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Morphometric diversity of some Nigerian accessions of Bambara groundnut (*Vigna subterranea*)

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Abstract

This study evaluated the morphological diversity of some Nigerian accessions of Bambara groundnut. Field experiments were conducted in Nigeria in two locations and the phenotypic variation of Bambara groundnut accessions evaluated in 3 years (2017–2020) using a randomized complete block design. Twenty-eight quantitative and 10 qualitative traits were observed. Twenty-three out of the 28 quantitative morphological traits showed significant differences. TVSu-589 (28.85) and TVSu-670 (28.57) had the highest plant height; TVSu-572 (121.52), TVSu-271 (113.10) and TVSu-336 (104.15) had the highest 100-seed weight. Genetic variations were also observed in seed colour, terminal leaflet shape, petiole colour and eye pattern. Principal component analysis showed PC1 constituting 23.36% and PC2 constituting 15.76% of the total variation, while the first eight principal components with eigenvalues ≥1 revealed 77.28% of the total variation. Cluster analysis grouped the accessions into four groups. Based on yield data in this study, accessions TVSu-594, TVSu-350, TVSu-336, TVSu-1242, TVSu-129, TVSu-14, TVSu-179, TVSu-2100, TVSu-261 and TVSu-589 were the best for yield and are recommended for further evaluation to improve yield. This study showed that a wide range of diversity exists in Bambara groundnut of Nigerian origin that could be useful for further utilization of genetic resources and improvement.

Introduction

Bambara groundnut has the potential to improve nutrition, boost food security, foster rural development and support sustainable land use. Bambara groundnut is indigenous to sub-Sahara Africa where it is widely cultivated. The centre of origin is North-Eastern Nigeria, in West Africa (Goli *et al.*, 1997; Xin *et al.*, 2020; Nomathemba *et al.*, 2021). This plant is referred to as a 'groundnut' because of the way it sets its pods, which is similar to groundnut (*Arachis hypogea*). The seeds of Bambara groundnut are consumed in several ways and at different stages of maturation, as a snack or vegetable. The young fresh seeds may be boiled and eaten as a snack in a manner similar to boiled peanuts, and are made into a pudding (or steamed paste) called Moi-Moi or Okpa (bean porridge) in some parts of Nigeria (Aremu *et al.*, 2022). In Zambia, Bambara groundnut is used for bread making (Mashau, 2022), and to produce legume milk (Ajilogba *et al.*, 2022). Dried seeds can be roasted and eaten as confectionery. For centuries, Bambara groundnut germplasm has been maintained as landraces, which are often phenotypically and genetically diverse (Hlanga *et al.*, 2022). All cultivated Bambara groundnut genotypes are from farmers' mass selection from landraces that have evolved directly from their wild relatives, and which have adapted to the natural environments (Muhammad *et al.*, 2020). Ahmad *et al.* (2015) reported that domesticated Bambara groundnut (*Vigna subterranea*var. *subterranea*) originated from its wild relative (*V. subterranea*var. *spontanea*) through a series of gradual natural and artificial selections that are still taking place. One example of such selection is a change from a spreading/trailing to a bunching growth habit, and reductions in leaflet area, pod thickness and days to flowering as a result of domestication.

Adaptation to harsh environmental conditions and yield stability are characteristics that made landraces of Bambara groundnut farmers friendly (Rex, 2020). The Bambara groundnut landraces can be systematically exploited in breeding programmes through a dedicated pre-breeding programme. Selection for genotypes will continue in mitigating the effects of climate change and enhancing the responsiveness of the crop to drought. Rex (2020) also reported that the selection of good parents is a key to success in plant breeding. This study evaluated the biodiversity of 100 Bambara groundnut of Nigerian origin and assessed the accessions for

28 quantitative and 10 qualitative agro-morphological traits. The study of the agronomic variability of these accessions is an important contribution to establishing the Bambara breeding programme in Nigeria for combating food and nutritional insecurity in Africa.

