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Characterization and Evaluation of Bambara Groundnut (*Vigna subterranea* (L.) Verdc.) for Yield and Related Traits in Assosa Zone, North Western Ethiopia

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Abstract: Bambara groundnut is a future emerging legume is usually known as a poor man's crop or as "women´s crop" and newly noted as crop for new millennium. It is highly nutritious nut with high content of essential amino acids such as methionine, leucine, isoleucine, lysine, phenylalanine, threonine, valine and tryptophan that makes the crop as an important for food security. In this context, a field experiment was conducted during 2019/20 cropping season at Sonka testing site of Asosa zone in north western Ethiopia with objective to estimate the variability of bambara groundnut genotypes with respect to important quantitative and qualitative traits. Treatments consisted in 20 accessions collected from five distracts of Benishangul Gumuze province in north western Ethiopia. The treatments were laid out in a randomized block design with three replications. All the qualitative characteristics recorded for genotypes showed different modalities and frequencies at vegetative stage with 70.12% of the fully expanded leaflet colour, 74.26% oval terminal leaflet shape, 76.24% petiole green colour, 78.22% stem green colour, 88.27% sparse hair on their stems, 70.41% spreading types, 81.33% rounded base with a point at the top, 90.11% yellowish brown pods at harvest and 90.06% oval shaped seeds. With respect to quantitative traits, genotypes AMN/04/013, AMN/04/014, AMN/04/015, AMN/04/019 and AMN/04/020 gave relatively higher grain yield (>2000 kg/ha) with the highest grain yield recorded for genotype AMN/04/016. Thus, these genotypes showed relatively better adaptation at tested location. Higher correlation values were observed for days to maturity, plant height, number of stems per plant, pods per plant, seed per pod and HSW indicating that these traits are very important to be used in selection for the crop improvement. Agronomic and morphological evaluations have provided more accurate estimation of genetic diversity, the raw material of plant breeding. In general this study enabled to determine how the influential traits direct to improve bambara groundnut genotypes.

Keywords: Crop, Genotypes, Grain Yield, Heritability, Legume

1. Introduction

Bambara groundnut (*Vigna subterranea* (L.) Verdc. L) is a future emerging legume grown in Africa and Asia. It is usually known as a poor man's crop or as "women´s crop" and newly noted as crop for new millennium. In drier parts of sub-Saharan Africa, bambara groundnut is mainly grown by female on a small scale in pure culture without improved techniques [13]. Bambara groundnut is one of the grain legumes which belongs to family *Papillionaceae* and

originates from north-eastern Nigeria and northern Cameroon [8]. Bambara groundnut seeds are rich in many components such as protein, carbohydrate [5] and have high antioxidant activity [12]. The word "bambara' comes from a place name near Timbuktu in central Mali, West Africa. The word "groundnut' is the causes of it pods setting occur under the ground soil, hence jointly its common name is 'bambara groundnut' [9]. The highly nutritious content of bambara groundnut and its high content of essential amino acids (methionine, leucine, isoleucine, lysine, phenylalanine,

threonine, valine and tryptophan) make it an important crop to consider for food security [17]. Bambara groundnut can possibly fulfill the regular demand of protein for the marginal users where the animal protein which not affordable with consumers with low incomes [16]. Seeds of bambara groundnut contain considerable amount of minerals such as Ca, K, Fe and Na. Moreover, the richness of K in seeds of bambara groundnut has ability to lessen diabetes by prompting the insulin hormone [4]. Bambara groundnut is a medicinal plant used to treat diarrhea, anemia, abscesses, internal injuries, ulcers, infected wounds, epilepsy, cataracts, menorrhagia during pregnancy, nausea in pregnant women, kwashiorkor and venereal diseases. Bambara groundnut also contains vitamin E, vitamin C and vitamin A indicating the crop has a potential for economic exploitation [1].

