found for principal component 5 (PC5) and comprised with D50%F (maximum 0.479), DTM, DSW and YLD (Kgha^{-1}). The last principal component 6 (PC6) accounted for 5.69% of the total variation and consisted of the traits DTE, DTM, NP, NL, BDW, NIP, PW and SL up to this principal component covered close to 86% of the cumulative variation. The two-dimensional (Figure 4) and three dimensional (Figure 5) graphical elucidation demonstrated that most of the accessions were dispersed at low distances whereas the few were dispersed at high distances as reflected by eigenvector (Table 10). The farthest accession from the centroid was G2, G3, G8, G9, G12 and G13 whereas other accessions were near to centroid. The proportion of variation for principal component (PC1) and (PC2) were 45.88% and 10.64% respectively, in which the first principal component occupied the topmost position of the total variation existed (Table 10).

3.7. Valuation of Shannon-Weaver diversity (H' Index)

The Shannon-Weaver diversity index was used to assess the phenotypic diversity for each trait. The estimation of the Shannon-Weaver diversity index (H) and Evenness (E_H) for the twenty-seven traits shown in Table 10. The Shannon–Weaver diversity index ranged from 2.57 for dry seed weight per plant to 2.71 for plant height, maturity date and shelling percent including the traits like fifty percent flowering date, nodes number per stem, internode length, pod width, seed length and seed width which indicated that maximum diversity ($H = 1.70$) was present among these traits. The equitability or evenness was found varied from 0.95 to 1.00. Similarly, maximum ($E_H = 1.00$) values of evenness was marked for the traits like fifty percent flowering date, maturity date, plant height, nodes number per stem, internode length, pod width, seed width, shelling percent whereas minimum ($E_H = 0.95$) was for biomass dry weight, dry pod weight, dry seed weight, yield kgha^{-1} .

164 Table 10: Eigenvectors and values for the first six principal component axes for 27 agronomic traits associated Bambara groundnut accessions

Characters	Eigenvectors								
	PC1	PC2	PC3	PC4	PC5	PC6			
Eigenvalue	12.39	2.87	2.37	2.21	1.82	1.54			
Proportion of Variance (%)	45.88	10.64	8.78	8.19	6.75	5.69			
Cumulative Proportion of Variance (%)	45.88	56.51	65.29	73.48	80.24	85.93	H index (H)	H _{max} = ln(N)	Evenness (E _H) = H/H _{max}
DTE	-0.003	-0.214	-0.072	-0.044	-0.407	0.579	2.69	2.71	0.99
D50%F	-0.141	0.093	-0.021	0.11	0.479	0.009	2.70	2.71	1.00
DTM	-0.189	-0.062	-0.086	-0.243	0.077	0.350	2.71	2.71	1.00
PH	0.151	0.205	0.31	-0.256	-0.193	-0.135	2.71	2.71	1.00
NB	0.165	-0.181	0.299	-0.022	-0.194	-0.249	2.67	2.71	0.99
NS	0.165	-0.234	-0.017	0.376	-0.171	-0.060	2.69	2.71	0.99
NP	-0.073	0.379	0.287	0.278	-0.091	0.270	2.67	2.71	0.99
NL	-0.073	0.379	0.287	0.278	-0.091	0.270	2.67	2.71	0.99
NNS	0.146	0.002	0.273	-0.318	-0.222	0.101	2.70	2.71	1.00
IL	0.055	0.111	0.472	-0.217	0.079	-0.117	2.70	2.71	1.00
BFW	0.178	-0.271	0.215	-0.028	0.37	0.053	2.62	2.71	0.97
BDW	0.193	-0.183	0.193	0.042	0.334	0.230	2.58	2.71	0.95
TNP	0.271	-0.033	-0.084	-0.092	-0.075	-0.076	2.69	2.71	0.99
NMP	0.269	-0.056	-0.032	0.026	-0.095	-0.150	2.68	2.71	0.99
NIP	0.085	0.058	-0.178	-0.377	0.036	0.195	2.68	2.71	0.99
FPW	0.244	0.157	-0.007	-0.056	0.059	0.087	2.62	2.71	0.97
DPW	0.254	0.201	-0.072	0.05	0.148	0.043	2.58	2.71	0.95
PL	0.186	-0.012	-0.214	-0.087	-0.03	0.055	2.68	2.71	0.99
PW	0.229	0.088	-0.064	-0.049	0.031	0.198	2.70	2.71	1.00
NSP	0.271	-0.033	-0.084	-0.092	-0.075	-0.076	2.69	2.71	0.99
DSW	0.257	0.176	-0.068	0.09	0.143	0.050	2.57	2.71	0.95
SL	0.256	0.067	-0.058	-0.018	-0.045	0.188	2.70	2.71	1.00
SW	0.212	-0.05	0.13	0.05	0.13	0.056	2.70	2.71	1.00
HSW	0.246	-0.013	-0.165	0.171	0.036	0.088	2.69	2.71	0.99
Shel%	0.144	-0.215	0.079	0.444	-0.182	0.015	2.71	2.71	1.00
HI	0.052	0.447	-0.302	0.024	-0.175	-0.242	2.68	2.71	0.99
Yld	0.254	0.201	-0.072	0.05	0.148	0.043	2.58	2.71	0.95

165 Legend: Days to emergence = DTE (d), Days to 50% flowering = D50%F (d), Days to maturity = DTM (d), Plant height (cm) = PH, Number of branches per plant = NB, Number of stems per plant = NS, Number of
166 petioles per plant = NP, Number of leaves per plant = NL, No. of nodes per stem=NNS, Inter nodes length = IL (cm), Biomass fresh weight per plant = BFW(g), Biomass dry weight per plant = BDW(g), Total no. of
167 pods per plant = TNP, Number of mature pods per plant = NMP, Number of Immature pods per plant = NIP, Fresh pods weight = FPW(g), Dry pods weight = DPW(g), Pod length = PL(mm), PW = PW (mm), No. of
168 seeds per plant = NSP, Dry seed weight per plant = DSW(g), Seed length = SL(mm), Seed width =SW (mm), Hundred seed weight = HSW(g), Shelling percent = Shel%, Harvest index = HI (%) and Yield (Kgha⁻¹) =
169 Yld

4. Discussion

4.1. Qualitative disparity

The existence of a significant qualitative variation was found for all the qualitative traits, supported by Gbaguidi *et al.* [46] he found significant variation among all the qualitative traits. We recorded three types of growth habit and similar observation were noticed by Ntundu *et al.* [1] in Tanzania and Azam-Ali *et al.* [47] in Cameroon. We categorized the vegetative growth of Bambara groundnut namely; bunches type, semi bunches type and spreading type which is matched by the result of Doku [48] and highly significant difference among the qualitative trait was noted by Egbadzor *et al.* [49].

4.2. Quantitative traits

The estimated 27 quantitative traits showed a massive genetic variation and similar variation was confirmed by Ntundu *et al.* [1] and Aliyu *et al.* [50] in *Vigna subterranean* (L.) Verdc and the cowpea (*Vigna unguiculata* L) [51]. The estimated high coefficients of variation (CV) in our study is the indication of vast scale of heterogeneity confirmed by Goli *et al.* [52] in Bambara groundnut. We found D50%F close to 39 days but [53] noticed close to 68 days in Ghana. The indeterminate [54] nature of flower bearing make it vital issue for adjustment mechanism to an environment [55]. The inconsistency of flowering time was reported by [52] from 38 to 68 days; Massawe *et al.* [10] from 64 to 76 days; Masindeni [56] reported 43-80 days and Ouedraogo *et al.* [8] from 32 to 53 days. Several climatic issues photoperiod, temperature, altitude and soil structure as well as genotypic nature is responsible to bearing flower in Bambara groundnut [24] and reported flowering happened between 36 to 53 days. In our study, genotype G1, G2, G3, G8, G9 and G10 identified as early flowering lines; early flowering ensures early maturity [57]. A significant difference ($P \leq 0.01$) was recorded for maturity (119.67 to 141.33) days is supported by Goli *et al.* [52] and Masindeni [56] and due to diverse cultivar along with multi-environmental factors maturation time varied from 90 to 180 days [58]. Plant height had no significant variation, supported by Ntundu *et al.* [1] in Tanzania and Shegro *et al.* [24] in south Africa. The yield and yield related traits like TNP, NSP, FPW, DPW, DSW, PL, PW, NMP, NIP and HSW showed high genetic discrepancy, similar variation stated by Shegro *et al.* [24] with a recommendation of variation happened due to effect of genotype by environment interaction Bambara yield. Hundred seed weight varied from 177.52g to 360.15g, is a vital factor for the measurement of morphological traits linked to yield ([1]; [8]; [10]; [56]; [53]; [59]) it also influence the yield directly. The yield of Bambara groundnut was recorded from 146.6 to 2678.6 kg ha^{-1} by Gbaguidi *et al.* [46]; average 703.3 kg ha^{-1} by FAO [19]; 1058.8 kg ha^{-1} by Dansi *et al.* [60] in west Africa whereas we calculated from 588.98 to 2991.77 kg ha^{-1} . Typically, FAO [19] estimated average yield Bambara groundnut is lower than our estimated yield 1180 kg ha^{-1} .