Materials and methods

Plant material and experimental location

The study was carried out at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria and IITA out station, located at the Institute of Agricultural Research and Training (IAR&T) Ikenne, Nigeria for 3 years (2017/2018, 2018/2019 and 2019/2020). Ibadan is located on coordinates 7.38°N and 3.94°E and it is situated at 181 m above sea level. The average annual temperature is 26.5 °C and about 1311 mm of precipitation falls annually with 81% mean relative humidity. Ikenne is on coordinates 6.87°N and 3.71°E and 235.2 m above sea level, has an annual rainfall of 1200 mm, 65% mean relative humidity and 21.4 °C mean temperature, respectively. Seeds of 100 accessions of Bambara groundnut were sourced from the list of Genetic Resources Center (GRC), of IITA and used for the field experiments. The accessions were previously reported by Osundare *et al.* (2022). The accessions were sourced to guide future research in the selection of genetic resources with thoroughly catalogued agronomic and genomic traits linked to GenBank accessions and to make data publicly available. The sourced accessions were also made to identify which of the thousands of accessions in a database is high yielding, as a critical step in food security.

Experimental design and field management

The experiments were laid out in a randomized complete block design with three replications. The total block size was (21 m × 50 m) and each plot was 1 m × 2.5 m. Inter and intra-row spacing was 1.00 m and 0.25 m. One seed was hand sown per hole, seed germination count was carried out and ungerminated supplied 2 weeks after planting. Herbicides such as paraquat was sprayed 2 weeks before ploughing and Metolachlor E.C was sprayed immediately after ridging the rate of 200 mg/20l to control weeds.

Data collection

Data were collected on 28 quantitative traits and 10 qualitative data using the procedure stated in the descriptor for Bambara groundnut (IPGRI, 2000). The experimental unit consisted of 10 plants per replicate. Data were collected from five tagged plants (at the middle of the row). The 10 qualitative traits are as follows; terminal leaflet colour, terminal leaflet shape (TLS), petiole colour, pod shape, dry pod colour, seed shape, growth habit, open flower colour, seed hilum colour and eye pattern.

Data analysis

Data collected in the three replications of the two locations and in the 3 years across locations were averaged and computed for all accessions, then subjected to analysis of variance (ANOVA) using the PROC GLM procedure on the statistical analytical system (SAS, version 9.4) (SAS, 2017). Treatment means were compared using Duncan multiple range test at 5 and 1% to separate the significant differences. Principal component analysis (PCA) was carried out using the PROC PRINCOMP procedure on SAS to determine the contribution of each trait to the total variation observed on the accessions used. Cluster analysis was carried out using the PROC CLUSTER procedure (Ward hierarchical clustering method) to show the distribution of the accessions into their different groups. Descriptive statistics were also employed to analyse qualitative data using frequencies and percentages. Pearson correlation was used to determine the relationships among the traits using PROC CORR in the SAS program.

Results

Quantitative traits

The ANOVA revealed highly significant ($P \leq 0.01$) differences for most of the quantitative traits studied (Table S3) in the 3 years for 23 traits, out of the 28 quantitative traits evaluated. The mean value of the accessions studied revealed that plant height (PH, cm) varied significantly from 28.85 to 18.27, while accessions TVSu-589, TVSu-670, TVSu-2109, TVSu-2106 and TVSu-285 had the highest plant height and accessions TVSu-1239, TVSu-662 and TVSu-647 had significantly short plant height. Terminal leaflet length (TLL, mm) varied significantly from 84.14 to 45.33; accessions TVSu-589, TVSu-2109, TVSu-2106, TVSu-2105 and TVSu-285 had the longest terminal leaflet length while accessions TVSu-662, TVSu-838, TVSu-275 and TVSu-1252 had the shortest terminal leaflet length. Terminal leaflet width (TLW, mm) varied significantly from 44.97 to 19.79; accessions TVSu-2109, TVSu-589, TVSu-2105 and TVSu-2106 had the widest terminal leaflet width while accessions TVSu-586, TVSu-647, TVSu-14 and TVSu-365 had significantly narrow terminal leaflet width. Petiole length (PetL, mm) varied significantly from 205.88 to 116.88; accessions TVSu-670, TVSu-589, TVSu-2109, TVSu-2100 and TVSu-331 had the longest petiole length while accessions TVSu-1239, TVSu-662, TVSu-2112 and TVSu-647 had the shortest petiole length. The number of trifoliate leaves (NTLs) varied significantly from 95.04 to 49.97; accessions TVSu-333, TVSu-838, TVSu-1242, TVSu-1245 and TVSu-633 had the highest number of trifoliate leaves while accessions TVSu-269, TVSu-627, TVSu-127, TVSu-675 and TVSu-173 had the lowest number of trifoliate leaves. Plant spread (PlanSpr, cm) varied significantly from 45.71 to 28.85; accessions TVSu-271, TVSu-2109, TVSu-2105, TVSu-331 and TVSu-2099 covered the widest area of land while accessions TVSu-365, TVSu-647, TVSu-348 and TVSu-1222 covered narrow area of land. Internodes length (IL, mm) varied significantly from 22.96 to 10.45; accessions TVSu-129, TVSu-589, TVSu-2106, TVSu-2109 and TVSu-572 had the longest internodes length while accessions TVSu-173, TVSu-650, TVSu-577 and TVSu-261 had the shortest internodes length. Banner length (BL, mm) varied significantly from 5.98 to 5.25; accessions TVSu-590, TVSu-346, TVSu-2104, TVSu-348 and TVSu-585 had the longest banner length while accessions TVSu-1252, TVSu-662, TVSu-334 and TVSu-576 had the shortest banner length. Peduncle length (PdclL, mm) ranged from 6.58 to 3.98; accessions TVSu-670, TVSu-1241, TVSu-2112, TVSu-589 and TVSu-647 had the longest peduncle length while accessions TVSu-662, TVSu-2102, TVSu-656, TVSu-271 and TVSu-178 had the shortest peduncle length. The number of days to first flowering observed among the selected accessions was 34–41 days and the number of days to maturity was 116–131 days. Pod length (PdL, mm) ranged from 24.68 to 14.96; accessions

