Agronomic and biochemical evaluation of fifteen exotic groundnut parameters (Arachis hypogaea L.) varieties grown in Northern Cameroon

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Abstract

Groundnuts (*Arachis hypogaea* L.) is a major oilseed and legume in semi-arid regions, yet limited information exists on the agronomic and biochemical performance of recently introduced varieties under the environmental conditions of Northern Cameroon. This study evaluated fifteen exotic groundnut genotypes across three agro-ecological sites (Gazawa, Bocklé and Dang) to assess variability in yield components, oil and protein content, total polyphenols and antioxidant activity. Significant differences were observed among varieties for all traits studied. Pod weight was strongly correlated with overall yield (0.97), indicating that seed mass is a key determinant of productivity. Lipid and protein contents showed a strong negative correlation (r = 0.90), suggesting trade-offs in metabolic partitioning between oil and protein biosynthesis. Total polyphenol content was positively associated with antioxidant activity (r = 0.91), highlighting the nutraceutical potential of some varieties. Based on multivariate clustering, genotypes were grouped into high protein, high polyphenol and high lipid types, indicating opportunities for targeted selection depending on end use. These findings provide a valuable baseline for varietal improvement programs aimed at enhancing yield, nutritional quality and environmental adaptation of groundnut in the semi-arid zone.

1. Introduction

Groundnut (*Arachis hypogaea* L.) is one of the world's most important leguminous oilseed crop, cultivated widely across tropical and subtropical regions for its edible seeds, oil and protein-rich meal. It plays a vital role in human nutrition, livestock feed and soil fertility management due to its ability to fix atmospheric nitrogen in association with *Rhizobium* spp. In Sub-Sahara Africa, particularly in Cameroon, groundnut contributes significantly to household food security and rural income, yet productivity remains low compared with global averages (FAO, 2023). This yield gap is largely attributed to the use of low-yielding landraces, limited genetic improvement and poor adaptation of introduced varieties to local agro-ecological conditions.

Groundnut yields and seed quality are influenced by both genetic and environmental factors. Traits such as pod weight, number of pods per plant are primary components determining yield, while seed composition especially oil, protein and phenolic content defines the crop's economic and nutritional value (Asibuo *et al.*, 2008; Noubissié *et al.*, 2012). However, trade-offs often exist between these traits. High oil content is frequently associated with reduced protein concentration due to competition for assimilates during seed development (Liu *et al.*, 2019). Understanding the magnitude and direction of such correlations is essential for designing breeding programs that combine high yield with superior seed quality.

Elsewhere macronutriment composition, biochemical constituents such as phenolics and flavonoids contribute to antioxidant activity, which is linked to health benefits and stress resilience. Recent studies highlight the importance of these metabolites in conferring tolerance to drought, heat and disease

(Tavares *et al.*, 2010). Therefore, integrating biochemical profiling with agronomic evaluation can provide a more comprehensive understanding of varietal performance.

Although several studies have evaluated local or improved groundnut genotypes in Cameroon (Noubissié *et al.*, 2012; Dolinassou *et al.*, 2016), information on recently introduced exotic varieties remains limited. Moreover, the relationships among yield, oil, protein and antioxidant traits under Northern Cameroonian conditions are poorly characterized. The present study was thus conducted to (i) assess the agronomic performance and biochemical composition of fifteen exotic groundnut varieties; (ii) determine correlations among key yield and biochemical parameters and (iii) classify varieties based on their biochemical profiles to identify promising genotypes for further improvement and adaptation in the semi-arid zone of Cameroon.

2. Materials and Methods

2.1. Study area

The experiment was conducted during the 2019 to 2021 cropping seasons across three agro-ecological sites in Northern Cameroun: Far-north (Gazawa), North (Bocklé) and Adamawa (Dang). These locations are representative of Sudanian and Sahelian zone and differ slightly in rainfall, temperature and soil characteristics. Annual rainfall ranges from 800 to 1 100mm, with average daytime temperatures between 27^{o}C and 34^{o}C. The soils are predominantly sandy loams with moderate organic matter content and slightly acid pH (5.8–6.4). The choice of site aimed to capture environmental variability relevant to peanut cultivation in the region.

2.2. Plant material

Fifteen exotic groundnut (*Arachis hypogaea* L.) varieties were evaluated (Table 1). These genotypes were introduced from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in Niger and selected for their reported variability in yield, oil content and disease tolerance. They were divided into two main groups:

- the Virginia group, which is creeping, has a longer vegetative cycle (120 to 150 days) and seeds that do not germinate prematurely;
- the Valencia and Spanish group, which is erect and has a shorter vegetative cycle (80 to 110 days).

