Estimates of phenotypic and genotypic variance and heritability in eighty-nine bambara groundnut [Vigna subterranea (L.) Verdcourt] accessions collected from six regions of Niger

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 ($\mathbf{H^2}$=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.

Keywords: *Vigna subterranea* L., Sahelian zone, diversity, genotypic, phenotypic, Niger.

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, the mainly contain healthy fatty acids such as omega-6 (n-6) and polyunsaturated fatty acids [12]. Despite, neglected 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 contributed 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 Bambara groundnut[16]. The National Institute of Agronomic Research of Niger (INRAN)gene bank includes 47 Bambara groundnutaccessions [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 thegenetic variability of Bambara groundnutaccessions in order to develop appropriate strategies for future improvement.

2. Material and methods

2.1.Material

The plant material is composed of seeds from 89 bambara groundnut accessions from six regions of Niger (table 1), taken from the collection of2012 and2013 [16] of the Department of Biology of the Faculty of Sciences and Techniques (FAST) of Abdou Moumouni University, 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.<u>Methods</u>

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.

2.2.1. 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.	
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

2.2.2.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 (AHC); which made it possible to assess the degree of similarity and dissimilarity between parameters. 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] showed 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 : σ^2_g **Phenotypic variance : σ^2_p** **Broad-sense heritability : H^2**	$\sigma^2_g = \frac{MSG - MSE}{r}$ $\sigma^2_p = \sigma^2_g$-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*. [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**	$PCV = \left(\sqrt{\sigma^2_p} / \bar{X}\right) \times 100$ $GCV = \left(\sqrt{\sigma^2_g} / \bar{X}\right) \times 100$ $RD = \left(\frac{PCV - GCV}{PCV}\right) \times 100$ $GA = K \times \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times H^2 \times 100$	
Shannon's diversity index denoted H'	$H' = -\sum Pi.log_2 Pi \; ; \quad Pi = \frac{ni}{\sum ni}$	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)	$Eq = \frac{H'}{log_2 S}$	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 showed significant differences between the minimums and maximums of the different parameters studied. The average performance across accessions were recorded as 7 days for days of seedlingsemergence, 33 days for entry into flowering, 35 days for 50% flowering and 85 days for maturity. The coefficients of variation ranged 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 wereclosed for all the parametersstudied.

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

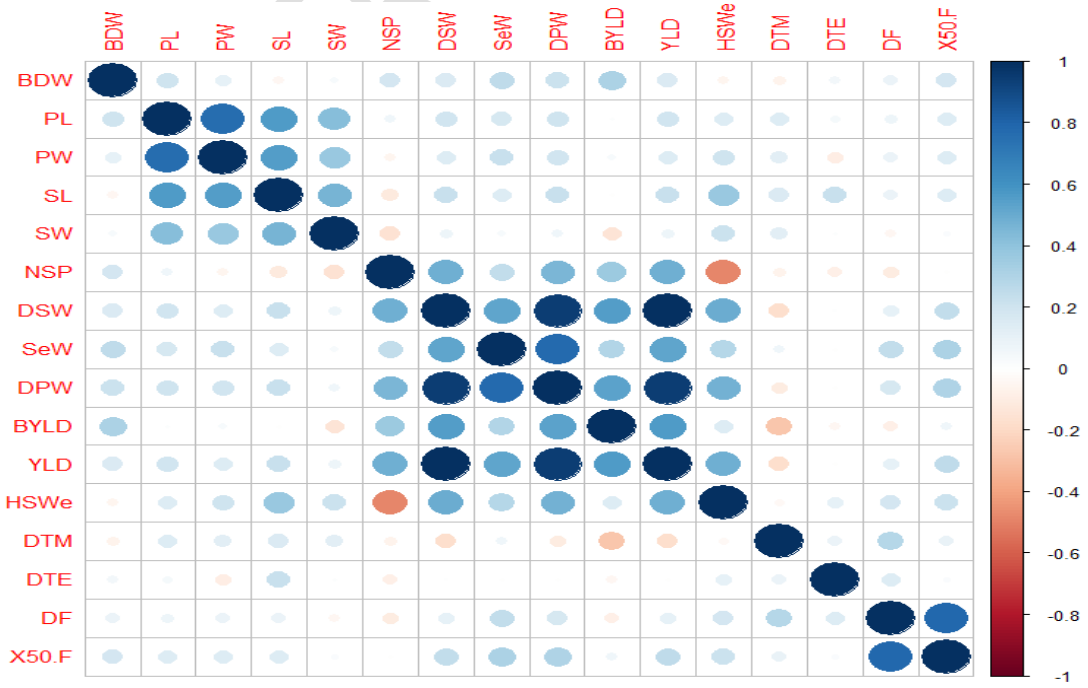
50%F(j)	35,25	31,00	34,92	38,50	1,894	3,586	5,46

