



Evaluation of agromorphological diversity of *Arachis hypogaea* accessions in central Côte d'Ivoire

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ABSTRACT

Peanuts (*Arachis hypogaea* L.) play an important role in West African agricultural systems, where improving yields is a major challenge for food security and producer incomes. With this in mind, a study was conducted to assess the agromorphological variability of twenty-nine accessions from Côte d'Ivoire and Mali and to identify high-performing varieties. The experiment was conducted using a completely randomized block design with three replicates, and nineteen (19) traits related to phenology and yield components were analyzed. Analysis of variance (ANOVA) showed that most traits discriminate between accessions at the 5% threshold, confirming the existence of significant genetic variability within the material studied. The study of diversity organization resulted in the division of accessions into four groups based on flowering time, number of seeds, pod weight, and seed weight. Group I contained accessions with a high number of seeds, while group III contained accessions with a low number of seeds. Group II consisted of late accessions (long flowering time) with a high pod and seed weight. Unlike group II, group IV consisted of early accessions (short flowering time) with low performance (low pod and seed weight). The genetic variability thus identified is a strategic asset for varietal improvement programs, particularly with a view to developing high-performance, resilient varieties adapted to the region's agroecological conditions.

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Keywords: *Arachis hypogaea*, Accessions, Agromorphological Diversity, Côte d'Ivoire.

INTRODUCTION

Agriculture is the main sector on which the survival of the majority of Africa's population, and particularly that of Côte d'Ivoire, depends. It employs over 60% of the working population and contributes over 27% of the country's gross domestic product (Sangaré et al., 2009). As a result, it remains the bedrock of the Ivorian economy, with export crops such as cocoa, coffee, oil palm, rubber and cotton playing a key role. With the implementation of a policy aimed at ensuring food security, agriculture has diversified with the promotion of market garden crops (dry

beans, groundnuts, cowpeas and potatoes). Groundnuts (*Arachis hypogaea*) play a vital role in human nutrition, and could play a major role in the Ivorian economy, especially for producers.

Groundnut (*Arachis hypogaea*) is one of the world's most widely cultivated legumes. With an annual production of some 11.6 million tonnes (around 60% of world production), China and India are the world's leading peanut producers. Africa, on the other hand, accounts for just 25% of global production, with Nigeria, Senegal and Sudan being the main producers (Noba et al., 2014).

Peanuts are cultivated and widely used in the oil industry for their oil-rich kernels. It contains 44 to 56% oil, 22 to 30% protein, potassium, phosphate and magnesium (Aleidi, 2016). They are a plant of choice because they adapt easily to many types of climates. The plant requires few inputs and has a good capacity to restore soil productivity (Bangata et al., 2013; Ama et al., 2022).

In Côte d'Ivoire, groundnut cultivation faces a number of constraints. It is practised by small-scale growers, particularly women in rural areas, using rudimentary methods and with no mastery of cultivation techniques (Koné et al., 2019). In addition to these structural constraints, pests and diseases cause significant yield losses, as do the effects of climate change, marked by irregular rainfall, rising temperatures, and more frequent droughts (Hamasselbe et al., 2011). Furthermore, these growers use “off-the-shelf” planting material contributes to the vulnerability of the crop to these biotic and abiotic stresses. All this could make peanut growing less profitable with low yields (Hamasselbe et al., 2012). It is therefore appropriate, in such circumstances, to remedy this situation by proposing improved groundnut varieties to growers. To meet these challenges, it is essential to adopt a rigorous approach to varietal improvement. This involves first establishing a sufficiently broad genetic base from a reference collection, followed by characterization of germplasm diversity in order to identify the most promising genotypes. Hence the present study, which is part of this approach, aimed to identify high-yielding peanut varieties that are tolerant to abiotic stresses.

This study, which is part of this approach, aims to identify peanut varieties with high yield potential that are more resistant to the main abiotic stresses and thus meet current production constraints.

