Estimates of Phenotypic and Genotypic Variance and Heritability in Eighty-Nine Bambara Groundnut [*Vigna subterranea* (L.) Verdcourt] Accessions Collected from Six Regions of Niger

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The bambara groundnut [Vigna subterranea (L.) Verdc. (Fabaceae)] is a legume mainly cultivated by women, for the nutritional quality of these seeds. It is a so-called minor culture and the improvement of the plant and its popularization remains to be promoted. The objective of this present work is to evaluate the genetic variability of bambara groundnut accessions. The experiment was carried out according to a completely randomized block device with four replications. Twenty-two (22) characters including four (4) phenological, four (4) morphological and fourteen (14) related to yield were evaluated for accessions characterization. Descriptive analysis showed significant differences. The coefficients of variation ranged from 3.51% (maturity date) to 38.87% (shell weight). Significantly high values (CV>20%) for 8 of the metric parameters were observed. Pod weight per plant and seed weight per plant (r=0.943), yield in kg/ha (r=0.943); seed weight per plant and yield in kg/ha (r=0.999) showed the strongest correlations. The phenotypic and genotypic coefficients of variation were high for dry biomass weight (PCV=42.23%; GCV=28.40%), shell weight (PCV=63.46%; GCV=22.46%) and 100-seed weight (PCV=25.57%; GCV=25.25%). Maturity date (95.77%) and 100-seed weight (99.84%) had high heritabilities. Broad-sense heritability and genetic gain are high for 100-seed weight (H^2=99.84%; GA=52.58%). The Ascending hierarchical classification produced four groups of which group 4 is the most efficient in yield with short (20.58cm) early accessions (80.32 days). Groups 1 and 2 include, late accessions (~22cm) with respectively maturity dates (DM=85.67 days and DM=86.53 days.

1. INTRODUCTION

Voandzou is a herbaceous plant whose chromosome set is 2n=22 as in most grain legumes [1]. Villages and countryside are the centers of origin and diversity of numerous cultivated and wild species. Voandzou has significant biodiversity across different agroecological zones in sub-Saharan Africa and around the world [2]. Indeed Kadams and Soja [3], Jonah et al., [4], Mahmudul et al., [5], Mahmudul et al., [6], Paulos et al., [7], Ibrahim et al., [8], and many other authors have highlighted this genetic diversity of the species vigna subterranea through various experiments. This immense potential gives it an abundant germplasm containing a wide range of genetic variability throughout its cultivation area [9]. Plant genetic resources form the basis of food and agricultural production worldwide and bring together wild and cultivated species selected by humans [10]. However, due to the genetic richness of Bambara groundnut, its seeds contain 64.4% carbohydrates, 23.6% proteins, 6.5% fats, 5.5% fibers, essential vitamins and minerals such as iron and zinc [11]. Also, they mainly contain healthy fatty acids such as omega-6 (n-6) and polyunsaturated fatty acids [12]. Despite neglect of the crop, it has been cultivated for several millennia in sub-Saharan Africa, particularly in harsh semi-arid savannah environments, where other grain legume crops perform dismal or fail completely [13]. Its ability to fix nitrogen in the soil gives the soil a certain fertility capacity, and can therefore contribute significantly to modern agriculture in the face of climate [14]. In sub-Saharan Africa, farmers have maintained this crop under their own care and management for many generations and there is a long list of entries characterized by different types of plants and seeds [15].

In Niger, very little information is currently available on the genetic diversity of voandzou [16]. The INRAN (National Institute of Agronomic Research of Niger) gene bank includes 47 voandzou accessions [17]. A collection of one hundred and fifteen (115) accessions is also located at the Faculty of Science and Technology of the Abdou Moumouni University of Niamey. But all these collections do not seem to represent all the variability of the national territory. The main objective of this present work is to evaluate the variability of some genetic parameters of voandzou accessions in order to develop appropriate strategies for future improvement.

2. MATERIALS AND METHODS

2.1 Materials

The plant material is composed of seeds from 89 bambara groundnut accessions from six regions of Niger (Table 1), taken from the collection from 2012 to 2013 [16] of the Department of Biology of the Faculty of Sciences and Techniques. (FAST) from the Abdou Moumouni University of Niger.

Table 1. Accessions and their provenance

N°	Varieties	Origins	N°	Varieties	Origins	N°	Varieties	Origins
1	Do 001	Dosso/Niger	31	Ti 043	Tillabéri/Niger	61	Ma 073	Maradi/Niger
2	Do 002	Dosso/Niger	32	Ti 044	Tillabéri/Niger	62	Ma 074	Maradi/Niger
3	Do 003	Dosso/Niger	33	Ti 045	Tillabéri/Niger	63	Ma 075	Maradi/Niger
4	Do 004	Dosso/Niger	34	Ti 047	Tillabéri/Niger	64	Ma 077	Maradi/Niger
5	Do 006	Dosso/Niger	35	Ti 048	Tillabéri/Niger	65	Di 081	Diffa/Niger
6	Do 007	Dosso/Niger	36	Ti 049	Tillabéri/Niger	66	Di-3 082	Diffa/Niger
7	Do 008	Dosso/Niger	37	Ti 050	Tillabéri/Niger	67	Di-4 082	Diffa/Niger
8	Do 009	Dosso/Niger	38	Ti 051	Tillabéri/Niger	68	Di 083	Diffa/Niger
9	Do 011	Dosso/Niger	39	Ti 052	Tillabéri/Niger	69	Di 084	Diffa/Niger
10	Do 013	Dosso/Niger	40	Ti 053	Tillabéri/Niger	70	Di 085	Diffa/Niger
11	Do 014	Dosso/Niger	41	Ti 054	Tillabéri/Niger	71	Di 086	Diffa/Niger
12	Do 015	Dosso/Niger	42	Ti 055	Tillabéri/Niger	72	Zi 087	Zinder/Niger
13	Do 016	Dosso/Niger	43	Ma 056	Maradi/Niger	73	Zi 088	Zinder/Niger
14	Do 017	Dosso/Niger	44	Ma 057	Maradi/Niger	74	Zi 091	Zinder/Niger
15	Do 018	Dosso/Niger	45	Ma 058	Maradi/Niger	75	Zi 092	Zinder/Niger
16	Do 019	Dosso/Niger	46	Ma 059	Maradi/Niger	76	Zi 093	Zinder/Niger
17	Do 022	Dosso/Niger	47	Ma-E 060	Maradi/Niger	77	Zi 094	Zinder/Niger
18	Do 023	Dosso/Niger	48	Ma 060	Maradi/Niger	78	Zi 095	Zinder/Niger
19	Do 024	Dosso/Niger	49	Ma-1 062	Maradi/Niger	79	Zi 096	Zinder/Niger
20	Do 025	Dosso/Niger	50	Ma-2 062	Maradi/Niger	80	Zi 097	Zinder/Niger
21	Do 029	Dosso/Niger		Ma-3 062	Maradi/Niger	81	Zi 098	Zinder/Niger
22	Do 030	Dosso/Niger	52	Ma 064	Maradi/Niger	82	Zi 100	Zinder/Niger
23	Do 031	Dosso/Niger	53	Ma-2 065	Maradi/Niger	83	Zi 101	Zinder/Niger
24	Do 035	Dosso/Niger	54	Ma-3 065	Maradi/Niger	84	Th 112	Tahoua/Niger
25	Do 036	Dosso/Niger	55	Ma 066	Maradi/Niger	85	Th 113	Tahoua/Niger
26	Do 037	Dosso/Niger	56	Ma 067	Maradi/Niger	86	Th 114	Tahoua/Niger
27	Do 038	Dosso/Niger	57	Ma 068	Maradi/Niger	87	Th 115	Tahoua/Niger
28	Do 040	Dosso/Niger	58	Ma 069	Maradi/Niger	88	Th 117	Tahoua/Niger
29	Do 041	Dosso/Niger	59	Ma 070	Maradi/Niger	89	Th 118	Tahoua/Niger
30	Ti 042	Tillabéri/Niger	60	Ma 072	Maradi/Niger			

