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Genetic Analysis and Variability Assessment of Bambara Groundnut (*Vigna subterranea* L.) Lines Based on Vegetative Traits

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ABSTRACT

Genetic diversity is essential to a plant species' ability to survive, adapt, and thrive in a constantly shifting environment. It also forms the basis for crop development's efficient selection process. Therefore, breeding programs that present a high level of genetic variability in germplasm collections benefit significantly from an understanding of the genetic processes responsible for the inheritance of this trait. Therefore, this research aims to estimate the genetic analysis and variability of Bambara groundnut based on vegetative components using multivariate analyses. A randomized complete block design, including three replications, was utilized to evaluate five genotypes of Bambara groundnuts. The seeds were divided into three groups: large, medium, and small seed sizes. Statistical analysis was conducted in SAS version 9.4 to estimate ten vegetative characters' variance components and heritability. Most vegetative variables in the current study showed significant variations between the five genotypes, fifteen combinations of seed size and genotypes, seed size categories, and the interaction between genotype and seed size categories. The estimation of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) varied from 0 to 20.36%. Moreover, the high values of GCV (20.36%) and PCV (28.18%) resulted from the wide canopy trait, while moderate GCV and high PCV were registered from the number of petioles, number of leaves, number of branches, and dried biomass. The low GCV and high PCV were recorded for fresh biomass and high plant growth. More research should be conducted to enhance these Bambara genotypes in various environments.

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INTRODUCTION

Bambara groundnut (*Vigna subterranean* (L.) Verdc.) is one of the grain legumes crops originally from Africa (Majola et al. 2021). It is a substitute food source producing protein and carbohydrates (Rahmah et al., 2020).

Consistent phenological development, such as susceptibility to extended photoperiods, a condition known as "hard-to-cook" during post-storage processing, and a lack of agricultural policy surrounding the value chain all impede the employment of Bambara groundnuts in enhancing food systems (Mateva et al., 2023).

Due to its ease of cultivation and resistance to drought, the Bambara groundnut can potentially displace soybean as a significant legume (Alhamdi et al., 2020).

Feldman et al. (2019) claim that the Bambara groundnut exhibits the most remarkable drought resistance, combining the three composite qualities of tolerance, avoidance, and escape. Furthermore, according to Mayes et al., (2019), Bambara groundnuts can further support climate change-ready agriculture.

Numerous studies have described the genetic diversity of Bambara groundnuts. Based on morphological characteristics, the results of multiple research show that the diversity of Bambara groundnuts is sufficiently wide (Gbaguidi et al., 2018). This crop's growth depends on identifying and choosing distinctive and trustworthy breeding lines under various conditions (Khan et al., 2022).

In addition to character identification, measurements of the Normalized Difference Vegetation Index (NDVI) can be performed to determine whether the NDVI value and the characteristics of the Bambara groundnut are correlated. N levels in a variety of plants, including rice (Jiang et al., 2021), wheat (Aranguren et al., 2020), and corn (Edalat et al., 2019), are measured using NDVI measurements.

To improve the crop, it is crucial to characterize, assess, and identify the best parents of Bambara groundnut germplasm; therefore, genetic variation can be an option for selecting appropriate parents. However, quantitative characters are highly influenced by environmental factors; hence, there is a need to partition total variances into heritable and non-heritable components for an efficient breeding program (Agajie, 2021). In crop improvement projects, identifying genetic diversity and breeding methodologies is vital (Khaliqi et al., 2021)[1].

To determine the benefits and drawbacks of various genotypes, it is crucial to identify Bambara groundnut's morphological and germination characteristics. One of the crucial phases of growing legumes is germination. It is essential to investigate the relationship between legume seed coat color and seed germination, as suggested by several studies (Alhamdi et al., 2024).

Genetic improvement must be made to provide high-yielding varieties with unique characteristics. Promising lines have been generated from the selection process (Saptadi et al., 2016). In order to improve the Bambara genotypes under various conditions, more research should be conducted on yield and yielding traits. Although some research has been done on the gene action of yield and features associated with yield in Bambara groundnuts, none of these studies have specifically examined seed size and weight (Khaliqi et al., 2021)[2].

Consistent Bambara groundnut improvement is essential for the crop's enhanced competitiveness. Selection of suitable parental materials has been achieved through significant genetic variability (Kakeeto et al., 2019).

Evaluation and selection of distinctive and reliable breeding lines in various conditions are essential to developing this crop (Olanrewaju et al., 2021). Considered a crop for the new millennium, Bambara groundnut has been identified as an emerging crop for the future. It is evident that by analyzing several genetic criteria, selection can be used to improve the morphological characteristics of Bambara groundnuts. Furthermore, the level of divergence was observed for nearly disparate geomorphic factors. Nonetheless, it may help plant breeders enhance the agromorphic characteristics of Bambara groundnut. (Khan et al., 2022).