MATERIALS AND METHODS

Material

The plant material used consisted of 29 groundnut accessions from the genebank collection of the Centre National de Recherche Agronomique (CNRA). Information on

registration codes in the genebank and the origin of accessions is detailed in Table 1.

Experimental site

The trial was conducted at the food crops research station of the Centre National de Recherche Agronomique of Bouaké, located at latitude 7°46'N, longitude 5°06' W and altitude 376 m (Brou et al., 2005).

Experimental design

The trial was set up as a randomized complete block design with three (3) replicates. The elementary plot consisted of 2 rows of seedlings 2 m long with a distance of 0.50 m between rows and 0.20 m between plants. That is 11 bunches per line and 22 bunches per accession.

Characteristics studied

Nineteen (19) variables were analyzed. With the exception of the number of plants at emergence (NoPE), emergence time (DeLe) and flowering time (DeFl), all the other variables were measured on 10 plants. These included plant height (HaPl) measured from the cotyledonary axil to the terminal bud, canopy width (CnPe) measured at the widest point from branch tip to branch tip, pod length (LoGo), pod width (LaGo), fresh pod weight (PoFG), nodule weight (PoNo), biomass (BiMa), number of nodules (NoNo), number of one-seeded pods (NoG1), number of two-seeded pods (NoG2), number of three-seeded pods (NoG3), number of seeds (NoGr), pod weight (PoGo), seed weight (PoGr), weight of 100 seeds (P100) and seed yield (Rdt).

Statistical analysis

The comparative analysis of accessions was carried out using a one-factor analysis of variance. Relationships between variables were studied using the correlation matrix. A principal component analysis (PCA) and the coordinates of the individuals were used to group the accessions using a hierarchical ascending classification (HAC). The groups resulting from the HAC were characterized using discriminant factor analysis (DFA). All these analyses were carried out using STATISTICA 7.1 software.

Table 1: List of *Arachis hypogaea* accessions used in the study of agromorphological diversity.

N°	Accession registration code	Country of Origin
1	ARA01/NIA16	Côte d'Ivoire
2	ARA02/FKE22	Côte d'Ivoire
3	ARA03/ ICR18	ICRISAT/Mali
4	ARA04/ ICR18	ICRISAT/Mali
5	ARA05/ ICR18	ICRISAT/Mali
6	ARA07/ OUA22	Côte d'Ivoire
7	ARA08/ ICR18	ICRISAT/Mali
8	ARA09/ ICR18	ICRISAT/Mali
9	ARA10/ ICR18	ICRISAT/Mali
10	ARA11/ ICR18	ICRISAT/Mali
11	ARA12/ TOU22	Côte d'Ivoire
12	ARA13/ KOR22	Côte d'Ivoire
13	ARA14/ ICR18	ICRISAT/Mali
14	ARA15/ ICR18	ICRISAT/Mali
15	ARA16/ ICR18	ICRISAT/Mali
16	ARA17/ ICR18	ICRISAT/Mali
17	ARA18/ ICR18	ICRISAT/Mali
18	ARA19/ ICR18	ICRISAT/Mali
19	ARA20/ ICR18	ICRISAT/Mali
20	ARA21/ ICR18	ICRISAT/Mali
21	ARA22/ ICR18	ICRISAT/Mali
22	ARA23/ ICR18	ICRISAT/Mali
23	ARA24/ ICR18	ICRISAT/Mali
24	ARA25/ ICR18	ICRISAT/Mali
25	ARA26/ ICR18	ICRISAT/Mali
26	ARA27/ ICR18	ICRISAT/Mali
27	ARA28/ ICR18	ICRISAT/Mali
28	ARA29/ ICR18	ICRISAT/Mali
29	ARA30/ BIAN22	Côte d'Ivoire

RESULTS

Comparative analysis of accessions

With the exception of fresh pod weight, biomass and 100-seed weight, the analysis of variance (Table 2) showed that the accessions were significantly different for all the characters.

