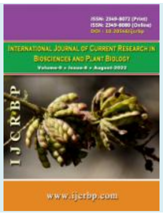
Int. J. Curr. Res. Biosci. Plant Biol. (2022) **9(8)**, 9-16

EXCELLENT PUBLISHERS

International Journal of Current Research in
Biosciences and Plant Biology

Volume **9** • Number **8** (August-2022) • ISSN: 2349-8080 (Online)

Journal homepage: www.ijcrbp.com



Original Research Article **doi:** https://doi.org/10.20546/ijcrbp.2022.908.002

Variability, correlations, genetic advance and heritability of physiological and agronomic parameters of Bambara groundnut (*Vigna subterranea* [L.] Verdc.) genotypes from Burkina Faso

Hervé Nandkangre[1]*, Diane Judicaëlle Kambou[2], Adjima Ouoba[3], Moussa N'Golo Konate[4], FidèleKoulibi Zongo[1], Ernest Renan Traore[2], AiméSévérin Kima[5], Boukaré Nikiema[1], Yannick Barkoindé Ilboudo[1] and Mahama Ouedraogo[6]

[1]*Centre Universitaire de Tenkodogo, Université Thomas SANKARA, 12 BP 417 Ouagadougou 12, Burkina Faso*
[2]*Unité de Formation et de Recherche - Sciences de la Vie et de Terre, Université Joseph KI-ZERBO, 03 BP 7021 Ouagadougou 03, Burkina Faso*
[3]*Centre Universitaire de Ziniaré, Université Joseph KI-ZERBO, 03 BP 7021 Ouagadougou 03, Burkina Faso*
[4]*Département des Sciences de la Vie et de la Terre, Université Norbert ZONGO, 01 BP 376 Koudougou 01, Burkina Faso*
[5]*Département Gestion des RessourcesNaturelles, Institut de l'Environnement et de Recherches Agricoles (INERA), 04 BP 8645 Ouagadougou, Burkina Faso*
[6]*Département Productions Végétales, Institut de l'Environnement et de Recherches Agricoles (INERA), 04 BP 8645 Ouagadougou, Burkina Faso.*

*Corresponding author; e-mail: hervenankangre@yahoo.fr

Article Info	Abstract
Keywords: Bambara groundnut Heritability Genotypic variance Phenotypic variation	Bambara groundnut is a seed legume of the Fabaceae family. It is the second most important food legume in Burkina Faso and is one of the main sources of income for women producers in rural areas. In Burkina Faso, research works on Bambara groundnut carried out to improve the performance of available landraces are very limited. For this purpose, agro-morphological characterization was carried out to contribute to a better knowledge of the diversity as well as the correlations between the characters, their mode of heritability and the genetic advance would make it possible to lay down milestones for a good strategy of conservation and improvement of the plant. Investigations were set up on the experimental site of the University Center of Tenkodogo following a completely randomized block design with four replications. A total of 20 genotypes were evaluated for this purpose. Nineteen (19) agronomic and physiological traits were recorded during the development stages of the plant and after harvest. The descriptive statistical analysis showed that there are strong amplitudes between the minimum and maximum values for all the studied characters. All the characters discriminate the accessions at the 5% threshold, except the plant spread. The cumulative values of the variance of the first four factorial axis (F1, F2, F3 and F4) for the 19 characters studied were 84.424%. The estimation of the genetic parameters showed slightly higher coefficients of phenotypic variation than the coefficients of genotypic variation for each of the 19 traits studied. The small differences between the phenotypic and genotypic coefficients of variation observed for all traits indicate that they are little influenced by the environment. The studied traits expressed a very high broad sense heritability with

certain characters (H^2 >30). These high heritability values allow for more reliable responses to selection. Moreover, when heritability is high, the influence of environmental factors acts in a not very significant way on the expression of the characters. The results obtained in this study should be taken into consideration for any Bambara groundnut improvement program in Burkina Faso.