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.*

3.1.2. Correlation matrix

Table 5 showed the Pearson correlation matrix between the studied traits. Strong correlations are observed between flowering 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 (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; the weight of seeds per plant and the yield. Negative correlations werealso observed between the weight of 100 seeds and the number of seeds.

Table 5: Interrelation between characters (Pearson Correlation Matrix).



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

The parameters 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 wereshowed in the table 7. Thus, the first axis explained 25.13% of the total variability observed, the second axis 15.46% and the third axis 15.46%.

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

The analysis of the correlations of each variable (parameter) with each of the axes indicated:

- On an axis 1, the 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.
- On an axis 2, the accessions with high 100-seed weights with long and wide pods and seeds often have the lowest yield.
- On an axis 3, the accessions with long height and long petioles, have a late flowering and 50% flowering date 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) wasobtained 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 showedthe lowest diversity (4.42 bits).

Pielou equitability (Eq) corresponds to the ratio between the diversity obtained and the maximum diversity. It expressed 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).

Table 7: Correlation 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.*

3.1.5. Ascending Hierarchical Classification (AHC)

The ascending hierarchical classification (AHC) (figures 1) showed thestructure of 89 bambara groundnut accessions 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, figures 1 and 2).

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.

Figure 1: Dendrogram from 3D HAC of bambara groundnut accessions.

