(RESEARCH ARTICLE)

Study of variability, correlation and heritability of physiological and yield related traits in Bambara groundnut [*Vigna subterranea* (L.) Verdc.] in Burkina Faso

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Abstract

Bambara Groundnut [*Vigna subterranea* (L.) Verdcourt] is one of the most consumed leguminous crops in Burkina Faso. Through its food and nutritional qualities, it is undeniably to be taken into account for the attack on the food and nutritional security of populations. This work aims to contribute to a better knowledge of correlations between parameters, their mode of heritability and genetic progress. Sixteen quantitative traits were used to evaluate ninety Bambara Groundnut genotypes from three agro-climatic zones. These genotypes were sown during 2018 campaign in Rollo (north-central region of Burkina Faso) following a Fisher block design with four repetitions. The analysis of variance showed that means of parameters were highly significant (P < 0.01) except for plant height implying existence of an important variation between genotypes for these parameters. Phenotypic coefficients of variation varied from 5.96% to 121% and genotypic ones from 3.26% to 175%. Generally, phenotypic coefficients of variation (PCV) generated more than genotypic coefficients (GCV). However, the small differences between the values of these data mean showed the weak influence of environment on gene expression. Heritability recorded values ≥ 20% and genetic advance varied from 57.96 to 2538.85. The parameters having recorded strong heritability's (20.35% to 97.95%) could be used in breeding and improvement programs of Bambara Groundnut by taking into account existing relations between these parameters. Programs to improve yield of Bambara Groundnut can only be envisaged after a good knowledge of the different relationships existing between yield parameters and their heritability.

1. Introduction

Bambara groundnut [*Vigna subterranea* (L.) Verdcourt] is an important legume crop in Burkina Faso and Sub-saharan Africa [1, 2, 3]. It contributes to the food security of the poorest populations of the planet [4]. It is much appreciated in the human diet and is full of enormous nutritional qualities (39% to 62.12% carbohydrates, 19.41% to 21.64% proteins, 6.43% to 7.35% lipids, 6.84 % to 8.38% fiber, 10.71 mg to 13.15 mg calcium, 1.39 mg to 2.60 mg iron, 2.26 mg to 2.73 mg zinc in 100 g of seeds) [5]. It also has proven agronomic potentialities thanks to its ability to trap atmospheric nitrogen. [6] have reported a fixation capacity of 100 kg N ha^{-1}.

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For several years in Burkina Faso, research works on Bambara groundnut are focused on several aspects such as identification of main fungal and viral diseases [7, 8, 9], conservation of Bambara groundnut seed [10], development of cultural options, in particular mounding periods [11] and mineral fertilizers utilisation [12] for enhancing and promote this culture. We can also report few works on genetic diversity assessment of cultivated accessions dealing with morphological and DNA markers (RAPD and SSR) [1, 13, 14, 15, 16] in order to deepen knowledge of this crop and highlight the diversity, which was hitherto not well known.

Despite its hardiness, forecasts in terms of Bambara groundnut yield remain difficult. The insufficiency and poor distribution of rainfalls, the decline in soil fertility are among other things, the major causes of the drop in yields. Setting up a breeding program based on varietal improvement in terms of productivity for yield and yield-related parameters of Bambara groundnut can be achieved through identification of traits showing high estimates of heritability and genetic advance [17]. In Burkina Faso, few studies have been focused on the relationship between yields related traits on Bambara groundnut accessions [18]. It is then necessary to deepen studies on different relationships between the parameters of yield and their heritability because information on phenotypic and genotypic relationships of physiological and yield related traits for yield in Bambara groundnut would be very useful to the breeders in developing an appropriate breeding strategy. The present work aims to study the variations of the parameters of the yield and to evaluate the heritability of these parameters in Bambara groundnut. The results of this research will make it possible to design effective programs to improve the yield of Bambara groundnut through releasing elite varieties with interesting agronomic characteristics.

2. Material and methods

2.1. Plant materiel and experimental site

Field evaluation was carried out on July 2018 in Rollo located in the North Central Region of Burkina Faso. Ninety Bambara groundnut genotypes used in this study were sourced from the Institute for the Environment and Agricultural Research (INERA) gene bank, Burkina Faso. Genotypes used were collected over different periods from the different phytogeographical zones. Six genotypes under selection by INERA, 18 genotypes collected from the Sahelian zone, 48 from Sudan-sahelian zone and 17 from Sudanian zone (Table 1).