• *Received: 08 June 2022* • *Revised: 15 July 2022* • *Accepted: 27 July 2022* • *Published Online: 6 August 2022*

Introduction

Bambara groundnut (*Vigna subterranea* [L.] Verdc.) is a seed legume belonging to the Fabaceae family. This legume is very well adapted to the growing conditions in savanna regions (Goli, 1997). It is the third most cultivated seed legume in West Africa after cowpea and groundnut (Touré *et al.,* 2013). In Burkina Faso, Bambara groundnut is the second most important food legume after cowpea (Ouédraogo *et al.*, 2008) and is one of the main sources of income for rural women producers. However, it has an unvalued status and is considered as food supplement but not a lucrative cash crop in Burkina Faso. Bambara groundnut is a complete food (Bamshaiye *et al.,* 2011) and is an important source of vegetable protein for humans (Embaby and Abdel-Galil, 2006). Seed is rich in protein (19%), carbohydrates (63%), fat (6.5%) and essential amino acids such as lysine, cysteine and methionine (Oliveira, 1976; Brough and Azam-Ali, 1992).

Agricultural production in Sub-saharan Africa is constrained by several factors such as insufficient rainfalls, low soil fertility and limited access to inputs (Nyamangara and Nyagumbo, 2010). In addition to these constraints, there is also the under-exploitation of certain crops such as Bambara groundnut, which stayed for a long time neglected by research institutions in Burkina Faso despite its enormous agronomic and nutritional potential. Few works have been done on the study of agromorphological variability (Kambou *et al.*, 2020), characterization and evaluation of Bambara groundnut accessions grown in Burkina Faso (Ouédraogo *et al.*, 2008).

In agronomy, identification of interesting traits within cultivated species is necessary for the development of varieties with high economic value (Setyawan *et al.*, 2014). This requires characterization of the genetic diversity, which is essential for the implementation of an efficient breeding strategy (Cooper *et al.*, 2001) as well as for the planning of variety improvement programs (Ravishanker *et al.*, 2013). Bambara groundnut has important agronomic, nutritional and economic value. A better knowledge of the morphological and agronomic diversity as well as the correlations between the characters, their mode of heritability and the genetic advance would allow us to lay the groundwork for a good conservation and improvement strategy for the plant. Indeed, any improvement program necessarily relies on agromorphological variability (Smith *et al.*, 1991; Nandkangré, 2016), which constitutes the raw material for the breeders. It is then imperative to characterize and preserve the variability of cultivated Bambara groundnut to prevent possible genetic erosion of the species. This study aims to characterize and evaluate the morpho-metric and agronomic variability of a Bambara groundnut collection in Burkina Faso through the study of phenotypic and genotypic variances, heritability and genetic advance for a better strategy for further breeding program.

Materials and methods

Study site

Field investigations were conducted on the experimental site of the University Center of Tenkodogo (11°48'37"N, 0°22'19"W) in the Center-east Region of Burkina Faso. Tenkodogo is located in the North Sudanianphytogeographical sector (Fontes and Guinko, 1995). The rainfalls are variable from one year to the next. The rainfalls recorded in Tenkodogo in 2021 were 787.7 mm from May to September with average minimum and maximum temperatures of 26°C (August) and 31°C (April), respectively. Soil characterization of the experimental site according to the FAO soil description guidelines (FAO, 1994) showed that the soil has a sandy texture in the 0 - 16 cm depth and a clayey-sandy texture in the 16 - 36 cm depth, all underlain by an iron shell. The drainage is excessive to perfect. The soil belongs to the class of iron-manganese sesquioxide soils and more specifically to a shallow leached ferruginous tropical soil according to the French classification (CPCS, 1967); and corresponding to an endo-petroplinthlixisol (WRB, 2015). The texture of the soil makes it potentially suitable for Bambara groundnut cultivation as it is better drained and facilitate pods penetration into the soil.

Plant material

The plant material used in this study consisted of 20 Bambara groundnut genotypes from the gene bank of the Institute of Environment and Agricultural Research (INERA: *Institut de l'Environnement et de Recherches Agricoles*) in Burkina Faso.These are the genotypes KVS109A, VARFOUR, KVS109B, KVS141-2, KVS97-3, KVS360, KVS314, KVS97-2, KVS311, KVSB24. P, 60GYF271, 60GYF439, 60GY301, 60GY-F80, KVS235-100GY, 60GYF276, KVS210 LR, 10VAR360, KVS075-1 and KVS075-2.

Experimental design and field management

The trials were set up following a randomized complete block design (RCBD) with four replications. Each block consisted of 20 lines of 4 m, with an interval of 1 m between blocks. Each line was randomly assigned with a genotype. The row spacing was 40 cm and the spacing between two holes on the row was 20 cm. The total area of the experimental plot was 136.8 m^2, 18 m long and 7.6 m wide.