2.2 Methods

The 192m² (16mx12m) plot, being heterogeneous (variable soil fertility), the test was carried out using the Fisher device (block device) with four (4) repetitions. Each block of 41.25m² (7.5mx5.5m), is subdivided into six (6) plots of 5.25m² (3.5mx1.5m). The distance between two repetitions (blocks) is 1m and between two plots is 0.50m. A plot has 105 pockets in 15 lines (15 accessions) including 7 pockets per line representing an accession. In a block there are 90 accessions, 630 pockets. Two seeds per pocket were sown (only one is left after germination and out of the ground). The total number of seeds sown per accession is 112, per plot 420, per block 2520 and for the experiment 10,080 seeds.

2.3 Data collection

Twenty-two (22) parameters were selected according to the bambara groundnut descriptor [18], presented in Table 2.

Table 2. Twenty-two (22) parameters studied and their different codes

Traits	Code		Unit
		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.	

Traits	Code		Unit
		Phenological traits	
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.	cm
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.	cm
		Yield and components traits	
Pod length	PL	Noted within two months of harvest; average length of 10 pods.	cm
Seed length	SL	Noted within two months of harvest; average length of 10 seeds	cm
Pod width	PW	Noted within two months of harvest; average length of 10 pods.	cm
Seed width	SWi	Noted within two months of harvest; average width of 10 seeds	cm
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 the all pods, randomly average values from 5 plants.	
Dry pod weigth	DPW	Data measured after drying of pods (12% moisture).	g
Seed weigth	SWe	Data measured after drying of seeds (12% moisture).	g
Hundred seed weigth	HSW	Observed within two months after harvest (with 12% moisture content).	g
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).	Kg/ha
Shell weigth	SW	Data measured within two months of harvest.	g
Biomass dry weigth per plant	BDW	Weight of dried plant, recorded after maintaining the harvested plant dried in sun.	g
Biological yield	BYLD	Weight of dry seeds + dry biomass	g

2.4 Statistical Analysis

The R 4.0.4 software (2021-02-15) was used to test for significant differences using the analysis of variance (ANOVA) procedure at the LSD level; $P \leq 0.05$ and to be compared between the mean of the significant characters. Correlations between quantitative variables were determined using Pearson's correlation coefficient formula. The same R software was used to perform the Pearson correlation test, principal component analysis (PCA) and ascending hierarchical classification (CHA); which made it possible to assess the degree of similarity and dissimilarity between the analyzed data. 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., [19], Assefa et al., [20]; Hosseini et al., [21] and Mahmudul et al., [6] shown in Table 3. Broad sense heritability was estimated using the formula given by Mahmudul et al., [5]. The diversity index of Shannon denoted H, Pielou equitability (Eq) and effective species richness (N) were calculated with the formulas used by Djego et al., [22] (Table 3).

Table 3. Formulas for the different estimated genetic parameters

Parameters	Formula	Meanings of terms
Genotypic variance : $\sigma^2{}_g$ Phenotypic variance : $\sigma^2{}_p$ Broad-sense heritability : H^2	$\sigma^2{}_g = \dfrac{MSG - MSE}{r}$ $\sigma^2{}_p = \sigma^2{}_g - MSE$ $H^2{}_b = \dfrac{\sigma^2_g}{\sigma^2_p} \times 100$	**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. [23], the rate is 2,06 at the point when the *K* is at 5%. $\bar{X}$ is the grand mean values of traits. The **GCV** and **PCV** 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 [5].
Genotypic coefficient of variation : GCV Phenotypic coefficient of variation : PCV Genetic Advance : GA	$PCV = \left(\sqrt{\sigma^2_p} \,/\, \bar{X}\right) \times 100$ $GCV = \left(\sqrt{\sigma^2_g} \,/\, \bar{X}\right) \times 100$ $RD = \left(\dfrac{PCV - GCV}{PCV}\right) \times 100$ $GA = K \times \dfrac{\sqrt{\sigma^2_p}}{\bar{\bar{X}}} \times H^2 \times 100$	
Shannon's diversity index denoted H'	$H' = -\sum Pi.\log_2 Pi$; $Pi = \dfrac{ni}{\sum ni}$	Pi = relative frequency of individuals of species i; ni = mean recovery of individuals of species i; n = total cover of the individuals of the plant formation. According to Djego et al.*,* [22], diversity is low when H' < 3 bits, medium if H' is between 3 and 4 bits, then high when H' ≥ 4 bits.
Pielou's Equitability (Eq)	$Eq = \dfrac{H'}{\log_2 S}$	Equitability is low when Eq < 0.6; average when Eq is between 0.6 and 0.8 and high if Eq ≥ 0.8 [22].
Effective specific richness (N)	$N = 2^{H'}$	2 designates the base of the logarithm used to calculate the Shannon diversity index H' [22].