4.3. Correlation coefficient

In plant breeding correlation matrix is a prominent approach for the judgement of degree of the association between two or more variables, is supported by Mohammed [53]. For superior genotype's selection programme consideration of correlation matrix can be a great scale of measurement [61]. Strong and positive significant correlation for total number of pods (TNP) was identified with the traits NMP, DPW, NSP, DSW and Yield this result is consistent with the study of Karikari [42] and Jonah *et al.* [63]. We got moderate and positively high significant association of plant height (PH) with TNP, NMP, FPW and yield can be proposed the selection based on these traits may be beneficial for yield enhancement of this crop as well as fodder production for animal feeding. Similar recommendation was stated by Mohammed [53] in Cote d'Ivoire and [64] in Cameroon.

4.4. Genetic components

For the selection program variation presents among the traits was taken into consideration which depends on the degree of heritability. To know the projected gain from selection, valuation of genetic advance with heritability can be a significant approach of crop improvement. Various research findings reported that the selection may be effective for a specific trait improvement using available genetic variation with the degree of heritability [25], [65]. Consideration of both heritability and genetic advance is more effective over the uniquely use of heritability [66,67]. Like the previous reporters Adebola *et al.* [68] findings, we disclose higher phenotypic variance values than genotypic variance for all traits, indicates the trait expression govern by the environment. The obtained GCV and PCV value was categorized based on the suggested index of 0%-10% for low, 10-20% for moderate and $\geq 20\%$ for high variation [31-33,69]. Intermediate to strong genetic advance with heritability was found for all yield related traits except seed width and shelling% is the indication of the traits have significant potential in the selection process due to low environmental influences, supported by Meena *et al.* [70] and Oladosu *et al.* [34]. The improvement of the traits with low heritability and genetic advance can be boost over heterosis breeding this is supported by Bijalwan & Madhvi [71]. The value of relative differences between GCV and PCV had higher for the trait plant height, seed width, days to 50% flowering, and seed length is the sign of higher environmental effect and the improvement of these traits are tough via direct selection whereas the trait with lower difference is the symbol of lower influence by the environment which may give desirable strong and significant output in crop improvement program, is supported by Umar *et al.* [25] and Usman *et al.* [35]. Direct selection can be effective considering the traits having low relative differences [72]. Considering the heritability and genetic advance index [37, 38] like as more than 60% for high, 30-60% for moderate, and 0-30% for low, we found the traits BFW (Hb = 97.68% GA = 88.82%), BDW(Hb = 89.91% GA = 106.66%), FPW (Hb = 99.55% GA = 93.54%), DPW(Hb = 98.10% GA = 113.94%), DSW (Hb

= 98.42% GA = 122.01%) and yield (Hb = 98.10% GA = 113.94%) were highly heritable together with high genetic advance value, recommended that for crop improvement direct selection can be effective based on these traits with effect of additive genes; similar findings documented by the previous researchers [65, 73]. Low to moderate heritability and genetic advance values may hindrance in the trait's betterment due to high environmental effects over the genetic effects on its stated by Ridzuan [74]. So, only an effective selection can be gained picking the traits with higher GCV, PCV, HB, and GA meaning that effect of additive genes is sufficiently robust than environmental effect [35].

4.5. Clustering patterns

Five clusters were constructed based on the 27 quantitative traits at 1.16 of the distant that indicates a degree of diversity among the genotypes. The cluster V considered as potential group of genotypes for the crop betterment associated with high yielding capacity. The findings of previous researchers [26, 46, 75, 76] stated that they constructed same type of cluster and found significant variation regarding morphological traits in Bambara groundnut. The study of Unigwe *et al.* [26] explored the four distinct groups of Bambara groundnut genotypes in south Africa using UPGMA model. The timing of flowering duration is a motivational factor for the final yield also play a positive role to the best yield of the group and selection could be effective from this class noted by Tourél *et al.* [77]. Flowering in Bambara groundnut is indeterminate up harvesting stage explained by Kumaga *et al.* [78]. However, early flowering has been considered as a well agronomic trait of crops to quick maturity, uniform yield as well as generally crop production [78] thus, accessions that have early flowering criteria should be treated as best to production of Bambara groundnut [79]. The groups achieved from the cluster analysis of quantitative characteristics illustrate the performances of Bambara groundnut accession cultivated in Benin would be the future guideline for this crop improvement [80, 81]. The clustering and characterization of accessions considering their agro-morphological traits and genetic similarity would be the crucial issue to identification and selection of the best parents for hybridisation [82]. Additionally, cluster IV produced 70.05% higher mean yield than the average grand mean yield of 1180 kg ha⁻¹ while the other groups gave lower yield and this finding were supported by Onwubiko *et al.* [73]. Therefore, current research represents significant information to the plant breeders based on their similarity and grouping of accessions through univariate and multivariate methods.

4.6. Principal Component Analysis.

The principal component analysis (PCA) is the re-validation instrument of cluster analysis. To estimate the total variation, exist in a set of characters, PCA is effective noted by Johnson [41].

The first axes (PC1) elucidate utmost portion of total variation in any PCA [83]. In our findings first principal component (PC1) accounted more proportion of variation (45.88%) than PC2 (10.68%). Similar result was identified by Mohammed *et al.* [84] of total variation at 19% (PC1) and 14% (PC2) in Bambara groundnut. The results of several researchers like Usman *et al.* [35], Farhad *et al.* [85] & Maqbool *et al.* [86] supported our findings. Shegro *et al.* [24] grouped the 20 Bambara groundnut accessions by PCA analysis using quantitative traits. For yield improvement the selection PC1 was revealed as the most powerful criterion concluded by the work of Adéoti *et al.* [87] and Mih *et al.* [88]. In my research total pod numbers, mature pods number, seed number, dry seed weight and yield kg/ha occupied high values in PC1. This finding supported by Stoilova & Pereira [81] described that the most significant components for yield are the pods number and seeds number per plant. The cluster analysis together with principal component analysis explored the common association among landraces in terms of seed yield and related agronomic traits.

4.7. Shannon diversity index (H) and Evenness (E)

Shannon's diversity index (H) is another index that is generally used to categorize the species diversity in a certain community. Shannon's diversity index is an account for both richness and evenness present in the species also used for a wide diversity of fields. The estimated H' Index varied from 2.57 for dry seed weight per plant to 2.71 for plant height, maturity date and shelling percent among the phenotypic traits. In our study the observed diversity index value was more than 2.50 for most of the traits evaluated. Olukolu *et al.* [80] reported H' Index of nineteen qualitative traits (0.1 to 0.15) and twenty-eight numerical traits (0.09 to 0.16) of Bambara groundnut that supported our findings. Bonny *et al.* [76] evaluated the diversity in qualitative traits of Bambara groundnut landraces of similar findings with our result.

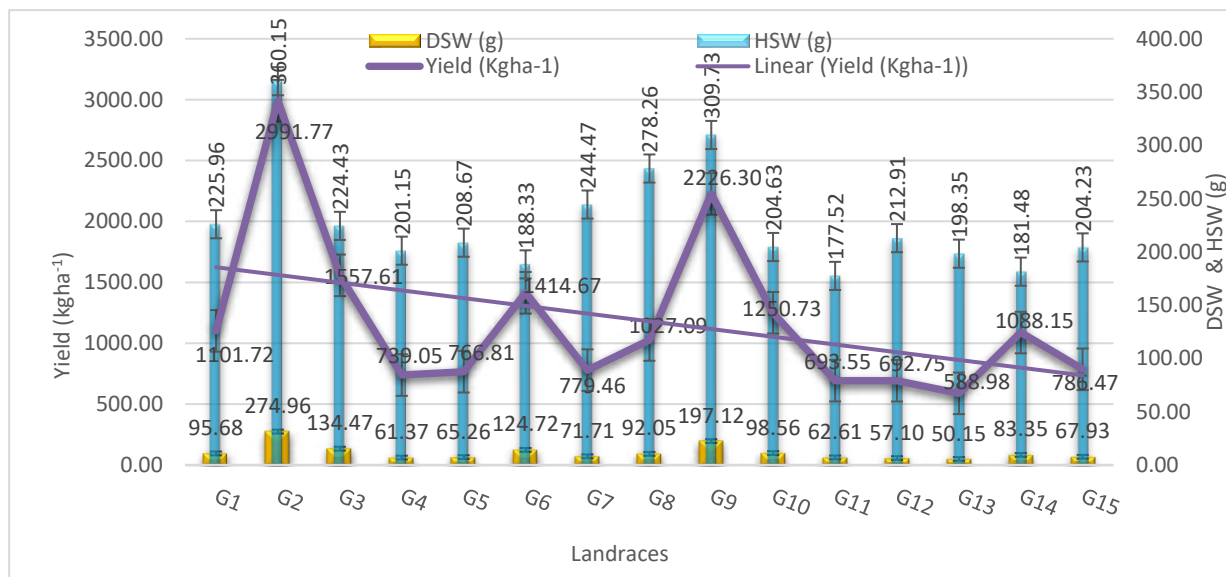


Figure 2: Graphical relationship of dry seed weight (DSW) and hundred seed weight (HSW) with yield (kg ha^{-1}) for Bambara groundnut landraces