The level of genetic variability present and the magnitude to which the traits are inherited influence the selection of superior genotypes (Scarano et al., 2014). As a result, the description and evaluation of Bambara groundnut genotypes and the selection of the best parents are critical for crop improvement (Unigwe et al., 2016). Since a new crop can boost genetic potential and encourage long-term research and development of new cultivars, a Bambara groundnut improvement project is necessary (Khan et al., 2022). Furthermore, heritability and genetic gain are used to assess the improvements in traits that can be achieved through direct selection (Khaliqi et al., 2021)[1].

Hence, by maximizing the use of scarce resources and preserving biodiversity, our findings will demonstrate the genetic enhancement of the accessions under study, enhance the data set, and offer suggestions for improved cultivation methods for the next breeding programs. Furthermore, the current experiment was carried out to assess the evaluation and genetic analysis yield performance of 28 Bambara groundnut lines selected based on vegetative traits with the specific objectives of determining phenotypic relationship, genetic components, heritability, genetic advance, and selection of superior lines based on vegetative traits for future evaluation.

MATERIALS AND METHODS

Twenty-eight lines of Bambara groundnut were selected based on top-yielder plants from each seed weight category (Table 1). The selection was based on individual yield performance consisting of ten from large seed weight, seven from medium, and 11 plants from small seed weight, respectively (Figure 1).

Experimental Design

This experiment was carried out at Field 15, University Putra Malaysia (UPM), in a randomized complete block design (RCBD) with three replications. Each experimental unit consists of five plants from each selected line.

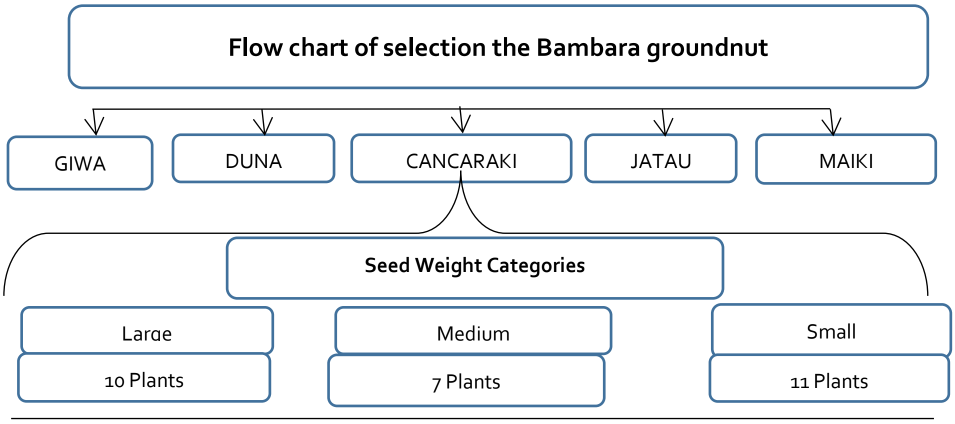

Figure 1: Flow chart of selection the Bambara groundnut

Table 1: Selected Bambara Groundnut Lines

NO	LINES Code	Genotype	Seed Size
1	G1LR1P3	GIWA	Large
2	G2LR3P2	DUNA	Large
3	G3LR2P1	CANCARAKI	Large
4	G4LR1P1	JATAU	Large
5	G4LR1P2	JATAU	Large
6	G4LR1P5	JATAU	Large
7	G4LR3P3	JATAU	Large
8	G5LR1P3	MAIKI	Large
9	G5LR3P3	MAIKI	Large
10	G5LR3P4	MAIKI	Large
11	G2MR1P2	DUNA	Medium
12	G3MR1P2	CANCARAKI	Medium
13	G3MR1P3	CANCARAKI	Medium
14	G4MR1P1	JATAU	Medium
15	G4MR1P2	JATAU	Medium
16	G4MR1P3	JATAU	Medium
17	G5MR1P1	MAIKI	Medium
18	G1SR1P3	GIWA	Small
19	G1SR2P4	GIWA	Small
20	G1SR3P1	GIWA	Small
21	G2SR1P1	DUNA	Small
22	G2SR1P3	DUNA	Small
23	G2SR2P3	DUNA	Small
24	G3SR1P1	CANCARAKI	Small
25	G3SR1P3	CANCARAKI	Small
26	G3SR1P4	CANCARAKI	Small
27	G4SR1P2	JATAU	Small
28	G5SR1P1	MAIKI	Small

Data Collection

Data were collected on ten vegetative attributes listed in Table 2. The quantitative data collected follows the Bambara groundnut descriptors (IPGRI, IITA, BAMNET, and Gonne et al., 2013). Growth parameters were directly recorded at different growth phases in the field and after harvest in the lab, as indicated in the following descriptors (IPGRI IITA, BAMNET).

