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Genetic Inheritance and Yield Performance of Bambara Groundnut Genotypes Based on Seed Weight

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Abstract— Though many studies on gene action of yield and yield related traits have been conducted on bambara groundnut, none of these focused on seed size and weight. Hence, this study was conducted to established inheritance pattern based on seed weight. Five bambara groundnut genotypes from Nigeria, namely Giwa, Duna, Cancaraki, Jatau, and Maiki were evaluated in randomized complete block design with three replication. The seeds of each genotype were grouped into three seed weight categories namely large, medium and small-seed size. Data were collected on 12 agromorphological traits and statistical analysis was conducted using SAS version 9.4 and variance component and heritability were estimated for each character. The present study revealed significant levels of variability among the five genotypes, fifteen combinations of seed size and genotypes, seed size categories and interaction of genotypes and seed size categories for most of the yield and yield components. High values of genotypic coefficient of variation (GCV) coupled with genetic advance (GA) were reported for the number of medium seed per plant, total large seed weight per plant, total medium seed weight per plant and hundred seeds weight, while moderate GCV was observed for the total number of seed per plant. But the phenotypic coefficient of variation (PCV) was higher than GCV for all characters. Moderate broad-sense heritability for 100SW is responsible for the selection of this particular trait. Among the combination, G5S is the best for yield and yielding traits, while genotypes G3 is the best for yield and yield components, whereas among the seed size categories small seed size showed the high yield and yielding components.

Keywords: Inheritance, yield performance, Bambara groundnut, seed weight.

I. INTRODUCTION

Global food demand is increasing due to a continuous increase in the human population [1]. The new agricultural approach based on intensive cultivation of existing crop will not be adequate to tackcle global food security. It is expected that the application of contemporary technology will play a critical role in the improvement of the underutilized Bambara groundnut in order to enhance productivity and feed the world's most famished and malnourished populations [2]. Bambara groundnut (*Vigna subterranea* L.Verdc.) is a tropical pulse with underground pods and is the third most essential food legume after groundnut (*Arachis hypogaea* L.) and Cowpea (*Vigna* *unguiculata* Walp.) [3]. It is one of the underutilized crops that could be an important future crop to cushion global food demand especially in Africa and the Asian continent [58], 4]. The seeds are rich source of protein (19%), carbohydrates (63%), fat (6.5%) and essential amino acids [3, 5, 6]. With a more inclusive nutritional information base, breeding strategies can be created for bambara groundnut that has verified promising plants such as chickpea and soybean [5, 6, 7]. The use of local lines is one of the causes of bambara groundnut's low productivity at the farm level [8]. Thus, intensifying research in this line might be astute because it will be a source of cheap input and better economic paybacks [9].

Seed weight/size is an important agronomic trait because it is positively associated with total yield, [10]. Generally, grain yield increases as the seed weight increases and *vice versa*. Plant breeders need genetic materials with maximum variability in new varietial development [11,12,13]. The average yield of bambara groundnut is considered low as compared with other leguminous crops; this however, is mainly attributed to the fact that most cultivated bambara groundnut are landraces. Overtime, no significant improved cultivars has been developed through selective breeding programme. Therefore, a thorough understanding on its genetic diversity is a prerequisite before setting up an efficient breeding program for bambara groundnut. Unlike many other underutilized crops, there are few studies on bambara groundnut genetic diversity based on seed weight. Little attention has been recorded on the impact of seed weight on yield in bambara groundnut [11,12,13]. However, the yield production of bambara groundnut is low due to a lack of breeding programs for varietal development. Also, there is very little information available on genetic diversity on bambara groundnut characteristics on yield and yield components [14]. The yield was described as a complex character; correlated with some traits contributing to the yield and polygenic character should be equally considered [10].

Genetic variation and the heritability of those attributes are among the key components for genetic improvement of crops for any trait [15,16]. Furthermore, highly correlated morphological characters with grain yield give breeders the choice to decide which traits to be used as selection criterials [17]. Characters affecting yield are inherited quantitatively and are affected by environmental interaction [18].

The performance of genotypes relies on the environment, and the effect of genotype-environment interaction on growth has been identified [19]. Traits responsible for the agro-morphological divergence among populations were phenological, vegetative and yield types [20]. Therefore, genetic variation can be a preference for selecting appropriate parents; however, quantitative characters are vulnerable to environmental influence requiring the partitioning of total variances as heritable and non-heritable components for the effective breeding program [21]. The success of the selection depends on the availability of a broad genetic variation in the breeding material for the target character and to what degree it is heritable [22].

Research seed size inheritance is important for taking appropriate breeding strategies to develop improved plant cultivar[23]. Superior genotypes are chosen in proportion to the amount of genetic variation present and the degree to which the characters are inherited [24]. The genotypic and phenotypic coefficient variation is useful in exploring the nature of variability in the breeding population [25].