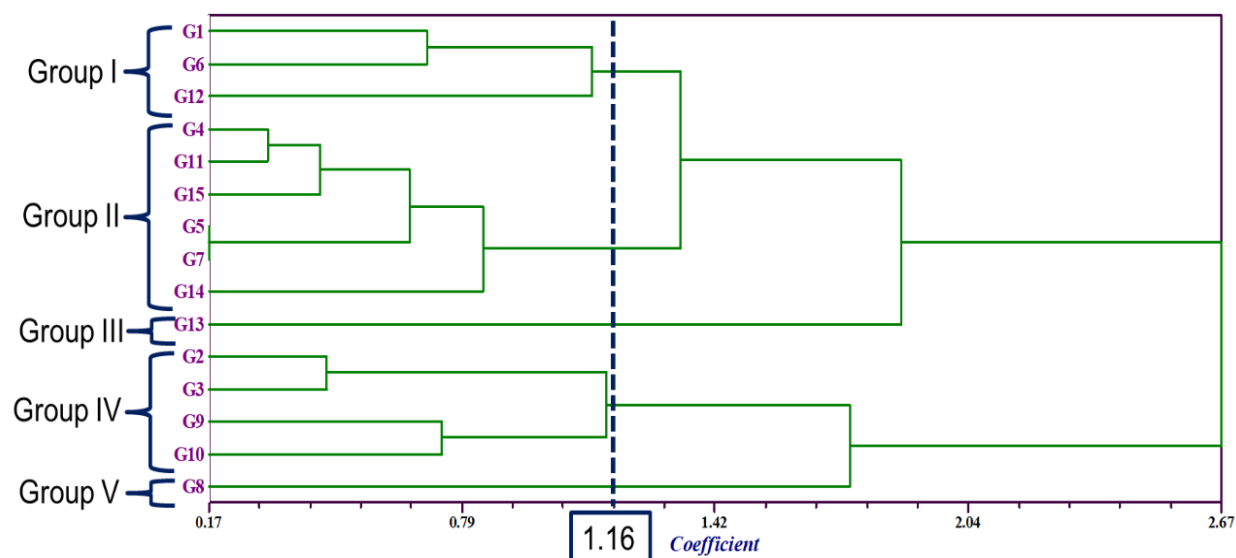


Figure 3: Dendrogram showing the relationship among the Bambara groundnut landraces revealed by UPGMA method

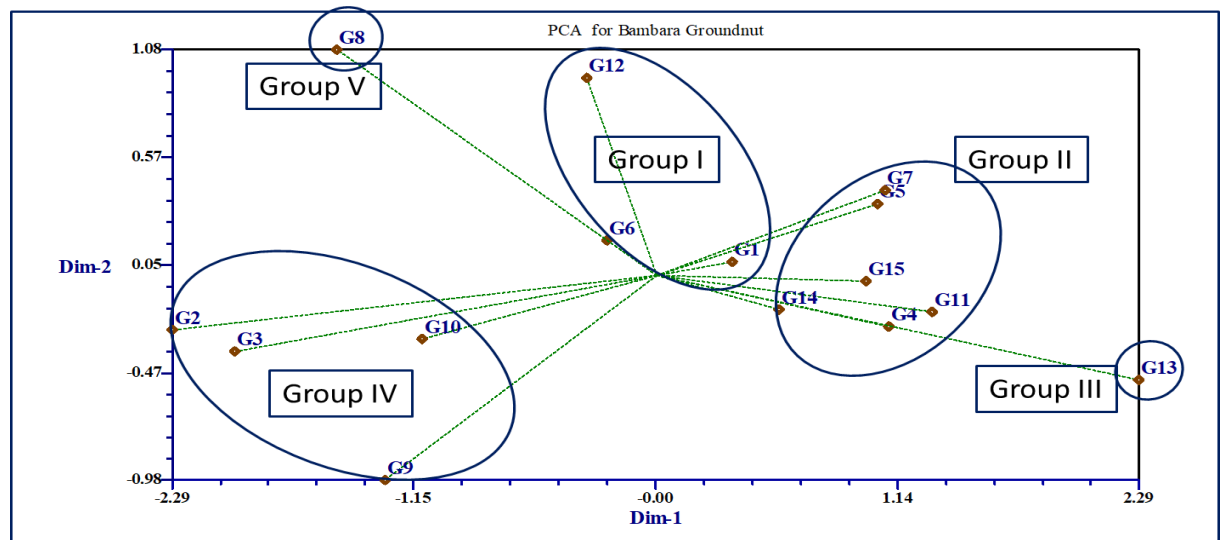


Figure 4: PCA - 2D graphical relationship among the Bambara groundnut accessions

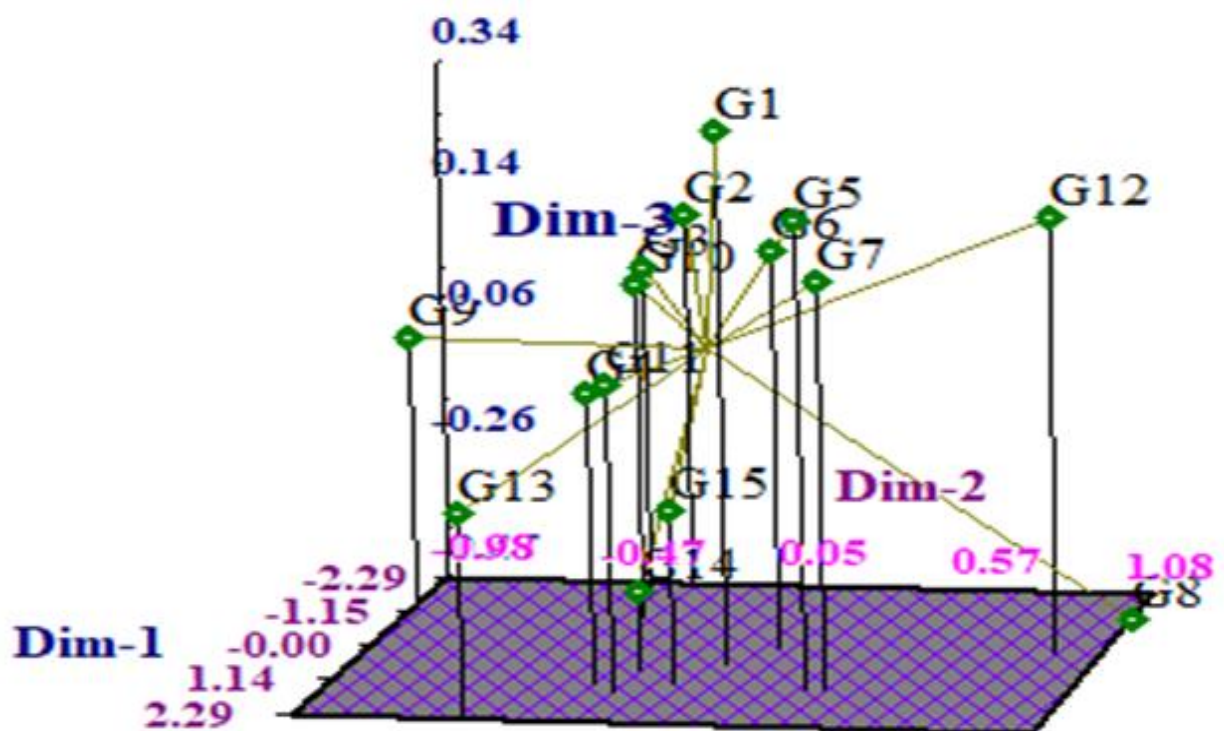


Figure 5: PCA -3D graphical relationship among Bambara groundnut accessions

5. Conclusion

From the present study finally an evident can be established that the enhancement of *Vigna subterranea* (L.) Verdc yield and its related traits can be gained via selection with the valuation of different genetic parameters analysis like GCV, PCV, HB, and GA. Based on the recorded data it can be stated that a considerable degree of variation exists in almost all the agronomic traits evaluated in this study. Moreover, this study also fixed a faultless association between the agronomic traits and grain yield. More than 20% PCV and GCV values were estimated for all traits excluding the traits like TNP, PW, NSP, SL, SW, and shell% besides this, the six traits like DSW, DPW, FPW, BDW, BFW, and Yield performed high ($\geq 20\%$) genetic advance (as percentage mean) with high heritable values. Additionally, it was declared that the landraces were diverse and depending on the similarity issues landraces are grouped into five clusters. Moderate to perfect significant association was noted between the yield and its related traits. The landraces G2, G3, G8 and G9 identified as high yielding promising lines and suggested that further research can be conducted to gain the homogeneity by providing emphasis on this potentially high yielding lines, following conventional breeding together with molecular approaches.

