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Evaluation and Genetic Analysis of Vegetative Traits in Different Genotypes of Bambara Groundnuts According to Seed Weight

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ABSTRACT

Analysis of genetic diversity in wild and cultivated plants is an essential requirement for any crop improvement involving genetic engineering, which includes evolution, ecological, geographical, and human factors, particularly in underutilized crops like Bambara groundnut. Therefore, knowledge of the genetic factors responsible for this character's inheritance is important for initiatives involving breeding that present significant genetic diversity in collections of germplasm. Five Bambara groundnut genotypes were evaluated using randomized complete block design with three replications. Three categories large, medium, and small seed sizes were used to group the seeds. For the majority of vegetative variables in the current study, significant differences were found across all 5 genotypes, 15 combinations of seed size and genotypes, seed size categories, and the interaction between genotype and seed size categories. For the overall variable, the impact of the environment on these traits was demonstrated by the fact that the phenotypic coefficient of variation was greater than the genotypic coefficient of variation. Moreover, low heritability and genetic advance were observed for whole vegetative traits. Both the phenotypic and genotypic coefficients of variation (GCV and PCV) estimation ranged from (0 to 10.71% and 3.84 to 48.36% respectively, for the vegetative parameters. Moderately GCV amounts (10.71%) and high PCV (24.77%) was recorded for the number of branches for each plant and the number of days to emergency. GCV (10.40%) and PCV (29.69%), while low GCV and high PCV have been recorded from rest vegetative variables except days to maturity that was low for both GCV and PCV. Further studies should be carryout for seeds weight on vegetative traits for improvement of these Bambara genotypes under different environments.

Keywords: Bambara Groundnut, Genetic Analysis, Seed Weight, Vegetative Traits.

INTRODUCTION

Bambara groundnut (*Vigna subterranea* L. (Verdc.) as a neglected crop, has the ability to increase the security in terms of nutrition and food while offering solutions for environmental sustainability and fairness in the accessibility and cost of food (Tan et al., 2020). Agroecological variables including environment (Berchie et al., 2016), fertility of the soil (Tyoakoso et al., 2019), accessibility to water (Chai et al., 2016), and the length of the day (Kendabie et al., 2020) have all been implicated in variations in Bambara groundnut production. Although several landraces have evolved to areas with a wide range of daylength, they are still considered autonomous short-day crops for pod set (Kendabie et al., 2020). In crop development initiatives, understanding genetic variability and breeding approaches is essential (Khaliqi et al., 2021)[1].

The phenotypic performance of seeds depends on three main factors viz; impacts of the environment, genotype, and genotype by interaction with the environment. The kernels possess the same genetic, psychological issues and biochemical characteristics of the embryo. The traits of seedlings that subsequently mature into juvenile and adult phases are mostly determined by the embryo and their surroundings (Tyagi, 2013).

Generally, kernel act as a significant phase in determining the ability of a seed batch to germinate under a variety of environmental circumstances. There are numerous parameters used to determine seed viability of crop which include dehydrogenase activity, accelerated aging, electrical conductivity, germination rate, seedling length, cold test, cool test, seedling dry weight, seedling mass, seed shape, and size (Sundaram et al., 2019). Although much investigation has been done on the gene action of yield and features associated to yield in Bambara groundnuts, none of these studies have specifically examined seed size and weight (Khaliqi et al., 2021)[2]

The factorial discriminatory evaluation demonstrated that agro-morphological variety was organized based on the populations' geographic origins and explained the overall variability. Phenological, vegetative, and yield types are attributes that cause agro-morphological variation amongst populations (Séverin et al., 2019). Research on how seed size is inherited is crucial for choosing the best breeding approach to create better plant cultivars. Similarly, the relationships of grain yield phenology and its constituent characteristics are important criteria for selection base on seed quality (Sundaram et al., 2019). The nature of diversity in the breeding population may be explored with the use of the genotypic and phenotypic coefficient variance (Acquaah, 2012).

To improve crop development, genotypic correlation is a useful technique for identifying the connections between agronomic variables in genetically varied populations (Bello et al., 2006). According to Addissu (2011), heritability quantifies the extent to which a certain trait is inherited by the next generation.