Heritability is the degree of genetic regulation linked to certain essential heritable traits [[58]26]. However, it has been stated that the best result in a crop improvement program is obtained when estimates of heritability are taken together with genetic advance [27, 28]. Generally, the selection of traits that indicated high values of heritability along with high values of genetic advance usually leads to better yield [29].

Genetic advance describes the degree of the benefit obtained in a character under given selection pressure [30]. However, the availability of genetic diversity would be beneficial for crop development through cross breeding as well as the plant breeders to prioritize favorable features in Bambara groundnut for the goal of further breeding. Selection with the value of several genetic parameters analysis can increase Bambara groundnut yield and related features [31]. Even though genetic variations allow for the development of recombinants, which are required for the development of new genotypes or lines, the production of Bambara groundnut genotypes that could lead to food security is solely based on the investigation of genetic factors of the crop's quantitative characteristics [32].

Therefore, the present experiment has been carried out to evaluate the genetic inheritance and yield performance of bambara groundnut genotypes selected based on seed weight with the specific objectives such as determining genetic components, heritability, genetic advance and selection of high yield lines based on seed weight in this generation for evaluation.

II. MATERIALS AND METHODS

A. Experimental Location and Station

The present study was conducted at experimental site Research Field 15, Faculty of Agriculture, Universiti Putra Malaysia (UPM). It is located on 3º02` N latitude and 101º 42` East longitude and altitude is 31 m above sea level.

B. Plant Materials

Five Bambara groundnut genotypes from Nigeria, namely Giwa, Duna, Cancaraki, Jatau & Maiki were used in this experiment (Fig 1). The seeds of each genotype were grouped into three seed weight categories namely large, medium, and small-seed weight. Fifteen combinations of genotypes based on seed weight categories and varieties presented in Table 1 were sown in trays with one seed per cell on mixed soil with peat

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moss. After 20 days in the trays, the seedlings were transferred into the experimental field.

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

C. Field Maintenance, experimental design and selection

The land was mechanically ploughed and harrowed and the bed was prepared in rows. According to [33], the seeds were planted at a planting distance of 30 cm, row to row distance of 1 m, and replication distance of 2 m, using a Randomized Complete Block Design (RCBD) with three replications. The experiment was conducted from November 2018 to March 2019. In this experiment, each experimental unit consists of five plants from 15 combinations of genotypes and seed weight categories (75 plants) for each replication. The same procedure was reported by [34]. Five randomly selected plants were chosen for data inquiry from the accessions analyzed to determine genetic divergence using morphophysiological variables [33]. From this experiment, selection has been carried out based on top yielder plants from each seed weight category per genotype.

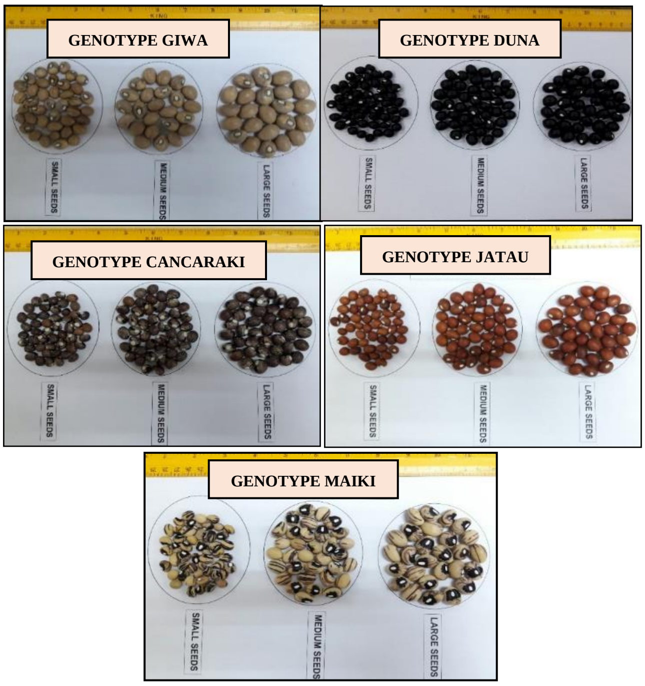

Fig 1: Five Bambara groundnut genotypes

The recommended fertilizer rates (100% N = 45 kg N/ha, 100% P = 54kgP_2O_5/ha, and 100% K = 45kgK_2O/ha). The total portion of phosphorus (100% P) and potassium (100% K) was applied during land preparation; hence, 70% N was applied two and six weeks after transplanting [35]. 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.

D. Data Collection

Data were collected on 12 agromorphological traits as described in Table 2. Data collection procedures was done following [36].