Bambara groundnut can well adapt to the tropical areas where cultivation of major crops like rice, wheat, maize, etc., are increasingly challenging due to drought and unpredictable rainfall patterns. In crop genetic variability, morphological method is considered as the first step in description and classification of germplasm [7]. Characterization and evaluation of genetic resources aid to identify differentiate and distinguish traits agronomic importance for improvement a crop in breeding scheme since they provide information on diversity within and between crop genotypes under consideration. Hence, this was initiated with objective to estimate the variability of bambara groundnut genotypes with respect to important quantitative and qualitative traits.

2. Materials and Methods

2.1. Description of the Experimental Site

A field experiment was conducted during 2019/20 cropping season at Sonka testing site of Asosa zone in north western Ethiopia. An approximate geographical coordinates of the site is 9°45'44" N latitude and 34°47'23" E longitude having an altitude of 1477 meters above sea level. The area is characterized by low and erratic rainfall with mean annual rainfall of 796 mm. The mean annual temperature is 21.2°C with a minimum of 14°C and maximum of 28.4°C.

2.2. Treatment and Experimental Design

The plant materials consisted of 20 accessions collected from five distracts of Benishangul Gumuze province in north western Ethiopia. Description the genotypes used in trial is shown in Table 1. The treatments were laid out in a randomized block design with three replications. Seeds were hand planted by placing two seeds per hill at row spacing of 50 cm and plant spacing of 20 cm. Thinning was after emergence to maintain the proposed plant density per plots. Crop management activities such as hoeing and weeding were carried out during crop growing season. Diseases and pest events visually monitored in the field.

2.3. Data Collection and Measurements

Agronomic traits recorded were days to flowering, days to maturity, plant height, number of branches, leaf number, terminal leaf length, number of nods, number stems, pods per plant, number of seeds per pod, hundred seed weight (HSW) and grain yield. Similarly, morphological traits recorded were terminal leaflet shape, petiole colour, stem colour, stem hairiness, growth habit, pod shape, pod colour, seed shape and pod hardness. The estimation of genetic parameters were done to identify and ascertain the genetic variability among the varieties and to determine the extents of environmental effect on various characters. Variance components due to phenotype $(\sigma 2p)$, genotype $(\sigma 2p)$ and the environment $(\sigma 2e)$ were calculated by adopting the following formula suggested by Burton and De vence [3].

$$Genotypic\ variance\ (\sigma 2g) = \frac{MSg - MSe}{r}$$

$$Phenotypic\ variance\ (\sigma 2p) = \sigma 2g + \sigma 2e$$

$$Environmental\ variance\ (\sigma 2e) = Error\ mean\ square$$

$$Where,$$

$$MSg = Mean\ squares\ due\ to\ genotypes$$

$$MSe = mean\ squares\ due\ to\ error$$

$$r = Number\ of\ replications$$

According to Sigh, (2001) the phenotypic genotypic coefficients of variances were expressed as:

$$PCV = \frac{\sqrt{Phenotypic\ variance}}{Population\ mean\ for\ trait}\ or\ PCV = \frac{\sigma 2P}{X}\ x\ 100$$

$$Where\ PCV = phenotypic\ coefficient\ of\ variation$$

$$GCV = \frac{\sqrt{Genotypic\ variance}}{Population\ mean\ for\ trait}\ or\ GCV = \frac{\sigma 2g}{x}\ x\ 100$$

$$Where\ GCV = Genotypic\ coefficient\ of\ variation$$

$$x = the\ grand\ mean\ of\ a\ character.$$

Heritability in broad sense was calculated for each trait by using the formula [2] as:

$$H^2\ (\%) = \frac{\sigma 2g}{\sigma 2p}\ x 1oo$$

Where: H=Heritability in broad sense
$\sigma^2 g$=genotypic variance
$\sigma^2 p$=Phenotypic variance
Genetic advance (GA) under selection, assuming the selection intensity of 5% was calculated as proposed by Johnson et al. [11] as:

$$GA = K.\sqrt{\sigma 2p}.\frac{\sigma 2g}{\sigma 2p} = K.H^*\sqrt{\sigma 2p}$$

Where: GA=Expected genetic advance
K=The selection differential (K=2.056 at 5% selection intensity)