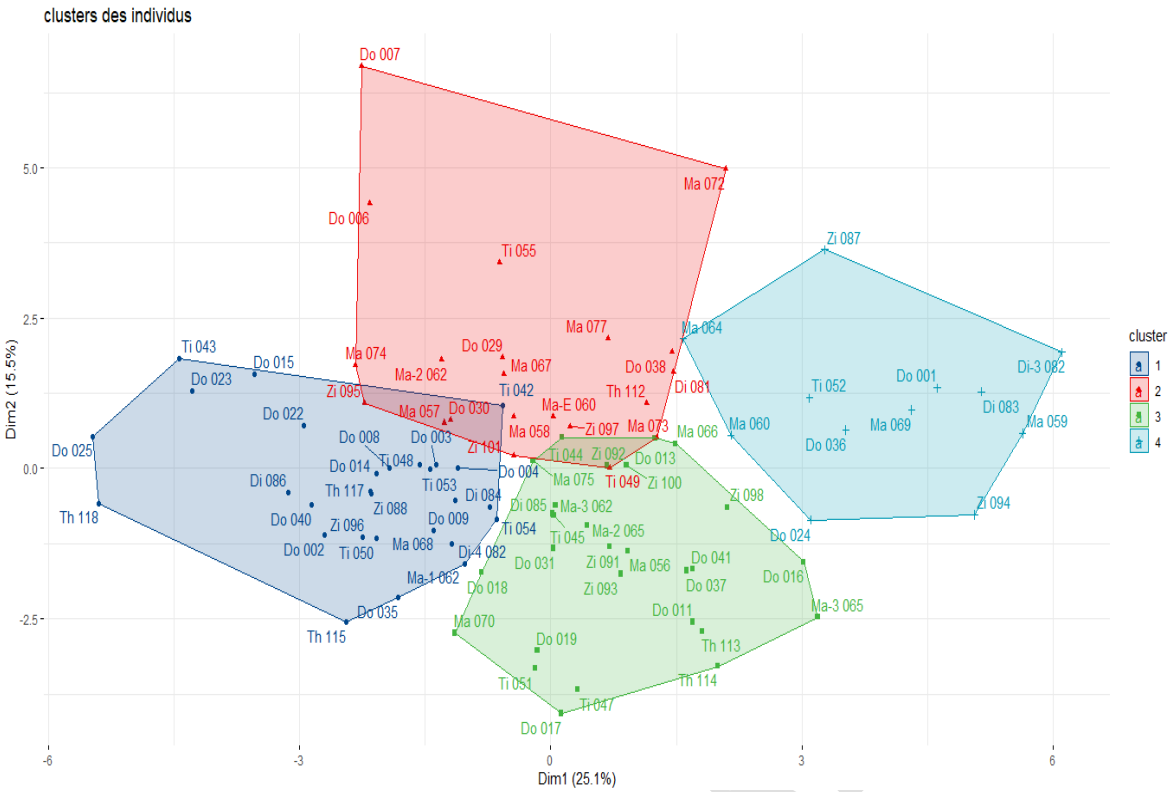


Figure 1: Distribution and grouping of individuals into different groups.

Group 4, is composed of 13.48% of accessions with high average yield (751.83 kg/ha) and group 1 of 32.58% of accessions with low 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 yield, 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 9: Caracteristics of the accessions groups according to some 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.*

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 showed the greatestphenotypic and genotypicvariance (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) 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) showedhigh phenotypic variances (>20%), four (4) moderate (10%<σ^2_p<20%) (Seed weight per plant, dry biomass weight, petiole length and plant height) andfinally the ten (10) have low phenotypic variances (<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). It should be noted thatforthe genotypic variance, forthree (3) parameters it ishigh (>20%) (Number of leaves, weight of 100 seeds and yield), four (4) moderate (10% < σ^2_g <20%) (number of pods, number of seeds, number of petioles per plant and biological yield) and for fifteen (15) 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 like 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 coefficients ofphenotypic and genotypic variation were observed at theflowering date, 50% flowering, maturity date and emergence date.

3.1.6.3. Broad-sense heritability

The results indicated 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 showed 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.

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

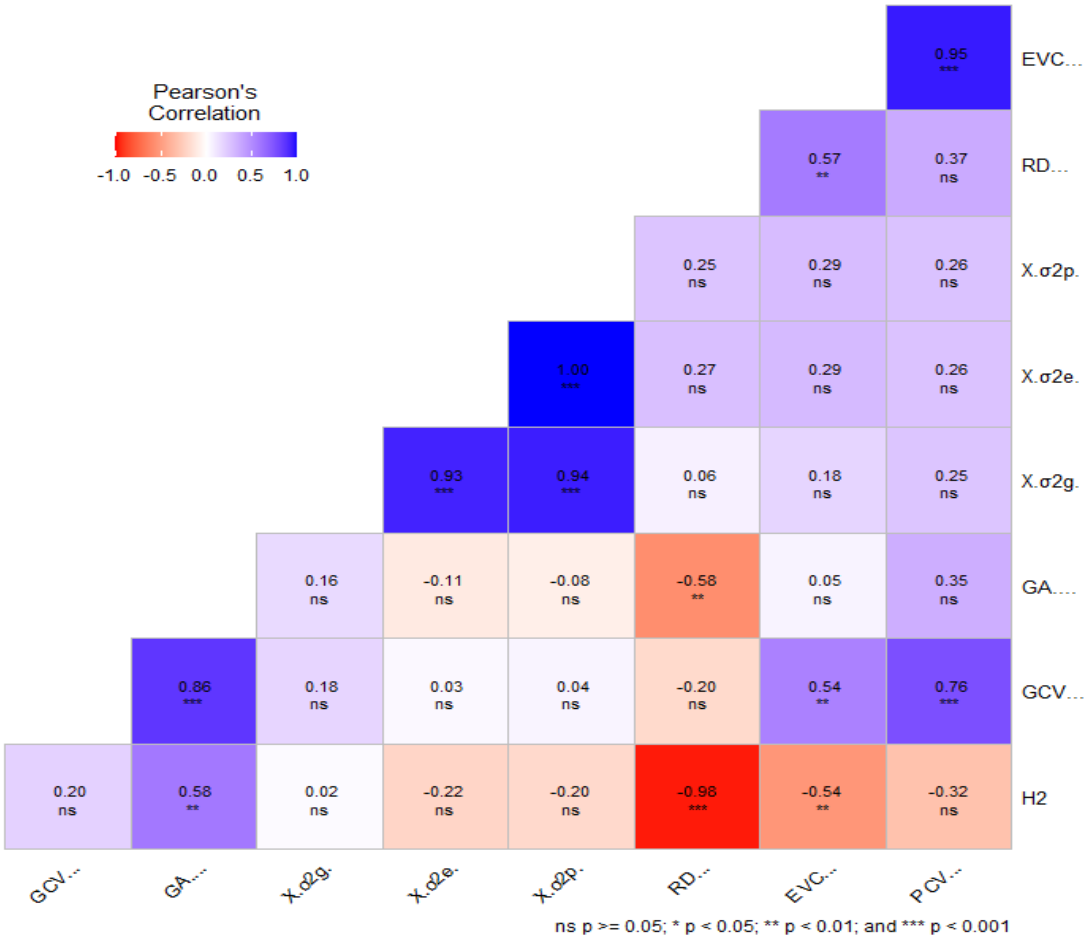
Traits	Mean	(σ^2_e)	(σ^2_g)	(σ^2_p)	EVC(%)	GCV(%)	PCV (%)	RD(%)	H^2 (%)	GA (%)
50%F	35.10	2.94	1.03	3.97	4.89	2.90	5.70	49.12	25.97	3.04
DF	33.00	4.17	0.27	4.44	6.19	1.58	6.39	75.27	6.10	0.80
DTM	84.62	0.39	8.77	9.15	0.73	3.50	3.57	1.96	95.77	7.05
PH	21.08	7.08	3.06	10.14	12.62	8.30	15.10	43.59	30.17	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	5055.80	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.*