3. RESULTS AND DISCUSSION

3.1 Results

3.1.1 Descriptive statistical analysis

The descriptive analysis in Table 4 shows significant differences between the minimums and maximums of the different parameters studied. The average performance across accessions were recoded as 7 days for days to emergence of seedlings, 33 days for entry into flowering, 35 days for 50% flowering and 85 days for maturity. The coefficients of variation range from 3.51% (maturity date) to 38.87% (shell weight). Nine (9) of the twenty-two (22) traits analyzed have significantly high values (CV>20%) with the highest being shell weight (38.87%), followed by biomass dry weight per plant (32.42%) and hundred seed weight (25.55%). Likewise, the median and the mean are close for all the characteristics studied.

3.1.2 Correlation matrix

Table 5 showed the Pearson correlation matrix between the studied traits. Strong correlations are observed between flowering date and 50% flowering date; the number of leaves per plant and the number of petioles per plant; the number of pods per plant and the number of seeds per plant; the number of pods per plant and the number of stems per plant; the number of seeds per plant and the yield in kg/ha; hull weight and pod weight per plant; hull weight and seed weight per plant; shell weight and yield; the weight of pods per plant and the weight of seeds per plant; pod weight per plant and yield in kg/ha; the weight of seeds per plant and the yield in kg/ha. Negative correlations are also observed between the weight of 100 seeds and the number of seeds.

3.1.3 Morphological diversity of bambara groundnut accessions from six regions of Niger

The parameters thus studied were grouped into principal components. The first three axes explain almost 53% of the total variability observed (Table 6). The characters responsible for these variabilities are grouped in Table 7. Thus the first axis explains 25.13% of the total variability observed, the second axis 15.46% and the third axis 15.46%.

At the level of Table 7, the analysis of signs of the correlations of each variable (parameter) with each of the axes indicates:

- ➢ On axis 1, accessions with the highest number of petioles, leaves and stems often have a high yield in pod number, seed number, seed weight, shell weight, pod weight, biological yield and yield in kg/ha.
- ➢ On axis 2, accessions with high 100-seed weights with long and wide pods and seeds often have low yield.
- ➢ On axis 3, accessions with long height and long petioles, have a flowering date and 50% late flowering and often a low yield.

3.1.4 Shannon diversity index, Pielou fairness and effective species richness (N)

The Shannon diversity index (H') was used to assess phenotypic diversity for each parameter (Table 7). It varies from 4.42 bits to 4.49 bits. The highest diversity (4.49 bits) is obtained by pod length, pod width, date of maturity, date of emergence, date of flowering and date of 50% flowering. The diversity that contains the maximum parameters is 4.48 bits: the number of petioles per plant, the number of leaves, the plant height, the petiole length, the number of stems per plant, the seed length, the seed width, number of pods and biological yield. The shell weight had the lowest diversity (4.42 bits).

Pielou equitability (Eq) corresponds to the ratio between the diversity obtained and the maximum diversity. It expresses the regularity or equitable distribution of individuals within species. Fairness ranges from 0.98 to 0.99. Only the dry biomass weight and shell weight parameters presented the smallest equitabilities, all the remains obtained high equitabilities (Eq> 0.8) (Table 7).

Effective species richness (N) indicates the number of species responsible for the observed diversity. Hull weight (24.04%) and dry biomass weight (24.38) presented the smallest numbers of species (Table 7).

3.1.5 Ascending Hierarchical Classification (CHA)

The ascending hierarchical classification (CHA) (Figs 1 and 2) provides a structure of 89 bambara groundnut accessions from the collection of eight regions of Niger into four groups. Group 1 (G1) is represented by 29 accessions ; group 2 (G2) by 20 accessions ; group 3 (G3) by 28 accessions and group 4 (G4) by 12 accessions (Table 8, Figs. 1 and 2). Group 4, made up of 13.48% of accessions, recorded the highest average yield (751.83 kg/ha) and group 1 of 32.58% of accessions had the smallest average yield (433.47 kg/ha) (Table 9).

- ➢ Group 3 and 4 are characterized by an early development cycle marked by an average flowering date of 31 days after sowing (DAS) and an average physiological maturity of 80 DAS with high yields, 563.89kg/ha and 751 .83kg/ha, respectively.
- ➢ Group 1 and 2 are characterized by a late development cycle marked respectively by an average flowering time of 35 DAS and an average physiological maturity of 86 DAS to 87 DAS.

Table 4. Analysis of variance of 16 traits studied

	Méd	Min	Moy	Max	SD	Var	CV (%)
NP	40,93	10,20	40,57	53,85	5,605	31,42	13,81
NL	122,19	77,25	122,02	161,55	16,704	279,025	13,69
PH (cm)	21,05	11,25	20,98	25,21	2,246	5,044	10,70
PeL (cm)	16,36	7,28	16,043	20,98	2,488	6,194	15,51
TNT	25,02	10,70	25,233	39,30	5,259	27,658	**20,84**
NS	9,10	4,47	9,150	12,60	1,488	2,214	16,26
BDW(g)	9,24	3,78	9,817	20,290	3,183	10,137	**32,42**
PL (cm)	1,640	1,150	1,648	2,080	0,137	0,0187	8,31
PW (cm)	1,280	0,830	1,283	1,590	0,094	0,009	7,32
SL (cm)	1,01	0,820	1,022	1,370	0,089	0,008	8,71
SW (cm)	0,660	0,440	0,676	1,170	0,093	0,009	13,75
NSP	19,7	9,61	20,17	33,15	5,13	26,320	**25,43**
DSW(g)	8,61	3,740	8,555	14,460	2,144	4,598	**25,06**
SeW (g)	2,670	1,380	2,866	8,090	1,114	1,241	**38,87**
DPW(g)	11,22	5,94	11,42	20,63	2,885	8,327	**25,26**
BYLD (kg/ha)	636,9	371,3	652,9	1033,9	133,813	17906,17	**20,5**
YLD (kg/ha)	533,4	233	532,3	899,7	133,39	17792,54	**25,04**
HSWe (g)	170,34	90,31	174,10	322,79	44,49	1979,15	**25,55**
DTM (j)	83,75	80,25	84,63	94,25	2,977	8,864	3,51
DTE (j)	7,00	6,250	7,183	9,750	0,453	0,206	6,306
DF (j)	32,75	30	33,00	36,25	1,144	1,137	3,46
50%F(j)	35,25	31,00	34,92	38,50	1,894	3,586	5,46

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 Lenght, 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 lenght, SW : Seed Width, HSWe : Hundred Seed Weight, HI : Harvest Index, YLD : Yield, SeW : Shell Weight, SWe : Seed Weight, BYLD : Biological Yield.