Genetic advance as percent of mean was calculated to compare the extent of predicted advances of different traits under selection, using the formula given by Falconer and Mackey [6] as:

$$GAM = \frac{GA}{x} X\ 100\ \text{(Source: [6])}$$

GAM=Genetic advance as percent of mean

GA=Genetic advance under selection

X=Mean value

3. Results and Discussion

3.1. Variation of Qualitative Traits

The data for frequencies of qualitative characters of bambara groundnut genotypes/accessions is depicted in Table 1. All the qualitative characteristics observed as well as the different modalities and their frequencies showed that at the vegetative stage 70.12% of the fully expanded leaflet colour of bambara groundnut exhibited green colour. About 74.26% of the genotypes had oval terminal leaflet shape. Information recorded on petiole and stem colour showed that 76.24% and 78.22% of genotypes exhibited green colour, respectively. With respect to stem hairiness, about 88.27% of genotypes showed sparse hair on their stems. Regarding the growth habit, genotypes with spreading growth habits dominated with 70.41%. And followed by bunch type growth habit with proportion of 20.68%. Likewise, genotypes with rounded base with a point at the top dominated with amounted to 81.33% and rounded base without a point at the top of 16.56%. After harvest, observation of the accessions showed mostly yellowish brown pods with proportion of 90.11% and brown pods 6.92%. Seed shape was dominated by oval with proportion of 90.06% and pod hardness was nearly in equal proportion with 55.56% hard and 43.46% was moderately hard.

Table 1. Frequencies of qualitative characters studied in 20 bambara nut accessions.

Character	Variable	Frequency (%)
Fully expanded leaflet colour	Dark green	4.88
	Green	70.12
	Light green	12.00
	Yellow green	3.90
Terminal leaflet shape	Round	17.82
	Oval	74.26
	Elliptic	0.99
	Lanceolate	6.93
Petiole colour	Green	76.24
	Pale Green	0.99
	Light Green	22.77
Stem colour	Green	78.22
	Pale green	1.98
	Dark green	19.80
Stem hairiness	Absent	4.80
	Sparse	88.27
	Dense	6.93
Growth habit	Bunch type	20.68
	Semi bunch type	8.91
	Spreading type	70.41
Pod shape	Rounded without point at the top	16.56
	Rounded base with a point at the top	81.33
	Elongated with rounded base	2.11
Pod colour	Yellowish brown	2.97
	Gray	90.11
	Brown	6.92
Seed shape	Round	8.04
	Oval	90.06
	Oblong	1.90
Pod hardness	Low	1.04
	Moderately hard	43.46
	Hard	55.56

Table 2. Mean performance of genotypes of bambara groundnut for phenological traits.

Genotype/Accession	Days to flowering	Days to maturity
AMN/04/001	58.57	122.17ef
AMN/04/002	59.80	124.00c-f
AMN/04/003	54.02	120.67f
AMN/04/004	59.27	125.33b-e
AMN/04/005	59.50	120.33f
AMN/04/006	58.40	123.81c-f
AMN/04/007	55.13	125.06b-e
AMN/04/008	58.80	123.13d-f
AMN/04/009	61.49	128.00b
AMN/04/010	60.20	126.33b-d
AMN/04/011	58.70	123.50c-f
AMN/04/012	57.00	123.67c-f
AMN/04/013	61.17	128.33b
AMN/04/014	60.83	127.17bc
AMN/04/015	60.00	127.13bc
AMN/04/016	59.27	132.53a
AMN/04/017	57.53	124.87b-e
AMN/04/018	55.56	125.00b-e
AMN/04/019	57.11	126.47b-d
AMN/04/020	57.40	125.67b-e
LSD	NS	3.72
CV (%)	5.75	1.80

Means followed by the same letters within a column are not significantly different at 5% probability level, NS=not significant.