Table 1
Characteristics of the 15 varieties of *Arachis hypogaea* selected for experimentation

Number	Accession	Alterid	Origin/Country	Growth babit	Branching	Vegetative Cycle (days)
1	GGP 687	C5	India	Erect/crawl	Alternate	101
2	GGP 1147	RCM439	Bolivia	Erect/crawl	Alternate	80
3	GGP 1360	JH24	India	Erect	Alternate	92
4	GGP 4964	U12-7-1	Brazil	Erect	Sequential	79
5	GGP 1365	EC2164	Indonesia	Erect	Alternate	90
6	GGP 1466	U 4-4-32	Congo	Erect	Irregular	102
7	GGP 3317	58–619	Argentina	Erect	Alternate	110
8	GGP 692	C29	Tanzania	Erect/crawl	Alternate	120
9	GGP 3743	AP80-43	Madagascar	Erect/crawl	Alternate	100
10	GGP 699	C75	India	Erect/crawl	Alternate	120
11	GGP 1454	R4-A	India	Erect	Sequential	90
12	GGP 1397	EC106965	USA	Erect	Sequential	90
13	GGP 1346	US17	Argentina	Erect	Alternate	91
14	GGP 927	55–437	Argentina	Erect	Sequential	85
15	GGP 434	SP2B	Brazil	Erect	Sequential	110

2.3. Experimental design and crop management

The experimental design was a Randomized Complete Block Design (RCBD) with three replications at each site. Each plot measured 3m × 2m ($6m^2$) and consisted of four rows, spaced 50 cm apart, with a plant spacing of 20 cm within rows.

The plot was cleaned, ploughed and the ridges were formed, the seeds were removed from their shells, and then the seeds suitable for sowing were selected. No chemical or organic treatments were applied to the plot.

The soils are clayey-sandy in the Far North, clay-loamy in the North region, and clay-siliceous in Adamawa. The climate is of the Sudano-Sahelian tropical type.

2.4. Agronomic and biochemical parameters measured

- *Agronomic parameters*:

- Number of pods per plant and number of seeds per plant.

These were determined on a sample of teen plants per variety and per repetition, then averaged for each variety according to the method described by Abdoul (2003).

NPP = ($\sum$ Pods on sampled plants)/n NSP= ($\sum$ Seeds on sampled plants)/n

NPP: Number of pods per plant NSP = Number of seeds per plant

n: number of plants sampled (n = 10)

- Weight of 100 pods

In each replicate, 100 pods were collected for each variety and weighed with an electronic balance (sensitivity: 0.01g).

- Pod yield in kilograms per hectare

The estimated pod yield was calculated based on a planting density of 90 000 plants/ha, using the formula of Mothilal *et al*. (2010):

Pod yield (kg/ha) = [(Pod weight × Number of pods / 10 000)] × 90 000

- *Biochemical parameters*

Biochemical analyses were performed on seeds that had been previously ground using a food processor. For this purpose, 10g of seeds from each variety were ground.

- Protein content (%)

The protein content was determined using the Kjeldahl method (AFNOR, 1981) for mineralization and the method of Devani *et al*. (1989) for nitrogen determination. The crude protein content was obtained by multiplying nitrogen content by the conventional factor of 6.25.

Protein (%) = Nitrogen (%) × 6.25

- Oil content : Soxhlet extraction (%)

The Franz Von Soxhlet method is a reference method used to determine the fat content in dehydrated solid foods. It is a gravimetric method, with the sample being weighed before extraction and the fat content at the end of extraction.

Oil content (%) = (Mass of extracted fat (g)) / (Mass of sample (g)) × 100

- Total polyphenol content

Polyphenols were determined by spectrophotometry, following the protocol applied by Goli *et al.* (2005). The calibration curve was performed using gallic acid at different concentrations (0-250µg/ml), under the same conditions and following the same dosage steps. The results were thus expressed in mg gallic acid equivalent per 100g dry matter (mg GAE/100gDM).

- Antioxidant activity (%)

Evaluated by the DPPH method (Meda *et al.* 2005). The results were expressed as a percentage (%).