Table 5. Interrelation between characters (Pearson Correlation Matrix)
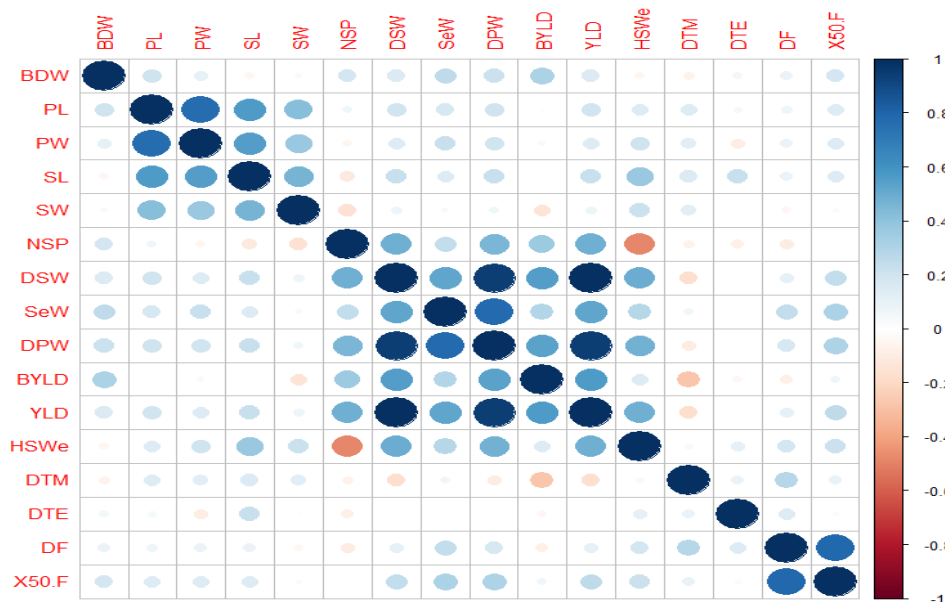
Table 6. Eigenvalues and contribution of variables (parameters) to PCA axes

Axes	Eigenvalues	Proportions (%)	Cumulative percentages (%)
1	5.528254	25,12843	25.12843
2	3.400416	15,45644	40.58486
3	2.633490	15,45644	52.55527

Table 7. Correlations between the starting variables (parameters) and each of the first three principal components and the indices

	Dim 1	Dim 2	Dim 3	Shannon index H' (bits)	Pielou's Equitability Eq	Effective specific richness N (%)
NP	**0.617**	-0.346	0.369	4,48	0,99	25,08
NL	**0.616**	-0.354	0.359	4,48	0,99	25,08
PH	0.080	-0.028	**0.561**	4,48	0,99	25,08
PeL	0.377	0.079	**0.752**	4,48	0,99	25,08
TNP	**0.642**	-0.452	-0.053	4,48	0,99	25,08
NS	0.474	-0.459	0.118	4,48	0,99	25,08
BDW	0.452	-0.128	0.321	4,44	**0,98**	**24,38**
PL	0.253	**0.625**	0.148	4,49	0,99	25,25
PW	0.227	**0.629**	0.140	4,49	0,99	25,25
SL	0.136	**0.771**	-0.025	4,48	0,99	25,08
SW	0.001	**0.582**	0.042	4,48	0,99	25,08
NSP	**0.556**	-0.418	-0.116	4,46	0,99	24,72
DSW	**0.839**	0.175	-0.431	4,46	0,99	24,72
SeW	**0.659**	0.214	-0.033	4,42	**0,98**	**24,04**
DPW	**0.880**	0.209	-0.332	4,46	0,99	24,72
BYLD	**0.606**	-0.149	-0.221	4,48	0,99	25,08
YLD	**0.846**	0.162	-0.419	4,46	0,99	24,72
HSWe	0.255	**0.607**	-0.299	4,46	0,99	24,72
DTM	-0.170	0.324	0.338	4,49	0,99	25,25
DTE	-0.033	0.171	0.087	4,49	0,99	25,25
DF	0.244	0.273	**0.554**	4,49	0,99	25,25
50%F	0.425	0.273	**0.518**	4,49	0,99	25,25

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 Lenght, 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 lenght, SW : seed width, HSWe : hundred seed weight, YLD : yield, SeW : shell Weight, SWe : Seed Weight, BYLD : Biological Yield

