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Assessment of Genetic Diversity of Bambara Groundnut Accessions [*Vigna subterranea* (L) Verdcourt] in Sahelian Zone of Niger

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Abstract

Original Research Article

The agro-morphological characterization of plant genetic resources is crucial to understand the phenotypic and genotypic relationships between different crop varieties. Bambara groundnut (*Vigna subterranea*) is a grain legume grown worldwide due to its high nutritional values, nitrogen-fixing ability, and drought tolerance. To assess the existing genotypic and phenotypic diversity within Bambara groundnut accessions and to estimate the genetic parameters guiding future varietal improvement programs, 22 Bambara groundnut accessions were characterized in the Sahelian zone of Niger. Thus, the coefficient of variation ranged from 2.42% to 48.25%, and 7 of the 22 parameters measured presented high coefficients of variation (CV>20%). Yield had positive high correlation with shell weight (r=0.56), 100-seed weight (r=0.61), and seed weight (r=0.99). The highest GCV and PCV were observed in number of seeds per plant (PVC=35.05% and GCV=22.65%), hull weight (PVC=85.91% and GCV=25.51%) and dry biomass weight (PVC=36. 61% and GCV=23.66%), for a respective heritability and genetic gain of: (h2b=41.58%; GA=30.03%), (h2b=8.82%; GA=15.60%) and (h2b=41.76%; GA=31.49%). The highest heritability is observed in the number of leaves (92.40%) and the date of maturity (92.08%). Emergence date revealed high heritability and genetic gain (h2b=78.77% and GA=20%). Parameters with high heritability and genetic gain (h2b≥60% and GA≥20%), are the least influenced by the environment. So, direct selection for improvement of these traits may be beneficial. To authenticate genetic inequality, principal component analysis (PCA) and hierarchical ascending clustering (HAC) were performed. The results showed a great agro-morphological diversity divided into four different groups, for the studied characters. Group 3 (4 accessions) and group 1 (3 accessions) are the high yielding accessions, while group 4 (8 accessions) and group 2 (7 accessions) are the lower yielding accessions. This great genetic diversity observed within the accessions studied has opened new possibilities for Bambara groundnut genetic selection in Niger. Group 3 accessions can serve as potential parents that can be used in improvement or varietal selection programs in Niger.

Keywords: Bambara groundnut, Sahelian zone, Genotypic, Phenotypic, Diversity, Niger.

1. INTRODUCTION

Bambara groundnut [*Vigna subterranea* (L.) Verdc.] is a grain legume of *papillionaceae* family and originates from Africa precisely from north-eastern Nigeria and northern Cameroon [1]. Bambara groundnut, an indigenous legume crop also known as a poor man's crop, is cultivated at low levels across the African continent, especially Sub-Saharan Africa [2]. These crops are often planted by small-holder farmers in degraded and marginal environments, without access to irrigation or fertilizers [3 ; 4]). Their cultivation has a positive impact on food security by generating income for subsistence farmers [5], reducing over-reliance on a limited number of crops for food, fuel and fodder [6] while requiring fewer inputs than conventional agriculture systems [7 ; 8]). This protein-rich (18–26%), drought tolerant, under-utilized legume species has several medicinal benefits and is rated as the third most produced and consumed crop after groundnuts and cowpea in semi-arid Africa with Nigeria as the largest producer in Africa [2]. Face to the substantial climatic variability in recent years, with significant annual rainfall variations, increasingly hot temperatures, drought, sudden and unpredictable floods, and soil depletion [9], the challenge for agricultural research is to contribute to increased crop yields and soil productivity while ensuring environmental sustainability. The popularization of Bambara groundnut cultivation and

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increasing its production could provide farmers with a substantial income and contribute to food safety in Africa [10].

Despite its numerous benefits, *Vigna subterranea* is a neglected and under-exploited species that has been cultivated for millennia and contributed to the food security of the world's poorest populations [11]. According to FAOSTAT [12], the worldwide production of dry Bambara groundnut seeds was 230,619 Mt covering 354,870 ha, with Africa accounting for more than 70% of this total. In 2020, Niger's production was estimated to be 55,570 tons for 81,240 ha [13]. However, little is known about voandzou cultivation, distribution, genetic diversity, and utilization in the country's major producing areas [14]. Furthermore, the breeding strategies that ought to be developed require a thorough understanding of the genetic diversity accumulated within traditional varieties because of natural and human selection. Therefore, the objective of this study was to assess the genetic diversity of a collection of traditional Bambara groundnut accessions in the Sahelian zone of Niger.

2. MATERIAL AND METHODS

2.1. Material

The data were collected through an agronomic trial conducted during the 2021 cropping season at the Radio-Isotope Institute (IRI) research station located on the campus of Abdou Moumuoni University (UAM) in Niger (13°29 North latitude and 2°10 East longitude). During this campaign, the rainfall recorded in the area was 512.5 mm collected in 38 rainy days.

The germplasm consisted of twenty-two (22) Bambara peanut accessions collected by the Biology Department of the Faculty of Science and Technology (FAST) of Abdou Moumouni University, in Maradi region (Table 1). These accessions were taken from the national collection conducted across the country from 2012 to 2013 [14].