Statistical Analysis

All morphological characteristics, as specified by Gomez (1984), were subjected to statistical analysis for analysis of variance (ANOVA) using the Statistical Analysis System (SAS) version 9.4. Duncan's New Multiple Range Test (DNMRT) was applied at 5% for the means comparison. The variance component and heritability were estimated for every character, including the seed weight. The variance component was estimated from the anticipated mean squares by utilizing PROC VARCOMP and SAS's Restricted Maximum Likelihood (REML) approach.

Table 2: List of quantitative traits

Character	Abbreviation	Method of evaluation
Days to Emergence	NDE	Number of days has been recorded from sowing to the first day of germination.
Days to 50% Flowering	NDF50%	Number of days from sowing to first flower opening on 50% of plants per plot was determined.
Plant Height (cm)	PH	The matured height of the plant was measured and conveyed in cm from the ground level to the tip of the main stem.
Wide Canopy (cm)	WC	Every plant's spread was determined at right angles as the mean of the two-canopy diameter and expressed in cm.
Days to Maturity (day)	DM	Number of days has been determined from planting to maturity.
Number of Petioles (no)	NP	At maturity, the number of petioles in each plant was recorded.
Number of Leaves (no)	NL	The number of leaves that were fully opened from the plants on each plant was counted.
Number of Branches (no)	NB	The number of branches was recorded in each plant at maturity.
Fresh Biomass (gr)	FB	Biological yield after harvesting was recorded in grams provided by each plant. The fresh materials were weighed, and the shoot's fresh weight was recorded.
Dried Biomass (gr)	DB	The biological yield produced by each plant after drying was recorded in grams. The dried materials were weighed, and the shoot dry weight was recorded.

RESULTS AND DISCUSSION

A highly significant difference in number of days to emergence was observed among the lines, genotypes, and seed size categories (Table 3). This result is consistent with the observation of morphological variation in selected accessions of Bambara groundnut obtained by (Unigwe et al., 2016), who reported a wide variation for days to emergence. The mean for the genotypes ranged from (7.19 to 8.92 days). G3 genotype had the shortest days to emergency (7.19 days after sowing), while the genotype G1 recorded the highest (8.92) days to emergency (Table 4, Figure 2). Among the lines, G3LR2P1 registered the lowest number of days to emergency (6.50 days after sowing), while G1SR3P1had the highest number of days to emergency (9.33 days after sowing) (Table 4, Figure 4). Among the seed size categories, large seed size recorded the lowest number of days to emergency (7.92 days after sowing). In comparison, small seed size registered the highest number of days to emergency (8.00 days after sowing) (Table 4, Figure 3).

The varietal effect on plant height was highly significant for all the genotypes and lines; however, no significant difference was observed among the seed size categories (Table 3). The increased variability offers scope for selection and improving the character in the desired direction. The same result for this character in agro-morphological divergence among the Bambara groundnut population was reported by (Bonny et al., 2019). The plant height for genotypes varied from 28.33 cm to 34.09 cm. The highest plant (34.09 cm) was from the G3 genotype, while the genotypes G1, G2, G4, and G5 were almost similar in height (Table 4, Figure 2). Among the lines, plant height ranged from 24.89 cm to 36.89cm. The shortest plant was registered by the G4LR3P3 line (24.89 cm), while the G3MR1P3 was recorded as the tallest plant (36.89 cm) among the lines (Table 4, Figure 4).

There was a highly significant difference among the genotypes and lines, but no significant difference was observed among the seed size categories for wide canopy (Table 3). This investigation is in harmony with agro-morphological divergence among four agroecological populations of Bambara groundnut with the works of (Bonny et al., 2019). The G2 genotype had the widest canopy spread (76.97 cm), statistically similar to the G3, while the least canopy spread (54.59 cm) resulted from G5. Among the lines, the wide canopy ranged from 30.00 cm to 85.17 cm. G5LR3P3 recorded the least canopy spread, whereas the widest canopy spread was registered by G2SR1P1 (Table 4, Figure 4).

Table 3: Mean squares of vegetative traits

SOV	df	NDE	NDF50%	PH	WC	DM	NP	NL	NB	FB	DB
Blocks	2	0	1.15ns	82.46*	940.52*	696.04*	29022.81*	261210.65*	684.05*	40818.75*	2756.77ns
Lines (L)	27	1.86**	16.58ns	32.61*	674.67**	31.00ns	5726.07**	51535.73**	82.78*	7501.45ns	1257.20ns
Genotypes (G)	(4)	5.59**	25.15ns	96.08**	2335.27**	57.07ns	26208.66**	235880.96**	159.18**	17445.98*	3548.48**
L (G)	(23)	1.21**	15.09ns	21.58ns	385.87**	26.46ns	2163.89ns	19475.69ns	69.49**	5771.96ns	858.72ns
Seed Sizes (S)	(2)	0.29**	32.72ns	6.47ns	179.61ns	96.83*	2153.45ns	19379.53ns	11.27ns	3670.13ns	998.77ns
L (S)	(25)	1.99**	15.29ns	34.71*	714.28**	25.73ns	6011.88**	54108.23**	88.50**	7807.95ns	1277.88ns
Error	54	0.00	23.46	17.56	157.90	24.13	2707.39	24366.29	32.20	6832.80	945.48