Analysis of correlations between traits

The correlation between the different variables studied was estimated using Pearson's r correlation coefficient (Table 3). Only correlations greater than or equal to 0.7 were taken into account. Most of the correlation coefficients were less than 0.7. Only the DeLe - NoPE pair showed a high correlation ($r = 0.73$). In this case, only the number of plants at emergence was considered in the principal component analysis to avoid redundancy.

Organization of variability: Principal Component Analysis (PCA)

Analysis of the factorial weight matrix resulted in the selection of the first two components, which explain 62.33% of the total variability (Table 4). Ten of the 19 descriptors were relevant in explaining the variability within the accessions used. The first component, which explained 37.84% of the variability, was defined by flowering time, plant height, canopy height, number of plants at emergence, number of seeds with three pods, number of seeds per plant and yield. The second component, defined by pod width, pod weight and seed weight, accounted for 24.25% of the total variability.

Structuring the variability of accessions

Hierarchical Ascending Classification (HAC) using the UPGMA method (Unweighted Pair Group Method with arithmetic Average) with truncation at 100 Euclidean distance units highlighted four groups of accessions (Figure 1). These four groups were made up of 4, 6, 11 and 8 accessions respectively. The origin of the accession played little part in the structuring of diversity. Of the ten characters used to distinguish between the four groups, four

(DeFl, PoGo, PoGr, NoGr) proved to be the most discriminating. The distribution of accessions and their characteristics are summarized in Table 5.

Discriminant factor analysis (DFA) was used to derive from all the initial variables a group of variables for discriminating between the groups defined above. Using the λ -Wilk test, the DFA revealed five discriminating descriptors for all the variables (Table 6). These were flowering time (DeFl), pod weight (PoGo), seed weight (PoGr), number of seeds (NoGr) and yield (Rdt). Projection of the variables on the canonical axes 1 and 2 indicates that these two axes have a discriminative power of 97.36%. The discriminant function derived from the variables to classify the units formed in the different groups is presented in Table 7. The first axis, which accounts for 64.55% of the total variability, discriminates against the number of seeds (NoGr). It is positively correlated with this axis. The second axis, which explains 32.81% of the total variability, discriminates between the variables pod weight (PoGo), seed weight (PoGr) and flowering time (DeFl). They are positively correlated with this axis. The relationship of the groups with the axes shows that groups I and III are opposite to axis 1 while groups II and IV are opposite to axis 2 (Figure 3). On the basis of the correlation circle between the variables and factorial axes 1 and 2 (Figure 2), accessions in group I, located in the positive part of axis 1 and 2, were characterized by late flowering. They were also distinguished by high pod and seed weight, high seed number and high yield. Group III, on the other hand, contains accessions with early flowering, low pod and seed weight, low seed number and low yield. Group II, located in the positive part of axis 2 and practically at the center of axis 1, contained late flowering accessions with high pod and seed weights. These accessions were also characterized by an average number of seeds and an average yield. Group IV was made up of early flowering accessions with an average seed number and low pod and seed weight.

Table 2: Mean values of 19 agro-morphological traits measured on 30 accessions of *Arachis hypogaea* and results of comparison tests.

Parameters	Minimum	Maximum	Mean	F	P
NoPE	04.67	20.33	15.30 ± 4.09	3.05	0.064
HaPl (cm)	29.00	56.03	36.91 ± 5.18	4.05	< 0.001
Cnpe (cm)	6.99	27.20	16.21 ± 3.46	7.15	< 0.001
DeLe (j)	4.92	13.33	8.16 ± 1.45	4.93	< 0.001
DeFl (j)	25.47	50.05	32.07 ± 6.79	12.78	< 0.001
LoGo	1.90	26.00	3.28 ± 3.98	126.45	< 0.001
LaGo	0.70	4.63	1.16 ± 0.64	81.15	< 0.001
PoFG	29.47	97.30	61.97 ± 47.74	2.22	0.128
BiMa	8.47	31.63	18.33 ± 4.46	2.42	0.108
PoNo	0.10	19.14	1.07 ± 3.33	163.44	< 0.001
NoNo	12.17	72.13	30.49 ± 14.34	135.60	< 0.001
NoG1	0.00	12.82	4.58 ± 2.74	39.74	< 0.001
NoG2	77.33	103.00	90.10 ± 5.39	4.77	< 0.001
NoG3	0.00	6.00	1.74 ± 1.53	81.39	< 0.001
PoGo	36.00	93.00	59.14 ± 13.03	34.80	< 0.001
PoGr	29.33	65.34	44.38 ± 8.98	20.88	< 0.001
NoGr	0.00	84.06	47.07 ± 14.79	83.69	< 0.001
P100	30.00	67.00	45.33 ± 8.53	2.04	0.149
Rdt	1.67	5.73	3.20 ± 1.01	13.41	< 0.001