Table 2: Data collection for yield and yield components traits

Character	Abbreviation	Method of evaluation
Number of Pods Per Plant (no)	Npod	At maturity, the number of pods in each plant was counted.
Dried Pods Weight(gr)	DPW	The weight of total pods per plant was recorded after optimal pod drying.
Number of Large Seeds Per Plant (no)	NLS	The number of large seeds in each plant was counted after drying.
Number of Medium Seeds Per Plant (no)	NMS	After drying, the number of medium seeds in each plant was counted.
Number of Small Seeds Per Plant (no)	NSS	The number of small seeds in each plant was counted after drying.
Total Large Seed Weight Per Plant (gr)	TLSW	Weight was measured in grams for the total number of large seeds per plant.
Total Medium Seed Weight Per Plant (gr)	TMSW	The weight was measured in grams of the total number of medium seeds per plant.
Total Small Seed Weight Per Plant (gr)	TSSW	The weight of the total number of small seeds per plant was recorded in grams.
100-seeds Weight(gr)	100SW	The weight of 100 seeds was determined by weighing 100 seeds from each genotype randomly and the weight was recorded as 100 seed weight in grams.
Total Seed Weight/Plant	TSW	The weight was measured in grams of the total number of seeds per plant.
Total Number of Seed/Plant	TNS	The number of total seeds in each plant was counted after drying.
Yield (ton/ha)	Ton/ha	The overall pod yield per hectare of the cultivars and seed yield were calculated. Seeds have been dried and weighted.

III. STATISTICAL ANALYSIS

Statistical analysis was conducted for analysis of variance (ANOVA) using Statistical Analysis System (SAS) version 9.4 for all the morphological traits as defined by Gomez [37], (Table 3). The means comparison was done using the Duncan's New Multiple Range Test (DNMRT) method at 5%. The variance component was estimated for each character including the seed weight from the expected mean squares using proc varcomp with Restricted Maximum Likelihood(REML) method in SAS.

Table 3: Keys-out of ANOVA table

Source of variation	df	MS	EMS
Blocks (R)	(r-1)	MSB	$\sigma^2e + {}_T\sigma^2_r$
Combinations (T)	(t-1)	MST	$\sigma^2e + {}_r\sigma^2_{G\times S} + rs\sigma^2_{T+}\ r_G\sigma^2_T$
Seed Sizes (S)	(s-1)	MSS	$\sigma^2e + {}_r\sigma^2_{G\times S} + r_T\sigma^2_G$
Genotypes (G)	(g-1)	MSG	$\sigma^2e + {}_r\sigma^2_{G\times S} + r_t\sigma^2_S$
S×G	(s-1)(g-1)	MSG ×P	$\sigma^2e + {}_r\sigma^2_{G\times S}$
Error	(r-1)(t-1)	MSE	σ^2e

Note: R= Blocks, G= Genotypes, S= Seed sizes, T= Combinations, MS = Mean squares, EMS = Expected mean squares, DF = Degree of freedom, SS = Sum of squares, SOV = Source of variation

A. Genetic variance, heritability, and genetic advance

Estimation of variance components were determine to quantified the genetic variation among varieties based on seed weight and to assess genetic and environmental influences on different traits.

The genotypic and phenotypic variance (GV and PV) were calculated as follows

$$\sigma^2_g = \frac{(MSG - MSE)}{r}$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

σ^2_e = MSE

Where: σ^2_g is the genotypic variance; σ^2_p is the phenotypic variance, σ^2_e is the error variance, MSG is the mean square of genotypes, MSE is the mean square of error and r = the number of replications.

The phenotypic and genotypic coefficient of variation (PCV and GCV) was calculated as described by Singh & Chaudhary [38] as follows.

$$PCV = \frac{\sqrt{\sigma^2_p}}{\overline{X}} \times 100$$

$$GCV = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100$$

Where: σ^2_p is the phenotypic variance; σ^2_g is the genotypic variance; $\overline{X}$ = mean of the trait. GCV and PCV values were

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characterized as low (0-10%), moderate (10-20%) and high (20% and above) as described by Subramanian & Menon [39].

a) Heritability broad sense was calculated as described by Falconer (1996) which is the ratio of genetic variance (σ_g^2) to phenotypic variance (σ_p^2). The formula for broad-sense heritability is as follows:

$$h_B^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} X100$$

Where: σ_g^2 is the genotypic variance; σ_p^2 is the phenotypic variance; h_B^2 = Broad-sense heritability, it is characterized as low (0-30%), moderate (30-60%) and high (≥60%) as given by [40].

b) Estimated and Expected Genetic Advance (GA). The amount of expected GA (as a percentage of mean) has been analyzed as described by Johnson [41] and selection intensity (K) was expected to be 5%. The genetic advance was characterized as low (0-10%), moderate (10-20%), and high (>20%) by following Johnson [41].

$$\text{GA\%} = \text{K} \times \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times h_B^2 \times 100$$

K is selection intensity (constant 5%, the value is 2.06); $\sqrt{\sigma_p^2}$ is the phenotypic standard deviation; h_B^2 is the heritability; $\bar{X}$ is the mean of traits.