Sowing was done on July 4, 2021 on a previously plowed flat field using a tractor. The different genotypes were sown at one seed per hole. At planting day, NPK mineral fertilizer (14-23-14) was applied at basal at the rate of 75 $kg.ha^{-1}$. Three manual weedings were performed on all plots as needed. Mounding was carried out on the 49th day after sowing (DAS) on all elementary plots.

Data collection and statistical analysis

A total of 19 characters, including 12 agronomic and seven physiological were recorded at different stages of plant development and after harvest. The characters were recorded according to the Bambara groundnut descriptor (IPGRI *et al.*, 2000). Statistical analyses were carried out with the average values obtained per row and per block.

Genotypes with less than 10 plants per row were excluded from the analyses. This was the case for the genotype KVS210 LR. Descriptive statistics such as mean, minimum, maximum and standard deviations for each trait were calculated. The Genstat 12ed software was used for this purpose at the 5% threshold. Five genetic parameters were estimated from the mean squares with all quantitative traits (Table 1) according to the formulas used by Jalata *et al.*, (2011) and Nwangburuka and Denton (2012).

Results and discussion

Variation of the studied traits

The minimum, maximum and mean values, standard deviations and Fisher P-value are reported in table 2. The results of the descriptive statistical analysis showed that there are high amplitudes between the minimum and maximum values for all the studied characters. Most of characters discriminate the genotypes (P = 5%) except the plant spread (PlS). Highly significant differences between the characters of the genotypes for almost all the characters studied indicates there is significant agromorphological diversity within this population of Bambara groundnut. Bonny and Djè (2011); Issa *et al.*, (2018); Khan *et al.*, (2021) also obtained similar results with Bambara groundnut accessions from various countries. This important agromorphological variability observed within different Bambara groundnut populations would result from the expression of important genetic heterogeneity under the influence of the environment.

Knowledge of the level of variability within a population is one of the most important step in the description and classification of crop germplasm (Manzano *et al.*, 2001; Radhouane, 2004). It also provided very useful information on the agromorphological diversity on Bambara groundnut genotypes, which is essential for the development, conservation and their use in the genetic improvement program in Burkina Faso.

Correlations and contribution of the variables to the axis of the principal component analysis

The principal component analysis (PCA) performed showed the variability within the Bambara groundnut genotypes. The cumulative variance values of the first four factorial axis (F1, F2, F3 and F4) were 84.424% (Table 3). The factor F1 presented an Eigen value of 9.679 and is positively and very strongly correlated with flowering (FFL and FLO50).

This factor is also very significantly correlated, but negatively, with the yield-related traits such as the number of seeds per pod (N1S and N2S), the number of pods per plant (NP/P) and the weight of pods per plant

(WP/P). There is also a strong correlation of this factor with the weight of seeds (W100S and WS/P) and the yield (YLD).

The factor F1account for 48.395% of the total variance and allows to discriminate the characters related to the sowing-flowering cycle in the positive abscissa and the yield as well as the yield-related traits in the negative abscissa. The correlations showed a clear relationship between physiological traits and plant yield and yield components. This helps to explain that genotypes with a high flowering cycle have low yield potentials. These results corroborate those of Ouédraogo *et al.*, (2008) who worked on 310 Bambara groundnut accessions from Burkina Faso. These authors reported that in Burkina Faso, late accessions gave the lowest yields. In contrast, Bonny and Djè (2011) results were not in accordance with Ivory Coast Bambara groundnut accessions, where rainfall is more abundant.

The F2 factor has an Eigen value of 3.052 and accounts for only 15.259% of the total variance. On the other hand, it is positively and very significantly associated with pod length (PLen), pod width (PWid) and seed length (SLen). The knowledge of the relationships between the traits is very important for the breeders in the choice of the traits to be integrated in the varietal improvement programs.

Estimation of genetic parameters

The genetic parameters are recorded in Table 4. The phenotypic coefficients of variation are slightly higher than the genotypic coefficients of variation for all the characters. The low coefficients of genotypic variation are recorded for pod filling ratio (PFR = 1.99%), pod width and length (PWid = 2.21%; PLen = 3.25%) and seed width (SWid = 3.62%). Contrariwise, these coefficients were high for the number of two-seeds per pod (N2S = 50.71), weight of pods per plant (WP/P = 21.39%) and number of leaves per plant (NL/P = 21.27%).