Table 1: Accessions and their provenance

Accession number	Villages	Communes	Abbreviations
056NeMa DOR271213	Dorama/Korama	Aguié	Ma 056
057NeMa DOR271213	Dorama	Aguié	Ma 057
058NeMa Z.M271213	Zabon Moussa	Tchadoua	Ma 058
059NeMa E.K291213	Elkolta	Maijirgui	Ma 059
060NeMa E.K291213	Elkolta	Maijirgui	Ma-E 060
060NeMa	Maradi	Maradi	Ma 060
062NeMa MA271211	Maradi	Maradi	Ma-1 062
062NeMa MA271212	Maradi	Maradi	Ma-2 062
062NeMa MA271213	Maradi	Maradi	Ma-3 062
064NeMa DOR271213	Dorama	Aguié	Ma 064
065NeMa D.S281212	Maradi	Maradi	Ma-2 065
065NeMa D.S281213	Dan Saa	Tessaoua	Ma-3 065
066NeMa	Maradi	Maradi	Ma 066
067NeMa DOR271213	Dorama	Aguié	Ma 067
068NeMa DOR271213	Dorama	Aguié	Ma 068
069NeMa DOR271213	Dorama	Aguié	Ma 069
070NeMa TC271213	Tchadoua	Tchadoua	Ma 070
072NeMa CH291213	Chabaré	Maijirgui	Ma 072
073NeMa HA271213	Halinkai	Say Saboua	Ma 073
074NeMa Z.M271213	Zabon Mussa	Tchadoua	Ma 074
075NeMa D.S281213	Dan Saa	Tessaoua	Ma 075
077NeMa D.S281213	Dan Saa	Tessaoua	Ma 077

2.2. Methods

The seeds are sown in pure culture on fallow land in July 2021. They are sown at a depth of 2 cm in the soil, with spacing of 25cm between plants and 50cm between plots. The experimental device consists of 4 blocks of 8.75m² (3.5m x 2.5m) spaced 1m apart. A block contains 2 plots of 3.75 m² (2.5m x 1.5m) containing at least 7 lines of accessions. Two seeds per accession are sown 7 times in a row (only one will be left after germination and out of the ground). Each accession is thus represented by 28 plants.

2.3. Data collection

Data was collected following the list of descriptors of Bambara groundnut (IPGRI *et al.*, [16]. Twenty-nine (29) traits were analyzed including 6 qualitative traits and 23 quantitative traits (9 phenological traits, 14 yield and yield related components traits) (Table 2).

Table 2: Qualitative and quantitative traits used for Bambara groundnut accessions' characterization

Traits	Code	
Qualitative traits		
Stem color	SC	Data recorded after 2 weeks of planting
Petiole pigmentation	PP	Data were taken after two weeks of sowing
Terminal leaflet shape	TL	Recorded 10 weeks after sowing.
Seed coat color	SCC	Recorded in two months after harvest
Eye shape	ES	Recorded in two months after harvest
Eye color	EC	Recorded in two months after harvest
Phenological traits		
Days to emergence	DTE	The number of days from planting to the arrival of 1st typical leaf on the soil surface.
Days to flowering	DF	This parameter corresponds to the number of days elapsed between sowing and the appearance of the first flower.
Days to 50% flowering	D50%F	Taken from seed germination to the arrival of 50% flowering(s)
Days to maturity	DTM	Days number from sowing to initial time of harvest
Quantitative traits		
Number of leaves	NL	Data counted 2 weeks later of 1st flowering, the average number of 5 plants.
Number of stems	NS	Recorded after harvest; average number of three stems of five healthy plants.
Number of petioles per plant	NP	Data counted 2 weeks later of 1st flowering, randomly from five healthy plants.
Petiole length	PeL	Recorded 10 weeks after planting; average length of three leaves at the fourth node of five healthy plants.
Plant height	PH	Measured from ground level (at the base of the plant) to the tip of the highest point, terminal leaflet included. Recorded 10 weeks after planting; average height of five plants.
Yield and components traits		
Pod length	PL	Noted within two months of harvest; average length of 10 pods.
Seed length	SL	Noted within two months of harvest; average length of 10 seeds
Pod width	PW	Noted within two months of harvest; average length of 10 pods.
Seed width	SWi	Noted within two months of harvest; average width of 10 seeds
Number of pods per plant	NPP	The number of individual pods of the 5 central plants after drying was used for the parametric measurements.
Number of seeds per plant	NSP	Data counted after dehusking all pods, randomly average values from 5 plants.
Dry pod weigth	DPW	Data measured after drying of pods (12% moisture).
Seed weigth	SWe	Data measured after drying of seeds (12% moisture).
Hundred seed weigth	HSW	Observed within two months after harvest (with 12% moisture content).
Yield	YLD	Data weighted of dried pods (at 12% moisture content) per plot, lastly converted the plot yield to a kilogram per hectare (kg/ha).
Shell weigth	SW	Data measured within two months of harvest.
Biomass dry weigth per plant	BDW	Weight of dried plant, recorded after maintaining the harvested plant dried in sun.
Harvest index	HI	Measured using the formula of the ratio of Grain yield (kg per ha.)/biological yield (grain + straw)
Biological yield	BYLD	Weight of dry seeds + dry biomass

2.4. Statistical Analysis

The software R 3.4.0 was followed to test the significant differences using the analysis of variance (ANOVA) procedure at the level of LSD; $P \leq 0.05$ and to compare among the mean of significant of traits. The correlations between the quantitative variables were determined using Pearson correlation coefficient formula. The estimated genetic parameters were used for dendrogram construction using R 3.4.0 software. Genotypic and phenotypic variances (VG and VP), genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (H2) and expected genetic gain (GA) were calculated according to the formulas used by Johnson *et al.*, [17], Assefa *et al.*, [18]; Hosseini *et al.*, [19] and Mahmudul *et al.*, [20] presented in (Table 3). Broad sense heritability was estimated using the formula given by Khan *et al.*, [21]. The same software was used to perform the Pearson coefficient of correlation, the principal component analysis (PCA) and ascending hierarchical classification (AHC) to assess the degree of resemblance and dissimilarity between the characters analyzed.