It provides the information required for the selection process and shows the proportion of genetic variability that has a genetic basis (Falconer, 1996). Additionally, it is contingent upon the strength and direction of the correlation between the desired attributes (More & Borkar, 2016). The extent of a character's gain under specific selection pressure is explained by genetic advancement (Shukla et al., 2006; Nwangburuka & Denton, 2012). According to several reports, combining genetic advancements with heritability estimations yields are the greatest results in crop development programs (Shukla et al., 2006; Asfaw et al., 2017). Improved yield is typically the result of selecting features with high heritability values and strong genetic advance values (Umar et al., 2014).

Correlation coefficient and path analysis are reliable statistical techniques for organizing and presenting the pattern of relationship between the predictor trait and response trait which can be used as selection criteria for enhancement of different traits (Mohan & Thiyagarajan, 2019). Therefore, the present experiment was carried out to assess the genetic inheritance on yield performance of Bambara groundnut genotypes selected based on seed weight with the specific objectives such as determining phenotypic relationship, genetic components, heritability, genetic advance, and selection of high yield lines.

Therefore, in order to understand genetic variability, heritability, and genetic advancement, a breeder must choose suitable genotypes for their enhancement. An overview of the relative significance of the many kinds of genetic factors determining the overall variability in plant character is given by estimates of genetic parameters (Nwosu et al., 2013).

MATERIALS AND METHODS

Experimental location and station

The current study was conducted at Universiti Putra Malaysia (UPM) Research Field 15, Faculty of Agriculture. Located at latitude 3°02′ N and longitude 101°42′ E, it is 31 meters above sea level.

The land was mechanically ploughed and harrowed and the bed was prepared in rows. The seeds were planted at a planting distance of 30 cm, row to row distance, using a Randomized Complete Block Design (RCBD) with three replications. The experimental fields were irrigated natural rainfall and supplementary irrigation using water sprinkler system. Weeding was controlled using silver shine mulching furrow bed weeds were controlled manually using hand hoeing and or hand pulling when was tendered. The recommended fertilizer were nitrogen, phosphorus and potassium were applied during land preparation and growth stages; hence, 70% N was applied two and six weeks after. The plants were checked for insects, pests, and diseases. Pesticides and fungicides were applied at different stages of growth for controlling fungi and insect pests at recommended rates when necessary.

In this experiment, five Nigerian Bambara groundnut genotypes, Giwa, Duna, Cancaraki, Jatau, and Maiki, were employed (Fig 1). Large, medium, and small are the three seed weight classifications, were created from the seeds of each genotype. One seed per cell was planted in trays containing fifteen genotype combinations depending on seed weight categories and genotypes listed in Table 1. The seedlings were placed in the trays with a mixture of soil and peat moss, and after 20 days, they were transferred to the experimental field.

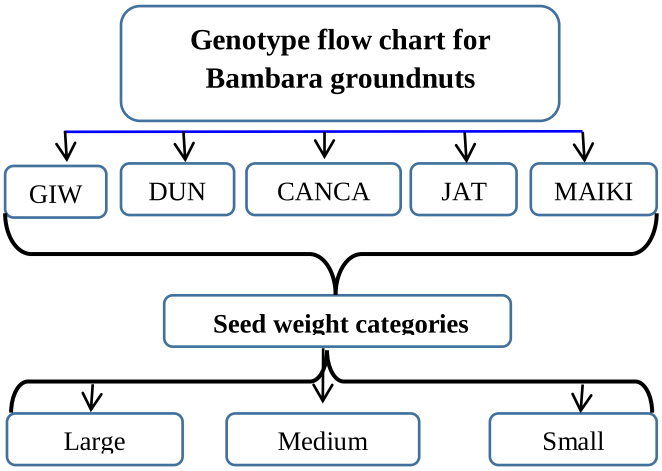

Figure 1. Genotype flow chart for Bambara groundnuts according to kernel weight.