Similar observations were recorded in the phenotypic coefficients of variation for all the traits. The small differences between phenotypic and genotypic coefficients of variation (PCV > GCV) observed for all traits indicate that the influence of environment was expected to be minimal. Similar results were reported by Aragaw *et al.*, (2011) and Nandkangré *et al.*, (2016) on ginger, but also in barley by (Nwangburuka and Denton, 2012). Broad-sense heritability (H²) ranged from 40.31% for plant width (PWid) to 90.01% for 100-seeds weight (W100S). The characters studied expressed high broad sense heritability in the majority of characters. High heritability value allow for more reliable responses to selection. Moreover, when heritability is high, the influence of environmental factors is not very significant on the expression of the characters.

The classification of Dabholkar (1992) allows to conclude that all the characters have a high heritability ($H^2 > 30\%$). However, heritability is affected by the selection plant, the traits considered and the environmental conditions of the study (Dabholkar, 1992).

The high heritability values obtained in this study would therefore be related to the good growing conditions and the adaptability of the genotypes in the Center-east Region in Burkina Faso. These high values could indicate the existence of the additive gene effect which is beneficial to selection. Indeed, the selection or improvement of varieties with interesting agronomic traits related to productivity requires a heritable variation of these traits.

Furthermore, the effectiveness of breeding depends on the control of actions that the breeder can exert on the components of phenotypic variability of the plant material (Kremer, 1981). One of the objectives of these actions is to decrease the part of environmental factors in the expression of the interesting traits. This will then predict the response to selection in breeding (Kremer, 1981).

The lowest value of expected genetic advance relative to the trait mean (GA/X) was recorded for pod width (PWid = 2.40%) and the highest value for number of two-seeds per pod (N2S = 73%). Fairly high values for some characters such as number of leaves per plant (NL/P = 38.17%), weight and number of pods per plant (WP/P = 37.04%; NP/P = 30.80%) as well as yield (YLD = 28.63%) were recorded. Combinations of high values of heritability (H^2), genotypic coefficient of variation (GCV) and expected genetic advance over the mean (GA/X) were obtained for the number of leaves per plant (NL/P), number of pods per plant (NP/P), number of two-seeds per pod (N2S), weight of pods per plant (WP/P), 100-seeds weight (W100S), seeds weight per plant (WS/P) and yield (YLD).

This indicates that these traits are under the control of more additive genetic effects (Jalata *et al.*, 2011) which are important in varietal improvement. In this case, selection could provide additional value compared to prediction based only heritability. This suggests that interesting genotypes can be identified on the basis of their phenotypic performance. Assefa *et al.*, (2001) reported that this provides a better estimation of genotype selection. These traits could therefore be useful for implementing effective strategies for selecting Bambara groundnut genotypes with high yield potential.

Table 1. Estimated genetic parameters.

Parameter	Formula	Significance of terms
Genotypic Variance (VG)	VG = (MSG – MSE)/r	MSG : Mean square of genotype
Phenotypic Variance (VP)	VP = VG + (MSE/r) = MSG/r	MSE : Mean square of error
Heritability broad sense (H^2)	H^2 (%) = (VG/VP)*100	r : nombre de répétitions
Genotypic Coefficient of Variation (GCV)	GCV (%) = (√VG/X)*100	√VG : Genotypic standard deviation
Phenotypic Coefficient of Variation (PCV)	PCV (%) = (√VP/X)*100	X : Mean of the character
Genetic Advance (GA)	GA = H^2*√VP*K	√VP : Phenotypic standard deviation; K = 2,06 (selection coefficient 5% threshold)

Table 2. Descriptive statistical analysis and variance of Bambara groundnut genotype traits.