Table 3: Genetic parameters formulas

Parameters	**Formula**	**meanings of terms**
Genotypic variance : σ^2_g Phenotypic variance : σ^2_p Broad-sense heritability : h^2_b	$\sigma^2_g=\frac{MSG-MSE}{r}$ $\sigma^2_p= \sigma^2_g$-MSE $h^2_b=\frac{\sigma^2_g}{\sigma^2_p} \times 100$	**MSG** is the genotypic mean square, **MSE** is the error mean square, and ***r*** is the replication number. ***K*** is the constant that indicates the intensity of selection. According to Adewale *et al.*, [22], the rate is 2,06 at the point when the *K* is at 5%. $\bar{X}$ is the grand mean values of traits.
Phenotypic Coefficient of Variation : **PCV** Genotypic Coefficient of Variation : **GCV** Relative Difference (RD) Genetic Advance : **GA**	PCV=$\left(\sqrt{\sigma^2_p} \,/\, \bar{X}\right) \times 100$ GCV=$\left(\sqrt{\sigma^2_g} \,/\, \bar{X}\right) \times 100$ RD=$\left(\frac{PCV-GCV}{PCV}\right) \times 100$ GA=K $\times \frac{\sqrt{\sigma^2_p}}{\bar{\bar{X}}} \times h^2_b \times 100$	The **PCV** and **GCV** values obtained were classified according to the suggested index from 0% to 10% for low variation, 10-20% for moderate variation, and ≥20% for high variation [21]. ***K*** is the constant that indicates the intensity of selection. According to Adewale *et al.*, [22], the rate is 2,06 at the point when the *K* is at 5%. $\bar{X}$ is the grand mean values of traits.

3. RESULTS

3.1. Qualitative Traits

The color of the stem, the pigmentation of the petiole, and the shape of the terminal leaflet are very diverse as indicated by the morphological observations in Table 3. According to the results, 18.2% of the accessions have red stems, 18.2% have green stems, and 63.63% have striped stems. The color of the petiole is greenish red for 63.63% of accessions and green for 32.4%. 90.91% of accessions have oval terminal leaflets, while 9.1% have lanceolate leaflets (Table 4). A brown seed coat with brown marbling is found in 13.63% of the accessions assessed, 31.82% of cream with brown dotted lines, 27.27% cream, 4.54% cream with black and brown marbling, and 13.63 % red with black dotted lines. In terms of eye color, 36.36% are black, 50% are brown, and 13.63% are red. Butterfly-shaped eyes account for 86.36% of accession eyes (Figure 1).

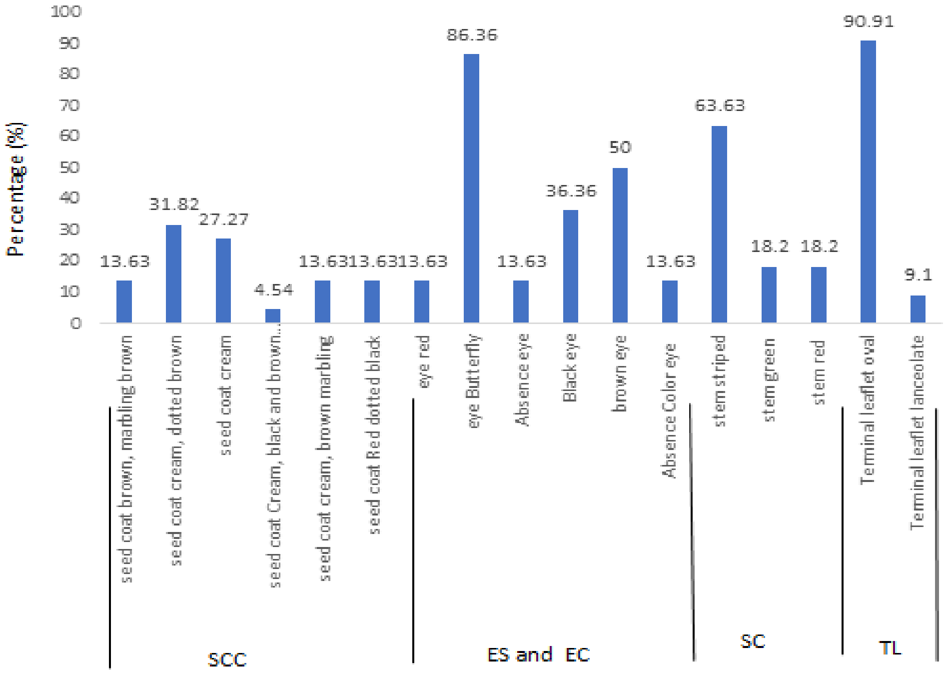


Figure 1: Frequency distribution of qualitative characteristics of the bambra groundnut accessions

3.2. Quantitative traits

In the current study, 22 quantitative characters were analyzed within the 22 accessions. The analysis of variance revealed significant variations inside the parameters (Table 4). Low variations between the minima and the maxima were observed for the morphological parameters, while substantial differences were observed between yield-related traits. The coefficients of variation ranged from 2.42% (date of 50% flowering) to 48.25% (shell weight). The greatest variability was observed in shell weight (CV=48.25%), dry biomass weight (CV28.50%), pod weight (CV=26.76%), number of seeds (CV=26.19%), 100 seed weight (CV=25.75%), seed weight (CV=21.87%), and yield (CV=23.26%) (Table 5). Weak variations (CV <20%) were observed for the other characters.