Acknowledgments and Funding

The author is thankful to the Ministry of Agriculture (MoA), Bangladesh Agricultural Research Council (BARC), Bangladesh Agricultural Research Institute (BARI) of the People's Republic of Bangladesh for adequate funding and other support through the Project of NATP Phase-II. The authors are grateful to all staff of ITAFoS, University Putra Malaysia, (UPM). Malaysia.aa

Author's contribution

The concept, design and methods of the paper were constructed by M.M.H.K.; M.Y.R.; M.J. and S.I.R. Data collection was carried out by M.M.H.K. Statistical analysis software and interpretation were undertaken by M.M.H.K., M.Y.R. and M.J. Writing—original draft preparation of the manuscript was carried out by M.M.H.K. Supervision by M.Y.R. Investigation by S.I.R. and M.J. Writing—review and editing by M.M.H.K. & M.M. All authors have read and agreed to the published version of the manuscript.

Conflict of Interests

The authors declare no conflict of interests.

References

- [1] Ntundu, W.; Shillah, S.; Marandu, W.; Christiansen, J.L. Morphological diversity of Bambara groundnut (*Vigna subterranea* [L.] Verdc.) landraces in Tanzania. *Genetic Resources and Crop Evolution*, **2006**, 53, 367-378.
- [2] Ahmad, N. Bambara groundnut, the crop for the new millennium: Molecular Techniques to Improve the Resiliency of Bambara Groundnut, Lamber Academic publishers, **2012**.
- [3] Verdcourt, B. The correct name for the Bambara groundnut, Kew Bulletin, Springer on behalf of Royal Botanic Gardens, Kew , **1980**, Vol.35 No.3 pp.474 ref.3, DOI : 10.2307/4110016.
- [4] Heller, J.; Begemann, F.; Mushonga, J. (Editors). Bambara groundnut *Vigna subterranea* (L.) Verdc. Promoting the conservation and use of underutilized and neglected crops. In Proceedings of the Workshop on Conservation and Improvement of Bambara Groundnut (*Vigna subterranea* (L.) Verdc.), 14–16 November 1995, Harare, Zimbabwe. Institute of Plant Genetics and Crop Plant Research, Gatersleben/Department of Research & Specialist Services, Harare/International Plant Genetic Resources Institute, Rome, Italy, **1995**, p.166.
- [5] Howell, J. A.; Eshbaugh, W. H.; Guttman, S.; Rabakonandrianina, E. Common names given to bambara groundnut (*Vigna subterranea*; *Fabaceae*) in Central Madagascar. *Economic Botany*, Springer on behalf of New York Botanical Garden Press, **1994**, 48, 217-221.
- [6] Linnemann, A. R. Bambara groundnut (*Vigna subterranea*) literature: a revised and updated bibliography. Tropical Crops Communication 7. Department of Tropical Crop Science, Wageningen Agricultural University, Netherlands, **1992**, pp.124.
- [7] Holm, J.N.; Marloth, B.W. The Bambara groundnut or njugo bean. *Farming in South Africa*, **1940**, Pamphlet No. 215, pp.195-198.
- [8] Ouedraogo, M.; Ouedraogo, J. T.; Tignere, J. B.; Bilma, D.; Dabire, C. B.; Konate, G. Characterization and evaluation of accessions of Bambara groundnut (*Vigna subterranea* (L.) Verdcourt) from Burkina Faso. *Sciences & Nature*, **2008**, 5(2), 191-197.
- [9] Amarteifio, J.O.; Tibe et. O.; Njogu R. M. The mineral composition of Bambara groundnut (*Vigna subterranea* (L.) Verdc) grown in Southern Africa. *African Journal of Biotechnology*, **2006**, 5, 2408-2411.
- [10] Massawe, F. J.; Mwale, S. S.; Roberts, J. A. Breeding in bambara groundnut (*Vigna subterranea* (L.) Verdc.): strategic considerations. *Afr J Biotechnol*, **2005**, 4, 463–471.
- [11] Singh, B. B.; Chambliss, O. L.; Sharma B. Recent advances in cowpea breeding. In: Singh B., B., Mohan Raj D., R., Dashiell, K., E., Jackai LEN (eds) Advances in cowpea research, Co publication of International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria and Japan International Research Centre for Agricultural Sciences (JIRCAS), Sayce Publishing, Devon, **1997**, 114–128.
- [12] Okpuzor, J.; Ogbunugafor, H.A.; Okafor, U.; Sofidiya, M.O. Identification of protein types in Bambara nut seeds: Perspectives for dietary protein supply in developing countries. *EXCLI Journal*, **2010**, 9, 17-28.

- [13] Heller J., Begemann F., et. al. & Mushonga J. Bambara groundnut *Vigna subterranean* (L.) Verdc. Conservation and improvement of Bambara groundnut (*Vigna subterranea* (L.) Verdc.). Harare, Zimbabwe: International Plant Genetic Resources Institute. pp 166, (1997).
- [14] Brink, M.; Ramolemana, G.M. et. al.; Sibuga K.P. *Vigna subterranean* (L.) Verde in Brink. M. & Belay. G. (éditeurs) PROTAI cereals and pulses/cereals et legumes secs. (CD-Room). *PROTA*, Wageningen, Pays Bas, **2006**.
- [15] Rungnoi, O.; Suwanprasert, J.; Somta, P.; Srinives, P. Molecular Genetic Diversity of Bambara Groundnut (*Vigna subterranea* L. Verdc.) Revealed by RAPD and ISSR marker Analysis. *Journal of Breeding and Genetics*, **2012**, 44, 87-10.
- [16] Ng, N.Q.; Osunmakinwa, A. A.; Begemann, F.; Goli, A. E. Germplasm maintenance/ preservation, characterization and documentation. GRU Annual Report, International Institute of Tropical Agriculture (IITA), Genetic Resources Unit, Ibadan, Nigeria., **1985**, pp.11-21.
- [17] Ntundu W.H.; Bach I.C.; Christiansen J.L.; Andersen S.B. Analysis of genetic diversity in Bambara groundnut (*Vigna subterranea* (L.) Verdc) landraces using amplified fragment length polymorphism (AFLP) markers. *African Journal of Biotechnology*, **2004**, 3, 220-225.
- [18] Sesay, A.; Kunene, I.S.; Earnshaw, D.M. Bambara groundnut (*Vigna subterranea*) cultivation in Swaziland. Report of a farmer's survey. Department of Biological Sciences, University of Swaziland, Kwaluseni, **1999**.
- [19] FAOSTAT, <http://www.fao.org/faostat/en/#data/QC>, **2017**.
- [20] Azam–Ali, S. N.; Aguilar-Manjarrez, J.; Bannayan-Avval, M. A. Global Mapping System for Bambara Groundnut Production. FAO Agricultural Information Management Series No.1, **2001** (Accessed 13th January 2017).
- [21] Anchirinah, V. M.; Yiridoe, E.K.; Bennett-Lartey, S.O. Enhancing sustainable production and genetic resource conservation of bambara groundnut: a survey of indigenous agricultural knowledge systems. *Outlook on AGRICULTURE*, **2001**, 30(4), 281-288.
- [22] Lacroix, B.; Assoumou, Y.; Sangwan, R.S. Efficient in vitro direct shoot organogenesis and regeneration of fertile plants from embryo explants of Bambara groundnut (*Vigna subterranea* L. Verdc.). *Plant cell reports*, **2003**, 21(12), 1153-1158.
- [23] Ayana, A.; Bekele, E. Geographical patterns of morphological variation in sorghum (*Sorghum bicolor* (L.) Moench) germplasm from Ethiopia and Eritrea: Quantitative characters. *Euphytica*, **2000**, 115, 91-104. <http://dx.doi.org/10.1023/A:1003998313302>.
- [24] Shegro, A. G.; Jansen Van Rensburg, W. S.; Adebola, P. O. Assessment of genetic variability in Bambara groundnut (*Vigna subterranea* [L.] Verdc.) using morphological quantitative traits. *Academia Journal of Agricultural Research*, **2013**, 1, 45-51.
- [25] Umar, U.U.; Ado, S.G.; Aba, D.A.; Bugaje, S.M. Genetic variability and heritability studies in maize (*Zea mays* L.) genotypes under three irrigation regimes. 38th Annual Conference of Genetic Society of Nigeria, 19th-23rd October 2014. Edo State, Nigeria., **2014**, pp. 381-386.