Characters	Minimum	Mean	Maximum	SD	*P-Value*
EMG50 (day)	5.25	6.60	8.00	0.77	0.001*
RES21 (%)	58.33	75.50	95.23	12.42	< 0.001**
FFL (days)	31.00	32.53	36.00	1.37	< 0.001**
FLO50 (days)	33.75	35.36	38.50	1.55	< 0.001**
NL/P	35.30	62.93	79.25	14.58	< 0.001**
PlH (cm)	17.20	19.50	22.25	1.25	< 0.001**
PlS (cm)	32.10	39.60	48.60	3.89	0.098 NS
N1S	0.24	2.10	5.85	1.35	< 0.003*
N2S	13.00	21.97	28.25	4.11	< 0.001**
NP/P	12.63	20.05	28.55	3.69	< 0.001**
WP/P (g)	11.66	20.02	25.71	4.22	< 0.001**
W100S (g)	40.50	53.80	62.25	7.03	< 0.001**
PLen (mm)	13.99	15.06	16.60	0.58	< 0.001**
PWid (mm)	11.44	12.19	12.81	0.37	0.020*
SLen (mm)	9.09	10.57	11.20	0.48	< 0.001**
SWid (mm)	7.97	8.78	9.35	0.39	< 0.001**
PFR (%)	33.25	61.02	145.00	23.09	0.033 *
WS/P (g)	8.78	15.55	20.06	3.57	< 0.001**
YLD (kg.ha^{-1})	692.18	1236.76	1650.00	315.71	< 0.001**

Legend:*EMG50* *: Number of days from sowing to 50% plantlet emergence ;* ***RES21*** *: Rate of emerged plants at 21 days after sowing ;* ***FFL*** *: Number of days from sowing to first flowering;* ***FLO50*** *: Number of days from sowing to 50% flowering;* ***NL/P*** *: Number of leaves per plant :* ***PlH*** *: Plant height ;* ***PlS*** *:Plant spread ;* ***N1S*** *: Number of pods containing one seed ;* ***N2S*** *: Number of pods containing two seeds ;* ***NP/P:*** *Number of pods per plant;* ***WP/P*** *:Weight of pods per plant ;* ***W100S*** *: Weight of 100 seeds ;* ***PLen*** *: PodeLenght ;* ***PWid*** *: Pod width ;* ***SLen*** *: Seed Lenght ;* ***SWid*** *: Seed width ;* ***PFR*** *: Pod fill rate ;* ***WS/P:*** *Weight of seed per plant ;* ***YLD*** *: Yield ; SD: Standard deviation ;* ***NS*** *: Not significant ; * : Significant difference at 5% ; ** : Hight significant difference at 5%.*

Table 3. Contribution of the variables to the axis of the principal component analysis,

Characters	**Principal factors**			
	F1	**F2**	**F3**	**F4**
EMG50 (day)	0.288	0.027	-0.751**	-0.522*
RES21 (%)	0.086	-0.323	0.843**	-0.002
FFL (days)	0.870**	-0.201	-0.096	-0.138
FLO50 (days)	0.953**	0.064	-0.056	0.031
NL/P	-0.636*	0.166	-0.095	0.684*
PlH (cm)	0.618*	0.412	0.188	0.473
PlS (cm)	0.460	0.447	-0.461	0.336
N1S	-0.791**	-0.122	-0.354	0.156
N2S	-0.737**	-0.226	-0.225	0.030
NP/P	-0.898**	-0.146	-0.130	0.251
WP/P (g)	-0.932**	0.082	-0.270	0.128
W100S (g)	-0.875**	0.157	0.219	-0.134
PLen (mm)	0.139	0.941**	0.177	0.054
PWid (mm)	-0.011	0.935**	-0.072	-0.107
SLen (mm)	-0.361	0.703**	0.233	-0.534*
SWid (mm)	-0.866**	0.337	0.161	-0.030
PFR (%)	-0.436	0.058	0.537*	0.085
WS/P (g)	-0.859**	0.076	-0.380	0.039
YLD ($kg.ha^{-1}$)	-0.850**	-0.104	0.238	-0.133
Eigen value	**9.679**	**3.052**	**2.465**	**1.689**
Variability (%)	**48.395**	**15.259**	**12.327**	**8.443**
% cumulative	**48.395**	**63.653**	**75.980**	**84.424**

Legend:*EMG50* *: Number of days from sowing to 50% plantlet emergence ;* ***RES21*** *: Rate of emerged plants at 21 days after sowing ;* ***FFL*** *: Number of days from sowing to first flowering;* ***FLO50*** *: Number of days from sowing to 50% flowering;* ***NL/P****: Number of leaves per plant :* ***PlH*** *: Plant height ;* ***PlS*** *:Plant Spread ;* ***N1S*** *: Number of pods containing one seed ;* ***N2S*** *: Number of pods containing two seeds ;* ***NP/P****: Number of pods per plant;* ***WP/P*** *:Weight of pods per plant ;* ***W100S*** *: Weight of 100 seeds ;* ***PLen*** *: Pod Length;* ***PWid*** *: Pod width ;* ***SLen*** *: Seed Length;* ***SWid*** *: Seed width ;* ***PFR*** *: Pod fill rate ;* ***WS/P****: Weight of seed per plant ;* ***YLD*** *: Yield ; * : Significant difference at 5% ; ** : Hight significant difference at 5%.*

Table 4. Genetic parameters of Bambara groundnut accessions.