Table 1. Bambara groundnut combination of genotypes and seed weight categories used in the first-generation

NO	Combination Code	Genotype	Seed Size
1	G1L	GIWA	Large
2	G2L	DUNA	Large
3	G3L	CANCARAKI	Large
4	G4L	JATAU	Large
5	G5L	MAIKI	Large
6	G1M	GIWA	Medium
7	G2M	DUNA	Medium

8	G3M	CANCARAKI	Medium
9	G4M	JATAU	Medium
10	G5M	MAIKI	Medium
11	G1S	GIWA	Small
12	G2S	DUNA	Small
13	G3S	CANCARAKI	Small
14	G4S	JATAU	Small
15	G5S	MAIKI	Small

Data collection

Ten vegetative attributes were the subjects of data collection; these are listed in Table 2. The quantitative information gathered adheres to the Bambara groundnut specifications (IPGRI, IITA, BAMNET & Gonne *et al*., 2013). Growth parameters estimate the rate of germination from four days following seed germination until all seeds have germinated., other variables were directly recorded at various growth stages in the field and in the laboratory following harvest, as shown by the following descriptions (IPGRI IITA, BAMNET).

Table 2. List of quantitative traits

Character	Abbreviation	Method of evaluation
Emergency Days	NDE	Number of days has been recorded from sowing to the first day of germination.
Flowering Days (50%)	NDF50%	It was calculated how many days it took for 50% of the plants in each plot to open their first flowers after being sown.
Height of Plant (cm)	PH	The mature height of the plant was measured and expressed in centimeters, starting from the ground and ending at 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.
Maturity Days (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 fresh weight was recorded.
Dried Biomass (gr)	DB	Biological yield produced by each plant after drying was recorded in grams. The dried materials were weighed and the shoot dry weight was recorded.

Statistical analysis

All morphological characteristics as specified by Gomez (1984) were statistically analyzed using the Statistical Analysis System (SAS) version 9.4 for analysis of variance (ANOVA). At 5%, Duncan's New Multiple Range Test (DNMRT) was used to compare means. For every character, including the seed weight, the variance component and heritability were estimated. The variance component was calculated from the expected mean squares using

SAS's Restricted Maximum Likelihood (REML) method and PROC VARCOMP.

RESULTS AND DISCUSSION

Significant differences were detected for the number of days to emergence among the genotypes, ranging from 7.50 days to 10.56 days. This shows that some Genotypes are more vigorous in terms of days to germination compared to other genotypes. In studies on Bambara groundnut genetic variability, heritability, and clustering patterns by Khan et al., 2020, in Malaysia, this finding was supported regarding quantitative characters for most vegetative traits. It was determined that the quantitative characteristics considered in the study exhibit a large amount of variance.

The potential for enhancing the genotypes studied for this character was suggested by such variation. This could be due to variations in their genetic make-up with respect to the evaluated character. This outcome was consistent with Suneetha's (2007) findings, and Sobda *et al*. (2013) studied genetic diversity among groundnuts using quantitative morphological traits, where the mean value for the number of days to emergence ranged from 7 to 15 days after sowing. Genotype G3 had the shortest days to emergency (7.50 days after sowing), followed by G1, G5, G4, and G2 (Table 4), however, no significant differences were observed among the combinations, seed size categories, and interaction of seed size and genotypes (Table 3, Table 4).

It was observed that there was a significant decrease in the mean value of combinations, seed size, and interaction for days to flowering (50%). Still, no significant variation was found amongst the genotypes. The Bambara groundnut accessions had a wide range of days to flowering (50%). The average days to 50% flowering were close to 44 days across the 28 accessions, with a range of 35 to 53 days after sowing in Malaysia, which is closer to the 38 days with a range of 25 to 51 days after sowing reported by (Khan *et al*., 2020). Variability in days to flowering was observed, which determines the earliness of the crop, even though it was not statistically different. This showed that most of the genotypes studied took the same number of days to flower, hence mature at more or less the same time. Masindeni (2006) also reported similar observations on assessing yield and yielding variables, where no significant difference between genotypes was observed. Bambara groundnut genotypes and seed size categories were significantly affected by the days to 50% flowering for large and medium seed size categories, but were not significant for the small seed size category (Table 4). The 50 percent of days to flowering among the genotypes for large seed size categories ranged between 35.00 and 46 days where G3 had the lowest (35 days), followed by genotypes G1, G2, G4, and G5 For medium seed size, G4 recorded the highest (50.33 days), while the other genotypes were similar (Table 4).