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TVSu-2105, TVSu-589, TVSu-2109, TVSu-336 and TVSu-2100 had the longest pod length while accessions TVSu-639, TVSu-640, TVSu-662 and TVSu-269 had the shortest pod length. Pod width (PdW, mm) ranged from 15.79 to 10.43; accessions TVSu-572, TVSu-368, TVSu-2099, TVSu-366 and TVSu-271 had the widest pod width while accessions TVSu-365, TVSu-662, TVSu-269 and TVSu-659 had narrow pod width. Grain yield per hectare (GYpHa, Kg) ranged from 1091.80 to 416.20; accessions TVSu-594, TVSu-261, TVSu-336, TVSu-350 and TVSu-1242 had the highest yield per hectare while accessions TVSu-285, TVSu-659, TVSu-359 and TVSu-268 had the lowest grain yield per hectare. Hundred seed weight (100-sdwt, g) ranged from 121.52 to 40.18; accessions TVSu-572, TVSu-271, TVSu-336, TVSu-368 and TVSu-83 had the highest 100-seed weight while accessions TVSu-287, TVSu-263, TVSu-178, TVSu-586 and TVSu-662 had the lowest 100-sdwt. Exceptional accessions with high-yielding characteristics above 800 kg per hectare in the locations and years include TVSu-594 (1091.80), TVSu-261 (966.20), TVSu-336 (917.80), TVSu-350 (903.30), TVSu-1242 (877.30), TVSu-2100 (855.40), TVSu-179 (848.20), TVSu-14 (834.30), TVSu-589 (820.70) and TVSu-129 (819.30) (Table S1).

Principal components

Comparison of the principal component's (PC) contribution to diversity in the 3 years revealed that PCs 1–8 constitute 77.28% of the total variation, where PCs 1, 2, 3, 4, 5, 6, 7 and 8 contributed 23.36, 15.76, 12.22, 6.86, 6.17, 4.72, 4.34 and 3.85, respectively. PCA showed PC1 constituted 23.36% and PC2 constituted 15.76%, while the first eight PCs that had eigen values ≥1 revealed 77.28% of total variation. Higher contribution to total variation was revealed by PCs 1 and 2. PC1 contributed 23.36%; these traits contributed to the variation plant height (0.28), terminal leaflet length (0.26), terminal leaflet width (0.26), petiole length (0.24), plant spread (0.25), internode length (0.19), yield per plant (0.19), yield per plot (0.19), pod length (0.28), pod width (0.29), seed length (0.30), seed width (0.24) and 100-seed weight (0.28). These components contributed positively to total variation. PC2 contributed 15.76%, yield per plant (0.29), number of pods per plot (0.34), yield per plot (0.38), yield per hectare (0.38), seed weight per plot (0.40), shelled harvest per plot (0.31) while shelling percentage (−0.30) contributed negatively (Fig. 1) (Table 1).