Table 4: Analysis of variance results of the 22 characters studied

Traits	Min	Max	SD	Mean	Var	CV (%)
NP	27.25	49.08	4.95	41.05	24.53	12.06
NL	81.75	144.39	15.05	123.52	226.46	12.18
PH (cm)	17.99	25.17	1.96	21.99	3.84	8.91
PeL(cm)	13.32	20.98	2.12	17.28	4.51	12.27
TNP	18.55	34.35	4.62	25.64	21.35	18.02
NS	4.47	11.57	1.57	8.96	2.46	17.52
BDW(g)	4.95	15.05	2.89	10.14	7.77	28.50
PL (cm)	1.53	1.90	0.10	1.67	0.011	5.98
PW (cm)	1.21	1.55	0.076	1.30	0.006	5.84
SL (cm)	0.87	1.24	0.08	1.03	0.006	7.76
SW (cm)	0.57	0.81	0.056	0.68	0.003	8.23
NSP	13.92	33.15	5.43	20.73	29.53	26.19
SWe (g)	5.92	12.54	1.91	8.73	3.66	21.87
SeW (g)	1.70	8.09	1.66	3.44	2.77	48.25
PW(cm)	7.62	20.63	3.26	12.18	10.65	26.76
BYLD (kg/ha)	476.6	889.1	115.18	670.9	13.267	17.16
YLD (kg/ha)	210.7	445.9	70.92	304.8	5029.17	23.26
HSW (g)	89.62	278.85	45.17	175.43	2040.16	25.75
DTM (day)	81.50	94.25	3.78	85.76	14.27	4.41
DTE (day)	6	8	0.44	7.17	0.20	6.13
DF (day)	31.25	35.25	0.99	33.17	0.99	2.98
D50%F (day)	33.25	37.25	0.86	35.51	0.73	2.42
P-values	0.00^{***}	0.00^{***}	0.00^{***}	0.00^{***}	0.00^{***}	0.022

Legend: **Max:** maximum; **Min**: minimum; **CV**: coefficient of variation, **Var**: Variance, **SD**: standard deviation, **DTE:** days to emergence, **DF:** days to flowering, **D50%F**: days to 50% flowering, **DTM**: days to maturity, **PH:** plant height, **NS:** number of stems per plant, **NP**: number of petioles per plant, **PeL:** petiole length, **NL**: number of leaves per plant, **BDW**: biomass dry weight per plant, **TNP**: total no. of pods per plant, **DPW**: dry pods weight, **PL**: pod length, **PW**: pod width, **NSP** : number of seeds per plant, **DSW**: dry seed weight per plant, **SL**: seed length, **SW**: seed width, **HSWe**: hundred seed weight, **HI**: harvest index, **YLD**: yield, **SeW**: shell weight, **SWe**: seed weight, **BYLD**: biological yield.

3.3. Correlation between parameters

To study the relationships between the parameters, a correlation matrix (Pearson's coefficient) was performed (Table 5). Positive correlations were obtained between: seed weight per plant with shell weight (r = 0.84), pod weight (r = 0.91) and yield (r = 0.99); the height of the plant with the length of the petiole (r=0.95); date at 50% flowering with seed length (r = 0.71); seed width with seed length (r = 0.67); pod width with pod length (r = 0.67); the number of leaves with the number of petioles (r=0.96); 100-seed weight with seed weight (r = 0.61), pod weight (r = 0.58) and yield (r = 0.61); shell weight with seed weight (r = 0.56), pod weight (r = 0.84) and yield (r = 0.56).

3.4. Agro-morphological diversity of Bambara groundnut accessions in the Sahelian zone of Niger

The principal component analysis (Table 6) reveals that the first three components with the twenty-two measured parameters explain 55.83% of the total variability, including 22.11% for axis 1, 19.85% for axis 1. axis 2, and 13.87% for axis 3. The overall variability is explained by 22 principal components with eigenvalues between 3.052 and 4.86. The first axis is defined by yield traits, but it is negatively correlated with plant height. Axis 2 is positively correlated with petiole length, pod length, seed length, pod width, seed width and maturity date. It is negatively correlated with the number of pods and the number of stems. The third axis is positively correlated with the number of petioles, the number of leaves, the number of seeds and negatively correlated with the weight of 100 seeds, date of flowering and date of 50% flowering.

Table 5: Pearson correlation between the evaluated characters

BDW	**HSW**	**NS**	**NP**	**NPP**	**NSP**	**NL**	**PeL**	**PL**	**PW**	**SL**	**SW**	**HI**	**PH**	**DTM**	**DTE**	**DF**	**D50%F**	
0.26	-0.08	-0.15	-0.02	-0.16	0.12	-0.02	0.31	0.21	0.11	**0.71**	0.24	-0.12	0.31	0.43	0.16	**0.69**	1	**D50%F**
0.23	0.03	-0.12	-0.05	-0.13	0.05	-0.05	0.35	0.24	0.27	-0.04	0.1	-0.06	0.34	0.41	0.04	1		**DF**
-0.01	-0.12	-0.32	0.08	-0.14	0.22	0.06	0.07	0.4	0.1	0.15	-0.06	0.04	0.13	0.3	1			**DTE**
0.25	0.07	-0.44	-0.03	-0.31	-0.02	-0.02	0.36	0.34	0.24	0.27	0.3	-0.07	0.36	1				**DTM**
0.304	0.107	0.001	0.404	-0.212	0.02	0.43	**0.95**	0.27	0.37	0.09	0.06	0.04	1					**PH**
-0.09	0.32	0.01	0.13	0.09	-0.01	0.17	-0.01	0.23	0.19	-0.02	0.08	1						**HI**
0.13	0.02	-0.17	-0.09	-0.06	0.06	-0.05	0.12	0.1	0.01	**0.67**	1							**SW**
0.16	-0.06	-0.09	0.03	-0.07	0.08	0.07	0.11	0.14	0.17	1								**SL**
0.36	0.439	0.087	0.19	0.005	-0.08	0.22	0.34	**0.67**	1									**PW**
0.26	0.28	-0.18	0.07	-0.19	-0.09	0.09	0.25	1										**PL**
0.3	0.14	0.03	0.38	-0.23	0.02	0.4	1											**PeL**
0.17	0.04	0.18	**0.96**	0.21	0.28	1												**NL**
0.22	-0.4	-0.1	0.33	0.42	1													**NSP**
0.13	-0.07	0.45	0.23	1														**NPP**
0.15	-0	0.12	1															**NP**
0.25	0.23	1																**NS**
0.12	1																	**HSW**
1																		**BDW**
																		SeW
																		SWe
																		DPW
																		YLD