NoPE: Number of emerged plants; Hapl: Plant height; CnPe: Canopy; DeLe: Emergence time; DeFl: Flowering delay; LoGo: Pod length; LaGo: Pod width; PoFG: Fresh pod weight; BiMa: Biomass; PoNo: Nodule weight; NoNo: Number of nodules; NoG1: Number of one-seeded pods; NoG2: Number of two-seeded pods; NoG3: Number of three-seeded pods; PoGo: Pod weight; PoGr: Seed weight; NoGr: Number of seeds; P100: Weight of 100 seeds; Rdt: Seed yield.

Table 3: Correlation matrix between 19 variables measured in 29 accessions of *Arachis hypogaea*.

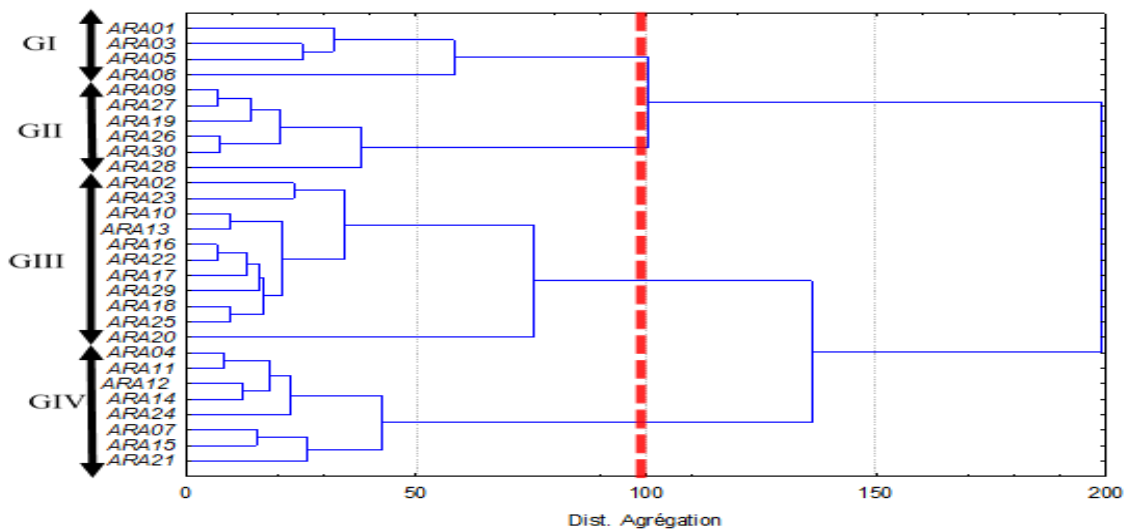
	NoPE	DeFl	HaPl	Cnpe	DeLe	LoGo	LaGo	PoFG	PoNo	BiMa	NoNo	NoG1	NoG2	NoG3	PoGo	PoGr	NoGr	P100	Rdt
NoPE	1,00																		
DeFl	0,34	1,00																	
HaPl	0,23	0,36	1,00																
Cnpe	0,45	0,47	0,56	1,00															
DeLe	-0,73*	-0,58	-0,48	-0,46	1,00														
LoGo	0,18	0,19	-0,01	0,12	0,02	1,00													
LaGo	0,23	0,25	0,09	0,48	0,08	0,25	1,00												
PoFG	0,06	0,04	0,18	0,18	-0,14	0,08	-0,05	1,00											
PoNo	-0,09	-0,09	-0,26	-0,26	0,09	-0,02	-0,05	-0,05	1,00										
BiMa	0,27	0,22	0,17	0,32	-0,14	-0,08	-0,05	0,19	-0,22	1,00									
NoNo	0,37	0,38	-0,20	0,02	-0,17	0,00	-0,02	0,00	0,11	0,35	1,00								
NoG1	0,05	0,06	0,08	0,07	-0,04	-0,22	-0,24	-0,12	-0,08	0,28	0,06	1,00							
NoG2	0,36	0,30	0,15	0,18	-0,46	0,22	0,02	0,13	0,06	-0,16	0,15	-0,26	1,00						
NoG3	-0,18	-0,40	-0,52	-0,42	0,56	-0,06	-0,03	-0,03	-0,04	-0,19	-0,21	0,00	-0,29	1,00					
PoGo	0,10	0,05	-0,32	0,11	0,21	0,08	0,45	-0,19	0,48	0,01	0,17	0,06	0,02	0,15	1,00				
PoGr	0,14	0,09	-0,42	-0,04	0,31	0,11	0,35	-0,12	0,42	-0,07	0,14	0,04	-0,02	0,24	0,69	1,00			
NoGr	-0,25	-0,33	-0,35	-0,14	0,49	0,01	0,15	-0,19	0,20	-0,36	-0,40	-0,04	-0,21	0,48	0,47	0,57	1,00		
P100	0,09	0,07	-0,15	-0,15	0,07	0,35	-0,01	-0,05	0,48	-0,37	-0,12	-0,10	0,22	0,02	0,20	0,22	0,07	1,00	
Rdt	0,37	0,34	0,31	0,47	-0,33	-0,14	0,09	0,33	-0,19	0,32	0,19	0,21	0,15	-0,22	-0,15	-0,14	-0,30	0,07	1,00