Variables	**GCV (%)**	**PCV (%)**	**H^2 (%)**	**GA**	**GA/X (%)**
EMG50 (day)	9,29	11,48	65,45	0,83	12,52
RES21 (%)	14,88	16,09	85,49	19,78	26,20
FFL (days)	3,81	4,03	89,53	2,16	6,64
FLO50 (days)	3,98	4,28	86,56	2,51	7,10
NL/P	21,27	22,78	87,13	24,02	38,17
PlH (cm)	5,45	6,40	72,43	1,59	8,13
PlS (cm)	6,17	9,71	40,31	2,03	5,12
N1S	18,77	22,55	69,29	70,27	26,79
N2S	50,71	60,67	69,88	19,58	73,00
NP/P	20,20	23,48	74,01	89,04	30,80
WP/P (g)	21,39	23,34	84,04	95,89	37,04
W100S (g)	12,08	12,73	90,01	12,05	22,39
PLen (mm)	3,25	3,79	73,59	0,74	4,93
PWid (mm)	2,21	3,05	52,59	0,29	2,40
SLen (mm)	4,01	4,49	79,56	0,69	6,57
SWid (mm)	3,62	4,34	69,58	0,46	5,19
PFR (%)	1,99	2,89	47,35	220,49	2,83
WS/P (g)	18,55	22,42	68,43	4,07	26,14
YLD ($kg.ha^{-1}$)	19,76	23,55	70,35	238,53	28,63

Legend:*EMG50* *: Number of days from sowing to 50% plantlet emergence ;* ***RES21*** *: Rate of emerged plants at 21 days after sowing ;* ***FFL*** *: Number of days from sowing to first flowering;* ***FLO50*** *: Number of days from sowing to 50% flowering;* ***NL/P*** *: Number of leaves per plant :* ***PlH*** *: Plant height ;* ***PlS*** *:Plant Spread ;* ***N1S*** *: Number of pods containing one seed ;* ***N2S*** *: Number of pods containing two seeds ;* ***NP/P****: Number of pods per plant;* ***WP/P*** *:Weight of pods per plant ;* ***W100S*** *: Weight of 100 seeds ;* ***PLen*** *: Pode Length ;* ***PWid*** *: Pod width ;* ***SLen*** *: Seed Length ;* ***SWid*** *: Seed width ;* ***PFR*** *: Pod fill rate ;* ***WS/P****: Weight of seed per plant ;* ***YLD*** *: Yield ;* ***NS*** *: Not significant ; * : Significant difference at 5% ; ** : Height significant difference at 5%.*

This study, carried out with a collection of 20 Bambara groundnut genotypes, revealed the existence of high variability. Environmental factors had little effect on the expression of the traits because of the high heritability expressed for all the traits and the small difference between the coefficients of phenotypic and genotypic variation. The combination of high heritability, genotypic coefficient of variation and expected genetic advance over the mean obtained for the traits number of leaves, 100-seeds weight, weight of pods per plant and yield indicate that these traits are under the control of additive gene effects that are important for Bambara groundnut improvement.

Conflict of interest statement

The authors declare that there is no conflict of interest regarding the publication of this article.

Acknowledgements

We appreciate the financial support of McKnight Foundation in this work

References

Aragaw, M., Allamerew S., Michael G. H., Tesfaye A., 2011. Variability of ginger (*Zingiber officinale*) accessions for morphological and some quality traits in Ethiopia. *Internatinal Journal of Agriculture Ressearch*, DOI: 10.3223/ijar.

Bamshaiye, O. M., Adegbola J. A., Bamishaiye E. I., 2011. Bambara groundnut: An Under Utilized Nut in Africa. *Adv. Agric. Biotechnol.*1: 60-72.