	D50%F	**DF**	**DTE**	**DTM**	**PH**	**HI**	**SW**	**SL**	**PW**	**PL**	**PeL**	**NL**	**NSP**	**NPP**	**NP**	**NS**	**HSW**	**BDW**	**SeW**	**SWe**	**DPW**	**YLD**
SeW	-0.03	0.06	0.07	0.04	0.079	0	0.04	0.06	0.34	0.16	0.12	0.2	0.23	0.27	0.19	0.26	0.39	0.15	1			
SWe	-0.05	0.02	-0.02	0.04	0.026	0.03	0.06	0.01	0.31	0.12	0.06	0.24	0.43	0.36	0.24	0.23	**0.61**	0.23	**0.56**	1		
DPW	-0.05	0.04	0.02	0.01	0.055	0.19	0.06	0.04	0.36	0.16	0.1	0.25	0.38	0.36	0.25	0.27	**0.58**	0.22	**0.84**	**0.91**	1	
YLD	-0.06	0.02	-0.02	-0.04	0.026	0.307	0.06	0.01	0.31	0.12	0.06	0.24	0.43	0.36	0.24	0.23	**0.61**	0.23	**0.56**	**0.99**	0.01	1

Legend: **DTE(day):** days to emergence, **DF(day):** days to flowering, **D50%F(day)**: days to 50% flowering, **DTM(day)**: days to maturity, **PH(cm):** plant height, **NS:** number of stems per plant, **NP**: number of petioles per plant, **PeL(cm):** petiole length, **NL**: number of leaves per plant, **BDW (g)**: biomass dry weight per plant, **TNP** : total no. of pods per plant, **DPW(g)**: dry pods weight, **PL(cm)**: pod length, **PW(cm)**: pod width, **NSP**: number of seeds per plant, **NPP**: number of pod per plant, **DSW(g)**: dry seed weight per plant, **SL(cm)**: seed length, **SW(cm)**: seed width, **HSW(g)**: hundred seed weight, **HI**: harvest index, **YLD(kg/ha)**: yield, **SeW(g)**: shell weight, **SWe(g)**: seed weight.

Table 6: Eigenvalues and contribution of variables to the different axes of PCA

Axes	**Eigen values**	**Proportions (%)**	**Cumulative percentages (%)**
1	4.863986	22.10903	22.10903
2	4.367111	19.85050	41.95953
3	3.052785	13.87629	55.83583

3.4.1. Analysis of genetic parameters

3.4.1.1. Phenotypic and genotypic variances

For all parameters, the phenotypic variance (σ^2_p) was greater than the genotypic variance (σ^2_g) (Table 7). The phenotypic variance ranged from 0.01 to 2544.04 while the genotypic variance (σ^2_g) ranged from 0.0003 to 65.54. The yield trait had the largest phenotypic variance (2544.04) and pod width had the smallest (0.01). Traits including yield (2544.04), number of leaves (709.35), the weight of 100 seeds (467.87), number of petioles (77.25), number of seeds (52.72), and number of pods (35.84) displayed high phenotypic variances ($\sigma^2_p > 20$). Maturity date (16.93), seedling height (10.82), seed weight (14.37), dry biomass weight (13.80), and petiole length (12.24) showed moderate phenotypic variances ($\sigma^2_p < 20$). The highest genotypic variance ($\sigma^2_g > 20$) was obtained with the number of leaves (65.54) followed by 100-seed weight (52.42), and the number of seeds (21.92). Maturity date (15.58), pod number (13.76), and yield (10.04) had moderate genotypic variances ($\sigma^2_g < 20$).

3.4.1.2. Phenotypic and genotypic coefficients of variation

For all traits, the phenotypic coefficient of variation (PVC) was higher than the genotypic coefficient of variation (GCV) (Table 7). The highest PVC and GCV values were obtained with the hull weight with 85.91% and 25.51%, respectively. The lowest values were found with maturity date for PVC (4.82%) and pod length for GCV (1.34%). High PVC and GCV values were found for traits like the number of seeds per plant (PVC=35.05% and GCV=22.65%), shell weight (PVC=85.91% and GCV =25.51%), and dry biomass weight (PVC=36.61% and GCV=23.66%). Emergence date and seed width showed moderate phenotypic and genotypic coefficients. The lowest phenotypic and genotypic coefficients of variation were observed for date to 50% flowering, date of maturity, date of flowering, length of pod, and width of pod.