Table 8. Accessions groups

Groups	Accessions
Group 1	Ti 043, Do 015, Do 022, Ti 042, Do 008, Do 003, Ti 048, Ti 053, Do 004, Di 084, Do 009, Ti 054, Di- 4082, Ma-1062, Do 035, Ma 068, Ti 050, Th 115, Do 014, Th 117, Zi 088, Zi 096, Do 002, Do 040, Di 086, Th 118, Do 025, Do 015, Do 023.
Group 2	Do 007, Do 006, Do 038, Do 030, Do 29, Ti 049, Ti 055, Ma 072, Ma 073, Ma 074, Ma 077, Ma 058, Ma-E- 60, Ma 057, Ma-2-062, Ma 067, Di 081, Zi 101, Zi 095, Zi 097.
Group 3	Do 013, Do 031, Do 018, Do 019, Do 017, Do 011, Do 037, Do 041, Do 016, Ti 044, Ti 045, Ti 051, Ti 047, Ma 066, Ma 075, Ma-3-062, Ma-2-065, Ma 070, Ma 056, Ma-3-65, Di 085, Zi 092, Zi 100, Zi 091, Zi 093, Zi 098, Th 113, Th 114.
Group 4	Do 024, Do 036, Do 001, Ti 052, Ma 059, Ma 060, Ma 064, Ma 069, Di-3-082, Di 083, Zi 087, Zi 094.
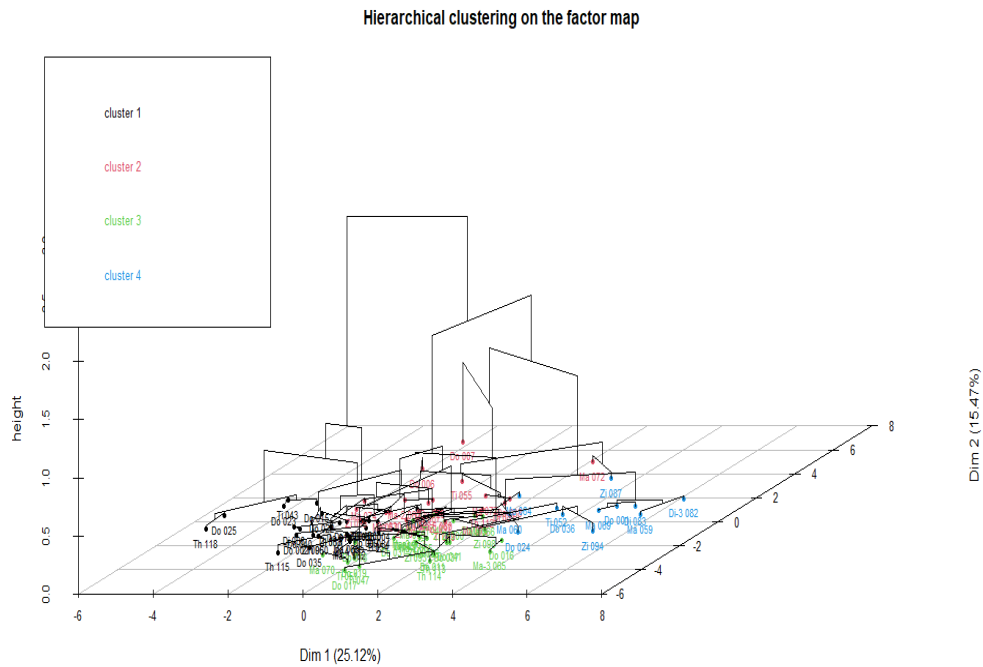
Fig. 1. Dendrogram from 3D HAC of bambara groundnut accessions
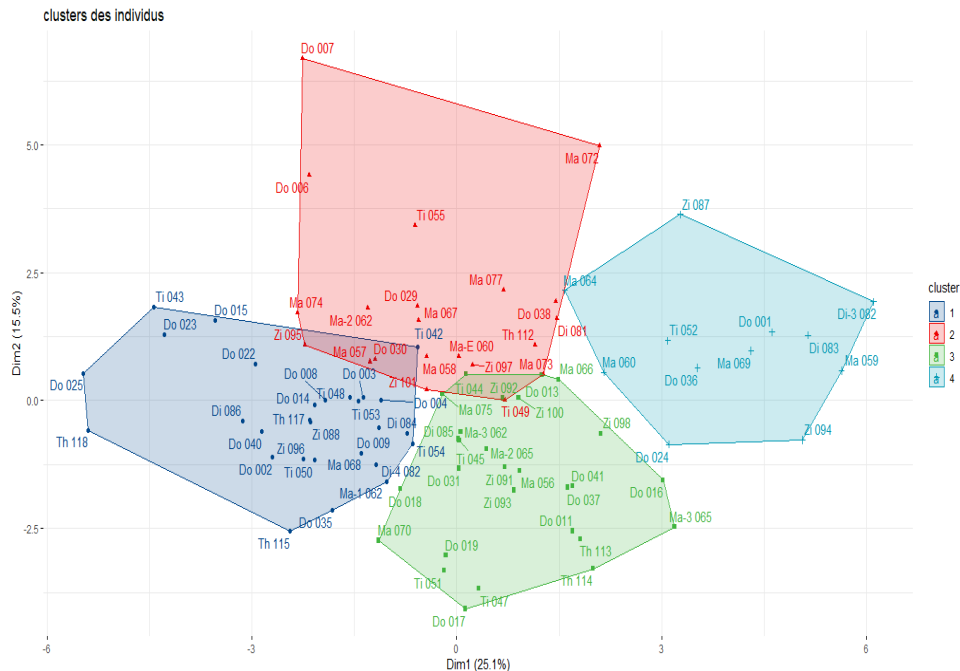
Fig. 2. Distribution and grouping of individuals into different groups

3.1.6 Genetic parameters

3.1.6.1 Phenotypic and genotypic variance

The analyzed results showed that the phenotypic variance (σ^2_p) is greater than the genotypic variance (σ^2_g) for all the parameters studied (Table 10). The phenotypic variance ranges from 0.014 to 54,296.52 and the genotypic variance from 0.005 to 5,055.80. Yield produced the highest phenotypic variance and genotypic variance (σ^2_p=54296.52 and σ^2_g=5055.80) followed by 100 seed weight (σ^2_p=1981.57 and

σ^2_g=1978.38) and number of leaf (σ^2_p =700.00 and σ^2_g=138.74). Eight (8) measured parameters (yield, number of leaves, number of pods, number of seeds, number of petioles per plant, weight of 100 seeds, weight of pods per plant, biological yield) have high phenotypic variances (>20%), four (4) moderate (10%<σ^2_p<20%) (seed weight per plant, dry biomass weight, petiole length and plant height) and ten (10) showed a low phenotypic variance (<10%) (50% flowering date, flowering date, maturity date, pod length, pod width, seed length, seed width, number of stems per plant, shell weight and date of emergence). For the genotypic variances three (3) are high (>20%) (Number of leaves, weight of 100 seeds and yield), four (4) are moderate (10% < σ^2_g <20%) (number of pods, number of seeds, number of petioles per plant and biological yield) and fifteen (15) are low (50% flowering, flowering date, maturity date, pod length, pod width, seed length, seed width seed, number of stems per plant, hull weight, date of emergence, seed weight per plant, pod weight per plant, dry biomass weight, petiole length and plant height).

3.1.6.2 Phenotypic and genotypic coefficients of variation

For all traits, the phenotypic coefficient of variation is higher than the genotypic coefficient of variation (Table 10). It was the hull weight trait that had the highest phenotypic coefficient of variation (PCV) (67.30%) and the dry biomass weight the highest genotypic coefficient of variation (GCV) (28.40%).). The lowest values for the phenotypic coefficient of variation are obtained with the maturity date (3.57%) and for the genotypic coefficient of variation with the flowering date (1.58%). The high PVC and GCV values were found at more than 20% for the parameters number of seeds (PVC=36.14% and GCV=20.68%), dry biomass weight (PVC=42.23% and GCV= 28.40%), 100 seed weight (PVC=25.57% and GCV=25.54%) and shell weight (PVC=67.30% and GCV=22.46%). The seed width presents moderate phenotypic and genotypic variation coefficients (PVC=17.82% and GCV=12.29%). The low phenotypic and genotypic coefficients of variation are flowering date, 50% flowering date, maturity date and emergence date.

3.1.6.3 Broad-sense heritability

The results indicate low (H^2<30%), moderate (30% < H^2 <60%) and high (H^2 >60%) heritability values in the broad sense. The broad-sense heritability range of all measured parameters ranges from 6.10% (flowering date) to 99.84% (100-seed weight). Maturity date (95.77%) and 100-seed weight (99.84%) have high broad-sense heritabilities (H^2>60%); seedling height (30.17%), pod width (31.52%), pod length (33.42%), seed width (47.62%), seed length the seed (33.96%), the length of the petiole (40.79%), the number of pods (37.55%), the number of seeds (32.74%) and the weight of dry biomass (45. 22%) have moderate broad-sense heritability (30%<(H^2)<60%); 50% flowering date, flowering date, number of leaves, number of stems per plant, hull weight, seed weight per plant, pod weight per plant, dry biomass weight, yield and date of emergence have low broad-sense heritability (H^2<30%) (Table 10).