Qualitative traits

Descriptive statistics on qualitative traits observed on terminal leaflet colour, growth habit and open flower colour were uniform in all the studied accessions as revealed in Table S2. The analysis of TLS revealed that 55% of the selected accessions are 'lanceolate', 44% 'oval' and 1% 'elliptic'. The analysis of petiole colour showed that 66% had 'whole green' petiole while 34% had 'base purple' petiole colour. The analysis of pod shape revealed that 57% had 'ending in a point with nook on the other side' while 41% had 'ending in a point round on the other side' while others also exited. The analysis of dry pod colour revealed that 82% had a 'yellowish brown' dry pod colour while 13% had a 'brown' dry pod colour, while others also existed. The analysis of the seed shape revealed that 89% had an 'oval' seed shape while 11% had a 'round' seed shape. The analysis of seed hilum colour showed that 51% had 'white' seed hilum colour while 49% had 'chalk white' seed hilum colour. The analysis of eye pattern showed that 'cream testa with grey butterfly-like eye' was highest at 21% while 'cream testa with brown butterfly-like eye' accounted for 16% of the selected accessions, while others also existed (Table S2). The analysis of seed colour revealed that 26% had a pale yellow colour, 11% had greyish yellow, 9% had light brown,

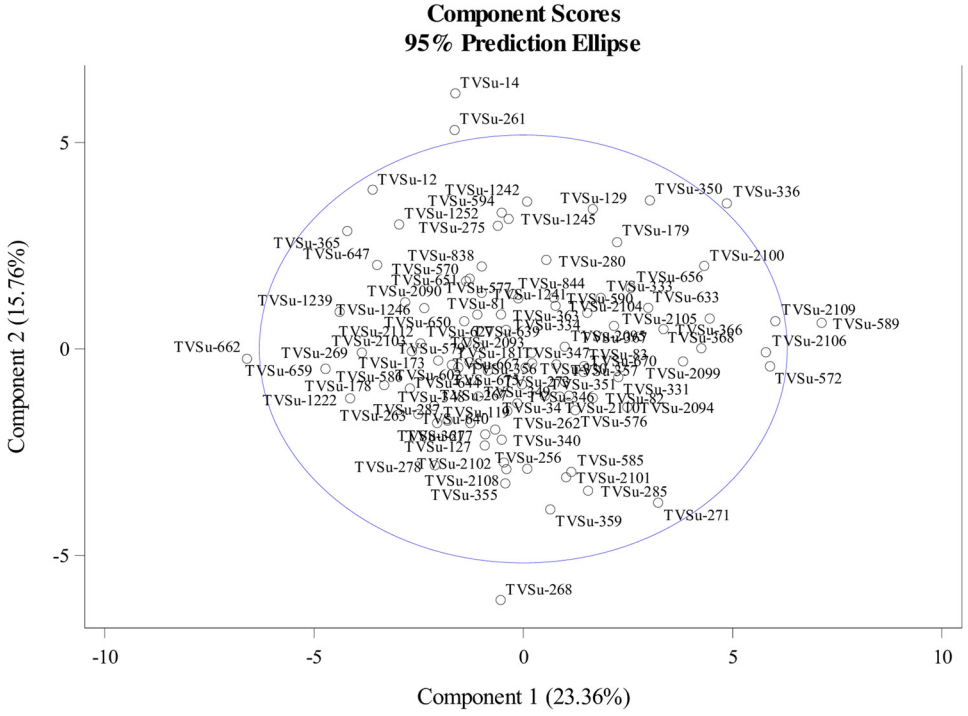

Figure 1. Contribution of PC1 and PC2 to variation.

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Table 1. Eigen values and contribution of first eight principal components axes to variation in 3 years