3.4.1.3. Broad-sense heritability

For all measured parameters, the broad-sense heritability (h^2_b) ranged from 0.4% (yield) to 92.4% (number of leaves per plant) (Table 7). The date of emergence (78.77%), the date of 50% flowering (66.10%), the date of maturity (92.08%) and the number of leaves per plant (92.4%) presented high broad-sense heritability values ($h^2_b > 60\%$) [20]. The number of pods (31.17%), the number of seeds (41.58%), the weight of dry biomass (41.76%), and the width of seed (53.27%) showed moderate broad-sense heritability values ($30\% < h^2_b < 60\%$), while the rest of the parameters displayed low broad-sense heritability values ($h^2_b < 30\%$).

3.4.1.4 Genetic Advance (GA)

Genetic gain ranged from 0.003% (harvest index) to 31.49% (dry biomass weight) (Table 7). Emergence date (20%), number of seeds (30.03%) and weight of dry biomass (31.49%) showed high genetic gains (GA≥20%); number of stems per plant (15.65%), number of pods per plant (16.64%), seed weight

(15.60%), seed width (17.10%) and weight of 100 seeds (11.10%) are moderate (10%<GA<20%) and the rest of the parameters have low genetic gains (GA<10%).

Table 7: Genetic parameters of bambara groundnut from the Sahelian zone of Niger

Traits	Mean	(σ^2_e)	(σ^2_g)	(σ^2_p)	EVC(%)	PCV(%)	GCV(%)	RD(%)	h^2_b (%)	GA (%)
DTE(d)	6.95	0.15	0.60	0.73	5.67	12.31	10.93	11.21	78.77	20
D50%F(d)	35.43	1.61	3.14	4.76	3.60	6.16	5.00	18.83	66.10	8.38
DTM(d)	85.27	1.34	15.58	16.93	1.36	4.82	4.63	3.94	92.08	9.15
DF(d)	33.11	2.92	1.17	4.10	5.16	6.11	3.28	46.31	28.74	3.62
PH(cm)	21.80	9.75	1.06	10.82	14.33	15.09	4.73	68.65	9.83	3.07
NP	41.05	70.29	6.96	77.25	20.42	21.41	6.43	69.96	9.01	3.97
NS	8.96	3.65	1.55	5.20	21.32	25.45	13.91	45.34	29.86	15.65
NPP	25.64	30.39	13.76	44.15	21.50	25.91	14.46	44.19	31.17	16.64
NSP	20.71	30.79	21.92	52.72	26.79	35.05	22.65	35.37	41.58	30.03
NL	123.52	643.80	65.54	709.35	20.54	21.56	6.55	69.61	92.4	4.10
SeW (g)	1,41	7.99	0.77	8.77	82.04	85.91	25.51	70.3	8.82	15.60
SWe (g)	1,88	14,28	0,1	14,36	43,27	43,40	3,36	92,26	0,6	0,53
DPW (g)	3.25	33.59	2.25	35.84	47.58	49.15	12.31	74.95	6.28	6.35
DSW (g)	8.73	14.28	0.09	14.37	43.27	43.40	3.36	92.26	0.6	0.53
BDW (g)	10.15	8.04	5.76	13.80	27.94	36.61	23.66	35.37	41.76	31.49
PeL (cm)	17.28	10.30	1.93	12.24	18.57	20.24	8.04	60.27	15.79	6.58
PL (cm)	1.67	0.02	0.005	0.03	8.97	9.92	4.23	57.36	18	3.72
SL (cm)	0.96	0.01	0.003	0.013	9.95	11.82	6.35	46.27	28.91	7.04
PW (cm)	1.29	0.01	0.0004	0.01	7.69	7.82	1.34	82.86	3.12	0.47
SW (cm)	0.66	0.005	0.006	0.011	10.67	15.56	11.57	25.64	53.27	17.10
YLD (kg/ha)	116.55	2534	10.04	2544.04	43.2	43.27	2.72	93.71	0.4	0.35
HI	0.65	0.033	0.0003	0.033	27.62	27.73	2.64	90.48	1.34	0.003
HSW(g)	45.03	415.45	52.42	467.87	45.27	48.04	16.08	66.52	11.02	11.10

Legend: σ^2_e :environmental variance, σ^2_g : genotypic variance**,** σ^2_p : phenotypic variance, h^2_b : heritability in broad sense, **PCV**: phenotypic coefficient of variation; **GCV**: genotypic coefficient of variation; **RD**: relative difference; **GA**: genetic advance**, DTE:** days to emergence, **DF:** days to flowering, **D50%F** : days to 50% flowering, **DTM**: days to maturity, **PH:** plant height, **NS:** number of stems per plant, **NP**: number of petioles per plant, **PeL:** petiole length, **NL**: number of leaves per plant, **BDW**: biomass dry weight per plant, **TNP**: total no. of pods per plant, **DPW**: dry pods weight, **PL**: pod length, **PW** : pod width, **NSP**: number of seeds per plant, **NPP**: number of pod per plant, **DSW** : dry seed weight per plant, **SL** : seed length, **SW** : seed width, **HSW**: hundred seed weight, **HI**: harvest index, **SeW(g)**: shell weight, **YLD**: yield, **SWe**: seed weight.