- [26] Unigwe, A. E.; Gerrano, A. S.; Adebola, P.; Pillay, M.; Monrovia, L. Morphological variation in selected accessions of Bambara groundnut (*Vigna subterranea* L. Verdc) in South Africa. *Journal of Agricultural Science*, **2016**, 8(11), 69-80.
- [27] Lestari, S. A. D. A. D.; Melati, M.; Purnamawati, H. Penentuan dosis optimum pemupukan n, p, dan k pada tanaman kacang Bogor [*Vigna subterranea* (L.) Verdcourt]. *Jurnal Agronomi Indonesia (Indonesian Journal of Agronomy)*, **2015**, 43(3), 193-200.
- [28] IPGRI, IITA, BAMNET. Descriptors for Bambara groundnut (*Vigna subterranea*). International Plant Genetic Resources Institute, Rome, Italy; International Institute of Tropical Agriculture, Ibadan, Nigeria. *The International Bambara Groundnut Network, Germany*, **2000**, 57.
- [29] Pearson, K. Correlation coefficient. In *Royal Society Proceedings*, **1895**, Vol. 58, P. 214.
- [30] Singh, R.K.; Choudhary, B.D. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani, New Delhi, **1985**.
- [31] Shabanimofrad, M.; Rafii, M.Y.; Wahab, P.M.; Biabani, A.R.; Latif, M.A. Phenotypic, genotypic and genetic divergence found in 48 newly collected Malaysian accessions of *Jatropha curcas* L. *Industrial Crops and Products*, 2013, 42, 543-551.
- [32] Sohrabi, M.; Rafii, M.Y.; Hanafi, MM.; Siti Nor Akmar, A.; Latif, M.A. Genetic diversity of upland rice germplasm in Malaysia based on quantitative traits. *The Scientific World Journal*, 2012. Article ID 416291, <https://doi.org/10.1100/2012/416291>
- [33] Robinson, H.F.; Comstock, R.E.; Harvey, P.H. Genotypic and phenotypic correlation in corn and their implications in selection. *Agronomy Journal*, 1951, 43(6), 282-287.
- [34] Oladosu, Y.; Rafii, M.Y.; Abdullah, N.; Abdul Malek, M.; Rahim, H.A.; Hussin, G. *et al.*; Genetic variability and selection criteria in rice mutant lines as revealed by quantitative traits. *Sci World J*, **2014**, 1-12.
- [35] Usman, M.G.; Rafii, M.Y.; Ismail, M.R.; Malek, M.A.; Abdul, L.M. Heritability and genetic advance among chili pepper genotypes for heat tolerance and morphophysiological characteristics. *Sci World J*, **2014**, 1-14.
- [36] Falconer, D. S. *Introduction to Quantitative Genetics*, Longman, **1981**.
- [37] Johnson, H.W.; Robinson, H.F.; Comstock, R.E. Estimation of genetic and environmental variability in soybeans. *Agron J*, **1955**, 47, 314-318.
- [38] Assefa, K.; Ketema, S.; Tefera, H.; Nguyen, H.T.; Blum, A.; Ayele, M. *et al.*, Diversity among ermplasm lines of the Ethiopian cereal tef *Eragrostis tef* (Zucc.) Trotter]. *Euphytica*, **1999**, 106, 87-97.
- [39] Juangsamoot, J.; Ruangviriyachai, C.; Techawongstien, S.; Chanthai, S. Determination of psaicin and dihydrocapsaicin in some hot chilli varieties by RP-HPLC-PDA after magnetic stirring extraction and clean up with C18 cartridge. *Int Food Res J*. **2012**, 19, 1217-1226.

- [40] Adewale, B.D.; Kehinde, O.B.; Popoola, J.O.; Aremu, C.O. Seed metrics of genetic and shape determination in Africa Yam Bean [Fabaceae] (*Sphenostylis stenocarpa* Hochst Ex. A. Rich) harms. *Afr. J. Plant Sci.*, **2010**, 4, 107-115.
- [41] Johnson, D. E. Applied Multivariate Methods for Data Analysis, **1998**, 26– 27.
- [42] NTSYS-pc, N. T.; Taxonomy, N. Multivariate Analysis System, version 2.2. *Exeter Software: Setauket, NY, USA*, **2005**.
- [43] Weaver, W.; Shannon, C.E. "The Mathematical Theory of Communication," Urbana, Illinois: *University of Illinois*, **1949**.
- [44] Shannon, C.E. "A mathematical theory of communication," *Bell System Technical Journal*, 1948, 27, 379–423 & 623–656.
- [45] Hennink, S.; Zeven, A.C. The interpretation of Nei and Shannon- Weaver within population variation indices. *Euphytica*, **1991**, 51(3), 235-240.
- [46] Gbaguidi, A. A.; Dansi, A.; Dossou-Aminon, I.; Gbemavo, D. S. J. C.; Orobiyi, A.; Sanoussi, F.; Yedomonhan, H. Agromorphological diversity of local Bambara groundnut (*Vigna subterranea* (L.) Verdc.) collected in Benin. *Genetic resources and crop evolution*, **2018**, 65(4), 1159-1171.
- [47] Azam-Ali, S. N.; Sesay, A.; Karikari, K. S.; Massawe, F. J.; Aguilar-Manjarrez, J.; Bannayan, M.; Hampson, K. J. Assessing the potential of an underutilized crop - a case study using bambara groundnut. *Exp. Agric.*, 2001, 37, pp. 433–472.
- [48] Doku, E.V. Growth habit and pod production in bambara groundnut (*Voandzeia subterranea*). *Ghana Journal of Agricultural Science*, **1969**, 2(2), 91-95.
- [49] Egbadzor, K.F.; Danquah, E.Y.; Ofori, K.; Yeboah, M.; Offei, S.K. Diversity in 118 cowpea [*Vigna unguiculata* (L.) Walp] Accessions assessed with 16 Morphological Traits. *International Journal of Plant Breeding and Genetics*, **2014**, 8(1),13-24.
- [50] Aliyu, S.; Massawe, F.; Mayes, S. Genetic diversity and population structure of Bambara groundnut (*Vigna subterranea* (L.) Verdc.): synopsis of the past two decades of analysis and implications for crop improvement programmes. *Genet Resour Crop Evol*, 2016, 63, 925–943. <https://doi.org/10.1007/s10722-016-0406-z>.
- [51] Gbaguidi, A.A.; Assogba, P.; Dansi, M.; Yedomonhan, H.; Dansi, A. Caracte´risation agromorphologique des varie´te´s de nie´be´ cultive´es au Be´nin. *Int J Biol Chem Sci*, **2015**, 729(2), 1050–1066.
- [52] Goli, A. E.; Begemann, F.; Ng, N. Q. Characterization and evaluation of IITA's Bambara groundnut collection. In J. B. F. Heller, & J. Mushonga (Eds.), Conservation and improvement of Bambara groundnut (*Vigna subterranea* (L.) Verdc.) (pp. 101-118). International Plant Genetic Resources Institute, 1997.
- [53] Mohammed, M. S. Pre-breeding of Bambara Groundnut (*Vigna subterranea* [L.] Verdc.) (Doctoral dissertation). University of KwaZulu-Natal, Durban, South Africa, 2014.