The highest correlations are shown in bold ($|r| \geq 0.7$), NoPE: Number of emerged plants; ; DeFl: Flowering delay; Hapl: Plant height; CnPe: Canopy; DeLe: Emergence time; LoGo: Pod length; LaGo: Pod width; PoFG: Fresh pod weight; PoNo: Nodule weight; BiMa: Biomass; NoNo: Number of nodules; NoG1: Number of one-seeded pods; NoG2: Number of two-seeded pods; NoG3: Number of three-seeded pods; PoGo: Pod weight; PoGr: Seed weight; NoGr: Number of seeds; P100: Weight of 100 seeds; Rdt: Seed yield.

Table 4: Eigenvalues and percentage of variation expressed by the first two axes in 29 accessions of *Arachis hypogaea* in Principal Component Analysis.

Principal component	Axe 1	Axe 2
Eigenvalue	3.78	2.43
Total variance (%)	37.84	24.25
Cumulative total variance (%)	37.84	62.09
DeFl	-0.58 *	-0.54
HaPl	-0.71 *	0.01
Cnpe	-0.62 *	-0.44
NoPE	0.76 *	0.19
LoGo	0.01	-0.39
LaGo	0.01	-0.61 *
PoFG	-0.31	0.03
PoNo	0.41	-0.40
BiMa	-0.44	0.01
NoNo	-0.24	-0.29
NoG1	-0.10	0.12
NoG2	-0.32	-0.38
NoG3	0.66 *	0.23
PoGr	0.56	-0.69 *
PoGo	0.54	0.70 *
NoGr	0.73 *	-0.16
P100	0.24	-0.38
Rdt	0.57 *	0.15

* Significant values: variables that contribute most to the formation of the axes. DeFl: Flowering delay; Hapl: Plant height; CnPe: Canopy; NoPE: Number of emerged plants; LoGo: Pod length; LaGo: Pod width; PoFG: Fresh pod weight; PoNo: Nodule weight; BiMa: Biomass; NoNo: Number of nodules; NoG1: Number of one-seeded pods; NoG2: Number of two-seeded pods; NoG3: Number of three-seeded pods; PoGr: Seed weight; PoGo: Pod weight; NoGr: Number of seeds; P100: Weight of 100 seeds; Rdt: Seed yield.