3.1.6.4 Genetic advance (GA)

The results show a large variation in expected genetic advance (GA) ranging from 0.80% (flowering date) to 52.58% (100 seed weight) (Table 10). Thus, the weight of 100 seeds (52.58%), the weight of dry biomass (39.35%), the number of pods (22.10%) and the number of seeds (24.38%) revealed high genetic advance. The parameters with moderate genetic gains are biological yield (19.37%), seed width (17.47%), petiole length (17.48%), hull weight (15.45%). and the number of stems (14.42%); and trait remnants have low genetic advance.

3.1.6.5 Matrix correlation coefficients between different genetic parameters of accessions

Table 11 presents the correlations between the different genetic variables. The environmental coefficient of variation is correlated with the phenotypic coefficient of variation (r=0.95), the genotypic coefficient of variation (r=0.54), the relative difference (r=0.57) and is negatively correlated with heritability in the broad sense (r=-0.54); the phenotypic coefficient of variation is correlated with the genotypic coefficient of variation (r=0.76); the relative difference is negatively correlated with heritability in the broad sense (r=-0.98) and genetic gain (r=-0.58); phenotypic variance is strongly and positively correlated with genotypic variance (r=0.94) and environmental variance (r=1); environmental variance is strongly correlated with genotypic variance (r=0.93); genetic gain is positively correlated with heritability in the broad sense (r=0.58) and the genotypic coefficient of variation (r=0.86).

3.2 Discussion

The study of the genetic variability of accessions from Niger revealed a rich and diverse genetic heritage. The descriptive analysis shows that the emergence time varies between 6 and 10 DAS (days after sowing). Sévérin et al., [24] obtained an emergence time varying between 6 to 11 DAS, Mahmudul et al., [6] between 5 to 13 DAS and Wassouo et al., [25] between 7 to 8 DAS; on the other hand Karikari [26] observed a longer emergence time of 14 to 25 DAS. The accessions from eight regions of Niger obtained a flowering date between 30 and 36 DAS, a height between 11 and 25 cm, a number of pods per plant between 11 and 39, an average yield of 532, 27 kg/ha and a weight of 100 seeds of 174.10 g. Massawe et al., [9] obtained a flowering time ranging from 64 to 76 days; Ouedraogo et al., [27] 32 to 53 days and Paulos et al., [7] 54 to 61 days. Shegro et al., [28], believe that this variability in the flowering date is due to climatic problems, photoperiod, temperature, altitude and soil structure as well as the genotypic nature of voandzou. It should be noted that during this experiment, some pods were empty, which suggests Autopolyploidies [34]. The 16 quantitative parameters measured showed large genetic variation. Such variation was reported by Aliyu et al., [29] and Mahmudul et al., [6] in vigna subterranea. The high coefficients of variation (>20%) observed in this study express a large scale of heterogeneity in the voandzou accessions confirmed by Harouna et al., [30], Moussa et al., [31], Baina et al., [32] and Ibrahim et al., [8]. Nine (9) of the sixteen (22) traits analyzed presented high coefficients of variation. These varied from 3.46% to 38.87%. Already in 2011, Sévérin et al., obtained coefficients of variation between 0% and 63.30%; in 2018, Harouna et al., between 10.3% and 72%; in 2019, Wassouo et al., between 1.79% and 37.08%. Only traits related to yield had high coefficients of variation. Indeed, according to Swanevelder [33], yield is very unstable in bambara groundnut. This variability can be justified by the fact that populations exchange seeds during the sowing period and select the seeds themselves without using sufficiently rigorous differentiation criteria. This therefore promotes the flow of genes which contribute to genetic variability. This explains the observations of Goli et al., [2], and Mahmudul et al., [5], which stipulate that the variations in the bambara groundnut are due to the existence of strong heterogeneity.

Table 9. List of groups of accessions for certain parameters

Parameters	G1 (32.58%)	G2 (22.47%)	G3 (31.46%)	G4 (13.48%)
YLD	433.47	500.45	563.89	**751.83**
BDW	8.85	9.19	10.56	11.80
TNP	17.30	17.67	22.98	24.45
NSP	22.53	22.62	27.85	29.64
DPW	9.24	10.93	11.85	16.49
DSW	6.96	8.06	9.06	12.08
PL	1,66	1,63	1,62	1,62
PW	1,31	1,29	1,27	1,27
SL	1,04	1	1,03	1,01
SW	0,7	0,7	0,67	0,64
HSWe	161.29	196.67	160.89	199.55
NL	112.07	120.38	131.34	129.86
PH	20.62	21.94	20.70	20.58
DTE	7.13	7.38	7.21	7.02
DF	34.73	35	31.46	31.54
50%F	36.34	36.60	33.28	32.65
DTM	85.67	86.53	80.46	80. 32

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 Lenght, 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 Lenght, SW : Seed Width, HSWe : Hundred Seed Weight, YLD : Yield, SeW : Shell Weight, SWe : Seed Weight

Table 10. Calculated genetic parameters of bambara groundnut accessions from 6 regions of Niger