Bonny, B. S., Djè Y., 2011. Variabilité morphologique et agronomique des variétés traditionnelles de Bambara groundnut [*Vigna subterranea* (L.) verdc. (fabaceae)] de Côte d'Ivoire. *Journal of Applied Biosciences*. 41: 2820 – 2835.

Brink, M., 1999. Development, growth and dry matter partitioning in bambara groundnut (*Vigna subterranea*) as influenced by photoperiod and shading. *Journal of Agricultural Science*. 133: 159-166

Brough, S. H., Azam-Ali S. N., 1992. The effect of soil moisture on the proximate composition of bambara groundnut (*Vigna subterranea* (L) Verdc). *J. Sci Food Agric*. 60(2), 197-203.

Collinson, S. T., Azam-Ali S. N., Chavula K. M., Hodson D. A., 1996. Growth, development and yield of bambara groundnut (*Vigna subterranea*) in response to soil moisture. *Journal of Agricultural Science*. 126: 307-318

Cooper, H. D., Spillane C., Hodgkin T., 2001. Broadening the genetic base of crops: *An overview. Pages 1-23. in Cooper, H. D., C. Spillane, and T. Hodgkin, editors. eds. Broadening the genetic base of crop production CABI. Wallingford, Oxon, U.K.*

CPCS (Commision de Pédologie et de cartographie des sols), 1967. Commission de Pédologie et de Cartographie des Sols. https://horizon.documentation.ird.fr/exl-doc/pleins_textes/divers16-03/12186.pdf

Dabholkar, A. R., 1992. Elements of Biometrical Genetics. Concepts publishing Company, New Delhi, India.138-140 pp.

Embaby, E. M., Abdel-Galil M. M., 2006. Seed born fungi and mycotoxins associated with some legume seeds in Egypt. *Journal of Applied Sciences Research*. 2(11), 1064-1071.

FAO, ISRIC (Centre International de Reference et d'Information des Sols), 1994. Directives pour la description des sols. 3rd Edn, Service des sols-ressources, aménagement et conservation, Division de la mise en valeur des terres et des eaux, 78p.

Fontes, J., Guinko S., 1995. Map of vegetation and land use in Burkina Faso. Explanatory note. Toulouse, Institute of International Map of the vegetation, Institute of Rural Development, Faculty of Science and Technology, University of Ouagadougou, Burkina Faso.

Goli, A. E., 1997. Bibliographical Review. In: Heller J, Begemann F, and Mushonga J, Eds. Conservation and improvement of bambara groundnut (*Vigna subterranea* (L.) Verdc). Harare, Zimbabwe, pp. 4-10.

IPGRI., IITA., and BAMNET., 2000. Descriptors for bambara groundnut (*Vigna subterranea*). International Plant Genetic Resources Institute, Rome Italy; International Institute of Tropical Agriculture, Ibadan, Nigeria; The International Bambara Groundnut Network, Germany. 57 pp.

Issa, H. A., Agali, A., Ousmane D. S., Kodo B. S., 2018. Variabilité morphologique et agronomique des morphotypes de Bambara groundnut (*Vigna Subterranea* (L.) cultivés dans la zone sahélienne du Niger. *European Scientific Journal*. 14: 377-393

Jalata, Z., Ayana A., Zeleke H., 2011. Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian barley (*Hordeum vulgare* L.) mandrake and crosses. *International Journal of Plant Breeding and Genetics*.**5**(1):44-52.

Kambou, D. J., Nandkangre H., Ouoba A., Konate N. M., Sawadogo N., Ouedraogo M., Sawadogo M., 2020. Agro-morphological characterization of Bambara nut accessions [*Vigna* subterranea (L) Verdcourt] from Burkina Faso. *Journal of Applied Biosciences*. 153: 15727 – 15744.

Khan, M. M. H., Rafii M. Y., Ramlee, S. I. Jusoh, M. Al-Mamun M., 2021. Bambara Groundnut (*Vigna subterranea* L. Verdc): A Crop for the New Millennium, Its Genetic Diversity, and Improvements to Mitigate Future Food and Nutritional Challenges. *Sustainability*, 13, 5530.

Kremer, A., 1981. Déterminisme génétique de la croissance en hauteur du Pin maritime (*Pinus* pinaster *Ait*) III. - Evolution des composantes de la variance phénotypique et génotypique. *Annales des sciences forestieres*. 38(3), 355-375.