GI: group I (4 accessions), GII: group II (6 accessions), GIII: group III (11 accessions), GIV: group IV (8 accessions)

Figure 1: Hierarchical bottom-up classification (UPGMA) of 29 *Arachis hypogaea* accessions based on Euclidean distances.

Table 5: Average performance of *Arachis hypogaea* groups formed by hierarchical ascending classification.

Variables	CAH Groups				<i>F</i>	<i>P</i>
	GI (N = 4)	GII (N = 6)	GIII (N = 11)	GIV (N = 8)		
NoPE	15.35±2.12 ^a	14.32±0.73 ^a	12.68±0.53 ^a	13.11±1.60 ^a	1.88	0.157
DeFl	25.67±6.31 ^b	49.45±4.53 ^a	43.73±5.65 ^a	28.33±9.48 ^b	22.91	< 0.001
HaPl	33.52±3.22 ^a	36.93±3.59 ^a	38.00±5.63 ^a	37.21±2.20 ^a	1.11	0.362
Cnpe	13.61±2.14 ^a	18.01±3.30 ^a	16.28±1.92 ^a	15.93±4.06 ^a	1.77	0.177
LaGo	1.00±0.01 ^a	1.72±1.33 ^a	1.01±0.03 ^a	0.99±0.01 ^a	2.31	0.100
NoG3	1.16±0.64 ^{a*}	1.37±1.12 ^a	2.18±2.09 ^a	1.69±0.64 ^a	0.57	0.634
PoGo	72.58±13.84 ^a	70.72±9.40 ^a	53.12±7.75 ^b	52.00±9.55 ^b	8.61	< 0.001
PoGr	53.75±9.17 ^a	53.80±5.12 ^a	39.87±5.26 ^b	38.83±3.52 ^b	15.08	< 0.001
NoGr	68.99±5.61 ^a	56.69±4.59 ^b	37.80±13.87 ^c	41.67±4.80 ^c	12.32	< 0.001
Rdt	3.89±0.74 ^a	3.29±0.94 ^{ab}	2.99±0.94 ^b	2.44±0.72 ^b	3.01	0.048

* For each character, values bearing the same letters are statistically equal; N: number of accessions. NoPE: Number of emerged plants; DeFl: Flowering delay; HapI: Plant height; CnPe: Canopy; LaGo: Pod width; NoG3: Number of three-seeded pods; PoGo: Pod weight; ; PoGr: Seed weight; NoGr: Number of seeds; Rdt: Seed yield.

Table 6: Discriminant analysis based on ten morphological characters analysed in 29 accessions of *Arachis hypogaea*.

Variable	Wilks (Lambda)	<i>F</i>	p-value
NoPE	0.815	1.886	0.158
DeFl	0.267	22.919	< 0.001
HaPl	0.882	1.114	0.362
Cnpe	0.824	1.778	0.177
LaGo	0.783	2.315	0.100
NoG3	0.935	0.578	0.635
PoGo	0.492	8.619	< 0.001
PoGr	0.356	15.082	< 0.001
NoGr	0.403	12.330	< 0.001
Rdt	0.734	3.014	0.049

NoPE: Number of emerged plants; ; DeFl: Flowering delay; HapI: Plant height; CnPe: Canopy; LaGo: Pod width; PoNo; NoG3: Number of three-seeded pods; PoGo: Pod weight; PoGr: Seed weight; NoGr: Number of seeds; Rdt: Seed yield.

Table 7: Eigenvalues, percentages of variability explained by the DFA factorial axes and correlation coefficients between variables and axes.