Traits	Mean	$(\sigma^2 e)$	$(\sigma^2 g)$	$(\sigma^2 p)$	EVC (%)	GCV (%)	PCV (%)	RD (%)	H^2 (%)	GA (%)
50%F	35.10	2.94	1.03	3.97	4.89	2.90	5.70	49.12	25.97	3.04
DF	33.00	4.17	0.27	4.44	6.19	1.58	6.39	75.27	6.10	0.80
DTM	84.62	0.39	8.77	9.15	0.73	3.50	3.57	1.96	95.77	7.05
PH	21.08	7.08	3.06	10.14	12.62	8.30	15.10	43.59	30.17	9.39
PW	1.28	0.01	0.005	0.02	8.29	5.61	10.00	43.90	31.52	6.50
PL	1.63	0.02	0.01	0.04	9.58	6.80	11.76	42.17	33.42	8.10
SW	0.68	0.008	0.007	0.014	12.92	12.29	17.82	31.03	47.62	17.47
SL	1.03	0.01	0.005	0.015	10.00	7.16	12.28	41.69	33.96	8.59
PeL	16.05	6.60	4.55	11.15	16.01	13.29	20.81	36.13	40.79	17.48
NL	122.02	561.26	138.74	700.00	19.41	9.65	21.68	55.49	19.82	8.85
TNT	25.24	32.48	19.53	52.02	22.58	17.51	28.58	38.73	37.55	22.10
NSP	20.17	35.73	17.40	53.13	29.64	20.68	36.14	42.77	32.74	24.38
NP	40.57	60.00	16.42	76.42	19.10	10.00	21.54	53.57	21.49	9.53
NS	9.15	3.31	1.39	4.70	19.87	12.87	23.67	45.63	29.57	14.42
SeW	174.10	3.19	1978.38	1981.57	1.03	25.54	25.57	0.12	99.84	52.58
BDW	9.82	9.42	7.78	17.20	31.26	28.40	42.23	32.75	45.22	39.35
HSWe	2.87	3.31	0.41	3.73	63.44	22.46	67.30	66.63	11.14	15.45
DPW	11.42	24.10	2.30	26.40	43.00	13.28	45.00	70.50	8.71	8.07
DSW	8.55	12.81	1.40	14.20	41.84	13.80	44.05	68.67	9.81	8.90
BYLD	18.38	26.22	10.50	36.70	28.00	17.60	32.95	46.58	28.54	19.37
YLD	533.31	49240.52	5055.0	54296.52	41.61	13.33	43.69	69.15	9.31	8.38
DTE	7.20	0.38	0.11	0.0	8.62	4.61	9.77	52.81	22.30	4.50

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 Lenght, 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 Lenght, SW : Seed Width, HSWe : Hundred Seed Weight, YLD : Yield, SeW : Shell Weight, SWe : Seed Weight, BYLD : Biological Yield

The first three components of the PCA with the twenty-two (22) parameters measured explain 53% of the total variability. Sévérin et al., [24], had with 4 main components almost 83.86% of the total variability from 25 quantitative parameters measured with 101 accessions in a similar experiment in Ivory Coast; Wassouo et al., [25] obtained 75% total variability with three first components of the PCA with 12 quantitative characters measured by working on 36 bambara groundnut accessions in the Far North region of Cameroon; Moussa et al., [31] obtained 81.40% with three first components of the PCA with 16 quantitative characters studied by working on the agro-morphological characterization of 30 accessions of bambara groundnut [*Vigna subterranea* (L.) verdc] cultivated in the Sudanian zone of Niger.

According to Dermaly [34], for a plant community to be able to cope with unforeseen variations in the environment, it is necessary for diversity to exist within the component populations of the community, the genotype which is best adapted to a generation n is no longer necessarily the best at a generation n + 1. The Shannon diversity index (H') is another index generally used to categorize the diversity of species in a certain population. It accounts for both the richness and uniformity present in species also used for a wide diversity of fields [5]. The Shannon diversity indices obtained in this study are between 4.42 and 4.49. All indices are high (>4), which explains the existence of diversity within the accessions studied. These results are close to those of Mahmudul et al., [5] who obtained diversities between 4.93 and 5.01 with 115 accessions and 27 quantitative parameters. On the other hand, smaller values were obtained by Olukolu et al., [35] between 0.09 and 0.16 with 124 accessions and twenty-eight (28) quantitative characters and by Mahmudul et al.,

[6] between 2 .57 and 2.71 with 15 accessions and twenty-seven (27) quantitative parameters, all with *vigna subterranea*. According to Assogbadjo [36] the Shannon index varies depending on the number of species. On the other hand, the number does not determine the evolution of the value of the diversity index, because a single species can dominate a population. Voandzou is a self-pollinating crop [37], therefore the level of diversity of this crop is influenced by farmers' agricultural practices as well as seed management techniques such as recycling, storage, exchange and new species introduction, supported by Alvarez et al*.,* [38] and Mahmudul et al*.,* [6]. Such diversity within *vigna subterranea* can allow the breeder to create heterozygous genotypes, among which there are types with characters of interest, which must therefore maintain a segregational charge. When a selection gives a privilege to individuals who provide greater segregation in the descendants, the heterozygous individual will accumulate, during evolution, the mechanisms which bring him a "more": it is this convergent set which constitutes heterosis [34].

Pielou's equitability (Eq) expresses the regularity or equitable distribution of individuals within species. For this study it varies between 0.98 and 0.99. Mahmudul et al*.,* [5] and Mahmudul et al*.,* [6] had very close results of 0.98 to 1. They obtained the same equitability (0.98) for the weight of dry biomass. The high equitabilities obtained for all parameters reflect a high abundance of these characters in the 89 accessions studied, supported by Dajoz [39], Henigfeld [41], Ousséni et al*.,* [42] and Assogbadjo [36].

The ascending hierarchical classification by the method Unweighted Pair-Group Method with Arithmetic mean (UPGMA) made it possible to group the accessions into 4 distinct groups according to the degree of similarity of the characters. Wassouo et al*.,* [25] obtained four groups by w orking on 36 accessions with 10 morphological characters measured ; Mahmudul et al*.,* [6] had 5 classes with 15 accessions for 27 quantitative parameters measured. All these results prove the morphological diversity that exists between the bambara groundnut

Table 11. Correlations of genetic parameters of accessions

ns p >= 0.05; * p < 0.05; ** p < 0.01; and *** p < 0.001
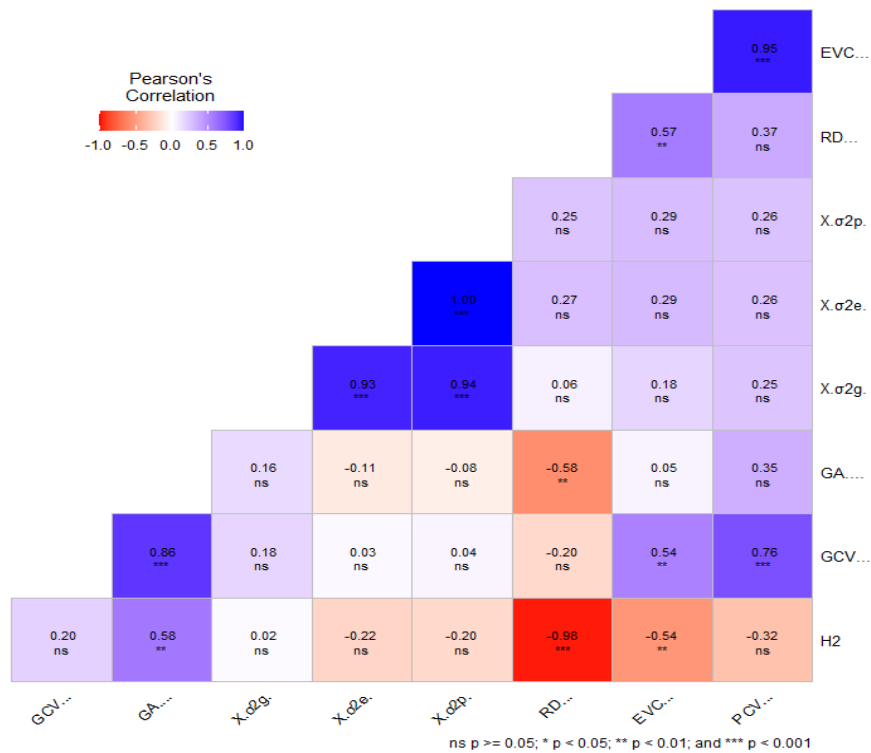
Légendes : GA : Genetic Advance ; EVC : Coefficient Environnemental Variation ; PCV : Coefficient Phenotypic Variation ; GCV : Coefficient Genotypic Variation ; σ^2_g : Genotypic Variance ; σ^2_p : Phenotypic Variance ; H2 : Broad-Sense Heritability ; RD : Relative Difference