Table 1 Genotypes studied and their origin

Origin	Genotypes
INERA	KVS 235, KVS 235 100 GY, KVS 246-1, KVS 246-2, KVS 246-3, Life 16-141
Sahelian	E 105b, E 108, E 110a, E 110b, E 111a, E 114, E 117, E 118, E 119, E 12, E 124a, E 124b, E 124c, E 125, E 126, E 13, E 59, E 61a
Sudan-sahelian	E 01, E 03, E 04, E 09, E 103a, E 103b, E 105a, E 107, E 111b, E 131, E 132, E 16a, E 48, E 49, E 51, E 53, E 56a, E 56b, E 56c, E 58, E 61b, E 62a, E 62b, E 62c, E 65, E 70b, E 71, E 72, E 75, Nob-Loc, E 76a, E 76b, E 78a, E 83a, E 83b, E 88b, E 89a, E 89b, E90, E 92, E 93b, E 94, E 95a, E 95b, E 97, E 98, ED8, KAYA 2014
Sudanian	E 101b, E 123, E 130, E 16b, E 20, E 22, E 23, E 25, E 26, E 27, E 28, E 44, E 76c, E 78b, E 83c, E 86, E 88a

2.2. Experimental design and agronomic practices

The experimental design used was a Completely Randomized Blocks device with four replications. Each Bambara groundnut genotypes was sowed on 4 m long as elementary plots. Seeds were sown on 4 m apart elementary plots with spacing of 40 cm between plot and 20 cm between the holes on the same plot. Twenty-one seeds were sowed in each plot. The replications were separated by 1 m. Recommended rate of 75 kg.ha^{-1} of NPK (14-23-14) fertilizer was applied as a broadcast fertilizer at basal. Mounding was carried out 7 weeks after sowing. Regular weeding was made as need.

2.3. Data collection and analysis

Sixteen quantitative traits were observed during different stage of development and after harvest in accordance with Bambara groundnut descriptor established by the International Plant Genetic Resources Institute [19] (Table 2). Data collected were subjected to Analysis of Variance (ANOVA) in order to estimate the difference between studied traits among Bambara groundnut genotypes. The software IBM SPSS Statistics 20 software was used for analysis, and the significance was determined using F-test at 95% confidence.

Table 2 Method of scoring and code of quantitative parameter studied

Quantitative Parameters studied	Code	Method of scoring
Emergence date (day)	EMG	Estimate using calendar
Emergence at twenty-one days after sowing (number)	ETO	Counted
Days to first flowering (day)	FFL	Estimate using calendar
Days to 50% flowering (day)	HFL	Estimate using calendar
Number of leaves per plant (number)	NLP	Counted
Plant height (cm)	PHT	Measured
Diameter of the plant (cm)	DPL	Measured
Pod weight (g)	PWE	Measured
Number of pods per plant (number)	NPP	Counted
Number of pods with one seed (number)	N1S	Counted
Number of pod with two seeds (number)	N2S	Counted
Weight of seeds per plant(g)	WSP	Measured
Seed length (mm)	SDL	Measured
Seed width (mm)	SDW	Measured
Weight of 100 seeds (g)	WHS	Measured
Yield per square meter (g.m^2)	YIE	Measured

Genotypic and phenotypic correlations were performed using the formula of [20]:

$$\mathbf{r_{x,y}} = \frac{COV(x,y)}{\sqrt{(\delta^2 x)(\delta^2 y)}}$$

Where $\mathbf{r_{x,y}}$ is either genotypic or phenotypic correlation between variables x and y. COV(x,y) is the genotypic or phenotypic covariance between two variables, $\delta^2 x$ is the genotypic or phenotypic variance of the variable x, $\delta^2 y$ is the genotypic or phenotypic variance of the yield y. The mean squares of the genotype and error for each character were used to calculate the genotypic variance ($\delta^2 g$), phenotypic variance ($\delta^2 ph$), Heritability (Broad sens) (H^2), Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV) and Genetic Advance (GA) (Table 3) according to [21].