	Axis 1	Axis 2
Eigenvalue	7.636	3.743
Percentage of inertia (%)	65.101	31.915
Cumulative percentage inertia (%)	65.101	97.016
NoPE	0.451	0.060
HaPl	-0.348	-0.033
DeFl	-0.607	0.720
Cnpe	-0.236	0.224
LaGo	0.062	0.403
NoG3	-0.252	-0.059
PoGo	0.546	0.558
PoGr	0.583	0.656
NoGr	0.739	0.384
Rdt	0.372	0.427

NoPE: Number of emerged plants; Hapl: Plant height;; DeFl: Flowering delay; CnPe: Canopy; LaGo: Pod width; NoG3: Number of three-seeded pods; PoGo: Pod weight; PoGr: Seed weight; NoGr: Number of seeds; Rdt: Seed yield.

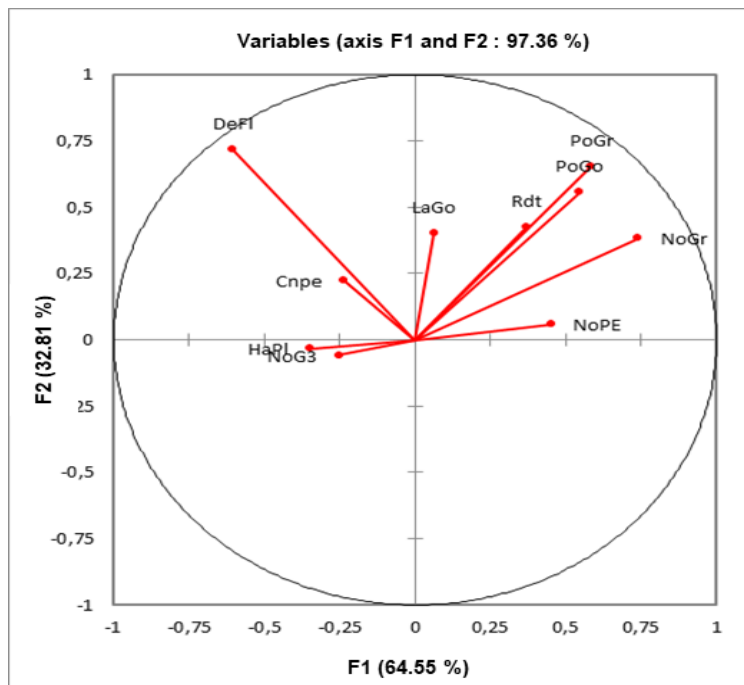


Figure 2: Distribution of variables in the 1-2 plane revealed from DFA for 29 accessions of *Arachis hypogea*.