	Contributing PCs							
	PCA 1	PCA 2	PCA 3	PCA 4	PCA 5	PCA 6	PCA 7	PCA 8
Eigen value	6.30	4.25	3.29	1.85	1.66	1.27	1.17	1.03
% Var. Exp.	23.36	15.76	12.22	6.86	6.17	4.72	4.34	3.85
Cum. Var. Exp.	23.36	39.12	51.35	58.21	64.38	69.1	73.43	77.28
PH (cm)	0.282	−0.089	0.276	−0.058	−0.048	−0.103	−0.236	−0.102
TLL (mm)	0.263	−0.124	0.264	0.037	−0.054	0.000	0.054	0.012
TLW (mm)	0.261	−0.076	0.281	0.129	−0.123	0.076	−0.034	−0.031
NTLvs	0.077	0.084	−0.192	−0.107	−0.014	0.571	−0.260	0.023
PetL (mm)	0.241	−0.066	0.242	−0.086	−0.021	−0.123	−0.322	−0.152
Plant Spr (cm)	0.253	−0.060	0.132	−0.091	−0.057	−0.028	−0.227	−0.108
IntL (mm)	0.194	0.021	0.147	0.104	−0.270	0.050	−0.075	0.160
BL (mm)	0.087	−0.041	0.021	0.323	0.066	−0.416	−0.038	−0.107
PdclL (mm)	0.062	0.102	0.196	0.248	−0.020	−0.160	0.200	0.341
NDtoFF	−0.088	−0.083	0.316	−0.223	0.528	0.036	0.068	0.061
NDto50%F	−0.088	−0.083	0.316	−0.223	0.528	0.036	0.068	0.061
NDtoM	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NFpP	0.111	−0.029	0.068	0.186	0.033	0.158	−0.024	0.740
Y/plant (g)	0.196	0.294	−0.030	0.098	0.229	0.034	−0.199	−0.149
NPdspP	−0.067	0.347	0.154	0.043	0.000	0.188	−0.041	0.124
YpP (g)	0.197	0.384	−0.045	0.082	0.140	0.032	−0.025	−0.005
Y/Ha (kg)	0.182	0.388	−0.024	0.091	0.169	0.001	−0.003	−0.044
NSdpPd	0.004	0.120	0.245	0.109	−0.208	0.305	0.526	−0.297
PdL (mm)	0.288	−0.041	0.124	−0.067	−0.007	0.195	0.424	−0.159
PdW (mm)	0.299	−0.111	−0.212	−0.122	0.076	−0.082	0.163	0.021
SdL (mm)	0.304	−0.020	−0.145	−0.234	0.045	−0.036	0.210	0.150
SdW (mm)	0.243	−0.049	−0.240	−0.206	−0.011	−0.157	0.205	0.148
Shthk (mm)	0.129	−0.148	−0.189	−0.069	0.144	0.273	−0.072	−0.108
Sdwt (g)	0.138	0.409	−0.046	0.004	0.086	−0.012	−0.052	−0.018
Chfwt (g)	0.007	0.089	−0.160	0.368	0.287	−0.176	0.175	−0.153
Shperc	0.106	−0.306	−0.109	0.404	0.184	0.209	−0.047	−0.049
Shdhv/P	−0.098	0.312	0.110	−0.389	−0.191	−0.211	0.042	0.047
100sdwt (g)	0.281	−0.029	−0.281	−0.165	0.045	−0.116	0.057	0.053

PH, plant height; TLL, terminal leaflet length; TLW, terminal leaflet width; NTLvs, number of trifoliate leaves; PetL, petiole length; Plan Spr, plant spread; IntL, pnternode length; BL, banner length; NDtoFF, number of days to first flowering, NDto50%F; PdclL, peduncle length; NDtoM, number of days to maturity; NFpP, number of flowers per peduncle; Yplant, yield per plant; NPdspP, number of pods per plot; YpP, yield per plot; YpHa, yield per hectare (kg); NSdpPd, number of seed per pod; PdL, pod length; PdW, pod width; SdL, seed length; SdW, seed width; Shthk, shell thickness; Sdwt, seed weight per plot; Chfwt, chaff weight; Shperc, shelling percentage; Shdhv/P, shelled harvest per plot; 100sdwt, 100-seed weight.

6% had reddish brown, 5% had light orange, 5% had brownish orange, 4% had dark brown, 4% had violet brown, 3% had greyish brown, 3% had yellowish brown, 2% had light yellow, 2% had orange white, 2% had pale violet while others had less than 2% occurrence (Table S2).

Correlation coefficients

Correlation coefficients revealed that plant height had a positive and significant correlation with yield per plant ($r = 0.23$), yield per plot ($r = 0.27$), yield per hectare ($r = 0.23$), pod length ($r = 0.54$), pod width ($r = 0.35$), seed length ($r = 0.39$), seed width ($r = 0.21$) and 100-seed weight ($r = 0.28$) (Table S4). The number of days to first flowering had a negative and significant correlation with yield per plot ($r = -0.28$), yield per hectare ($r = -0.22$), pod width ($r = -0.23$), seed width ($r = -0.27$), seed weight per plot ($r = -0.29$) and 100-seed weight ($r = -0.32$). Yield per plant had a positive and significant correlation with the number of pods per plot ($r = 0.28$), yield per plot ($r = 0.78$), yield per hectare ($r = 0.81$), pod length ($r = 0.25$), pod width ($r = 0.25$), seed length