3.1.6.5. Matrix correlation coefficients between different genetic parameters of accessions

Table 11 shows 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). However,itis 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). The 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).

Table 11 : correlations of genetic parameters of 89 accessions.



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.*

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.

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 [42], 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 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).

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. H^2 values give an indication of the accuracy with which selection will take place. However, the low H2 values indicaded that the phenotypic differences observed among the bambara groundnut accessions were mainly caused by

environnemental effects, which further suggested that selection under such circumstances will not be very effective [63]. 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].

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 thestructuring of 89 accessions into four groups. Group 4 is composed of the most interesting performance accessions. This group could therefore be used for bambara groundnut improvement. The estimation of genetic parameters also made it possible to highlight theweak 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. Thehigh heritability ofthe broad sense coupled with the high genetic gain was obtained for the weight of hundred seeds, thus showedthe effectof additive genes in its expression, so that the direct selection maybe applied for this trait improvement..

References

1. Koné M, Patat-Ochatt EM, Conreux C, Sangwan RS & Ochatt SJ (2007). In vitro morphogenesis from cotyledon and epicotyl explants and flow cytometry distinction between landraces of bambara groundnut (Vigna subterranea (L.) Verde.), an underutilised grain legume. Plant Cell Tissue Organ Culture 88: 61-75.

2. Goli, A.E., Begemann, F., Ng, N.Q. (1997). Caracterization and evaluation of IITA's bambara groundnut collection. In Heller J., Begemann E., Mushonga J,(Eds).Promotion of the conservation and use of underutilized and neglected crops.9.Proceedings of the workshop on conservation and improvement of bambara groundnut (Vigna subterranea (L.) Verdc).14-16.Harare.Zimbabwe. pp.101–118.

3. Kadams, A.M. and A.A. Sajo, (1998). Variability and correlation studies in yield and yield components in Bambara groundnut (Vigna subterrenea L. Verdc). Journal of Applied Science and Management, 2: 66-70.

4. Jonah, P. M., B. Aliyu, GG Jibung, (2013). Estimations de la variance phénotypique et génotypique et de l'héritabilité chez l'arachide bambara (Vigna subterranea [L.] Verdc) à Mubi, État d'Adamawa, Nigéria. Journal international de recherche en informatique, ingénierie et sciences appliquées (IJIEASR) ISSN : 2319-4413.