The variance component was estimated from the expected mean squares using proc varcomp with Restricted Maximum Likelihood (REML) method in SAS.

IV. RESULTS AND DISCUSSION

A. Yield and yielding traits

Statistical analysis revealed a significant and highly significant (p <0.05, p <0.01) difference for most of the parameters studied (Table 4). The mean performance, for the 12 yield and yield components characters of fifteen combinations, genotypes, seed size and interactions of (genotypes and seed size categories) presented respectively in (Tables 5).

B. Yield and yield components

The results on the number of pods per plant were presented in (Table 4). There were significant (P<0.05) differences among the combinations and interaction of genotypes and seed size categories. But no significant difference was observed among the genotypes and seed size categories. The number of pods per plant is related to the number of flowers produced, the proportion of flowers that initioated pods, and proportion of pods that survived to produce grain-bearing pods [42]. The current observations were in agreement with the findings on variability studies M3 mean value generation and screening of bambara groundnut by Pranesh [43], relationship and path coefficient analysis between yield of seed and its component character in M4 and M5 of bambara groundnut by Naik [44], Due to this wide variation improvement can be made for this character which directly added to the total yield of

the plant. Individual pod weight mainly determines the yield of this crop.

The number of pods per plant for combinations varied from 41.11 to 139.50. The highest number of pods per plant (139.50) was found in G3L, while the lowest number of pods (41.11) was observed in G1M, statistically similar to others (Table 5). For interaction, seed size categories within genotypes affected significantly on the number of pods per plant. The large seed size recorded the lowest number of pods per plant among all five genotypes, while medium and small seed size categories registered the highest number of pods, were statistically similar to each other (Table 5).

Table 4: Mean squares of yield and yield traits

SOV	df	Npod	DPW	NLS	NMS
Replications	2	1312.82^{ns}	8430.94^{*}	24.64^{ns}	388.82^{ns}
Combinations	14	1249.83^{*}	1222.28^{ns}	44.53^{*}	524.99^{ns}
Seed Sizes(S)	(2)	1045.24^{ns}	1190.52^{ns}	60.94^{*}	339.9^{ns}
Genotypes(G)	(4)	1136.47^{ns}	459.34^{ns}	31.49^{ns}	957.13^{*}
S×G	(8)	1357.65^{*}	161170^{ns}	46.95^{*}	355.19^{ns}
Error	27	550.38	1218.10	18.55	275.07

SOV		NSS	TLSW	TMSW	TSSW
Replications	2	254.07^{ns}	81.13^{ns}	359.83^{ns}	52.43^{ns}
Combinations	14	308.35^{*}	144.64^{*}	161.47^{ns}	74.50^{*}
Seed Sizes(S)	(2)	723.25^{**}	84.37^{ns}	62.57^{ns}	199.55^{**}
Genotypes(G)	(4)	110.99^{ns}	173.53^{**}	301.88^{ns}	61.74^{ns}
S×G	(8)	303.31	145.26^{**}	115.99^{ns}	49.63^{ns}
Error	27	134.46	32.72	125.87	30.75

SOV		100SW	TSW	TNS	Ton/ha
Replications	2	278.58^{ns}	1320.55^{*}	1680.60^{ns}	5.88^{ns}
Combinations	14	830.57^{**}	411.96^{ns}	1265.80^{ns}	1.83^{ns}
Seed Sizes(S)	(2)	87.43^{ns}	427.91^{ns}	1054.04^{ns}	1.89^{ns}
Genotypes(G)	(4)	2110.10^{**}	477.90^{ns}	1403.28^{ns}	2.13^{ns}
S×G	(8)	376.60^{*}	375.01^{ns}	1250.01^{ns}	1.67^{ns}
Error	27	133.07	402.18	811.11	1.77

Note: * Significant at 5%, ** highly significant at 1%, ns = not significant, SOV = source of variation, G = genotypes, DF = degree of freedom, Npod= number of pod per plant, DPW= dried pod weight, NLS= number of large seed per plant, NMS= number of medium seed per plant, NSS= number of small seed per plant, TLSW= total large seed weight per plant, TMSW= total medium seed weight per plant, TSSW= total small seed per plant, 100SW= hundred seed weight, TSW= total seed weight per plant, TNS= total number of seed per plant, Ton/ha= yield ton per hectare.