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($r = 0.36$), seed width ($r = 0.21$), seed weight per plot ($r = 0.78$) and 100-seed weight ($r = 0.30$). The number of pods per plot had a positive and significant correlation with yield per plot ($r = 0.47$), yield per hectare ($r = 0.45$), number of seeds per pod ($r = 0.24$), seed weight per plot ($r = 0.45$) and shelled harvest per plot ($r = 0.45$), but had a negative and significant correlation with pod width ($r = -0.36$), seed width ($r = -0.27$), shelling percentage ($r = -0.45$) and 100-seed weight ($r = -0.27$). Yield per plot had a positive and significant correlation with yield per hectare ($r = 0.93$), pod length ($r = 0.30$), pod width ($r = 0.29$), seed length ($r = 0.43$), seed width ($r = 0.26$), seed weight per plot ($r = 0.87$), chaff weight ($r = 0.26$), shelled harvest per plot ($r = 0.20$) and 100-seed weight ($r = 0.41$). Yield per hectare had a positive and significant correlation with pod length ($r = 0.27$), pod width ($r = 0.26$), seed length ($r = 0.37$), seed width ($r = 0.23$), seed weight per plot ($r = 0.83$), chaff weight ($r = 0.26$), shelled harvest ($r = 0.23$) and 100-seed weight ($r = 0.34$), but had a negative and significant correlation with shelling percentage ($r = -0.21$). The number of seeds per pod had a positive and significant correlation with pod length ($r = 0.42$) but had a negative and significant correlation with pod width ($r = -0.21$), seed width ($r = -0.21$) and 100-seed weight ($r = -0.28$). Pod length had a positive and significant correlation with pod width ($r = 0.54$), seed length ($r = 0.63$), seed width ($r = 0.34$) and 100-seed weight ($r = 0.39$). Pod width had a positive and significant correlation with seed length ($r = 0.74$), seed width ($r = 0.74$), shelling percentage ($r = 0.32$) and 100-seed weight ($r = 0.78$), but had a negative and significant correlation with shelled harvest ($r = -0.31$). Seed length had a positive and significant correlation with seed width ($r = 0.67$), seed weight per plot ($r = 0.29$) and 100-seed weight ($r = 0.77$). Seed width had a positive and significant correlation with 100-seed weight ($r = 0.71$). Seed weight per plot had a positive and significant correlation with shelled harvest per plot ($r = 0.35$), and 100-seed weight ($r = 0.30$) had a negative and significant correlation with shelling percentage ($r = -0.32$). Chaff weight had a positive and significant correlation with shelling percentage ($r = 0.22$) and 100-seed weight ($r = 0.19$), but had a negative and significant correlation with shelled harvest per plot ($r = -0.21$). Shelling percentage had a negative and significant correlation with shelled harvest per plot ($r = -0.98$).

Cluster analysis of quantitative traits

Cluster analysis was used to assess the genetic differences of the observed quantitative traits, where individuals with related descriptions are grouped into the same cluster. The similarity, relatedness and distance of the varieties are the foundation of this method, where similar accessions were grouped into the same cluster, and dissimilar accessions were grouped differently. The length between the lines (distance between two points) was calculated using standardized morphological data, and a dendrogram was constructed using these values (Fig. 2). The selected population was grouped into four subpopulations, cluster 1 had 9 accessions, cluster 2 had 41 accessions, cluster 3 had 16 accessions and cluster 4 had 34 accessions (Fig. 2). Accession with the highest yield components and highest agronomic traits responses fell into clusters 2 and 4 as revealed through the means.

Discussion

The results of this study demonstrated morphological diversity among the sourced accessions of Nigerian Bambara groundnut, with the different groupings of the distribution of the accessions through the dendrogram and the distribution of data. We identified TVSu-589 and TVSu-670 as accessions that could be used in the improvement of the plant height in future breeding research. We also identified TVSu-572, TVSu-594 and TVSu-336 as Bambara groundnut accessions with high yield. The traditional farmers in West Africa and the formal seed system will have access to seeds of Bambara groundnut with higher potential for yield. Further investigation into the genetic makeup will reveal specific genes responsible for individual differences and the effects of such genes in the development of targeted traits.