Table 3 Genetic parameters estimation

Parameter	Formula	Significance of terms
Genotypic variance ($\delta^2 g$)	$\delta^2 g = (MSG - MSE)/r$	MSG: Mean Square of Genotype
Phenotypic variance ($\delta^2 ph$)	$\delta^2 ph = \delta^2 g + (MSE/r) = MSG/r$	MSE: Mean Square of error r: Number of replications
Heritability (Broad sense) (H^2)	H^2 (%) = ($\delta^2 g / \delta^2 ph$)*100	δg: Genotypic standard deviations δph: Phenotypic standard deviations
Genotypic Coefficient of Variability (GCV)	GCV (%) = ($\delta g/X$)*100	X: Mean of the character
Phenotypic Coefficient of Variability (PCV)	PCV (%) = ($\delta ph/X$)*100	
Genetic Advance (GA)	GA = H^2* δph*K	K = 2,06 (Selection coefficient)

3. Results and discussion

3.1. Genetic variability of Bambara groundnut

Mean squares and genetic parameters estimated of 90 Bambara groundnut genotypes are given in table 4. Analysis of results showed that all the characters are discriminant ($P < 0.05$) except plant height. This diversity implies not only a heterogeneity within genotypes, their diverse origins, but can also be attributed to the interaction genotypes-environment. [1, 16] had reported similar results on respectively 310 and 20 Bambara groundnut accessions in Burkina Faso. This studied population, with a broad genetic base could offer possibilities for improving Bambara groundnut through classic selection method.

The phenotypic coefficients variation (PCV)are higher than the genotypic coefficients variation (GCV)for all 16 traits studied. This would mean that genotype was influenced by environment in the phenotype expression. [22] classified values of GCV and PCV. Values greater than 20% indicated high variation, between 10 to 20% are moderated and less than 10% showed low variation. Low GCVs were recorded for plant height at maturity (3.26%), seed width (4.89%), days to 50% flowering (5.43%), seed length (5.54%), the first flowering (6.10%), emergence date (7.39%) and the diameter of the plant (9.67%). In contrast, higher values were recorded for yield (175.00%) and the number of pods containing a seed (121.00 %). Lower PCVs were recorded for seed dimensions (SDW = 5.96%, SDL = 6.62%) and flowering (FFL = 7.46%, HFL = 7.68%) and higher values with yield (261%), pods weight (121%) and number of pods (105%). High genotypic and phenotypic coefficient of variation indicates the presence of considerable amount of genetic variability for these characters in the material studied. [23] and [24] reached to the same findings respectively on *Arachis hypogea* and 33 lines of *Vigna subterranea* obtained from the germplasm collection of the International Institute of Tropical Agriculture, Ibadan in Nigeria. Our findings related to the results of [25] who worked on 12 Bambara groundnut cultivars from Nigeria. The relatively small difference observed between PCV and GCV may be due to the little influence of environment on character expression as found earlier [26, 27].

Heritability in broad sense is very important to predict the dependability of phenotypic traits. In fact, according to [28], heritability estimates are useful for quantitative selection because they provide information on the extent to which a particular trait can be inherited through generations. Following to the classification of [29], very high values were recorded for traits such as number of pods containing one seed (97.95%), weight of 100 seeds (91.54%) and emergence on the 21st day after sowing (81.67%) and moderate values for number of leaves per plant (55.75%), number of pods per plant (55.30%), days to 50% flowering (50.04%), pod weight (48.62%), yield (45.20%), and plant height (20.35%). High values of heritability in broad sense indicate the possibility of high genetic gain from selection for these characters [30]. These results are closed to [31] on *Vigna unguiculata* accessions. According to [32], a heritability of 100% implies that the phenotype could provide a perfect measure of the value of genotypes; therefore, these traits are very informative for desired traits. However, the breeding material could affect heritability, the traits taken into account and the environmental conditions of the study [33].

High genetic advance values were recorded for weight of 100 seeds (2538.85), number of leaves per plant (983.06), yield (876.43), number of pods with one seed (647.25) and diameter of plant (517.60). According to [29], high heritability combined with high genetic advance is indicative of additive gene action. High heritability coupled with low genetic advance would be the result of non-dependence genetic effects while low heritability coupled with low genetic

gain suggests that phenotypic selection may not be effective in improving these traits [27]. Moreover, selection based on both high values of heritability in broad sense and genetic advance would be more reliable in the expression of traits in offspring [34, 35].