- [54] Dimakatso, R.M. Evaluation of Bambara groundnut (*Vigna subterranea*) for yield stability and yield related characteristics. Thesis M.Sc. Agric. degree in the Faculty of Natural and Agricultural Sciences, **2006**.
- [55] Ndiang, Z.; Bell, J.M.; Missoup, A.D.; Fokam, P.E.; Amougou, A. Etude de la variabilité morphologique de quelques variétés de voandzou au Cameroun. *Journal of Applied Biosciences*, 2012, 60: 4394-4409.
- [56] Masindeni, D. R. Evaluation of Bambara groundnut (*Vigna subterranea*) for yield stability and yield related characteristics (Master's Thesis). University of the Free State, Bloemfontein, South Africa, 2006.
- [57] Shegro, A.G.; Atilaw A.; Pal, U.R.; Geleta N. Influence of varieties and planting date on productivity of soybean in Metekel Zone, North Western Ethiopia. *Journal of Agronomy*, **2010**, 9, 146-156, <http://dx.doi.org/10.3923/ja.2010.146.156>.
- [58] Swanevelder, C.J. *Bambara—food for Africa: Vigna subterranean bambara groundnut*. National Department of Agriculture, South Africa, **1998**.
- [59] Shegro, A.G.; Van Rensburg, J.S.; Adebola, P.O. Genetic diversity of *Amaranthus* species in South Africa. *South African Journal of Plant and Soil*, **2015**, 32, 39-46. <http://dx.doi.org/10.1080/02571862.2014.973069>.
- [60] Dansi, A.; Vodouhe, R.; Azokpota, P.; Yedomonhan, H.; Assogba, P.; Adjatin, A.; Loko, Y.L.; Dossou-Aminon, I.; Akpagana, K. Diversity of the neglected and underutilized crop species of importance in Benin. *Sci World J*, **2012**, Article ID 932947.
- [61] Adebisi, M. A.; Ariyo, O. J.; Kehinde, O. B. Variation and correlation studies in quantitative characters in Soybean. *The Ogun Journal of Agricultural Science*, 2004, 3, 134-142.
- [62] Karikari, S. K. Variability between local and exotic Bambara groundnut landraces in Botswana. *African Crop Science Journal*, 2000, 8, 145-152. <http://dx.doi.org/10.4314/acsj.v8i2.27704>.
- [63] Jonah, P. M.; Abimiku, O. E.; Adeniji, O. T. Multivariate Analysis and Character Association on the Growth and Yield of Bambara Groundnut in Mubi, Adamawa State, Nigeria. *International Journal of Management and Social Sciences Research*, 2014, 3, 2.
- [64] Ndiang, Z.; Bell, J.L.; Fokam, P.E.; Ouattara, B.; Simo, C.; Dibong, D. S. Agro-morphological variability in twelve Bambara groundnuts (*Vigna subterranea* (L.) Verdc.) accessions in Cameroon *Sciences. Technol Dev*, 2014, 16, 38–45.
- [65] Langat, C.; Ombori, O.; Leley, P.; Karanja, D.; Cheruiyot, R.; Gathaara, M., *et al.* Genetic variability of agronomic traits as potential indicators of drought tolerance in common beans (*Phaseolus vulgaris* L.). *International Journal of Agronomy*, **2019**, Article ID 2360848.
- [66] Mazid MS, Rafii MY, Hanafi MM, Rahim HA, Shabanimofrad M, Latif MA. Agro-morphological characterization and assessment of variability, heritability, genetic advance and divergence in bacterial blight resistant rice genotypes. *South African Journal of Botany*. 2013; **86**:15-22.

- [67] Asfaw, A.; Ambachew, D.; Shah, T.; Blair, M.W. Trait associations in diversity panels of the two-common bean (*Phaseolus vulgaris* L.) gene pools grown under well-watered and water-stress conditions. *Front. Plant Sci.*, 2017, 8, 733.
- [68] Malek MA, Rafii MY, Afroz SS, Nath UK, Mondal M. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. *The Scientific World Journal*. 2014; **2014**: 12. Article ID 968796 <https://dx.doi.org/10.1155/2014/968796>.
- [69] Sabri RS, Rafii MY, Ismail MR, Yusuff O, Chukwu SC, Hasan NA. Assessment of Agro-Morphologic Performance, Genetic Parameters and Clustering Pattern of Newly Developed Blast Resistant Rice Lines Tested in Four Environments. *Agronomy*. 2020; **10**(8); 1098.
- [70] Meena, M.L.; Kumar, N.; Meena, J.K.; Rai, T. Genetic variability, heritability and genetic advances in chilli, *Capsicum annuum*. *Biosci Biotechnol Res Commun*, 2016, 9, 262–266.
- [71] Bijalwan, P.; Madhvi, N. Genetic variability, heritability and genetic advance of growth and yield components of chilli (*Capsicum annuum* L.) genotypes. *Int J Sci Res*, 2013, 5, 1305–1307.
- [72] Fakuta, N.M.; Ojiekpon, I.F.; Gashua, I.B.; Ogunremi, O.C. Genetic variability, heritability and genetic advance in gum arabic (*Acacia senegal* (L) Wild) provenances, 38th Annual GSN conference, 19th -23rd October 2014. Edo State, Nigeria., 2014, 405-409.
- [73] Onwubiko, N. C.; Uguru, M. I.; Chimdi, G. O. Estimates of Genetic Parameters in Bambara Groundnut [*Vigna subterranea* (L.) Verdc.]. *Plant Breeding and Biotechnology*, 2019, 7(4), 295-301.
- [74] Ridzuan, R.; Rafii, M. Y.; Mohammad Yusoff, M.; Ismail, S. I.; Miah, G.; Usman, M.; Genetic diversity analysis of selected *Capsicum annuum* genotypes based on morphophysiological, yield characteristics and their biochemical properties. *Journal of the Science of Food and Agriculture*, 2019, 99(1), 269-280.
- [75] Sobda, G.; Wassouo, F.A.; Koubala, B.B. Assessment of twenty bambara groundnut (*Vigna subterranea* (L.) Verdcourt) landraces using quantitative morphological traits. *International Journal of Plant Research*, 2013, 3(3), 39-45.
- [76] Bonny, B. S.; Dagou, S. E. K. A.; Ajoumani, K.; Koffi, K. G.; Kouonon, L. C.; Sie, R. S. Evaluation of the diversity in qualitative traits of Bambara groundnut germplasm (*Vigna subterranea* (L.) Verdc.) of Côte d'Ivoire, 2019.
- [77] Tourél, Y.; Koné, M.; Tanoh, H.K.; Koné, D. Agromorphological and Phenological Variability of 10 Bambara Groundnut [*Vigna subterranea* (L.) Verdc. (Fabaceae)] landraces cultivated in the Ivory Coast, *TROPICULTURA*, 2012, 30(4): 216-221.
- [78] Kumaga, F.K.; Adiku, S.G.K.; Ofori, K. Effect of post-flowering water stress on dry matter and yield of three tropical grain legumes. *Int. J. Agric. Biol.*, 2003, 5: 405-407.
- [79] Onwubiko, N.I.C.; Odum, O.B.; Utazi, C.O.; Poly-Mbah, P.C. Studies on the adaptation of Bambara groundnut [*Vigna subterranea* (L.) Verdc.] in Owerri Southeastern Nigeria. *New York Science Journal*, **2011**, 4(2), 60–67.
- [80] Olukolu, B. A.; Mayes, S.; Stadler, F.; Ng, N. Q.; Fawole, I.; Dominique, D.; et al., Kole, C. Genetic diversity in Bambara groundnut (*Vigna subterranea* (L.) Verdc.) as revealed by phenotypic descriptors

and DArT marker analysis. *Genetic resources and crop evolution*, **2012**, 59(3), 347-358. DOI 10.1007/s10722-011-9686-5.

[81] Stoilova, T.; Pereira, G. Assessment of the genetic diversity in a germplasm collection of cowpea (*Vigna unguiculata* (L.) Walp.) using morphological traits, *African Journal of Agricultural Research*, 2013, 8(2), 208-215,

[82] Souza, E.; Sorrells, M. E. Relationships among 70 American oat germplasm. I. Cluster analysis using quantitative characters. *Crop Science*, 1991, 31, 599-605. <http://dx.doi.org/10.2135/cropsci1991.0011183X003100030010x>

[83] Lezzoni, F.A.; Pritts, M.P. Application of Principal components analysis to Horticulture Research. *Horticulture*, **1991**, 26(4), 334-338.

[84] Mohammed, M. S.; Shimelis, H. A.; Laing, M. D. Preliminary morphological characterization and evaluation of selected Bambara groundnut [*Vigna subterranea* (L.) Verdc.] genotypes for yield and yield related traits, **2019**, DOI: 10.18805/LR-475.