5. Md Mahmudul H. K., Mohd Y. R., Shairul I. R., Mashitah J., and Al Mamun, (2020). Genetic Variability, Heritability, and Clustering Pattern Exploration of Bambara Groundnut (Vigna subterranea L. Verdc) Accessions for the Perfection of Yield and Yield Related Traits. Hindawi. BioMed Research International. Volume 2020, Article ID 2195797, 31 pages https://doi.org/10.1155/2020/2195797.

6. Md Mahmudul H. K., Mohd Y. R., Shairul I. R., Mashitah J. & Md Al Mamun., (2021). Genetic analysis and selection of Bambara groundnut (Vigna subterranea [L.] Verdc.) landraces for high yield revealed by qualitative and quantitative traits. Scientific Reports, 11:7597.

7. M. Paulos, Gobeze L., Mesfin K. (2022). Characterization and Evaluation of Bambara Groundnut (Vigna subterranea (L.) Verdc.) for Yield and Related Traits in Asosa Zone, Northwestern Ethiopia. Applied and Environmental Soil Science Volume 2022, Article ID 8533233, 7 pages https://doi.org/10.1155/2022/8533233.

8. A. Z. Y. Ibrahim, Alhassane A., Idi S. S., and Harouna I. A., (2023). Etude de la variabilité génétique de 19 accessions de voandzou « Vigna subterranea (L.) Verdcourt » de l'extrême et du centre Est du Niger. International Journal of Innovation and Applied Studies. ISSN 2028-9324. pp. 682-694.

9. Massawe, F. J., Mwale, S. S. & Roberts, J. A. (2005). Breeding in bambara groundnut (Vigna subterranea (L.) Verdc.) : Strategic considerations. Afr. J. Biotechnol. 4, 463–471.

10. N. Kameswara, (2004). Plant genetic resources : advancing conservation and use through biotechnology. Academic jounals.

11. Majola, N., Gerrano, A.S., Shimelis, H., (2021). Bambara groundnut (Vigna subterranea [L.] Verdc.) Production, utilisation and genetic improvement in sub-Saharan Africa. Agronomy 11, 1345.

12. Mbuma, N.W., Labuschagne, M., Siwale, J., Hugo, A., (2022). Diversity in seed protein content, selected minerals, oil content and fatty acid composition of the Southern African bambara groundnut germplasm collection. J. Food Compos. Anal. 2022, 109, 104477.

13. Khan, F., Azman, R., Chai, H.H., Mayes, S., Lu, C., (2016). Genomic and transcriptomic approaches towards the genetic improvement of an underutilised crops: The case of bambara groundnut. Afr. Crop Sci. J., 24, 429–458.

14. Mayes, S., Ho, W.K., Chai, H.H., Song, B., Chang, Y., Massawe, F., (2019). Bambara Groundnut (Vigna Subterranea (L) Verdc) A Climate-Smart Crop for Food and Nutrition Security. In Genomic Designing of Climate-Smart Pulse Crops, 1st ed.; Kole, C., Ed.; Springer International Publishing: Cham, Switzerland, pp. 397–424.

15. J. Siwale, M. Labuschagne, Abe Shegro G., and Ntombokulunga W. M., (2022). Phenotypic Diversity and Characterization of the Southern African Bambara Groundnut Germplasm Collection for Grain Yield and Yield Components. Agronomy, 12, 1811.

16. Harouna, A. I., Bakasso, Y., Zoubeirou, A., M., Doumma, A., Maiboucar, I. (2014). Diagnostic participatif de la diversité de morphotypes et des connaissances locales en matière de culture du Voandzou (Vigna Subterranea L,) au Niger.nternational Journal of Innovation and Applied Studies. pp.1915-1925.

17. MDA, Ministère de développement agricole du Niger (2007). Rapport national sur l'état des ressources phytogénétiques pour l'alimentation et pour l'agriculture, 43 Pages.