Note: * Significant at 5%, ** highly significant at 1%, ns = not significant, SOV = source of variation, G = genotypes, DF = degree of freedom, NDE= number of days to emergency, NDF50% = number of days to 50% flowering, PH = plant height, WC= wide canopy, DM=days to maturity, NP= number of petioles, NL= number of leaves, NB= number of branches, FB= fresh biomass, DB= dried biomass.

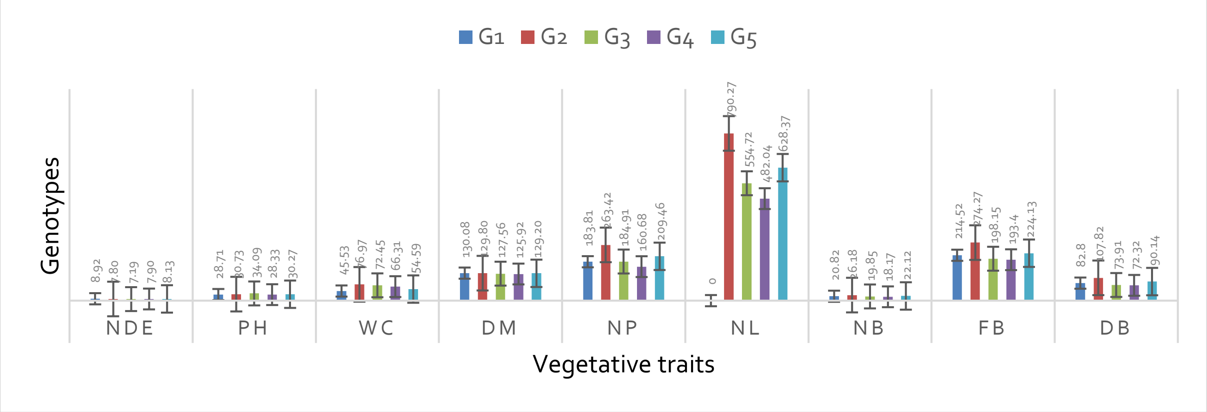

Figure 2: Variability among 5 genotypes of Bambara groundnut for vegetative traits. Note: G1= Giwa, G2, Duna, G3= Cancaraki, G4= Jatau, G5= Maiki, NDE= number of days to emergency, PH = plant height, WC= wide canopy, DM=days to maturity, NP= number of petioles, NL= number of leaves, NB= number of branches, FB= fresh biomass, DB= dried biomass.

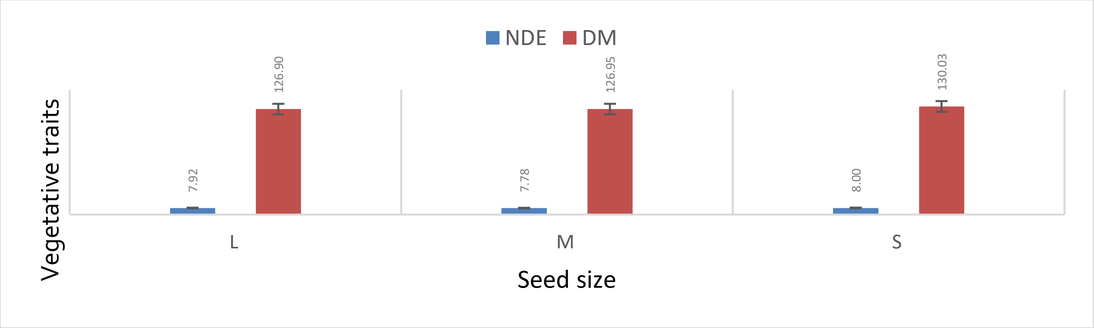

Figure 3: Variability among 3 seed size category of Bambara groundnut for vegetative traits. Note: L= large seed sizes, M= medium seed sizes, S= small seed sizes, NDE= number of days to emergency, DM=days to maturity.