AA (%) = ((Abs C – Abs E) / Abs C) × 100

AA (%) = Percentage reduction in DPPH

Abs C = Absorbance of the control

Abs E = Absorbance of the sample

All analyses were conducted in triplicate to ensure accuracy

2.5. Statistical analysis

Data were analyzed by ANOVA using STATGRAPHICS version 5.0. Means separation was performed using the Less Significant Difference (LSD) test at $p \leq 0.05$. The Pearson correlation coefficient (r) was used to assess relationships between parameters. The formula used is as follows:

$r = \Sigma [(Xi - Xm) \times (Yi - Ym)] / [\Sigma (Xi - Xm) 2 \times \Sigma (Yi - Ym) 2]^{1/2}$

r = Correlation coefficient ($-1 \leq r \leq 1$)

Xi, Yi = Values of variables X and Y for variety i

$\overline{\varvec{X}}, \overline{\varvec{Y}}$: Means of Xi and Yi for all varieties studied

Significance thresholds: $p < 0.05$ (*) and $p < 0.01$ (**).

The XLSTAT software was also used for correlations and Hierarchical Ascending Classification (HAC) were performed to classify genotypes based on their yield and biochemical profiles.

3. Results

3.1. Agronomic parameters

- Number of pods per plant

The mean number of pods per plant ranged from 26.50 to 105.50 among the 15 varieties studied (Table 2). Varieties 55–437 and U12-7-1 recorded the highest values (105.50 and 87.50 pods/plant, respectively). Conversely, the lowest values (26.50 and 35.50) were recorded in genotypes AP80-43 and U4-4-32, followed by variety C75 with 39.50 pods/plant.

- Number of seeds per plant

The number of seeds per plant varies between 42.00 and 130.50. The best performances were obtained in varieties 55–437, 58–619, C5, R4-A and US17. In contrast, U12-7-1 and AP80-43 had the lowest averages.

- Weight of 100 pods

The weight of 100 pods reveals that varieties 58–619 and AP80-43 stand out with high average weights. In contrast, varieties EC106965 and C5 have the lowest weights (42.57 g and 43.52 g). The other genotypes, notably JH24 and US17, have values that are close to the overall average (Table 2).

- Pod yield in kg/ha

Pod yield varied significantly among varieties. 58–619, AP80-43 and C75 ranked highest with 4 767, 4 541 and 4 064 kg/ha respectively (Table 2). Intermediate yields were recorded in R4-A (3 521 kg/ha), SP2B (3 462 kg/ha), C29 (3 386 kg/ha), JH24 (3 099kg/ha) and US17 (3 077 kg/ha). The lowest yields were observed in C5 (1 958 kg/ha) and EC106965 (1 916 kg/ha).

Table 2
Variability of agronomic parameters of 15 exotic varieties of *Arachis hypogaea* in Northern Cameroon

Parameters / Genotypes	Number of pods per plant	Number of seeds per plant	Weight of 100 pods (g)	Pod yield in kg/ha
C5	42.00 ± 2,82b	96.00 ± 7.31e	43.52 ± 0.38a	1 958 ± 43a
RCM439	45.00 ± 5,65bc	67.50 ± 9.89cd	60.54 ± 15.63b	2 725 ± 138b
JH24	52.00 ± 2,82cd	76.00 ± 36.76de	68.87 ± 3.90bcd	3 099 ± 234bcd
U12-7-1	87.50 ± 21,21f	42.00 ± 14.14a	61.29 ± 7.33b	2 758 ± 240b
EC21164	53.00 ± 22,62c	76.00 ± 4.42de	63.97 ± 5.13bc	2 879 ± 308bc
U4-4-32	35.50 ± 11,31ab	50.50 ± 11.20abc	64.17 ± 13.17bc	2 888 ± 290bc
58–619	69.50 ± 7,07d	113.00 ± 31.11g	105.93 ± 20.32fg	4 767 ± 219g
C29	47.50 ± 12,72bc	73.00 ± 4.41cd	75.25 ± 13.80bcd	3 386 ± 228cde
AP80-43	26.50 ± 1,41a	48.00 ± 9.50a	116.40 ± 11.96g	4 541 ± 227g
C75	39.50 ± 7,07b	68.00 ± 5.43cde	90.32 ± 4.79ef	4 064 ± 287f
R4-A	68.50 ± 1,41d	95.00 ± 12.62f	78.24 ± 10.43de	3 521 ± 326e
EC106965	50.00 ± 5,67c	64.50 ± 8.38bc	42.57 ± 2.37a	1 916 ± 142a
US17	62.50 ± 12,72d	93.00 ± 8.48f	68.38 ± 12.20bcd	3 077 ± 472bcd
55–437	105.50 ± 25,45g	130.50 ± 8.38h	63.63 ± 12.75bc	2 863 ± 125bc
SP2B	42.50 ± 4,24bc	61.50 ± 9.89b	76.94 ± 5.28cde	3 462 ± 317de
Means	55.13 ± 9,61	76.96 ± 13.47	72.00 ± 13.30	3 194 ± 565
CV (%)	17.43	17.50	18.47	13.55

NPP: Number of pods per plant; NSP: Number of seeds per plant; W100P: Weight of 100 pods; PY: Pod yield in kilograms per hectare; %L: Lipid content; %P: Protein content; PPT: Total polyphenol content; AOA: Antioxidant activity; CV: Coefficient of variation.