Among the combinations, G3L recorded the lowest (35 days), while the highest 50% flowering (53 days) was recorded in G3S (Table 4). The range illustrated for days to 50% flowering in seed size categories (42.86 to 47.27 days) indicated variability. The highest mean for 50% flowering was observed for small seed size, while no significant differences were observed between the large and medium seed size categories (Table 4). Bambara groundnut landraces flowering times in Burkina Faso were varied from 32 to 53 days, according to Ouedraogo *et al*. (2008), and 36 to 53 days were reported among twenty genotypes of Bambara groundnut which were under identical environments of Pretoria, South Africa (Shegro *et al*., 2013).

Flowering in *V. subterranea* is influenced by a variety of ecological aspects, including warming, height, the condition of soil and germplasm. According to reports, as a short-day crop, cultivating Bambara groundnut will cause delayed or absent flowering during long days, hence the number of days to flowering is considered cultivar-dependent (Swanevelder,1998; Shegro *et al*., 2013).

Table 3. Mean squares of vegetative traits

SOV	df	NDE	NDF50 %	PH	WC	DM	NP	NL	NB	FB	DB
Replications	2	2.64ns	7.45ns	56.93*	729.18*	58.12*	2135.59ns	19220.28ns	128.70ns	27153.57*	5398.39*
Combinations	14	6.54ns	51.78*	8.76ns	91.12ns	41.90**	3716.56**	33448.99**	52.20ns	12739.99*	1241.18*
Seed Sizes(S)	(2)	3.80ns	85.33*	0.85ns	92.87ns	62.74*	3067.06ns	27603.52ns	4.27ns	5838.09ns	299.27ns
Genotypes(G)	(4)	12.48*	22.00ns	19.49*	25.81ns	61.70**	4067.09*	36603.07*	87.72ns	8146.100ns	801.68ns
S×G	(8)	4.27ns	58.28*	5.37ns	123.33*	26.79ns	3703.67**	33333.32**	46.42ns	16761.97**	1696.42*
Error	27	4.14	22.26	6.49	46.1	13.05	1216.03	10944	43.19	5564.38	566.59

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

Combine Treatment	NDE	NDF50%	PH	WC	DM	NP	NL	NB	FB	DB
G1L	11.00a	44.00a-d	20.58a	59.39a	125.78a	202.06b-d	606.17b-c	24.94a	171.82bc	65.21bc
G2L	8.00a	43.33b-d	23.53a	59.07a	124.39ab	155.15c-e	465.45c-e	19.01a	179.60bc	68.32bc
G3L	7.50a	35.00d	27.25a	84.00a	113.50c	266.50a	799.50a	34.50a	415.53a	139.04a
G4L	7.33a	42.67b-d	24.12a	63.84a	120.94ab	160.90c-e	482.70c-e	24.71a	189.09bc	79.06bc
G5L	10.67a	46.67a-c	23.90a	65.15a	114.33c	153.92c-e	461.75c-e	17.08a	179.94bc	68.17bc
G1M	10.00a	41.67b-d	22.83a	61.86a	125.17ab	199.50b-d	598.50b-c	26.67a	188.56bc	75.78bc
G2M	8.67a	42.67b-d	24.90a	63.23a	121.58ab	196.13b-d	588.40b-c	22.73a	257.18b	100.39ab
G3M	7.00a	43.33b-d	25.20a	55.72a	118.50bc	136.56de	409.67de	23.22a	114.46bc	50.71c
G4M	11.33a	50.33ab	23.51a	61.54a	124.89ab	182.67b-e	548.00b-e	23.20a	230.79bc	84.99bc
G5M	11.00a	39.00cd	21.17a	58.25a	124.00ab	119.50e	358.50e	16.67a	92.25c	42.89c
G1S	8.67a	46.00a-c	21.69a	60.63a	125.50ab	217.99a-c	653.97a-c	22.10a	185.28bc	84.21bc
G2S	8.67a	46.67a-c	23.67a	64.73a	125.67ab	230.47ab	691.40ab	28.73a	226.39bc	87.40bc
G3S	8.00a	53.00a	25.38a	61.98a	122.00ab	173.68b-e	521.05b-e	24.17a	159.25bc	60.62bc
G4S	7.67a	48.00a-c	21.30a	59.53a	124.00ab	177.12b-e	531.35b-de	22.55a	180.43bc	73.66bc
G5S	10.00a	42.67b-d	23.83a	60.17a	124.67ab	178.00b-e	534.00b-e	20.00a	155.65bc	68.55bc
Genotype										
G1	9.90a	43.89a	21.70b	60.63a	125.48a	206.52a	615.54a	24.57a	181.89a	75.07a
G2	8.44ab	44.22a	24.03ab	62.35a	123.88ab	193.92a	581.75a	23.49a	221.06a	85.37a
G3	7.50b	44.88a	25.78a	65.14a	118.56c	182.97ab	548.89ab	26.40a	206.52a	76.51a
G4	8.78ab	47a	22.98ab	61.64a	123.28ab	173.56ab	520.68ab	23.49a	200.10a	79.24a
G5	10.56a	42.78a	22.97ab	61.19a	121.00bc	150.47b	451.42b	17.92a	142.61a	59.87a
Seed Categories										
Large	9	42.86b	23.64	65.03	120.24b	182.08	546.23	23.3	213.74	80.03
Medium	9.6	43.40b	23.52	60.12	122.83ab	166.87	500.61	22.5	176.65	70.95
Small	8.6	47.27a	23.17	61.41	124.37a	195.45	586.35	23.51	181.4	74.89
Mean	9.07	44.55	23.44	62.12	122.53	181.45	544.36	23.1	190.07	75.18
SE	0.33	0.84	0.47	1.45	0.75	6.86	20.59	1.07	14.23	4.79
CV	24.3	12.54	13.2	15.53	4.04	25.09	25.09	30.64	49.65	42.29