Table 4 Mean squares, variance components heritability and genetic advance of 90 Bambara groundnut genotypes from Burkina Faso

Parameter	Mean	Mean Square	PCV (%)	GCV (%)	H^2 (%)	GA
EMG	5.47	0.97**	9.00	7.39	67.39	68.33
ETO	16.17	19.19**	13.56	12.25	81.67	368.78
FFL	27.80	17.04**	7.46	6.10	66.96	285.97
HFL	31.87	23.72**	7.68	5.43	50.04	252.19
PHT	19.11	7.42ns	7.23	3.26	20.35	57.96
DPL	30.16	45.53**	11.22	9.67	74.23	517.60
NLP	54.14	291.70**	15.81	11.81	55.75	983.06
PWE	13.12	76.32**	121.00	84.00	48.62	212.95
NPP	17.91	65.10**	105.00	78.00	55.30	262.12
N1S	15.71	76.57*	111.00	110.00	97.95	647.25
N2S	0.56	0.93**	78.00	64.00	67.65	124.18
WSP	9.02	37.14**	68.00	56.00	70.71	419.16
WHS	57.62	645.68**	23.37	22.36	91.54	2538.85
SDL	11.16	1.96**	6.62	5.54	70.01	106.55
SDW	9.26	1.09**	5.96	4.89	67.29	76.48
YIE	59.32	1607.40**	261.00	175.00	45.20	876.43

Legend : EMG: Emergence date, ETO: Emergence at twenty-one days after sowing, FFL: Days to first flowering, HFL: Days to 50% flowering, PHT: Plant height, DPL: Diameter of the plant, NLP: Number of leaves per plant, PWE: Pod weigh, NPP: Number of pods per plant, N1S: Number of pods with one seed, N2S: Number of pod with two seeds, WSP: Weight of seeds per plant, WHS: Weight of 100 seeds, PWE: Pod weigh, SDL: Seed length, SDW: Seed width, YIE: Yield per square meter, ns: not significant, *: Indicate significant difference at 5%, ** indicate significant difference at 1%. PCV: Phenotypic coefficient variation, GCV: Genotypic coefficient variation, H2: Heritability in broad sense, GA: Genetic advance

3.2. Phenotypic and genotypic correlations among physiological and yield related traits

Phenotypic and genotypic correlations between the different characters are indicated in the table 5. The results showed negative and positive values for both genotypic and phenotypic correlations. In general, genotypic correlations were higher than their related phenotypic correlations for respective characters. This show a strong association between the characters taken in pair. This means that the environment has weak influence on the expression of traits and selection could be based on phenotypic traits. Significant and very significant positive correlations were recorded between weight of 100 seeds and emergence date (rp = 0.662; rg = 0.965), days to 50% flowering (rg = 0.500), diameter of the plant (rp = 1.453; rg = 2.021), number of leaves per plant (rp = 1.604; rg = 2.575), seed length (rp = 3.1682; rg = 4.637) and seed width (rp = 3.850; rg = 5.567). Weight of seed per plant exhibited positive and significant correlations with number of leaves per plant (rp = 0.367; rg = 0.289), seed length (rp = 0.428; rg = 0.618) and seed width (rp = 0.646; rg = 0.962). Selection based on one or more of these parameters leads to improved yield performance. Some authors such as [36] and [26] have reached the same results. Correlation gives magnitude of association of different component traits. According to [37], the significant positive correlation among the yield-related traits suggest that these characters also make positive indirect contribution to the final grain.

Negative and strong genotypic correlations were observed between days to 50% flowering and yield parameters such as number of pods (rp = - 0.385; rg = - 0.655), number of pods with one seed (rp = - 0.356; rg = - 0.606), weight of seed per plant (rg = - 0.314) and weight of 100 seeds (rg = - 0.500). Reducing flowering time positively influences the yield parameters such as the number of pods number of pods with one seed, weight of pods, weight of seeds per plant and weight of 100 seeds. These correlations are particularly interesting in view of the short rainy seasons observed in

Burkina Faso. Selection based on genotypes with a short semi-flowering cycle enables early pod formation. Pods formed in this way will have sufficient time to fill with seeds before the rains shorten. [18] worked on the agronomic performance of eight Bambara groundnut genotypes reached to the similar findings. Emergence date was also negatively and strongly correlated to emergence at 21st DAS (r_p = - 0.333; r_g = - 0.486), number of pods (r_g = - 429) and number of pods with one seed (r_g = - 0.324). The earlier the emergence of the seedlings, the lower the performance of the pods and seeds. That is to say that the plants with late emergence have recorded good performance and vice versa.