This study demonstrated diversity in plant height, seed weight and 100-seed weight, confirming the results of Nabuuma *et al.* (2022). Other studies have also reported morphological variations of the quantitative and qualitative traits of Bambara groundnut accessions (Ntundu *et al.*, 2006; Ullah *et al.*, 2011; Shegro *et al.*, 2013; Tafadzwanashe and Albert, 2013; Zenabou *et al.*, 2014; Mohammed *et al.*, 2016; Atoyebi *et al.*, 2017; Adikuru *et al.*, 2017; Odongo *et al.*, 2018; Mohammed *et al.*, 2019; Nomathemba *et al.*, 2021; Mesay *et al.*, 2022). However, this research demonstrated that variability existed among Bambara groundnut accessions of Nigeria origin, which has not been reported before. The accessions showed no significant difference in the number of days to maturity. This agrees with Berchie *et al.* (2010) who also observed no significant difference in the number of days to maturity. Earliness to maturity may be a useful trait to escape drought in erratic heightening moisture stress environment and insect infestation as supported by Shumba-Mnyulwa (2002) and Toure *et al.* (2012) (Khan *et al.*, 2021a). The accessions showed significant differences in yield per hectare, in the observed years with an average of 641.59 kg per hectare. This confirmed the report of Khan *et al.* (2021a) and Hailegiorgis *et al.* (2011) that Bambara groundnut can grow and produce reasonable yield in Africa. This was also reiterated by Khan *et al.* (2021b) and Oluwaseyi *et al.* (2021).

PC1 and PC2 had the highest contribution to variation, indicating that they are key factors to reveal diversity in the selected accessions. Similar results were also reported by Ntundu *et al.* (2006), Hailegiorgis *et al.* (2011) and Ravishanker *et al.* (2013). However, this study demonstrated that plant height, seed weight and yield per hectare are important diversity traits among Bambara groundnut of Nigerian origin which has not been reported before. The level of morphological similarity shown by accessions within the same cluster indicated that the accessions may not have a common ancestry, similar to the results reported by Ntundu *et al.* (2006), Ullah *et al.* (2011), Olukolu *et al.* (2012) and Mohammed *et al.* (2016). The dendrogram analysis in this study identified four subpopulations based on morphological traits, which indicated high genetic variation, which has potential for future breeding programmes in other ecological zones in Nigeria.

The analysis of 'locations' showed significant variations for 20 out of the 28 traits evaluated in the years. A similar result was obtained by Esan *et al.* (2023) who reported significant differences in traits of Bambara groundnut evaluated in different regions in Cote d'Ivoire. Yield per plant varied significantly among accessions in the years from 12 to 42 g/plant, indicating that the yield of Bambara groundnut varied widely depending on accessions and environmental conditions. The results are in agreement with previous studies (Shumba-Mnyulwa, 2002; Shareef and Krishnaraj, 2013; Chai *et al.*, 2017; Mayes *et al.*, 2019; Oluwaseyi *et al.*, 2021; Khan *et al.*, 2021a; Hlanga *et al.*, 2022;