Table 5: Means comparison for yield and yield traits

Combination. Trt	Npod	DPW	NLS	NMS
G1L	44.83b	80.22a	6.94bc	11.94a
G2L	56.67b	76.44a	9.67bc	24.33a
G3L	139.50a	150.89a	17.00b	75.50a
G4L	60.63b	87.79a	14.00b	31.56a
G5L	47.42b	80.06a	10.42bc	22.94a
G1M	41.11b	84.87a	9.50bc	12.33a
G2M	49.92b	59.88a	4.75c	16.08a
G3M	43.81b	55.83a	11.06bc	27.78a
G4M	63.64b	83.34a	10.33bc	29.00a
G5M	44.17b	86.59a	10.33bc	23.67a
G1S	45.93b	88.68a	12.22bc	13.80a
G2S	68.73b	88.07a	11.92bc	27.00a
G3S	60.97b	76.43a	13.13bc	33.00a
G4S	65.33b	70.49a	10.50bc	24.89a
G5S	61.50b	114.96a	30.00a	14.33a
Genotype				
G1	43.96a	84.59a	10.22a	13.25b
G2	58.44a	74.80a	8.78a	22.47b
G3	74.17a	87.32a	13.32a	41.67a
G4	63.20a	80.54a	11.61a	28.48a
G5	51.03a	93.87a	13.18a	20.31b
Seed Categories				
Large	64.83	91.09	11.65ab	30.60
Medium	48.53	74.10	9.20b	21.77
Small	60.49	87.73	13.33a	22.61
Mean	57.80	84.15	11.29	24.86
SE	4.30	5.94	0.81	2.87
CV	49.35	46.86	46.62	76.50

Note: Means with the same letter are not significantly different, Npod= number of pods per plant, DPW= dried pod weight, NLS= number of large seeds per plant, NMS= number of medium seeds per plant, 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.

Significant (P<0.05) difference was observed among the combinations, seed size categories, and interaction for number of large seed per plant, but no significant differences were observed among the genotypes (Table 4). The mean values of combinations for this parameter ranged from 4.75 to 30. The G5S registered the highest number of large seed per plant, while the G2M was registered the lowest number of large seed per plant, which was statistically similar to the most of others (Table 5).

Table 5: Continued

Combination. Trt	NSS	TLSW	TMSW	TSSW
G1L	21.67d	14.05bc	13.18a	11.23bc
G2L	24.75cd	9.49bc	17.153a	15.97bc
G3L	51.00ab	16.15bc	45.965a	15.63bc
G4L	26.83cd	14.25bc	19.64a	11.81bc
G5L	25.78cd	14.39bc	21.403a	11.81bc
G1M	22.89cd	16.52bc	13.913a	13.06bc
G2M	34.58a-d	4.36c	9.647a	7.74c
G3M	18.17d	11.32bc	22.06a	6.65c
G4M	33.27a-d	10.62bc	21.743a	12.14bc
G5M	26.50cd	15.62bc	22.717a	15.77bc
G1S	35.15a-d	20.33b	15.503a	21.09ab
G2S	45.00a-c	11.51bc	19.65a	17.43a-c
G3S	29.62b-d	14.65bc	25.973a	13.24bc
G4S	35.75a-d	8.40bc	14.97a	12.46bc
G5S	53.50a	50.88a	16.507a	26.63a
Genotype				
G1	26.57a	16.97ab	14.20a	15.13a
G2	34.78a	8.45c	15.48a	13.71a
G3	30.67a	13.77bc	29.50a	11.37a
G4	31.95a	11.09bc	18.78a	12.14a
G5	35.26a	20.13a	20.20a	18.07a
Seed Categories				
Large	28.51b	13.49	21.86	13.12b
Medium	27.08b	11.69	18.02	11.07b
Small	39.80a	16.58	18.52	18.17a
Mean	31.87	13.80	19.41	14.14
SE	2.11	1.32	1.84	1.02
CV	44.00	62.03	62.74	47.95

Note: Means with the same letter are not significantly different, NSS= number of small seeds per plant, TLSW= total large seed weight per plant, TMSW= total medium seed weight per plant, TSSW= total small seed per plant, 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.

For seed size categories, the lowest number of large seed per plant was recorded by the medium seed size which statistically similar with the large seed size category, while the highest number was registered by the small seed size, which was statistically similar with large seed size category (Table 5). Small seed size was recorded the lowest number of large seed per plant within all five genotypes, but there were no statistical differences between large and small seed size categories among the genotypes (Table 5). There were significant (P<0.05) differences among the genotypes, but no significant difference was observed among the combinations, seed size categories and interaction for the number of medium seed per plant (Table 4).

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The genotype G3 recorded the maximum number of mediums (41.67) which was statistically similar to the G4 genotype, while the minimum number of medium seed per plant has been registered by the G1 (13.25) that statistically similar with G5 and G2 genotypes (Table 5).