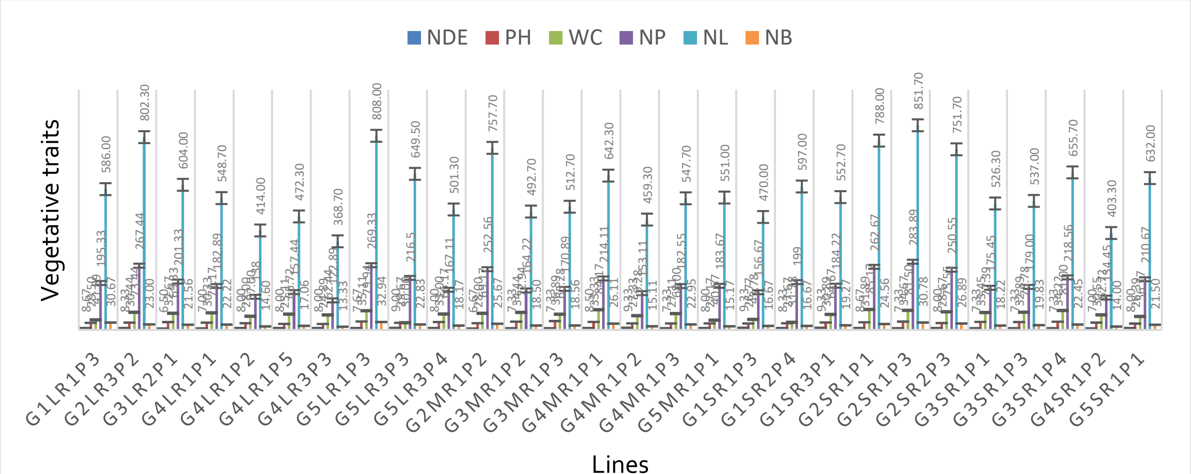

Figure 4: Variability among 28 of Bambara groundnut for vegetative traits. Note: NDE= number of days to emergency, PH = plant height, WC= wide canopy, NP= number of petioles, NL= number of leaves, NB= number of branches.

Days to maturity varied significantly among the seed size categories, while no significant difference was observed among the genotypes and lines (Table 3). Almost similar results on morphological variation in selected accessions of Bambara groundnut were obtained by (Unigwe et al., 2016)**.** According to Swanevelder (1998), the maturity of the Bambara groundnut varies from three to six months, depending on cultivar and climatic conditions. Photoperiod, on the other hand, has an impact. The mean number of days to maturity among types of seed size varied from 126.90 to 130.03 days. Large and medium seed sizes recorded the earliest maturity (126.90 and 126.95 days), respectively, which was statistically the same, whereas small seed size registered the maximum days to maturity (130.03 days) (Table 4, Figure 3).

A highly significant difference was observed among the genotypes and lines for the number of petioles per plant, while no significant difference was recorded among the seed size categories (Table 3). Similar reports on estimates of genetic parameters in Bambara groundnut have been published by Onwubiko *et al.* (2019), who reported a significant difference among the Bambara accessions for such related traits. The highest number was G2 reported, while G4 reported the lowest, dynamically similar to G1 and G3 (Table 4, Figure 2). Line mean values for this attribute ranged from 122.89 to 283.89; the G4LR3P3 line recorded a lower mean of (122.89) almost significantly the same with most of the other lines, while the maximum number of petioles was observed by line G2SR1P3 (283.89) Table 4, Figure 3.

A significant difference was observed among the genotypes and lines for the number of leaves per plant, but no significant difference was recorded among the seed size categories (Table 3). This was in agreement with the findings of Bonny et al. (2019), who reported vast differences in vegetative traits, including the number of leaves per plant among four agroecological populations of Bambara groundnut. Mean performance among the genotypes ranged from 482.04 to 790.27. Genotype G2 recorded the maximum leaves number per plant, while the minimum leaves number per plant was observed in G4, which is statistically comparable with the genotypes G1, G3, and G5 (Table 4, Figure 2). G2SR1P3, amongst the lines, resulted in the highest number of leaves per plant (851.70), while G4SR1P2 registered the minimum number of leaves per plant (430.30) (Table 4, Figure 4).

The results of the branch number per plant are presented in (Table 3). Varietal differences were highly significant among the genotypes, while significant differences were observed among the lines, but no significant difference was observed among the seed size. Agreement with this research finding can be found in the work on estimates of genetic parameters in Bambara groundnut Onwubiko et al. (2019), who reported significant differences among quantitative traits, including several branches per plant. Mean performance among the genotypes ranged from 18.17 to 26.18. The G2 has the most significant number of branches per plant (26.18), while the G4 has the smallest number of branches per plant (18.17), which was statistically the same as the G1, G3 and G5 genotypes (Table 4, Figure 2). Mean values among the lines ranged from 13.33 to 32.94. G4LR3P3 resulted in the lowest number of branches per plant, whereas G5LR1P3 registered the highest number of branches per plant, statistically similar to most other lines.