3.2. Phenological Traits

Analysis of variance showed that genotypes were significantly differed for days to maturity and did not significant differences on days to flowering (Table 2). Thus, all the genotypes (entries) were characterized by their relative homogeneity in flowering. Ouedraogo *et al.* [14] reported that all the entries that characterized exhibited their relative homogeneity in flowering. In general days to maturity for bambara groundnut genotypes ranged from 120.33 to 132.53. The longest days to maturity (132.53) was recorded for genotype AMN/04/016. The shortest days to maturity (120.33) was seen for genotype AMN/04/005. As this investigation indicated that, genotypes AMN/04/001, AMN/04/002, AMN/04/003, AMN/04/005, AMN/04/006, AMN/04/008, AMN/04/011, AMN/04/012 and AMN/04/017 took relatively shorter days to maturity. Conversely, genotypes AMN/04/004, AMN/04/007, AMN/04/009, AMN/04/010, AMN/04/013, AMN/04/014, AMN/04/015, AMN/04/016, AMN/04/018, AMN/04/019 and AMN/04/020 exhibited relatively longer days to maturity. The difference of 12.20 days was observed between the longest and shortest days to maturity. This is an indication that there was relatively a wide range of variability among genotypes for days to maturity. Judicaëlle *et al*. [10] reported that days to maturity was significant for genotypes with non significant of days to flowering for genotypes studied in Brurkina Faso.

Table 3. Mean performance of genotypes of bambara groundnut for growth traits.

Genotype/Accession	Plant height (cm)	Branches	Leaf number	Terminal leaf length (cm)	Stems per plant	Nodes per stem
AMN/04/001	171.53e	2.34	48.89	54.47e-g	5.83e	2.93c-e
AMN/04/002	181.33b-d	2.41	48.73	58.43b-e	7.87c-e	2.87de
AMN/04/003	178.67b-e	2.50	44.00	55.20c-f	7.63de	2.72e
AMN/04/004	183.33bc	3.21	54.09	60.00b	8.77cd	3.46a-c
AMN/04/005	177.40c-d	2.95	48.80	50.82g	8.47cd	3.26b-e
AMN/04/006	179.67b-d	2.45	51.47	58.73b-d	8.05c-e	3.50ab
AMN/04/007	182.67b-d	2.16	50.80	57.17b-e	8.30c-e	3.46a-c
AMN/04/008	181.00b-d	2.44	48.00	57.67b-e	9.70b-d	3.22b-e
AMN/04/009	183.67bc	3.10	54.93	59.62b	8.90cd	3.44a-c
AMN/04/010	183.13bc	2.75	50.00	56.73b-e	9.78b-d	3.42a-d
AMN/04/011	184.67a-c	2.29	47.67	59.33bc	8.60cd	3.57ab
AMN/04/012	175.33de	2.70	47.53	51.60fg	7.33de	3.32a-d
AMN/04/013	183.67bc	2.39	54.50	57.27b-e	9.27cd	3.77ab
AMN/04/014	184.00a-c	2.64	55.89	57.35b-e	8.88cd	3.75ab
AMN/04/015	185.00ab	3.56	55.50	59.59b	12.15ab	3.37a-d
AMN/04/016	191.33a	3.77	47.13	64.27a	12.49a	3.87a
AMN/04/017	178.50b-e	3.23	55.57	57.93b-e	9.27cd	3.52ab
AMN/04/018	180.47b-d	3.18	55.89	58.54b-e	8.10c-e	3.66ab
AMN/04/019	182.17b-d	3.36	56.79	57.39b-e	8.67cd	3.48a-c
AMN/04/020	180.67b-d	3.44	56.60	55.13d-f	10.27a-c	3.50ab
LSD	7.51	NS	NS	4.18	2.63	0.57
CV (%)	2.51	22.68	14.52	4.42	17.85	10.16

Means followed by the same letters within a column are not significantly different at 5% probability level, NS=not significant.