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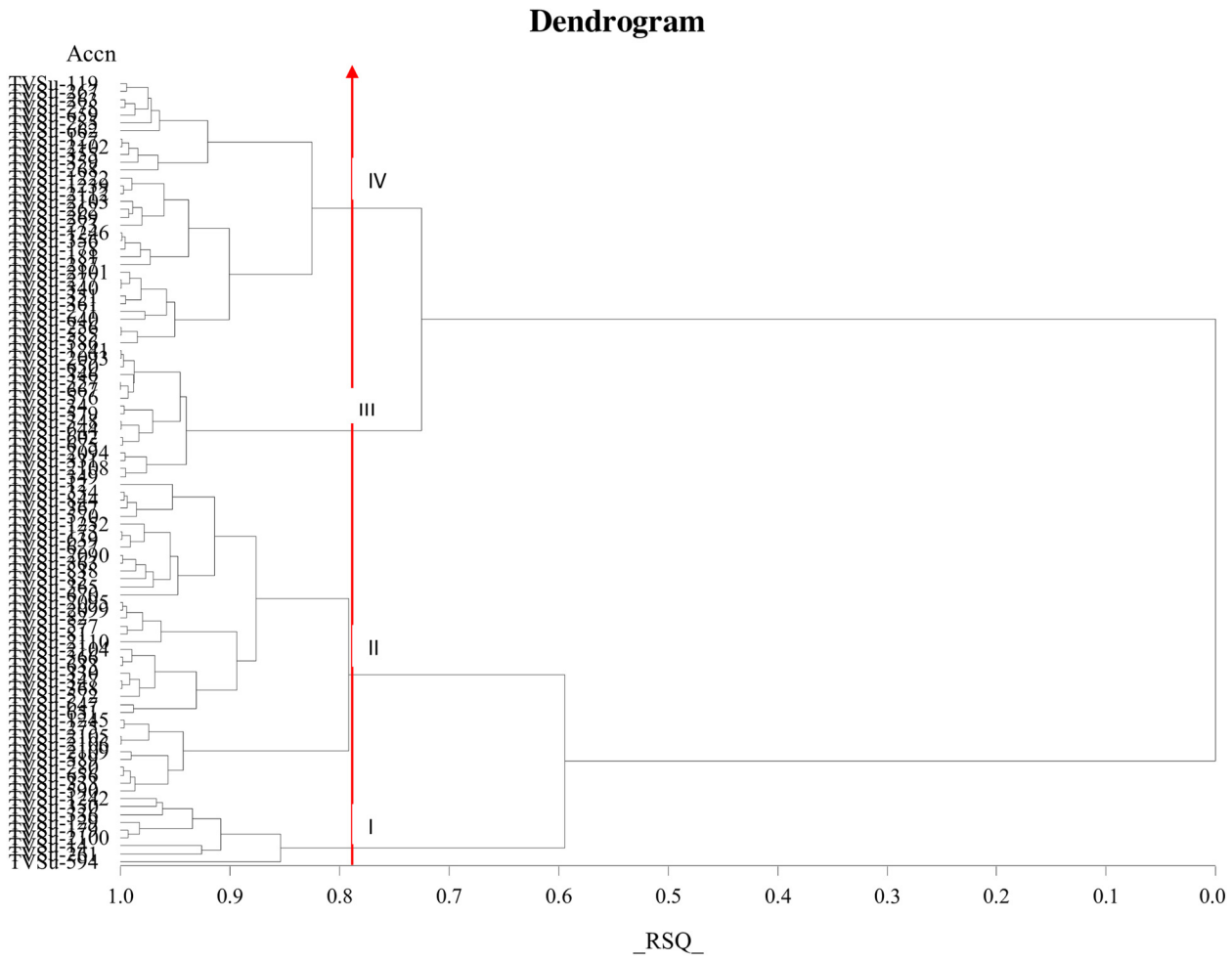

Figure 2. Dendrogram showing the group classification of the accessions.

Esan *et al.*, 2023).The interaction of 'accession × location' also indicated that traits responsible for diversity in Bambara groundnut showed significant differences in the locations. This was also reported by Muhammad *et al.* (2020). Some of the non-significant quantitative traits are less influenced by location and may express their genetic potential at any particular location. The interaction of 'accession × location × year' showed that accessions of Bambara groundnut express its morphological traits differently in locations, hence, diversity among the 'accessions' is genetically and environmentally controlled.

Qualitative traits analysis showed that all the sourced accessions for this research had green leaves confirming a previous report (Basu *et al.*, 2007). Mohammed *et al.* (2016) also reported variations in the TLS, pod shape, pod texture, seed shape and seed colour of 49 Bambara groundnut landraces. However, only 2% of the accessions in this study had pods without a point while 57% of the pods had a point with a nook on the other side. These results contrast with the finding of Mohammed *et al.* (2016) who reported that none of the pods of the Bambara groundnut landraces used had a point. Open flower colour for all the 100 accessions used for this study was yellow, seed colour was dominated by pale yellow at 26%, and seed eye pattern was dominated by cream testa with grey butterfly-like eye at 21%. The findings corroborated the report of Goli *et al.* (1997) that Bambara groundnut varies in seed morphological features. This study identified TVSu-336, TVSu-350, TVSu-261, TVSu-594 and TVSu-589 as high-yielding accessions of Bambara groundnut that originated in Nigeria with above 800 kg/ha. This study also confirmed that positive correlation existed between yield-contributing traits and yield per hectare, which indicated the improved performance of the associated traits in this research. These traits characterized in the study will provide valuable information for future breeding programmes to improve yield of Bambara groundnut in Nigeria.

Conclusions

This study concluded that morphological variability existed among Bambara groundnut in Nigeria and that such variation existed in plant height, petiole length, pod width, plant spread, yield per hectare, yield per plot, yield per plant, number of pods per plot and terminal leaflet length, and are important traits that should be given attention in making effective selection for parents in Bambara groundnut breeding. Further studies should also make use of high-throughput sequencing markers to dissect the level of diversity established in this study in the genomic constituent of Bambara groundnut.

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/S1479262123001028.

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Competing interest. None.

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