accessions. This diversity will undoubtedly allow breeders to choose the parents that best meet the needs of the populations. This choice could be oriented in this present work towards the accessions of group 4 which present accessions performing in average grain yields higher than the total average yield obtained (532.27 kg/ha) [40].

Strong correlations are observed between the flowering date and the date of 50% flowering (r=0.783). Accessions that quickly reach 50% flowering are those that have started flowering early. Wassouo et al., [25] also obtained a strong correlation between the flowering date and the date of 50% flowering (r=0.937) and drew the same conclusion. Strong correlations are also observed between performance-related parameters. Mahmudul et al., [6], Pranesh et al., [42] and Jonah et al., [43] found strong correlations between number of pods per plant and number of seeds per plant, seed weight per plant, weight of pods per plant, yield. Wassouo et al., [25], also observed a strong correlation between seed weight and number of pods. Ouedrago et al., [27] state that traits such as number of pods per plant, number of seeds per plant and 100-seed weight are positively correlated with yield in bambara groundnut. Oyiga and Uguru [44] thus see the possibility of using these variables to estimate yield.

The estimated genetic parameters showed that the genotypic variance is lower than the phenotypic variance of all observed traits, often with significant deviations. These results confirm, in agreement with those of Malek et al., [45], Danbe et al., [46], Mahmudul et al., [5], Mahmudul et al., [6], Paulos et al., [7] and Ibrahim et al., [47], a strong impact of environmental factors on the expression of the characters studied and therefore difficult genetic control over their expressions. Selection is inefficient if environmental variation is very large and masks genetic variation [48].

The genotypic coefficients of variation are lower than the phenotypic coefficients of variation, with significant differences between the two coefficients. The maturity date and the weight of 100 seeds had close estimates, so these characters are very little influenced by the environment as reported by Baninga et al., [49] and Ibrahim et al., [8]. PCV and GCV values are classified according to the suggested index of 0% to 10% for low variation, 10 to 20% for moderate variation and greater than or equal to

20% for high variation [5]. This classification made it possible to have an appreciation of the results obtained. The coefficients of phenotypic and genotypic variations are high for the traits number of seeds (PVC=36.14% and GCV=20.68%), weight of dry biomass (PVC=42.23% and GCV=28.40%), hundred seed weight (PVC=25.57% and GCV=25.54%) and shell weight (PVC=67.30% and GCV=22.46%). This explains a high environmental effect and therefore the improvement of these traits is difficult through direct selection [47]. Bonaiti [50] thinks Too much environmental effect can reduce the overall efficiency of the selection scheme.

Maturity date (RD=1.96%) and hundred seed weight (RD=0.12%) gave small relative differences. A trait with a lower difference reflects the weak influence of the environment, which can give a strong and significant result desirable in the crop improvement program. These claims are supported by Umar et al., [51], Usman et al., [52], Mahmudul et al., [6] and Paulos et al., [7]. For Fakuta et al., [53] direct selection can be effective for traits with small relative differences. According to Drabo et al., [54], the coefficient of variation does not indicate the heritable and non-heritable part of a genotypic variability although it indicates the existing level of variability. Heritability estimation indicates the degree of variability that has been transmitted from parents to offspring [55]. Therefore, for better information on the parents to be hybridized in order to obtain the desired characters, an estimation of the genotypic coefficient of variation and heritability is necessary [56]. The number of seeds (GCV=20.68%-H^2=32.74%), weight of dry biomass (GCV=28.40%- H^2=45.22%) and weight of 100 seeds (GCV=25, 54% - H^2=99.84 gave moderate to high coefficients of variation and heritabilities in the broad sense. Selection is all the more effective when the heritability of the traits is high (Néverwendé et al., [57] and Ibrahim et al., [8]), because a strong heritability in the broad sense of traits reflects a weak influence of environmental factors on their expressions ([54], [46], [7]). The higher the heritability of a character, the more likely it is that the performance will be the same for the offspring [58]. hundred seed weight and maturity date had high broad-sense heritabilities. Unfortunately, heritability alone does not predict whether selection will bring a substantial improvement [56]. However, the joint estimation of heritability and genetic gain can provide more reliable information ([59], [49]). The hundred seed weight had high broad-sense heritability and high

genetic gain (H^2=99.84% and GA=52.58%), indicating the additive action of genes, supported by Kashif et al*., [60]. Ridzuan et al., [61] and Mahmadul et al., [6]* argue that low to moderate heritabilities and genetic gain values can hinder trait improvement due to high environmental effects compared to genetic effects on its state. According to Huby et al*., [62]*, very low heritability values reflect the difficulty of selection. The performance of an individual is expressed as the sum of genetic and environmental effects. Thus, only efficient selection can be achieved by choosing the parameters with higher phenotypic and genotypic coefficient of variation, broad-sense heritability and genetic gain, which means that the effect of additive genes is robust enough that the environmental effect [52].

4. CONCLUSION

This study highlighted the existence of genetic diversity within the collection of bambara groundnut accessions of Niger. This variability is organized around vegetative characteristics and yield and a structuring of 89 accessions into four groups. Group 4 presents the most interesting performance performances. This group could therefore be used in improving the plant. The estimation of genetic parameters also made it possible to highlight a weak influence of environmental factors on the expression of characters such as the date of maturity and the weight of hundred seeds which resulted in low relative differences (RD) between PCV and GCV. Also, a high heritability in the broad sense coupled with a high genetic gain was obtained only for the weight of hundred seeds, thus showing the intervention of additive genes in its expression. Improvement by direct selection is therefore possible for this trait.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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