18. IPGRI/IITA/BAMNET. (2000). Descriptors for bambara groundnut : 48. Rome.Italy.

19. Johnson H. W., H. F. Robinson et Comstock, R. E., (1955). Estimates of genetic and environmental variability in Soybeans. Agronomy Journal 47, no. 7: 314–318.

20. Assefa K., Tefera H., Merker A., Kefyalew T. and Hundera F., (2001). Variability, heritability and genetic advance in Phenomorphic and agronomic traits of Tef [Eragrostis tef (Zucc.) Trotter] germplasm from eight Regions of Ethiopia. Hereditas 134, no. 2:103–113.

21. Hosseini S. J., Sarvesta ni Z. T., Pirdashti H., Afkhami A. and Hazrati S., (2012). Estimation of heritability and genetic advance for screening some rice genotypes at salt stress conditions. International journal of Agronomy and Plant Production. Vol., 3 (11), 475 482.

22. J. Djego, M. Gibigaye, B. Tente, B. Sinsin, (2012). Ecological and structural analyzes of the Kaodji community forest in Benin. Int. J. Biol. Chem. Sci. 6(2): 705-713. ISSN 1991-8631.

23. Adewale, B. D., Kehinde, O. B., Aremu, C. O., Popoola, J. O., & Dumet, D. J. (2010). Seed metrics for genetic and shape determinations in African yam bean [Fabaceae] (Sphenostylis stenocarpa Hochst. Ex. A. Rich.) harms. African Journal of Plant Science, 4, 107-115.

24. Sévérin, B., and Yao, D. (2011). Morphological and agronomic variability of traditional varieties of voandzou (Vigna subterranea L. verdc,) from Ivory Coast.Journal of Applied Biosciences. 41:2820-2835.

25. Wassouo F. A., Madi A., Sobda G., Koubala B. B., Mvondoawono J. P., (2019). Agro morphological diversity of thirty-six accessions of voandzou [Vigna subterranea (L.) Verdcourt] cultivated in the Far North region of Cameroon. Journal of Applied Biosciences 140: 14227 - 14234.

26. Karikari KS, 2000. Variability between local and exotic Bambara groundnut landraces in Botswana. Afr. Crop Sci. J. 8:153-157.

27. Ouedraogo, M., Ouedraogo, J. T., Tignere, J. B., Bilma, D., Dabire, C. B. & Konate, G., (2008). Characterization and evaluation of accessions of Bambara groundnut (Vigna subterranea (L.) Verdcourt) from Burkina Faso. Sci. Nat. 5(2), 191–197.

28. Shegro, A. G., Jansen Van Rensburg, W. S. & Adebola, P. O. (2013). Assessment of genetic variability in Bambara groundnut (Vigna subterrenea [L.] Verdc.) using morphological quantitative traits. Acad. J. Agric. Res. 1, 45–51.

29. Aliyu. E. Goli, F. Begemann, and N. Q. Ng, (1997). "Characterization and evaluation of IITA's Bambara groundnut collection," in Conservation and Improvement of Bambara Groundnut (Vigna subterranea (L.) Verdc.), International Plant Genetic Resources Institute, pp. 101–118.

30. Harouna, A.I., Alhassane, A., Daouda, O.S., Boureima, K.S. (2018). Morphological and Agronomic Variability of Morphotypes of Voandzou (Vigna Subterranea (L.) Cultivated in the Sahelian Zone of Niger. European Scientific Journal, 14: 377-393.

31. S. Moussa D., Amadou H. I., Boubacar M. M., and Boukar K. K. K., (2022). Agro-morphological characterization of 30 accessions of voandzou [Vigna subterranea (L.) verdc] cultivated in the Sudanian zone of Niger. International Journal of Innovation and Applied Studies ISSN 2028-9324 Vol. 36 No. 2 May. 2022, p. 553-563.

32. D-j. Baina, I. Z. M. Mourtala, M. M. Abdou and A. R. I. B. Yerima, (2023). Study of the agro morphological variability of 81 accessions of Voandzou [Vigna subterranea (L.) Verdc] in Niger. Journal of Applied Biosciences 183: 19181–19196. ISSN 1997-5902.