Significant differences have been found amongst the genotypes for fresh biomass and highly significant differences for dried biomass per plant traits. However, no significant difference was observed among the lines and seed size categories (Table 3). These results align with the works on morphological variation in selected accessions of Bambara groundnut by (Unigwe et al., 2016), who reported that a highly significant difference between fresh and dried wight indicated high genetic variation for this trait. Wide ranges of variation for fresh biomass from 193.40 g to 274.27 g per plant and for dried biomass from 72.32 g to 107.82 g per plant were observed among the genotypes. The G2 recorded the highest weight of fresh and dried biomass (274.27 g, 107.82 g), respectively, while the lowest fresh and dried biomass was registered by the G4 genotype (Table 4, Figure 2). There were no significant differences among the lines, genotypes, and seed size categories for the number of days to 50% of flowering (Table 3), which was supported by (Valombola et al., 2019**)**; he found no significant difference in agronomic and morphological diversity of Bambara groundnut accessions in North-Central Namibia for this trait and the same result on estimating heritability and genetic advance in Bambara groundnut reported by (Namo & Damfami, 2020). Photoperiod, temperature, altitude, and soil structure, as well as genotypic character, are all factors that influence flowering in Bambara groundnut (Shegro et al., 2013).

Table 4: Means comparison for vegetative traits

Line	NDE	NDF50 %	PH	WC	DM	NP	NL	NB	FB	DB
G1LR1P3	8.67c	51.67a	29.50a-e	41.89f-h	130.00a	195.33a-e	586. a-e	30.67ab	217.86a	83.52a
G2LR3P2	8.33e	49.00a	30.44a-e	73.44a-d	131.00a	267.44a-c	802.30a-c	23.00a-f	293.17a	156.43a
G3LR2P1	6.50k	48.67a	32.67a-e	69.33a-d	127.33a	201.33a-e	604. a-e	21.56b-f	217.11a	79.84a
G4LR1P1	7.00i	44.00a	30.33a-e	71.17a-d	123.33a	182.89a-e	548.70a-e	22.22a-f	233.85a	85.48a
G4LR1P2	8.00f	45.67a	28.00b-e	57.00c-g	122.67a	138.00e	414.00e	14.61ef	150.52a	62.01a
G4LR1P5	8.00f	46.00a	25.11de	65.72a-f	124.67a	157.44de	472.30de	17.06c-f	166.02a	63.18a
G4LR3P3	8.00f	49.00a	24.89e	62.44a-g	124.00a	122.89e	368.70e	13.33f	133.59a	58.50a
G5LR1P3	7.67g	48.33a	35.11ab	79.94a-d	126.67a	269.33ab	808.ab	32.94a	264.9a	104.73a
G5LR3P3	9.00b	52.33a	29.67a-e	30.00h	127.00a	216.50a-e	649.50a-e	22.83a-f	216.85a	97.18a
G5LR3P4	8.00f	52.67a	33.00a-e	66.17a-f	132.33a	167.11b-e	501.30b-e	18.17c-f	224.76a	88.21a
G2MR1P2	6.67j	49.00a	28.00b-e	69.17a-d	128.33a	252.56a-d	757.70a-d	25.67a-e	222.63a	78.92a

G3MR1P2	7.33h	48.67a	34.44a-c	72.94a-d	129.00a	164.22c-e	492.70c-e	18.50c-f	189.63a	70.36a
G3MR1P3	7.33h	49.33a	36.89a	65.28a-f	124.67a	170.89b-e	512.70b-e	18.56c-f	156.91a	60.05a
G4MR1P1	8.50d	51.00a	33.33a-d	84.17ab	131.33a	214.11a-e	642.30a-e	26.11a-d	294.52a	98.28a
G4MR1P2	9.33a	48.33a	27.33b-e	59.28b-g	121.33a	153.11de	459.30de	15.11d-f	164.17a	61.98a
G4MR1P3	7.33h	49.33a	27.11b-e	68.00a-e	128.33a	182.55a-e	547.70a-e	22.95a-f	256.30a	91.08a
G5MR1P1	8.00f	46.67a	27.17b-e	40.67gh	125.67a	183.67a-e	551.00a-e	15.17d-f	166.86a	67.90a
G1SR1P3	9.33a	54.00a	26.77b-e	43.78e-h	130.00a	156.67de	470.00de	16.67c-f	182.36a	72.64a
G1SR2P4	8.33e	47.33a	27.67b-e	31.78h	131.67a	199.00a-e	597.00a-e	16.67c-f	231.50a	90.15a
G1SR3P1	9.33a	52.33a	30.89a-e	64.67a-g	128.67a	184.22a-e	552.70a-e	19.27c-f	226.36a	84.90a
G2SR1P1	8.67c	47.33a	31.89a-e	85.17a	130.67a	262.67a-c	788.00a-c	24.56a-f	300.62a	107.11a
G2SR1P3	7.33h	50.67a	34.67a-c	81.5a-c	128.33a	283.89a	851.7a	30.78ab	325.49a	104.62a
G2SR2P3	8.00f	52.33a	28.67a-e	75.55a-d	130.67a	250.55a-d	751.70a-d	26.89a-c	229.46a	92.04a
G3SR1P1	7.33h	50.33a	33.45a-d	72.39a-d	126.00a	175.45b-e	526.30b-e	18.22c-f	190.10a	76.72a
G3SR1P3	7.33h	49.67a	32.89a-e	73.78a-d	128.33a	179.00b-e	537.00b-e	19.83b-f	194.44a	75.09a
G3SR1P4	7.33h	50.33a	34.22a-c	81.00a-d	130.00a	218.56a-e	655.70a-e	22.45a-	240.72a	81.40a
G4SR1P2	7.00i	51.00a	30.55a-e	62.72a-g	131.67a	134.45	403.30e	14.00f	148.26a	58.03a
G5SR1P1	8.00f	51.33a	26.39c-e	56.17de-g	134.33a	210.67a-e	632.00a-e	21.50b-f	247.27a	92.66a