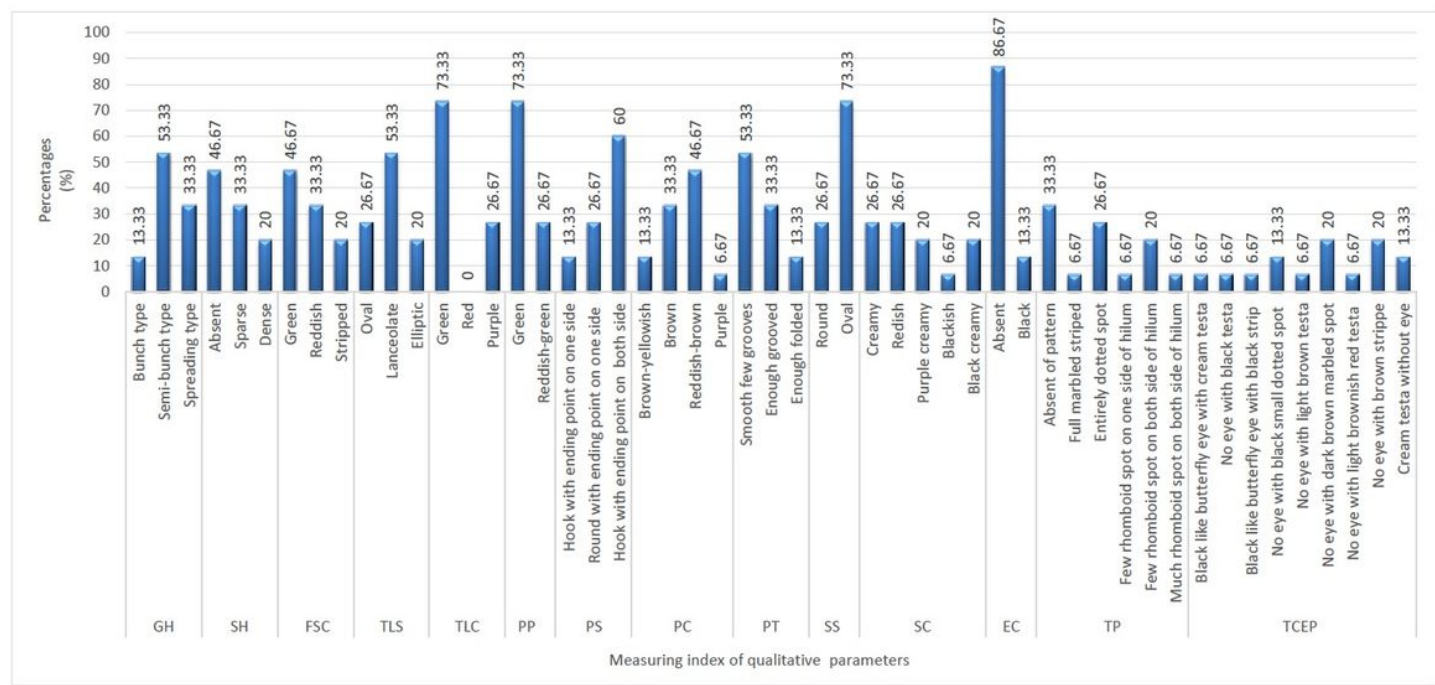
[85] Farhad, M.; Hasanuzzaman, M.; Biswas B.; Azad, A.; Arifuzzaman, M. Reliability of yield contributing characters for improving yield potential in chilli (*Capsicum annuum*), *International Journal of Sustainable Crop Production*, **2008**, 3(3), 30–38.

[86] Maqbool, R.; Sajjad, M.; Khaliq, I.; Rehman, A.; Salam, K. A.; Khan H. S. Morphological diversity and traits association in bread wheat (*Triticum aestivum* L), *American-Eurasian Journal of Agricultural & Environmental Sciences*, **2010**, 8(2), pp. 216– 224.

[87] Adéoti, K.; Dansi, A.; Ahoton, L.; Vodouhè, R.; Ahohuendo, B.C.; Rival, A A.; Sanni, A. Agromorphological characterization of *Sesamum radiatum* (Schum. and Thonn.), a neglected and underutilized species of traditional leafy vegetable of great importance in Benin. *African Journal of Agricultural Research*, 2012, 7(24), 3569-3578.

[88] Mih, A.M.; Tonjock, K.R.; Ndam, L.M. Morphological characterization of four selections of *Vernonia hynenolepis* A. Rich. (Asteraceae). *World Journal of Agricultural Sciences*, 2008, 4(2), 220-223.

Figures



Legend: GH = growth habits; SH = Stem hairiness; FSC = Color of first stem; TLS = Shape of terminal leaflet; TLC = Terminal Leaf color; PP = Petiole pigmentation; PS = Pod shape; PC = Pod color; PT = Pod texture; SS = Seed shape; SC = Seed color; EC = Eye Color; TP = Testa pattern; TCEP = Testa color with eye pattern round hilum

Figure 1

Graphical display of qualitative traits' frequency distribution of Bambara groundnut accessions

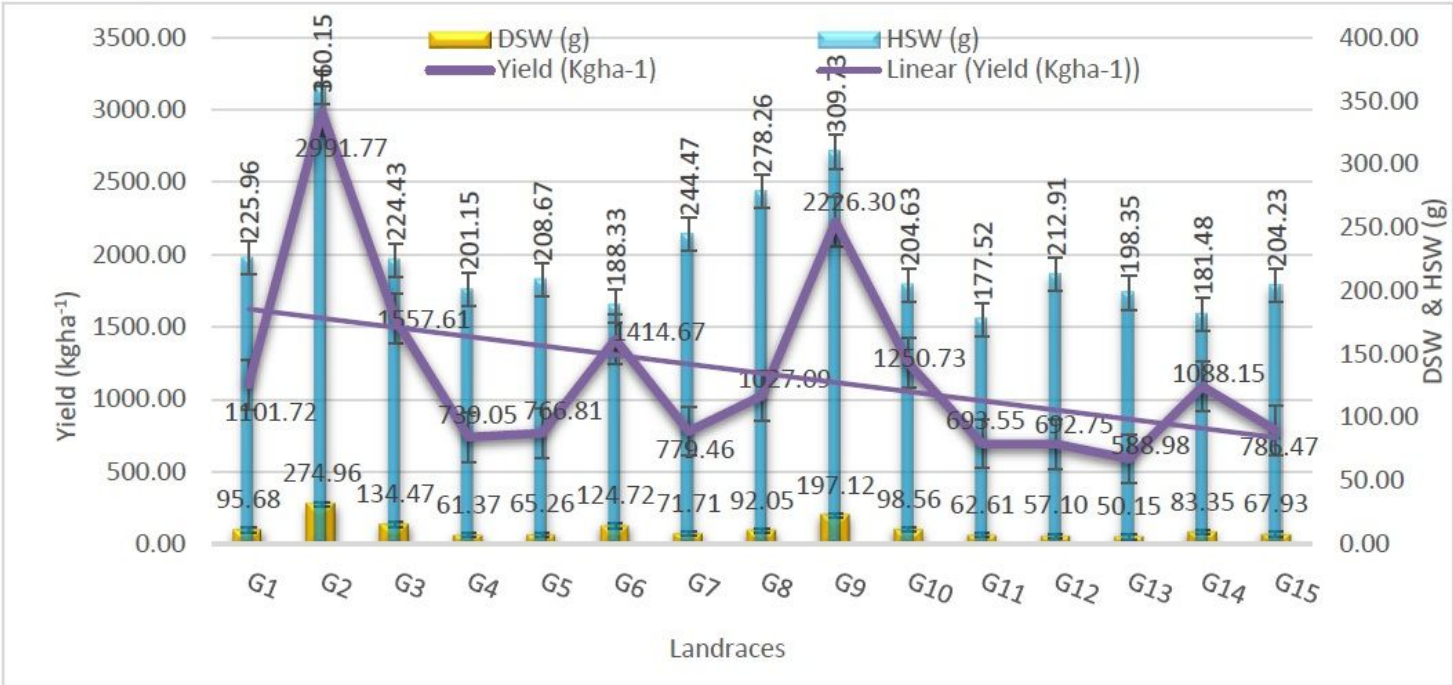


Figure 2

Graphical relationship of dry seed weight (DSW) and hundred seed weight (HSW) with yield (kgha-1) for Bambara groundnut landraces