3.3. Growth Traits

The data of growth traits for varieties is depicted in Table 2. Analysis of variance indicated that genotypes were significantly differed for plant height, terminal leaf length, number of stems per plant and nodes per stem (Table 3). Plant height for genotypes ranged from shortest (171.53 cm) for AMN/04/001 and the tallest height (191.33 cm) for

AMN/04/016. Similarly, terminal leaf length ranged from 50.82 to 64.27 cm with the longest for genotype AMN/04/016 and the least for AMN/04/005. As this result showed that plant height and terminal leaf length measured were significantly differed due to effect of genotypes which might be attributed to their inherent differences. Number of stems per plant is one of the growth traits varied from 5.83 to 12.49 with the greatest number of stems per plant (12.49) for AMN/04/016 and the lowest (5.83) for AMN/04/001 (Table 2). In line with this, number of nodes per stem was varied from 2,72 to 3.87 with greatest number of nodes per stem (3.87) was observed for genotype AMN/04/016 and least number of nodes per stem (2.72) was seen for genotype AMN/04/003. As this result showed that plant height, terminal leaf length, number of stems per plant and nodes per stem measured were significantly differed for genotypes which might be attributed to their inherent variability. On the other hand, number of branches per plant and leaf number were not significantly different for genotypes (Table 3).

3.4. Yield Components and Yield

Analysis of variance revealed that genotypes of bambara groundnut were significantly differed for yield components and yield (Table 4). Number of pods per plant was varied from 20.00 to 41.87 with the highest number of pods per plant (41.87) was recorded for genotype AMN/04/016. The lowest number of pods per plant (20.00) was seen for genotype AMN/04/003. Genotypes had variable HSW which ranged from 16.00 to 22.00 g where the highest HSW (22.00 g) was achieved from genotype AMN/04/016 and the lowest HSW (16.00 g) was obtained from AMN/04/005 (Table 4). Grain yield for genotypes varied from 1107 to 3163 kg/ha. The highest grain yield (3163 kg/ha) was obtained from genotype AMN/04/016 and the lowest (1107 kg/ha) from genotype AMN/04/003.

Table 4. Mean performance of genotypes of bambara groundnut for yield components and yield.

Genotype/Accession	Pods per plant	Seeds per pod	HSW (g)	Grain yield (kg/ha)
AMN/04/001	23.07[f-h]	1.45	17.36[g-i]	1310[g-j]
AMN/04/002	29.00[b-g]	1.62	18.58[d-g]	1673[d-g]
AMN/04/003	20.00[h]	1.35	16.59[i]	1107[j]
AMN/04/004	26.75[c-h]	1.53	18.25[f-h]	1547[f-i]
AMN/04/005	24.17[e-h]	1.43	16.00[i]	1177[ij]
AMN/04/006	26.08[c-h]	1.48	18.13[f-h]	1383[g-j]
AMN/04/007	26.83[c-h]	1.59	18.77[d-g]	1503[g-i]
AMN/04/008	20.77[gh]	1.45	16.83[hi]	1358[g-j]
AMN/04/009	27.00[c-h]	1.57	19.43[b-f]	1655[d-g]
AMN/04/010	24.40[e-h]	1.53	18.50[f-h]	1950[de]
AMN/04/011	21.80[gh]	1.46	17.37[g-i]	1575[e-h]
AMN/04/012	22.83[f-h]	1.39	16.52[i]	1199[h-j]
AMN/04/013	25.93[d-h]	1.55	20.35[bc]	2700[bc]
AMN/04/014	33.83[a-d]	1.53	20.02[b-d]	2690[bc]
AMN/04/015	37.87[ab]	1.56	20.80[ab]	2881[ab]
AMN/04/016	41.87[a]	1.79	22.00[a]	3163[a]
AMN/04/017	32.73[b-d]	1.42	18.46[e-g]	1462[g-j]
AMN/04/018	34.83[a-c]	1.47	19.17[c-f]	1895[d-f]
AMN/04/019	31.33[b-f]	1.47	19.92[b-e]	2027[d]
AMN/04/020	26.55[c-h]	1.59	19.89[b-e]	2450[c]
LSD	8.88	NS	1.47	384
CV (%)	19.27	6.76	4.79	12.67