Genotype	NDE	NDF50%	PH	WC	DM	NP	NL	NB	FB	DB
G1	8.92a	51.33a	28.71b	45.53d	130.08a	183.81bc	551.42bbc	20.82b	214.52ab	82.80b
G2	7.80d	49.67a	30.73b	76.97a	129.80a	263.42a	790.27a	26.18a	274.27a	107.82a
G3	7.19e	49.50a	34.09a	72.45ab	127.56a	184.91bc	554.72bc	19.85b	198.15b	73.91b
G4	7.90c	48.04a	28.33b	66.31b	125.92a	160.68c	482.04c	18.17b	193.40b	72.32b
G5	8.13b	50.27a	30.27a	54.59c	129.20a	209.46b	628.37b	22.12b	224.13ab	90.14ab
Seed Categories										
Large	7.92b	48.73a	29.87a	61.71a	126.90b	191.83a	575.48a	21.64a	211.86a	87.91a
Medium	7.784c	48.91a	30.61a	65.64a	126.95b	188.73a	566.19a	20.29a	207.29a	75.51a
Small	8.00a	50.61a	30.73a	66.23	130.03a	205.01a	615.03a	20.99a	228.78a	85.03a
Mean	7.92	49.51	30.39	64.47	128.14	196.23	588.70	21.05	217.37	83.68
SE	0.08	0.50	0.53	2.03	0.71	7.17	21.52	0.88	9.68	3.60
CV	9.83	9.19	16.12	28.81	5.09	33.51	33.51	38.12	40.81	39.46

Note: Means with the same letter are not significantly different, SE= standard error, C.V= coefficient variation G1= Giwa, G2, Duna, G3= Cancaraki, G4= Jatau, G5= Maiki, NDE= number of days to emergency, NDF50% =

number of days to 50% flowering, PH = plant height, WC= wide canopy, DM=days to maturity, NP= number of petiole, NL= number of leaves, NB= number of branches, FB= fresh biomass, DB= dried biomass.

Genetic variability, heritability, and genetic advance as criteria for morphological traits selection in Bambara groundnut

The estimation of genetic variables viz., variability in the phenotypic and genotypic coefficients, heritability in a specific sense, and genetic advancement for ten characters of vegetative studied are presented in (Table 5).

Genetic Variability

The extent of variability concerning phenotypic and genotypic variances, phenotypic and genotypic coefficients of variance, heritability broad sense, and genetic advance for the ten vegetative traits are presented in (Table 5) respectively. The phenotypic coefficient of variation value was higher than the genotypic coefficient of variation for all the characters, indicating the influence of the environment on the expression of these parameters. A similar result was reported by Onwubiko et al. (2019), who reported that phenotypic variances were slightly higher than the corresponding genotypic variances in all the phenotypic descriptors.

The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) estimate ranged from (GCV= 0 to 20.36%) and (PCV= 0 to 38.71%), respectively, among the vegetative parameters (Table 5). Moreover, the high values of GCV (20.36%) and PCV (28.18%) resulted from the broad canopy trait. In contrast, moderate GCV and high PCV were registered from the number of petioles, number of leaves, number of branches, and dried biomass (GCV=16.16, 16.17, 19.51 and 12.18%), (PCV= 31.05, 31.05, 33.28 and 38.71%) respectively. Whereas the low GCV (6.87%) and high PCV (38.64%) were recorded for fresh biomass, while the plant high trait had low GCV (7.37%) and moderate PCV (15.63%), but for the days to maturity and number of days to 50% of flowering, both GCV and PCV were low (Table 5).