3.4.2. Cluster Analysis

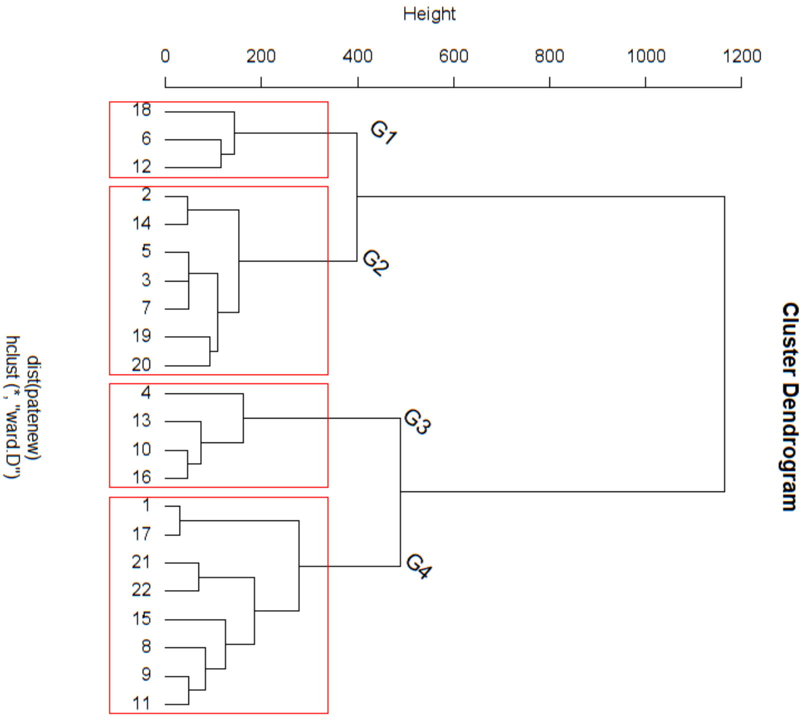
In this study, the homogenized data was used to calculate Euclidean distances among the 22 Bambara groundnut accessions. The Agglomerative Hierarchical Clustering (AHC) analysis following the Unweighted Pair-Group Method with Arithmetic mean (UPGMA) clustered the different accessions into 4 groups (clusters) based on the twenty-two measured traits at the dissimilarity level of 348.7 (Figure 2). Group 1 (G1) was made up of three (3) accessions, group 2 (G2) with seven (7) accessions, group 3 (G3) with four (4) accessions, and group 4 with eight (8) accessions (Table 8). Group 4 with the largest number of accessions produced more yield (2414.28 kg/ha) and group 1 consisting of the smallest number of accessions gave the lowest yield (1513.58 kg/ha). It should be noted that group 3 containing four accessions gave a yield (2029.3kg/ha) close to that of group 4.

Table 8: Characteristics of the groups of Bambara groundnut accessions

Traits	**Group 1**	**Group 2**	**Group 3**	**Group 4**
	Ma 072, Ma 060, Ma-3 065	**Ma 057, Ma 067, Ma-E 060, Ma 058, Ma-1 062, Ma 073, Ma 074**	**Ma 059, Ma 066, Ma 064, Ma 069**	**Ma 056, Ma 070, Ma 075, Ma 077, Ma 068, Ma-2 062, Ma-3 062, Ma-2 065.**
DTE(d)	7	7.25	7.62	7.25
D50%F(day)	35.42	36.04	35.75	34.97
DTM(day)	88.17	87.43	84.56	84.00
DF(day)	33.17	33.86	31.2	32.59
PH (cm)	20.14	22.20	21.03	22.99
NP	44.43	41.19	38.89	40.74
NS	9.28	8.12	9.63	9.24
NPP	29.54	25.06	28.18	23.42
NSP	23.56	19.10	24.94	19.00

Traits	**Group 1**	**Group 2**	**Group 3**	**Group 4**
	Ma 072, Ma 060, Ma-3 065	**Ma 057, Ma 067, Ma-E 060, Ma 058, Ma-1 062, Ma 073, Ma 074**	**Ma 059, Ma 066, Ma 064, Ma 069**	**Ma 056, Ma 070, Ma 075, Ma 077, Ma 068, Ma-2 062, Ma-3 062, Ma-2 065.**
NL	131.26	123.56	116.69	123.99
SWe (g)	3.89	3.27	5.58	2.35
DPW (g)	14.54	10.51	16.99	10.34
DSW (g)	10.64	7.23	11.41	7.98
BDW (g)	11.38	8.85	10.70	10.53
PeL (cm)	18.80	17.28	16.05	17.32
PL (cm)	1.68	1.68	1.70	1.63
SL (cm)	1.10	1.00	1.05	1.02
PW (cm)	1.32	1.31	1.31	1.28
SW (cm)	0.72	0.69	0.68	0.65
YLD (kg/ha)	1513.58	2057.91	2029.3	2414.28
HSW (g)	199.94	160.56	183.89	174.93
BYLD (kg/ha)	1856.17	3792.24	3246.91	5865.2

Legend: DTE: days to emergence, **DF:** days to flowering, **D50%F**: days to 50% flowering, **DTM**: days to maturity, **PH:** plant height, **NS:** number of stems per plant, **NP**: number of petioles per plant, **PeL:** petiole length, **NL**: number of leaves per plant, **BDW**: biomass dry weight per plant, **TNP**: total no. of pods per plant, **DPW**: dry pods weight, **PL**: pod length, **PW** : pod width, **NSP**: number of seeds per plant, **NPP**: number of pod per plant, **DSW**: dry seed weight per plant, **SL**: seed length, **SWi**: seed width, **HSW**: hundred seed weight, **HI**: harvest index, **YLD**: yield, **SW**: shell weight, **SWe**: seed weight, BYLD: biological yield.



Ma 056 =1, Ma 057=2, Ma 058=3, Ma 059=4, Ma-E 060=5, Ma 060=6, Ma-1 062=7, Ma-2 062=8, Ma-3 062=9, Ma 064=10, Ma-2 065=11, Ma-3 065=12, Ma 066=13, Ma 067=14, Ma 068=15, Ma 069=16, Ma 070=17, Ma 072=18, Ma 073=19, Ma 074=20, Ma 075=21, Ma 077=22.