Table 4. Means comparison for vegetative traits

NDE= number of days emergenc, NDF50% = number of days to 50 percent 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, SE= standard error, C.V= coefficient variation, L= large seed sizes, M= medium seed sizes, S= small seed sizes, G1= Giwa, G2, Duna, G3= Cancaraki, G4= Jatau, G5= Maiki.

Among the genotypes, the variabl effect on height plant has been substantial. The height of the plants ranged from 21.70 cm to 25.78 cm. The highest plant (25.78 cm) was observed in genotype G3, while genotypes G1, G2, G4, and G5 were similar in height with no significant difference (Table 4). The interaction of genotypes and seed size as well as seed sizes were not significantly different (Table 3). Plant height is primarily determined by the genotype's genetic makeup, but it is also influenced by environmental conditions Pranesh (2015), reported a significant decrease in the mean value for plant height when screening for genetic variability on M3 generation of Bambara groundnut.

Significant variation has been observed for canopy amongst the seed size categories for individual genotypes, while no substantial variation was found amongst the genotypes and combinations (Table 3). Large seed size had the widest canopy spread, while the medium and small seed size categories recorded the least spread among all genotypes (Table 4). Maturity days attribute varied significantly among the combinations and genotypes ($p \leq 0.01$), while a significant variation ($p \leq 0.05$) was recorded among the seed size categories (Table 3). These results are consistent with those of Alake, (2017), who found significant variability among the genotypes studied for this character with regard of variation in genetics, selection gains and linkage of genetic for nutritional characteristics in accessions of Bambara groundnut which arrived from Africa. This could be due to differences in the genotypes studied' genetic sources.

The mean number of maturity days among the combinations varied from 125.78 to 114.33 days. G5L and G3L recorded the earliest maturity at 114.33, and 114.50 day respectively, while G1L, G2L, G4L, G1M, G2M, G3M, G4M, G5M, G1S, GS2, G3S, G4S, and G5S had similar mean number of days to maturity (Table 4). Amongst the genotypes, the earliest maturing genotype was G3(118.56 days) followed by G5(121 days) whereas the longest days to maturity was observed in G1 (125.48 days) followed by G2 and G4 at 123.88, and 123.28 days respectively (Table 4). For seed size categories, small seed size recorded the maximum days to maturity (124.37 days) followed by medium seed size (122.83 days), while large seed size recorded the minimum days to maturity which not significantly different from medium seed size category (Table 4).