Means followed by the same letters within a column are not significantly different at 5% probability level, NS=not significant.

3.5. Variance Components

3.5.1. Phenotypic and Genotypic Variations

Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population under consideration [3]. Phenotypic variance varied from 0.01 for number of seeds per pod to 91.02 for grain yield (Table 5). In line with this, relatively higher magnitude of difference between genotypic and environmental variance was observed for the characters number of pods per plant and grain yield. This implies greater influence of environmental factors for the phenotypic expression of these characters [3]. In contrast, relatively lower phenotypic variance (<50) was recorded for other traits. Genotypic variance ranged from 0.01 to 36.64 with relatively higher genotypic variance for number of pods per plant and grain yield. In general phenotypic coefficient of variation (PCV) varied from 0.52 for grain yield to 26.25 for number of pods per plant (Table 5). According to Sivasubramanian and Madhavamenon (1973) PCV categorized as high if PCV>20%, moderate if PCV is 10-20% and low if PCV is below 10%. Based on this categorizing, traits number of branches, number of stems and number of pods per plant had higher PCV. Conversely, traits leaf number and number of nodes per stem exhibited moderate PCV whereas days to flowering, days to maturity, plant height, terminal leaf length, number of seeds per pod, HSW and grain yield showed lower PCV with PCV value below 10%. This reflected the pronounced influence of environmental factors for the expression of these characters.

In line with this, genotypic coefficient variance (GCV) varied from 0.33 to 17.82% (Table 5). The lowest GCV (0.33%) was recorded for grain yield while the highest GCV (17.82%) for number of pod per plant. As this investigation indicated that moderate GCV (10-20%) was recorded for traits number of branches, number of stems and number of pods per plant. On the other hand, lower GCV (<10%) was seen for days to maturity, days to maturity, plant height, leaf number, terminal leaf length, number of stems per plant, number of seeds per pod, HSW and grain yield.

3.5.2. Broad Sense Heritability and Genetic Advance

Different characters have different levels of heritability that can contribute for yield improvement in breeding programs. In general heritability in broad sense (H^2) ranged from 2.25% for days to flowering which was the lowest to 73.93% for HSW which was the highest value. Johnson et al. [11] classified heritability estimates as low (<30%), moderate (30-60%) and high (>60%). Based on this classification, only HSW exhibited high H^2 estimate. This result revealed that environment had low influence for the expression of the trait

which suggests direct selection using this character as major contributor of yield components to improve yield of the study area. Thus, selection could be effective in genotypes for this trait and the possibility of improving bambara groundnut grain yield through direct selection for grain yield related trait. Relatively moderate H^2 was recorded for traits days to maturity, plant height, terminal leaf length, number of stems, number of pods per plant and grain yield which may be occurred due to influence of the environment on the polygenic nature of these traits. It was observed that heritability (H^2) was low for traits number of branches, leaf number, number of nodes per stem and number of seeds per pod. Low heritability that occurred for these traits limits the possibility of including the traits in order to select desirable genotypes. This may be due to the higher influence of environment for the expression of phenotypic variation than genotypic variation. Genetic advance as a percent mean was ranged from 1.95% for leaf number to 26.95% for days to flowering (Table 5). This result indicated that selecting the top 5% of the genotypes could result in an advance of 2.23% to 74.52% over the respective population mean.