33. Swanevelder, C.J., (1998). Bambara-Food for Africa: Vigna subterranea Bambara groundnut (National Department of Agriculture).

34. Y. Demarly, (1984). Genetic mechanisms of adaptation in plants. Bull. Soc. bot. Fr., 131, Actual. bot., 125-137.

35. Olukolu B.A., Mayes S., Stadler F., (2012). "Genetic diversity in Bambara groundnut (Vigna subterranea (L.) Verdc.) as revealed by phenotypic descriptors and DArT marker analysis," Genetic Resources and Crop Evolution, vol. 59, no. 3, pp. 347–358.

36. B. Assogbadjo (2021). Diversity and endogenous knowledge of useful species from riparian agroforestry systems in the central core of the Lama Classified Forest in southern Benin. Thesis dissertation, Jean LOROUGNON GUEDE University, Plant ecology.

37. Thomas M., Demeulenaere E., Dawson J.C., (2012). "On-farm dynamic management of genetic diversity: the impact of seed diffusions and seed saving practices on a population-variety of bread wheat," Evolutionary Applications, vol. 5, no. 8, pp. 779–795.

38. Alvarez N, Garine E, Khasah C, Dounias E, Hossaert-Mckey M, and Mckey D, (2005). "Farmers' practices, metapopulation dynamics, and conservation of agricultural biodiversity on farm: a case study of sorghum among the Duupa in sub-Sahelian Cameroon," Biological Conservation, vol. 121, no. 4, pp. 533–543.

39. Dajoz R, (1985). Summary of ecology. Bordas, Paris, France, 504 p.

40. C. Henigfeld, (2014). Effects of agricultural practices and agroecological infrastructures on the diversity of Chiroptera. Internship dissertation, University of Lorraine, livestock institute.

41. A. Ousséni, E. C. Gervais, I. Dramane, (2016). Dynamics of land use and state of flora and vegetation in the upper Alibori basin in Benin. Journal of Applied BioSciences. Volume 108, ISSN: 1997-5902.

42. Pranesh, H., Nandini, R., Chandra, K., Rangaiah, S. & Nagaraju, N. (2017). Character association and path analysis of yield and yield components in m

3 generation of Bambara groundnut (Vigna subterranea (L.) verdc.) treated with ethyl methane sulphonate (EMS). Int. J.Pure Appl. Biosci. 5(3), 306–311.

43. Jonah, P.M., B. Aliyu, GG Jibung, (2013). Estimates of phenotypic and genotypic variance and heritability in Bambara groundnut (Vigna subterranea [L.] Verdc) in Mubi, Adamawa State, Nigeria. International Journal of Computer Science, Engineering and Applied Sciences Research (IJIEASR) ISSN: 2319-4413.

44. Oyiga BC. and Uguru M.I, (2011). Interrelationships among Pod and Seed Yield Traits in Bambara Groundnut (Vigna subterranea L. Verdc) in the Derived Savanna Agro-Ecology of South-Eastern Nigeria under Two Planting Dates. International Journal of Plant Breeding 5(2):106-111.

45. Malek, M.A., Rafii, M.Y., Afroz, S.S., Nath, U.K. & Mondal, M., (2014). Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. Sci. World J., article ID 968796, https://doi. org/ 10. 1155/ 2014/ 968796.

46. Danbe, N., Yakouba, O., Sobda, G., Basga, S. D., Lendzemo, V., Kaouvon, P., ... & Kaboui, A. (2018). Characterization of the phenotypic and genotypic diversity of rainfed sorghum in the Sudano-Sahelian zone of Cameroon. Journal of Applied Biosciences, 129, 12973-12981.

47. A. Z. Y. Ibrahim, H. I. Amadou, A. Alhassane (2022). Assessment of Genetic Diversity of Bambara Groundnut Accessions [Vigna subterranea (L) Verdcourt] in Sahelian Zone of Niger. Sch Acad J Biosci, 2022 Sept 10(9): 218-229.

48. H.B. Dounia, (2021). Genetic improvement of plants. Democratic and Popular Algerian Republic Ministry of Higher Education and Scientific Research, Constantine University Faculty of Natural and Life Sciences Department of Biology and Plant Ecology.