Table 5: Estimates of variability, heritability, and genetic advances of vegetative traits for five genotypes of Bambara

Traits	$\sigma^2{}_g$	$\sigma^2{}_e$	$\sigma^2{}_p$	GCV (%)	PCV (%)	$h^2{}_{B\%}$	GA%
NDF50%	0	20.69	20.69	0	9.19	0	0
PH	5.02	17.56	22.58	7.37	15.63	22.23	7.16
WC	172.26	157.9	330.16	20.36	28.18	52.17	30.29
DM	2.29	24.13	26.42	1.18	4.01	8.66	0.72
NP	1006.2	2707.4	3713.6	16.16	31.05	27.1	17.33
NL	9056.5	24366.3	33422.8	16.17	31.05	27.1	17.33
NB	16.86	32.2	49.06	19.51	33.28	34.36	23.56
FB	222.88	6832.8	7055.68	6.87	38.64	3.16	2.51
DB	103.91	945.48	1049.39	12.18	38.71	9.9	7.9

Note: $\sigma^2 g$= Genotypic variance, σ^2s= Seed weight variance, σ^2e= Error of variance, σ^2p= Phenotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2B= Broad sense heritability, GA= Genetic advance, NDE= number of days to emergency, NDF50% = number of days to 50% flowering, PH = plant height, WC= wide canopy, DM=days to maturity, NP= number of petioles, NL= number of leaves, NB= number of branches, FB= fresh biomass, DB= dried biomass.

Similar findings were also reported for most of the characters on estimates of genetic parameters in Bambara groundnut, variation in pod yield characters, and heritability estimates in some cultivars of Bambara groundnut by Onwubiko et al. (2019) (Jonah et al., 2012) respectively.

Broad-sense Heritability and Genetic Advance

Heritability is known as the fraction of overall variance of phenotypic features between individuals in a particular group due to genetic variation. Individual features provide stronger signals than higher GCV combined with high heritability and GA. The broad-sense heritability of the examined vegetative features ranged from 0 to 52.17%. The two variables with intermediate heritability (52.17% and 34.3%, respectively) were wide canopy and number of branches (Table 5), showing that the environment less influences the magnitudes of heredity. In contrast, other characters had low heritability (0 to 30%). Prior research has found that traits with high estimates of heritability and high values of genetic progress can be subjected to direct selection (Langat et al., 2019). The same result for the wide canopy, which had a moderate heritability estimate, was recorded by Onwubiko et al. (2019).

Furthermore, the genetic advance (GA) calculated expressed the high genetic advance values (≥20%) for wide canopy (30.29%), number of branches (23.56%) (Table 5), total small seed weight per plant (23.56%), (Table 5). In contrast, moderate values resulted in the number of tiny seeds per plant (19.19%), 100-seed weight (18.73%) respectively (Table 5), number of petioles, and number of leaves (17.33%) (Table 5). In the selection processes, these characters were essential, with little influence from the setting. Similar findings on assessments of genetic parameters in Bambara groundnut, variability in pod yield characteristics, and estimates of heritability in some Bambara groundnut cultivars were also reported for most of the characters by Onwubiko et al. (2019) (Jonah et al., 2012) respectively. This is consistent with prior heredity research, which found that trait development selection is influenced not just by available genetic variation but also by the level of heritability (Langat et al., 2019). The current study shows that improving yield and other associated parameters of Bambara groundnut can be accomplished through selection based on heritability and genetic advance estimates.

Furthermore, the magnitude of changes detected for practically all agronomic properties was significant, which can be used to plant breeders' advantage in improving the agronomic characteristics of this crop.

CONCLUSION

The only basis for developing Bambara groundnut genotypes that may contribute to food security is the study of the genetic components of the crop's quantitative characteristics. Significant levels of variability were found in the five genotypes, fifteen combinations of genotypes and seed size categories, and the interaction between genotypes and seed size categories for the highest levels of vegetative characters in the current study.

It is evident from the second experiment that the improvement of related characters of *V. subterranean* can be achieved through selection by the estimates of heritability and genetic advance. Moderate broad sense heritability coupled with high genetic variance for growth traits such as wide canopy and number of branches and low for other traits are responded selection for these particular traits. The development of Bambara groundnut genotypes that could lead to attaining food security solely rests on exploring genetic aspects of the crop's quantitative traits because genetic variations provide room for recombinants essential for developing new genotypes or lines. Most of the lines showed variations for vegetative. It was concluded from this investigation that a considerable amount of variation exists among Bambara groundnut cultivars for vegetative traits.

Subsequently, a new crop could enhance the genetic potential and inspire long-term research and development of new genotypes; therefore, the Bambara groundnut improvement project is essential. Furthermore, the current experiment was carried out to assess the evaluation and genetic analysis yield performance of 28 Bambara groundnut lines selected based on vegetative traits with the specific objectives of determining phenotypic relationship, genetic components, heritability, genetic advance, and selection of superior lines based on vegetative traits for future breeding program.

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