Table 5. Phenotypic and genotypic coefficient of variability, heritability and genetic advance for genotypes.

Trait	$\sigma2p$	$\sigma2g$	$\sigma2e$	PCV (%)	GCV (%)	H^2 (%)	GA (%)
Days to flowering	11.56	0.26	11.3	5.81	0.87	2.25	26.95
Days to maturity	11.23	6.16	5.07	2.68	1.98	54.85	3.03
Plant height	30.51	9.82	20.69	3.05	1.73	32.19	2.02
Number of branches	0.51	0.09	0.42	25.15	10.56	17.65	9.14
Leaf number	49.63	3.44	46.19	13.64	3.59	6.93	1.95
Terminal leaf length	13.12	6.70	6.42	6.31	4.51	51.07	6.64
Number of nodes	0.17	0.05	0.12	12.01	6.35	28.00	6.99
Number of stems	3.98	1.45	2.53	22.37	13.52	36.49	16.81
Pods per plant	53.57	24.69	28.88	26.25	17.82	46.09	24.91
Seeds per pod	0.01	0.01	0.01	7.65	3.82	25.00	3.41
HSW	3.03	2.24	0.79	9.33	8.03	73.93	14.21
Grain yield	91.02	36.64	54.38	0.52	0.33	40.25	6.42

As suggested by Sivasubramanian and Madhavamenon (1973), genetic advance as percent of mean was classified as low (<10%), moderate (10-20%) and high (> 20%). Based on this classification, traits like days to flowering and number of pods per plant exhibited high genetic advance. Traits number of nodes per stem and HSW attained moderate genetic advance. In contrast, traits number of branches per plant, leaf number, terminal leaf length, number of nodes per stem, number of seeds per pod and grain yield had low genetic advance. Trait like HSW exhibited high heritability coupled moderate genetic advance whereas pods per plant had moderate heritability coupled with high genetic advance. Moreover, trait number of stems per plant showed moderate heritability coupled with moderate genetic advance. Hence, these traits should be given top priority during selection breeding in bambra groundnut because they are the major portion of genetic variation attributable to additive gene action and selection may be effective in early generations for these traits. Moderate heritability accompanied with moderate genetic advance as percent of mean was an indication that additive and non-additive gene actions are involved in the expression of the traits. The correlation of

selected agronomic traits with grain yield is presented in Table 6. In general, correlation coefficient (r) of agronomic traits with grain yield ranged from 0.42 to 0.92. With exception of days to flowering, all other traits were significantly and positively correlated with grain yield (Table 5). Higher correlation (r) values were observed days to maturity, plant height, number of stems per plant, pods per plant, seed per pod and HSW.

Table 6. Correlation of selected agronomic traits with grain yield.

Trait	Grain yield
Days to flowering	0.42[NS]
Days to maturity	0.84*
Plant height	0.71*
Number of branches	0.52*
Leaf number	0.44*
Terminal leaf length	0.52*
Number of nodes	0.63*
Number of stems	0.76*
Pods per plant	0.74*
Seeds per pod	0.72*
HSW	0.92*

4. Conclusion

Bambara groundnut genotypes exhibited differently for qualitative and quantitative traits recorded and measured due to their genetic variability. Genotypes AMN/04/013, AMN/04/014, AMN/04/015, AMN/04/019 and AMN/04/020 gave relatively higher grain yield (>2000 kg/ha) with the highest grain yield recorded for genotype AMN/04/016. Thus, these genotypes showed relatively better adaptation at tested location. Higher correlation values were observed for days to maturity, plant height, number of stems per plant, pods per plant, seed per pod and HSW indicating that these traits are very important to be used in selection for the crop improvement. Agronomic and morphological evaluations have provided more accurate estimation of genetic diversity, the raw material of plant breeding. In general this study enabled to determine how the influential traits direct to improve bambara groundnut genotypes.

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