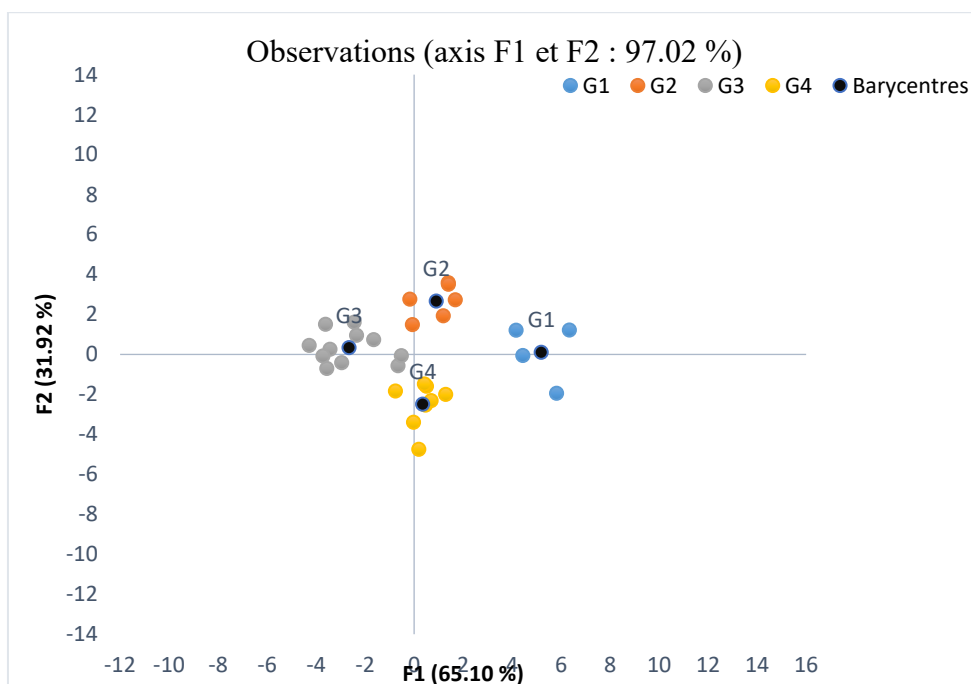


Figure 3: Projection of the groups of *Arachis hypogaea* accessions from the AHC onto planes 1 and 2 of the discriminant factorial analysis.

DISCUSSION

The agromorphological variability of 29 groundnut accessions was analysed using 19 agromorphological descriptors. Analysis of the results showed that 4 of the 19 descriptors revealed variability between accessions. The descriptors linked to phenology and yield were the most discriminating of those studied. These were flowering time (DeFl), pod weight (PoGo), number of seeds (NoGr) and seed weight (PoGr). This predominance of phenological traits and yield components in the structuring of diversity confirms that, in *Arachis hypogaea*, traits directly associated with productivity are generally the main factors of genetic differentiation (Zaman et al., 2011; Banla et al., 2020). These results are in line with those obtained by Montcho et al. (2021) who showed that the most discriminating traits in *Arachis hypogaea* were flowering time, emergence rate, pod weight and seed weight. Desmae et al. (2019) emphasized the importance of flowering time in the agroecological adaptation of peanut genotypes.

Indeed, earliness plays a decisive role, as it determines the length of the crop cycle, helps avoid water stress at the end of the season, and thus contributes to greater yield stability. However, the results showed that there was very little variability in vegetative development. Most of the accessions used in this study came from Mali. This could have resulted in poor discrimination between accessions for these traits. Also, as demonstrated by Bertoli et al. (2019), genetic diversity within cultivated peanuts is generally limited due to their allotetraploid origin.

Hierarchical clustering analysis (HCA) coupled with discriminant factor analysis (DFA) showed that the accessions studied fell into four groups. The grouping was done independently of geographical origins. This similarity could be explained by the fact that the accessions used in these two countries are descended from a common ancestor or come from an exchange of material between the two countries. The results obtained are similar to those of Garba et al. (2015). These authors

evaluated the morphological variability within accessions originating from Niger, Burkina Faso, Spain, Nigeria, Russia, Mali, America and India and concluded that the descriptors used did not allow accessions to be classified according to their origin. Similarly, Banla et al. (2020) emphasized in their study that the difference between populations was more based on their genetic differences than based on their geographical origin

Group I contained late-flowering accessions with a high number of seeds, while group III contained early-flowering accessions with a low number of seeds. Early flowering would allow early maturity and early harvesting, sometimes preventing the influence of environmental factors at the end of the season. Group III with early accessions could be useful in breeding programmes for water stress tolerant varieties. However, in our study, group I varieties, which turned out to be late, had a high number of seeds and a high yield. These results are in line with those obtained by Yol et al. (2018). These accessions should be grown in areas with a longer rainy season as the use of these accessions in areas with a short rainy season could reduce their performance.

Conclusion

The study showed that there is agromorphological diversity between the different accessions evaluated. The analyses carried out made it possible to classify the accessions into four groups. Late accessions with a high number of seeds and good yields could be included in varietal selection programmes.

COMPETING INTERESTS

The authors declare that they have no competing interests.

AUTHORS' CONTRIBUTIONS

This work was carried out in perfect collaboration between all the authors. FLAN developed the protocol, conducted the field and post-harvest agricultural activities, conducted the statistical analyses of the data collected, and drafted the manuscript. DNC contributed to the implementation of the protocol,

statistical analyses of the data collected, helped draft the manuscript, and participated in translating the manuscript into English. PKNK contributed to the statistical analysis of the data, edited the manuscript, and translated the manuscript into English. GAG, LCO and LF corrected the manuscript in French and English.

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