49. Béninga M. B., Sangaré A., Nguetta A. S. P., Zoro B. I. A. and Coulibaly Y. M., (2011). Estimation of the genetic parameters of some agromorphological descriptors in millet [Pennisetum glaucum (L.) R. Br.,]. Journal of Applied Biosciences 43: 2891 – 2898. ISSN 1997–5902.

50. Umar, U.U., Ado, S.G., Aba, D.A. & Bugaje, S.M. (2014). Genetic variability and heritability studies in maize (Zea mays L.) genotypes under three irrigation regimes. In 38th Annual Conference of Genetic Society of Nigeria, 19th-23rd October 2014. Edo State, Nigeria. 381–386.

51. B. Bonaiti, (1982). Genotype environment interaction on milk production in cattle. Ann. Broom. Salt. Anim. , 14 (4), 441-452.

52. Usman, M. G., Rafii, M. Y., Ismail, M. R., Malek, M. A. & Abdul, L. M. (2014). Heritability and genetic advance among chili pepper genotypes for heat tolerance and morphophysiological characteristics. Sci. World J. 1–14.

53. Fakuta, N. M., Ojiekpon, I. F., Gashua, I. B. & Ogunremi, O. C. (2014). Genetic Variability, Heritability and Genetic Advance in Gum Arabic (Acacia senegal (l) Wild) Provenances, 38th Annual GSN Conference, 19th–23rd October 2014 405–409

54. I. Drabo, Roger G. Z., M. Sawadogo, M. Ouedraogo. (2013). Genetic variability and estimates of Genetic Parameters in Burkina Faso's Pearl Millet Landraces. International Journal of Agriculture and Forestry 3(7): 367-373.

55. Visscher, P. M., Hill W. G., & Wray, N. R. (2008). Heritability in the genomics era-concepts and misconceptions. Nat Rev Genet, 9, 255-266.

56. Burton G.W. and Devane E.M., (1953). Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material. Agronomy Journal, 45, 478-481.

57. Nerbéwendé S., Romaric K. N., Pauline B., Renan E. T., Baloua N., Djakaridia T., Mahamadou S., Jean-Didier Z. (2014). Evaluation of the genetic diversity of sweet grain sorghums (Sorghum bicolor (L) Moench) from northern Burkina Faso. Journal of applied Biosciences 84:7654-7664.

58. Margot Sabbagh - F.J., (2021). Heritability. French Institute of Horses and Riding. ifce. www.equipedia.ifce.fr

59. Govindaraj M., Selvi B., Rajarathinam S. and Sumathi P., (2011). Genetic Variability and Heritability of Grain Yield Components and Grain Mineral Concentration in India's Pearl Millet (Pennisetum Glaucum (L) R. Br.) Accessions. African Journal of Food, Agriculture, Nutrition and Development 11, no. 3.

60. Kashif M., Ahmad J., Chowfdhry M.A, Perveen K, (2003). Study of genetic Architecture of some Important Agronomic Traits in Durum Wheat (Triticum durum). Asian Journal of plant Sciences, 2(9): 708-712.

61. Ridzuan, R., Rafii, M. Y., Mohammad Yusoff, M., Ismail, S. I., Miah, G., & Usman, M., (2019). Genetic diversity analysis of selected Capsicum annuum genotypes based on

morphophysiological, yield characteristics and their biochemical properties. J Sci Food Agriculture, 99(1), 269-280.

62. Huby M., Gogué J., Maignel L., Bidanel J., (2003). Genetic correlations between the numerical and weight characteristics of the litter, the variability of piglet weight and their survival between birth and weaning. INRA, Station of Quantitative and Applied Genetics, 78352 Jouy-en-Josas Cedex. INRA, Domaine de Galle, 18520 Avord. ITP, Animal Improvement Center, B.P. 35104, 35651 Le Rheu Cedex.

63. Julius S., Maryke L., Abe S. G., Ntombokulunga W. M., (2022). Pheneotypic Diversity and Characterization of the Southern African Bambara Groundnut Germplasm Collection for Grain Yield and Yield Components. Agronomy 12. 1811