Highly significant (P<0.01) difference was found among the seed size categories, while significant (P<0.05) differences were among the combination, but there was no significant difference among the genotypes and interactions for the number of small seeds per plant (Table 4). The range observed for the number of small seeds was higher in seed size categories (28.5 to 39.80). The highest mean registered for this trait by small seed size, whereas the lowest number recorded by medium seed size which statistically similar to the large seed size category (Table 5). The mean values of this trait for combinations range from 18.17 to 53.50. The G5S (53.50) was recorded the highest number of small seeds which statistically similar to G3L, G2M, G4M, G1S, G2S and G4S. While the lowest number of small seeds was observed by G3M (18.17) which statistically similar to most of the others (Table 5).

Among the combinations there was significant (P<0.05) difference, while among the genotypes and interaction highly significant (P<0.01) differences were observed, but no significant difference was found among the seed size categories for total large seed weight per plant (Table 4). For combinations, the range of mean values for this trait was 4.36g to 50.88 g. The G5S recorded the highest large seed weight (50.88 g), while G2M registered the lowest large seed weight (4.36 g) which was statistically similar to others except for G1S and G5S (Table 5). The mean values of this character among the genotypes ranged from 8.45 to 20.13 g. The genotypes G5 (20.13 g) recorded higher large seed weight which was statistically similar to the G1 genotype, whereas the G2 (8.45 g) registered the lowest large seed weight that statistically similar to G3 and G4 genotypes (Table 5). For interaction, among the genotypes for large seed size, there was no significant difference observed, while medium and seed size was significantly different. Small seed size was recorded the highest total large seed weight among the seed size categories within G1 (20.33 g) and G5 (50.88 g) genotypes (Table 5).

Highly significant (P<0.01) difference was recorded among the seed size categories, while significant (P<0.05) differences were among the combination, but there was no significant difference among the genotypes and interactions for total small seed weight per plant (Table 4).

Table 5: Continued

Combination. Trt	100SW	TSW	TNS	Ton/ha
G1L	87.99ab	38.46a	40.44a	2.56a
G2L	72.01b-d	42.62a	58.75a	2.84a
G3L	55.85de	77.74a	143.50a	5.19a
G4L	65.01cd	45.7a	72.39a	3.05a
G5L	80.48a-c	47.61a	59.14a	3.18a
G1M	98.07a	43.5a	44.72a	2.90a
G2M	37.25e	21.75a	55.42a	1.45a
G3M	63.72cd	40.02a	57.00a	2.67a
G4M	64.09cd	44.50a	72.60a	2.97a
G5M	90.35ab	54.10a	60.50a	3.61a
G1S	91.80ab	56.92a	61.17a	3.79a
G2S	57.66de	48.59a	83.92a	3.24a
G3S	70.94b-d	53.87a	75.75a	3.59a
G4S	52.33de	35.83a	71.14a	2.39a
G5S	69.93b-d	60.09a	77.67a	4.00a
Genotype				
G1	92.62a	46.29a	50.04a	3.09a
G2	55.64c	46.29a	66.03a	2.51a
G3	64.46c	54.643a	85.66a	3.64a
G4	60.48c	42.01a	72.04a	2.80a
G5	80.25b	53.932a	65.77a	3.60a
Seed Categories				
Large	73.44	48.47	70.75	3.23
Medium	70.70	40.77	58.05	2.72
Small	68.53	51.06	73.93	3.40
Mean	70.83	46.73	67.50	3.12
SE	2.89	3.19	4.77	0.21
CV	27.04	45.30	46.84	45.30

Note: Means with the same letter are not significantly different, 100SW= hundred seeds weight, TSW= total seed weight per plant, TNS= total number of seeds per plant, Ton/ha= yield ton per hectare, 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.

There was a wide difference observed in the range of this trait (11.07 to 18.17 g) for seed size categories. The mean for this trait was higher in small seed size category (18.17 g) than large and medium seed size categories. While between large and medium seed size categories no significant difference was recorded (Table 5). The mean of total small seed weight range from 6.65 g to 26.63 g for combinations. The highest total small seed weight was registered in G5S (26.63 g) which was statistically similar to G1S and G2S, while the G3M

(6.65 g) recorded the lowest total seed weight, which was statistically similar to all others combination (Table 5).

There was a highly significant (P<0.01) difference among the genotypes and combinations, while significant (P<0.05) differences were registered for interaction, but there was no significant difference found among the seed size categories for this trait (Table 4). Hundred seed weight is an indication of the seed size of a genotype and does not give the measure of average seeed yield. The current observations were in agreement with the findings on evaluation of bambara groundnut for yield stability and yield related characteristics by [42] that reported that hundred seed weight was significantly affected by genotype.