For the petioles number and leaves number, high significant difference in the mean value of combinations and interactions, while significant difference was observed for genotypes, and no significant differences were found among the seed size categories (Table 3). Amongst the combinations, a varied range of differences was obtained ranging from 119.50 to 266.50. Highest petioles number has been registered by G3L, while the lowest was registered in G3M (Table 4). The average values of genotypes for this character ranged from 150.47 to 206.52. The genotypes G5 recorded a lower mean of 150.47 which is not significantly different from G3 and G4 while G1 registered the maximize petioles number, similar to other genotypes except for G5 (Table 4). A high range of variation was observed for this parameter amongst the seed weight classes within varieties, large seed size within G1 genotypes no variation was found, while large seed dimensions in G2 and G4 genotypes registered the lowest number, but the maximum values were recorded with G3. Medium seed size was recorded the lowest number with G3 and G5 genotypes. Small seed size verified the uppermost petioles number within G1, G2, and G5 genotypes (Table 4).

The leaves number of plant varied highly significantly among the combinations, while among the genotypes were significantly different, however, there were no discernible variation amongst the seed weight groups (Table 3). Mean performance amongst the combinations for leaves number, G3L observed the high leaves number (266.50) followed by G1S and G2Sat 230.47 and 217.99 respectively, while the G5M recorded the lowest leaves number (Table 4). The maximum number of leaves per plant was registered by the genotype G1 (125.48) which is statistically the same with other genotypes except for G5, while the minimum number recorded for genotype G5 (150.47) (Table 4). A high range of variation was observed for this trait among the seed size categories within genotypes, for large seed size, genotypes G1 had no variation, while large seed size in G2 and G4 genotypes registered the lowest number at 465.45 and 482.70, however, G3 had the maximum values of 799.50. Medium seed size recorded the lowest number of 409.67 and 358.50 for genotypes G3 and G5 respectively. Small seed size registered the maximum petioles number in G1, G2 and G5 at 653.97, 691.40, and 534.00 respectively (Table 4). According to research by Onwubiko et al (2019), who studied estimates of variables of genetic in Bambara groundnut and suggested a significant variation which could be served as basis for this crop. The result of branches number has been presented in Table 3.4. The combination, genotypes, seed sizes groups, and genotype-seed size interaction did not show any significant differences. This study mean values for these features are consistent with those found in a pre-breeding study of Bambara groundnut Mohammed, (2014).

Significant differences were found among the combinations and genotypes interaction and seed size groupes for fresh biomass and dried biomass traits, but no significant difference was observed among the genotypes and seed size groupes (Table 3). Variation for fresh biomass ranged from 92.25 to 415.53 g per plant, while dried biomass ranged from 42.89 to 139.04 g per plant. The G3L recorded the highest weight of fresh and dried biomass at 415.53, 139.04 g respectively, while the lowest fresh and dried biomass were registered by G5M (Table 4). For interaction, fresh and dried biomass result of plants from the various seed sizes and genotypes are presented in (Table 4).

For large seed size genotype G1, G2 and G4 recorded the lowest whereas genotype G3 registered the highest fresh and dried biomass per plant. Among the medium seed size within genotypes, the lowest fresh and dried biomass was recorded with G3 and G5 genotypes, but small seed size within genotypes for this trait, all the genotypes were the same. Genotypes that demonstrated high seed yield performance and greater biomass production could examined for maximum amount yield, breeding or germplasm preservation, according to a similar diversity study that used morphological and characterization and evaluation of selected Bambara groundnut genotypes for yielding related traits Mohammed *et al.*, (2019). No significant variation amongst the combinations, genotypes, seed weight groups, and interaction for the branches number (Table 3).

Selection criteria for morphological features in Bambara groundnuts including genetic variation, heritability and genetic advancement

The estimations of genetic character viz., genetic advancement, broad-sense heritability, variance in phenotypic and genotypic coefficients for 10 vegetative characters was presented in Table 5.