Figure 2: Dendrogram of the 22 accessions of Bambara groundnut cultivated in the Sahelian zone of Niger

4. DISCUSSION

The study of the 22 accessions made it possible to evaluate the existing genetic variability within the species of *Vigna subterranea* in the Sahelian zone of Niger.

4.1. Qualitative parameters

The results showed high variability in the coloration of the tegument, and shape and color of the seed eye. Similar results were reported by Mahmudul *et al.*, [23], indicating high variability in the coloration of the tegument, and shape and color of the seed eye.

Significant variations among all the qualitative traits studied were also revealed by Gbaguidi *et al.*,[24]. Wassouo *et al.,* [25] believe that this difference in coloration would be linked to biological factors. According to Ndiang *et al.,* [26] the resemblance between varieties and characters shows that there are characters that are specific to certain varieties. According to Anchirinah *et al.,* [27], voandzou genotypes are distinguished based on plant habits and seed characteristics. In this study, seed coats were all smooth; a complete absence of roughness was noticed. These results converge with those of Ndiang *et al.,* [26] and Mahmudul *et al.,* [23].

4.2. Quantitative parameters

The descriptive analysis of the quantitative traits showed that the emergence time for the evaluated accessions varied between 6 and 8 DAS. This result is consistent with those of Djé *et al.,* [28] and Wassouo *et al.,* [25] who reported similar emergence times of 6 and 8 DAS, and 6 and 7 DAS, respectively. Furthermore, Touré *et al.,* [10] revealed an emergence time interval of 6 to 15 DAS. However, Karikari [29] observed a higher time of emergence of 14 to 24 DAS. These variations can be explained by the genotype makeup of each accession, the environmental conditions, and the storage conditions of the seeds [25].

A very significant difference was observed between the minima and the maxima of the parameters analyzed. This corroborates the results of Harouna *et al*., [15], who reported significant differences between minima and maxima in a study involving 14 morphotypes in Niger. The coefficients of variation ranged from 2.42% (date of 50% flowering) to 48.25% (shell weight). Seven (7) of the 22 metric characters analyzed showed significantly higher coefficients of variation (CV>20%). Previously, Sévérin *et al.,* [30], obtained coefficients between 0% and 63.30%, Amadou *et al.,* [15] between 10.3% and 72%, Moussa [31] between 4.16% and 72.51%, Wassouo *et al.,* [25] between 1.79% and 37.08%, and Mahmudul *et al.,* [23] between 13.17 and 41.21%. Remarkably, high coefficients of variation were obtained for yield parameters, indicating significant yield variability within the accessions investigated. Consistent results were obtained by several authors [32; 15; 23]. It is also in line with the observation of Swanevelder [33] who indicated that the yield of Bambara groundnut is very unstable.

4.3. Correlation between parameters

In plant breeding, correlation matrix is an important tool for determining the degree of association between two or more variables [34; 20]). The greatest correlations were obtained between shell weight and seed weight (r=0.84), seed weight per plant and pod weight (r=0.91), seed weight per plant and yield (r=0.99), and seedling height and petiole length (r=0.95). These results are close to those of Harouna *et al.,* [15], who obtained a strong correlation between the weight of seeds per plant and the weight of pods (r=0.96). Wassouo *et al.,* [25] also obtained a strong correlation between the seed weight and the number of pods (r=0.945). It was previously indicated that traits like the number of pods per plant, the number of seeds per plant, and 100-seed weight are positively correlated with yield in Bambara groundnut [35].

4.4. Genetic components

For all traits studied, the genotypic variance was significantly lower than the phenotypic variance. This result is like those of Mahmudul *et al.,* [23], Danbe *et al.,* [36] and Malek *et al.,* [37]. This significant difference reflects a strong impact of environmental factors on the expression of these traits. High heritability plays a crucial role in trait selection [38]. In this study, the parameters date of emergence (78.77%), date of flowering at 50% (66.10%), date of maturity (92.08%) and number of leaves (92.4%) were presented high heritability values, implying the low impact of the environment on the expression of these traits (Visscher *et al.,* [39]. High heritability values for yield-related traits were recently reported by Mahmudul *et al.,* [23]. Moderate heritability values were observed for pod number (31.17%), seed number (41.58%), dry biomass weight (41.76%) and seed width (53.27%). Emergence date had high heritability and genetic gain (78.77% and 20%). Low to moderate heritability and genetic advance values may hamper genetic improvement of the trait due to strong environmental effects [40]. According to Nerbéwendé *et al.,* [38], heritability alone does not predict whether selection will result in significant improvement. Therefore, joint estimation of heritability and expected genetic gain can provide more reliable information for genetic improvement [41].

CONCLUSION

This study revealed a large agro-morphological variability within the investigated accessions of the Sahelian zone of Niger. The 22 accessions were clustered into four (4) groups for the different traits evaluated. Group 3 (4 accessions) followed by group 1 (3 accessions) consisted of accessions with the highest average yield while group 4 (8 accessions) and group 2 (7 accessions) were made up of accessions with the lowest average yield. A strong influence of environmental factors on the expression of the performance of certain accessions was observed. This was illustrated by significant differences between the phenotypic and genotypic coefficients of variation as well as differential broad-sense heritability values (low to high) for the different traits evaluated. These findings can play a crucial role for Bambara groundnut genetic breeding in Niger. However, to be more comprehensive, this study should be followed by a molecular characterization and a biochemical evaluation of the grains.

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