Table 5 Estimated phenotypic (P) and genotypic (G) correlation coefficients

Parameters		ETO	FFL	HFL	DPL	PHT	NLP	PWE	NPP	N1S	N2S	SDL	SDW	WSP	WHS
EMG	rp	-0.333	0.350	0.302	0.372	0.099	0.689	0.081	-0.295	-0.222	-0.056	0.024	0.037	-0.053	0.662
	rg	-0.486	0.517	0.441	0.542	0.145	1.004	0.118	-0.429	-0.324	-0.081	0.034	0.054	-0.078	0.965
ETO	rp		-0.122	-0.076	-0.001	-0.019	-0.363	0.068	0.203	0.162	0.034	-0.014	0.038	0.136	0.005
	rg		-0.162	-0.100	-0.001	-0.025	-0.480	0.091	0.268	0.215	0.045	-0.018	0.050	0.181	0.006
FFL	rp			0.060	0.044	0.009	0.094	-0.015	-0.051	-0.047	-0.004	0.002	-0.001	-0.021	0.005
	rg			0.893	0.653	0.134	1.412	-0.221	-0.768	-0.708	-0.055	0.033	-0.016	-0.313	0.077
HFL	rp				0.403	0.126	0.610	-0.178	-0.385	-0.356	-0.014	0.013	-0.007	-0.185	-0.294
	rg				0.686	0.215	1.037	-0.303	-0.655	-0.606	-0.024	0.023	-0.012	-0.314	-0.500
DPL	rp					0.319	1.804	0.630	0.037	0.088	-0.021	0.104	0.081	0.290	1.453
	rg					0.444	2.510	0.877	0.052	0.122	-0.029	0.145	0.113	0.403	2.021
PHT	rp						1.526	0.596	0.113	0.157	-0.018	0.109	0.076	0.295	1.361
	rg						4.352	1.700	0.322	0.447	-0.050	0.312	0.218	0.840	3.880
NLP	rp							0.662	0.206	0.249	-0.001	0.094	0.057	0.367	1.604
	rg							1.063	0.331	0.400	-0.001	0.151	0.092	0.589	2.575
PWE	rp								0.055	0.056	0.000	0.008	0.008	0.055	0.179
	rg								0.076	0.077	0.001	0.011	0.011	0.076	0.249
NPP	rp									0.070	0.003	0.000	0.001	0.040	0.030
	rg									0.104	0.004	0.000	0.001	0.060	0.044
N1S	rp										0.002	0.001	0.001	0.041	0.040
	rg										0.003	0.001	0.001	0.049	0.048
N2S	rp											-0.004	-0.002	0.010	-0.079
	rg											-0.008	-0.004	0.019	-0.146
SDL	rp												0.161	0.422	3.168
	rg												0.235	0.618	4.637
SDW	rp													0.646	3.850
	rg													0.967	5.767
WSP	rp														0.148
	rg														0.212

4. Conclusion

Research carried out to determine the level of variability, the different types of correlation between characters and heritability has shown that there is considerable phenotypic diversity among Bambara groundnut accessions from

Burkina Faso. The significant correlations observed between studies at the level of genotypes and phenotypes offer possibilities of varietal selection because environment do not influence significantly the expression of the characters, mainly those related to yield. In order to improve the productivity of Bambara groundnut, it would be necessary to rely on the significant and positive correlations between the components of the yield and yield because for a good yield improvement program, the mode of inheritance of yield components must be understood. In addition, traits with high heritability coupled with high genetic advance values must be taken into consideration in a varietal improvement program.

Compliance with ethical standards

Acknowledgments

Disclosure of conflict of interest

This work was carried out in collaboration between all the authors. Author DJK collected the data, did the literature search and wrote the manuscript. The author HN carried out the statistical analyses and the correction of the manuscript. The author MNK participated in the set-up of the study and the data collection. Author AO wrote the protocol. The author MO and MS supervised the study. All authors have read and approved the final manuscript.

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