Hundred seeds weight mean value ranged from 37.25 g to 98.07 g for combinations. G1M recorded the highest 100-seeds weight (98.07 g), which was statistically similar to G1S, G5M, G5L and G1L, while the G2M registered the lowest 100-seeds weight (37.25 g), which was statistically similar to G4S, G2S and G3L, Table 5). A wide range was observed among the genotypes (55.64 g to 92.62 g). The highest 100-seeds weight was recorded by the G1 (92.62 g) genotype, while the lowest 100-seeds weight was registered by the G2 (55.64 g) genotype which was statistically similar to G3 and G4 genotypes (Table 5). For interaction, among the genotypes and seed size categories, G1genotyp had the higher 100-seeds weight which was statistically similar with G5 and G2 genotypes in large seed size category, while for medium seed size category also G1 had the highest 100-seeds weight similar to G5 genotype, whereas the G1 had the high 100-seeds weight that was statistically similar with G3 and G5 genotypes. But within the genotype, seed size categories just were significantly differenced with G2 and G3 genotypes, therefore large seed size category recorded the highest 100-seeds weight than medium and small seed size categories for genotype G2, while in G3 the highest 100-seeds weight was registered by small seed weight category (Table 5). The bambara groundnut genotypes exhibited considerable variation among the morphological and seed traits [45]. Besides, variation in yield-related traits has also been reported by Shegro[46], who showed that cultivar and environment may influence performance. These reports suggested that morphological and seed traits are useful for the characterization of bambara groundnut and selection of desirable genotypes suitable for breeding, conservation, and mass production. [47] showed on a study of morphological variability and phylogenetic analysis in the common bean that contribution due to character divergence varies from crop to crop.

Among the combinations, genotypes, seed size categories and interaction for fresh pod weight, dried pod weight, total mediums seed weight per plant, total seed weight per plant, the total number of seed per plant and yield (Ton per hectare) traits (Table 4). The result of these traits was disagreement in the previous study of genetic diversity in bambara groundnut as revealed by phenotypic descriptors and dart marker analysis by [4] and estimates of genetic parameters in bambara groundnut by Onwubiko [48]. These traits were not affected by genotype, this means that there was no variation among the genotypes for characters mentioned above.

C. Genetic variability, heritability and genetic advance as criteria for yielding traits selection in bambara groundnut.

The estimates of genetic parameters viz., phenotypic and genotypic coefficient variation, heritability in the broad sense and genetic advance for 12 characters of yield and yield components studied are presented in Table 6.

D. Genetic variability

The extent of variability in respect of phenotypic and genotypic variances, phenotypic and genotypic coefficients of variance, heritability broad sense and genetic advance for the 12 yield and yield component traits are shown in Table 6. The phenotypic coefficient of variation was of a high significance than the genotypic coefficient of variation for all the traits suggesting the environmental effect in the expression of those parameters. A similar result was reported on evaluation of genetic variability, heritability, genetic advance and correlation for agronomic and yield components in common bean landraces from South western Kenya by Anunda [49] and assessment genotypes of groundnut for pod yield and its component traits for pod yield and its component traits by Kavitha, [50]. and eminence apparatuses under organic and conservative fertilizer managements in organic and conformist nourishment managements in groundnut by Bhargavi, [51]. Those who reported higher phenotypic coefficient of variation the genotypic coefficient of variation. The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) estimate ranged from (GCV= 0 to 36.76) and (PCV= 22.59 to 77.01) respectively among the yield and

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yield components traits (Table 6). High GCV and PCV were detected for these traits such as the number of medium seed per plant (GCV=36.76, PCV=77.01), total large seed per plant (GCV=30.34, PCV=67.12), total medium seed per plant (GCV=25.25, PCV=61.32) and hundred seed weight (GCV=20.02, PCV=28.18). Whereas moderate GCV (11.34) and high PCV (46.10) for the total number of seed per plant and low GCV and high PCV were registered for other yielding traits. The same result on variabitliy in yield of pod characteristics and heritability evaluations in particular cultivars of bambara groundnut was reported for the number of days to emergency, hundred seeds weight and shelling percentage by [52]. Similar kind of observations was also reported for most of the characters on genetic variation and association educations for selection of multipledisease resilient lines in two crosses of peanut by Narasimhulu [53] and estimates of genetic parameters in bambara groundnut by Onwubiko [48]. Thus, selection in this population of bambara would prove successful once the fixed genetic component is freed from environmental influence. Hence, selection may be effective for improving these traits in bambara groundnut.

E. Broad-sense heritability and genetic advance

The heritability in the broad sense is the amount of total variation or phenotypic characters between individuals in an assumed population due to genetic variation. Higher GCV, combined with high heritability and high GA, gives better signs than individual traits. The broad-sense heritability for the yield and yielding studied characters ranged from 0% to 50.45%. Hundred seeds weight was the only trait that exhibited moderate heritability (50.45%) (Table 7), signifying that the magnitudes of heritability are less influenced by the environment. While other characters were recorded the low heritability (0% to 30%).