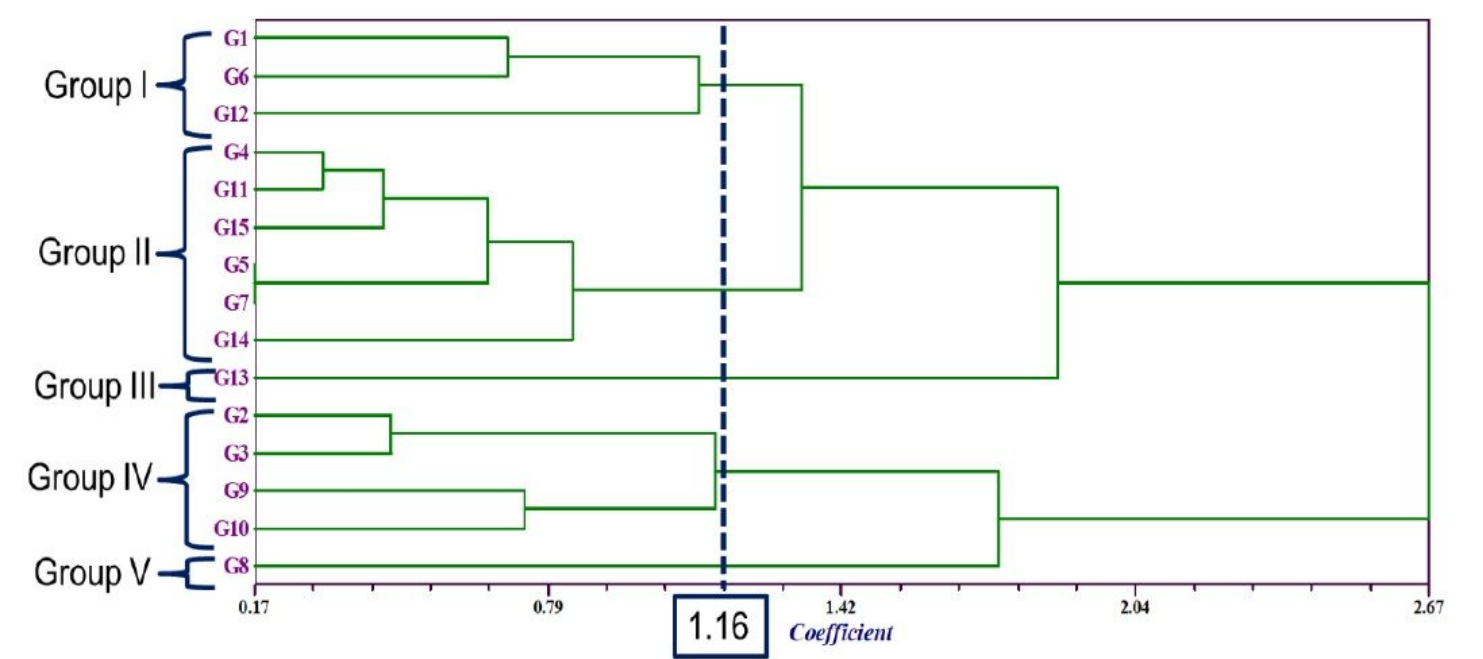


Figure 3

Dendrogram showing the relationship among the Bambara groundnut landraces revealed by UPGMA method

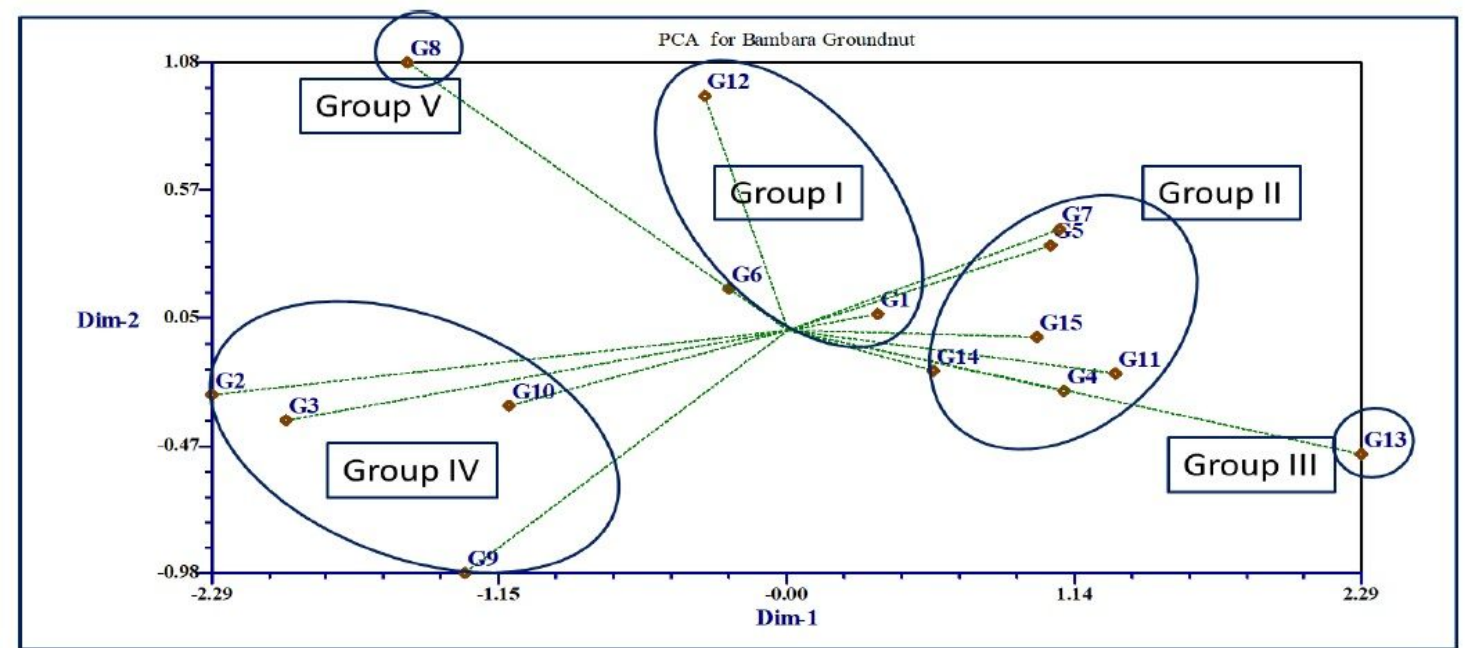


Figure 4

PCA - 2D graphical relationship among the Bambara groundnut accessions

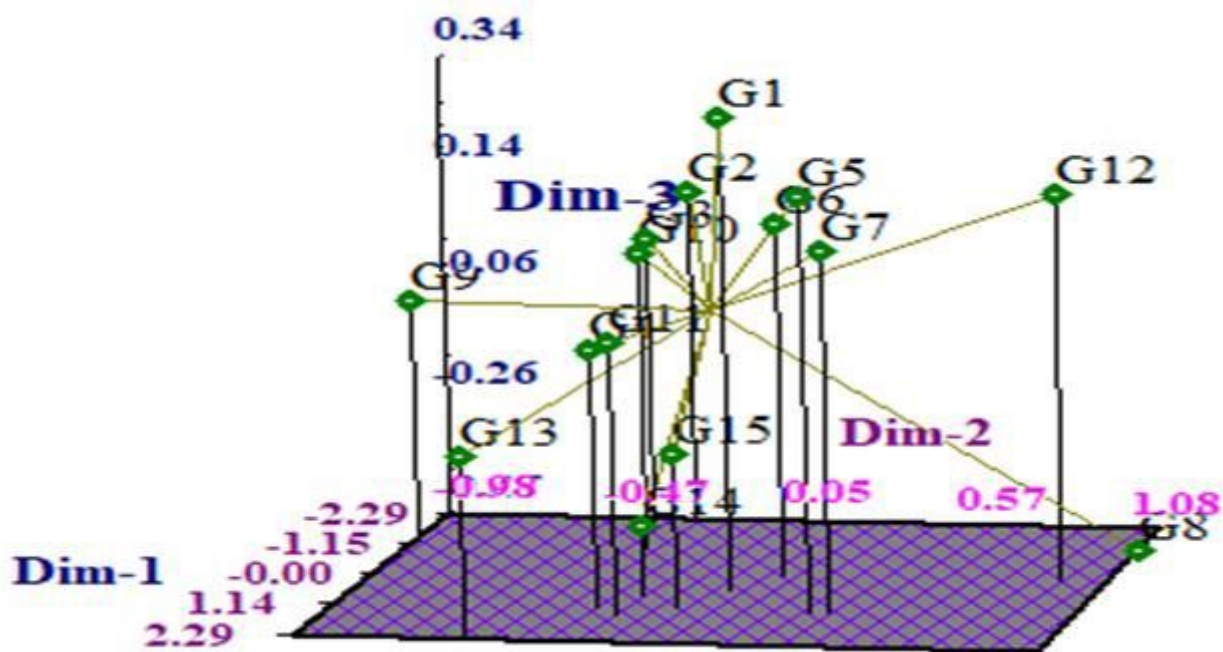


Figure 5

PCA -3D graphical relationship among Bambara groundnut accessions