Genetic variability

The phenotypic coefficient of variation for the overall variable was greater than the genotypic coefficient of variation, suggesting that the environment has an impact on these traits. Like other researchers (Malek *et al.*, 2014, Unigwe *et al.*, 2016 & Khan *et al.*, 2020), we find that the phenotypic variation for all characteristics. This suggests that trait expression is influenced by the environment. The resulting GCV and PCV value have been grouped using the proposed index of 0% -10% for low variation, 10-20% for reasonable variation, and 20% for high variance (Sabri *et al.*, 2020), according to this categorized explanation those traits which recorded 0 values, no genetic effects and the environmental factors can be affected highly on that. The assessment of genetic variation, heritability, genetic advancement, and association for morphological and yield variables in common bean landraces also produced similar results from Southwestern Kenya by Anunda *et al*., (2019) superior apparatuses under organic and conservative fertilizer managements in organic and conformist nourishment managements in groundnuts, as well as assessment genotypes of groundnut for its crop yield. Those who reported higher variation of phenotypic and genotypic coefficient. The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) estimation ranged from (0 to 10.71% and 3.84 to 48.36% respectively, for the vegetative parameters (Table 5). Moreover, the modest value of GCV (10.71%) and high PCV (24.77%) were recorded for number of days to emergency and branches number GCV (10.40%) and PCV (29.69%), while low GCV and high PCV have been recorded from the all-other vegetative traits except days to maturity that was low for both GCV and PCV.

Table 5. Estimations of variability, heritability, genetic advancement of vegetation attributes for five Bambara groundnut genotypes

Traits	σ^2_g	σ^2_s	σ^2_e	σ^2_p	**GCV (%)**	**PCV (%)**	$h^2_{B\%}$	**GA%**
NDE	0.94	0.09	4.01	5.04	10.71	24.77	18.72	9.55
NDF50%	0	8.17	21.66	29.83	0	12.26	0	0
PH	1.93	0	5.65	7.58	5.93	11.75	25.48	6.17
WC	0	33.76	33.3	67.06	0	13.18	0	0
DM	4.72	3.03	14.38	22.13	1.77	3.84	21.33	1.69
NP	31.15	937.18	1153	2121.33	3.08	25.38	1.47	0.77
NL	280.23	8434.7	10377.1	19092.03	3.08	25.38	1.47	0.77
NB	5.77	0	41.25	47.03	10.4	29.69	12.27	7.51
FB	0	3525.8	4924	8449.8	0	48.36	0	0
DB	0	375.37	465.87	841.24	0	38.58	0	0

Note. σ^2_g= Genotypic variance, σ^2_s= Seed weight variance, σ^2_e= Error of variance, σ^2_p= Phenotype variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, $h^2_{B=}$ 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.

As a result, once the fixed genetic component is free of environmental impact, selection in this Bambara population will be effective. finally, selection might be a good way to improve these qualities in Bambara groundnut.

Broad-sense heritability and genetic of advance

The amount of overall variation of phenotype features between individuals in a particular group due to genetic variation is known as broad-sense heritability. Individual features provide stronger signals than higher GCV combined with high heritability and GA. The broad-sense heritability for the vegetative studied characters ranged from 0 to 25.48%, moreover, the genetic advance (GA) estimate shown low values for all vegetative traits, indicating that the magnitudes of heritability are influenced by the environment. The results of this study were almost identical to those of Pranesh (2015)'s variation revisions M3 mean value production and evaluation of Bambara groundnut, Kakeeto *et al*., (2019), genetic variability, correlation, and path analysis investigations for vegetative and yield attributes in groundnuts by Hampannavar et al., 2018, as well as genetic variation and heritability of kernel physical quality variables and their link with specific agronomic traits in groundnut genotypes from Uganda. Therefore, preference for selection ought to be given to those parameters which documented higher estimations heritability attached with much genetic advance and the percent of selection mean according to the mentioned variables which could be beneficial in comprehending better gain by selection.

CONCLUSION

A significant amount of variation was found among the 5 genotypes in the current investigation, based on three different seed size categories, were evaluated for vegetative, yield, and yield component characters. Both the number of branches and days to emergence showed moderate GCV; however, for all traits, the phenotypic coefficient of variation was greater than the GCV. Therefore, these traits might be underscored during the selection process to enhance the vegetative stage of Bambara groundnut genotypes. Among the combinations, further studies should be carried out on seed weight, vegetative traits, yield, and yielding traits for the improvement of these Bambara. genotypes under different environments.

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