Furthermore, the genetic advance (GA) intended had exposed the high genetic advance values (≥20%) for number of medium seed per plant (36.15%), hundred seeds weight (29.29%), total large seed weight (28.26%) and total medium seed weight (21.42%) (Table 7). The yield and yield characteristics in this study showed high genetic advance interest. Those traits were significant in the selection process and had a little environmental effect. The finding of the present research was almost accordance with the findings on variability studies M3 mean value generation and screening of bambara groundnut by Pranesh [43], genetic variation and heritability of kernel physical quality traits and their association with selected agronomic traits in groundnut genotypes from Uganda by Kakeeto [54]. and genetic variability , correlation and path analysis studies for yield and yield attributes in groundnut by Hampannavar [55]. Consequently, gathering, characterizing, analyzing, and storing Bambara groundnut germplasms are important steps in developing a crop enhancement program that will provide appropriate parent materials [56].

Therefore , preference for selection ought to be given to those parameters which documented higher estimations heritability coupled with high genetic advace as percent mean and selection based on these traits might be useful in comprehending better gaian by selection.

Table 6: Estimates of variability, heritability, genetic advances of vegetative traits for 5 genotypes of bambara groundnut

Traits	σ^2_g	σ^2_s	σ^2_e	σ^2_p
Npod	20.15	285.31	524.6	830.07
DPW	0	0	1211.9	1211.9
NLS	1.07	0	25.06	26.12
NMS	83.56	0	283.1	366.66
NSS	0	38.53	133.62	172.15
TLSW	17.54	22.94	45.35	85.82
TMSW	24.02	0	117.66	141.68
TSSW	0.84	7.24	30.54	38.62
100SW	201.07	61.21	136.27	398.55
TSW	13.49	0	390.71	404.2
TNS	58.62	48.07	861.91	968.61
Ton/ha	0.06	0	1.74	1.8

Note: σ^2_g= Genotypic variance, σ^2_s= Seed weight variance, σ^2_e= Error of variance, σ^2_p= Phenotypic variance, Npod= number of pod per plant, DPW= dried pod weight, NLS= number of large seed per plant, NMS= number of medium seed per plant, NSS= number of small seed per plant, TLSW= total large seeds weight per plant, TMSW= total medium seeds weight per plant, TSSW= total small seeds per plant, 100SW= hundred seeds weight, TSW= total seed weight per plant, TNS= total number of seeds per plant, Ton/ha= yield ton per hectare.

Table 6: Continued

Traits	GCV (%)	PCV (%)	$h^2_{B\%}$	GA%
Npod	7.77	49.85	2.43	2.49
DPW	0	41.37	0	0
NLS	9.14	45.26	4.08	3.8
NMS	36.76	77.01	22.79	36.15
NSS	0	41.17	0	0
TLSW	30.34	67.12	20.44	28.26
TMSW	25.25	61.32	16.96	21.42
TSSW	6.47	43.94	2.17	1.97
100SW	20.02	28.18	50.45	29.29
TSW	7.86	43.02	3.34	2.96
TNS	11.34	46.1	6.05	5.75
Ton/ha	7.86	43.06	3.33	2.96

Note: PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, $h^2_{B=}$ Broad sense heritability, GA= Genetic advance, Npod= number of pod per plant, DPW= dried pod weight, NLS= number of large seed per plant, NMS= number of medium seed per plant, NSS= number of small seed per plant, TLSW= total large seeds weight per plant, 100SW= hundred seeds weight, TSW= total seed weight per plant, TNS= total number of seeds per plant, Ton/ha= yield ton per hectare.

V. CONCLUSION

The current research exposed significant levels of variability among the five genotypes, fifteen combinations of seed size categories and genotypes, seed size categories and interaction of genotypes and seed size for most of the yield and yield component characters. High values of genotypic coefficient of variation (GCV) coupled with genetic advance (GA) were documented for the number of medium seed per plant, total large seed weight per plant, total medium seed weight per plant and hundred seed weight, while moderate GCV were observed for the total number of seed per plant. But the phenotypic coefficient of variation (PCV) was higher than GCV for all characters. Moderate broad-sense heritability for 100SW is responsible for the selection of this particular trait. Therefore, during the selection process, these characters could be focused to increase the yield potential of Bambara groundnut genotypes. Among the combination, G5S is the best for yield and yielding traits, while among the genotypes G3 is the best intern of yield and yield components, whereas among the seed size categories small seed size showed the high yield and yielding components. Further studies should be carryout for seeds weight, yield and yielding traits for improvement of these Bambara genotypes under different environments.

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