Linnemann, A. R., Westphal M., Wessel E., 1995. Photoperiod regulation of development and growth in bambara groundnut (*Vigna subterranea*). *Field Crops Research*, 40: 39- 47.

Manzano, A. R., Nodals R. A. A., Gutiérrez R. A. I. M., Mayor F. Z., Alfonso C. L., 2001. Morphological and isoenzyme variability of taro (*Colocasia esculenta* L. Schott) germplasm in Cuba. *Plant Genetic Resources Newsletter*. 126 : 31-40.

Nandkangré, H., 2016. Caractérisation génétique et identification de variétés de gingembre *Zingiber officinale* Rosc.) adaptées au système de production au Burkina Faso. Thèse de Doctorat Unique, Université Ouaga I Pr Joseph KI-ZERBO. 101 p.

Nandkangré, H., Ouedraogo, M., Nanema, K.R., Bado, S., Ouedraogo, N., Sawadogo, M. 2016. Variability, correlations, heritability and genetic advance of rhizome yield and yield related traits in ginger (*Zingiber officinale* Rosc.) Landraces from Burkina Faso. *J. Appl. Environ. Biol. Sci*. 6(8), 54–60.

Nwangburuka, C.C., Denton O.A., 2012.Heritability, characters association, and genetic advance in six agronomic and yield related characters in leaf *Corchorus olitorius*. *International Journal of Agricultural Research*, DOI: 10.3923/ijar.

Nyamangara, J., Nyagumbo I., 2010. Interactive effects of selected nutrient resources and tiedridging on plant growth performance in a semi-arid small holder farming environment in central Zimbabwe. Innovations as Key to the Green Revolution in Africa, pp. 357-363.

Oliveira, J. S., 1976. Grain legumes of Mozambique. Trop. Grain Legume Bull. 3: 13-15.

Ouedraogo, M., Ouedraogo J. T., Tignere J. B., Balma D., Dabire B.C., Konate G., 2008. Characterization and evaluation of accessions of bambara groundnut (*Vigna subterranean* (L.) Verdc.) from Burkina Faso. *Sciences &Natur*. 5:191-197.

Radhouane, L., 2004. Etude de la variabilité morpho-phénologique chez *Pennisetum glaucum (L.)* R. Br., *Plant Genetic Resources Newsletter*, 138, 18-22.

Ravishanker, Kumar S., Chatterjee A., Baranwal D. K., Solankey S. S., 2013.*Genetic* variability for yield and quality traits in ginger (*Zingiber officinale* Roscoe). *The Bioscan*.8(4), 1383-1386.

Setyawan, A. D., Wiryanto S., Bermawie N., 2014. Variation in isozymic pattern of germplasm from three ginger (*Zingiber officinale*) varieties. Short communication, *Bioscience*. **6**(1), 86-93.

Smith, S. E., DossA. A., Warburton M., 1991. Morphological and agronomic variation in North African and Arabianalfalfas, *Crop Science*. 31, 1159- 1163.

Toure, Y., Koné M., Silué S., Kouadio Y. J., 2013. Prospection, collecte et caracterisation agro-morphologique des morphotypes de Bambara groundnut (*Vigna subterranea* (L.) Verdc) de la zone savanicole en côte d'Ivoire. *European scientific journal*. 9: 308-325.

WRB (World Référence Bases), 2015. Base de référence mondiale pour les ressources en sols 2014. Système international de classification des sols pour nommer les sols et élaborer des légendes de cartes pédologiques. Mise à jour 2015. 203 p. Classification, corrélation and communication, 2nd édition. World Soil Resources Reports No.103, FAO, Rome, 145 p.

How to cite this article:

Nandkangre, H., Kambou, D.J., Ouoba, A., Konate, M. N., Zongo, F., Traore, E. R., Kima, A., Nikiema, B., Ilboudo, Y. B., Ouedraogo, M., 2022. Variability, correlations, genetic advance and heritability of physiological and agronomic parameters of Bambara groundnut (*Vigna subterranea* [L.] Verdc.) genotypes from Burkina Faso. Int. J. Curr. Res. Biosci. Plant Biol., 9(8): 9-16. **doi:** https://doi.org/10.20546/ijcrbp.2022.908.002