3.2. Biochemical parameters

- Protein content

Analysis of the protein content of exotic peanut varieties grown in the Northern Zone reveals significant variability (Table 3). The highest values were recorded in US17 (28.73%) and RCM439 (27.66%). These values suggest interesting potential for selection programs aimed at protein enrichment. However, the SP2B and 58–619 varieties have lower protein contents than the previous ones, with values of 19.80% and 19.40%, indicating lower nutritional quality in terms of protein. The US17 variety produced the highest protein level throughout the study area (28.73%).

- Lipid content

Lipid levels ranged from 37.76% to 55.33%. Varieties 58–619 and U4-4-32 showed the highest contents (55.33% and 51.53%), suggesting particular interest for industrial use geared towards oil production. In contrast, the RCM439 and US17 varieties have lower values, ranging from 37.76% to 40.10%, reflecting a more moderate lipid composition.

- Total polyphenol content

The results of the analysis of variance show a statistically significant difference in total polyphenol content between varieties ($p < 0.05$). Genotypes 58–619 and R4-A stand out with high contents, ranging from 1.73 to 1.67 mg GAE/100g, reflecting good potential in antioxidant compounds. The EC21164 and C75 varieties followed with an average content of 1.57mgGAE/100g. The ten other varieties had concentrations ranging from 1.51mgGAE/100g (RCM439) to 1.16mgGAE/100g (SP2B), reflecting notable biochemical diversity.

- Antioxidant activity

The evaluation of the antioxidant activity of the seeds, measured by the DPPH radical scavenging method, highly significant differences between genotypes ($p < 0.01$). Variety 58–619 has the highest antioxidant activity, reaching 79.33%, which indicates high functional potential. Varieties EC21164 and R4-A follow closely behind, with levels of 77.76% and 76.73% respectively. In contrast, the SP2B and 55–437 varieties had the lowest capacities, ranging from 56.33% to 55.16% (Table 3). These results highlight the potential of certain genotypes for nutritional or nutraceutical applications related to their antioxidant properties.

Table 3
Variability of biochemical parameters of 15 exotic varieties of *Arachis hypogaea* in northern Cameroon

Parameters Genotypes	Protein content	Lipid content	Total polyphenol content	Antioxidant activity in seeds
C5	26.26 ± 1,05hg	41.10 ± 0,95bc	1.41 ± 0.11bcd	73.16 ± 1,15e
RCM439	27.66 ± 2,23g	37.76 ± 1,15a	1.51 ± 0.07cd	71.83 ± 0,83e
JH24	25.83 ± 0,23f	41.36 ± 0,66bcd	1.47 ± 0.09cd	66.16 ± 0,58d
U12-7-1	25.03 ± 1,05efg	46.00 ± 1,78ef	1.37 ± 0.11bcd	62.30 ± 0,36c
EC21164	22.93 ± 0,61cde	44.26 ± 1,35de	1.57 ± 0.12de	77.76 ± 0,72f
U4-4-32	20.06 ± 1,20ab	51.53 ± 2,40g	1.33 ± 0.06ab	61.03 ± 0,63d
58–619	19.40 ± 0,70a	55.33 ± 2,30h	1.73 ± 0.12e	79.33 ± 0,70f
C29	24.06 ± 1,20def	43.53 ± 1,30cde	1.38 ± 0.06bcd	71.00 ± 0,34e
AP80-43	20.86 ± 1,05abc	48.76 ± 1,56fg	1.33 ± 0.05ab	59.16 ± 0,32b
C75	24.46 ± 1,15ef	40.83 ± 0,55ab	1.57 ± 0.11de	70.96 ± 0,41de
R4-A	23.53 ± 2,30def	44.06 ± 0,37cde	1.67 ± 0.12e	76.73 ± 0,51f
EC106965	23.83 ± 2,05def	42.03 ± 0,40bcd	1.36 ± 0.04abc	65.23 ± 0,73c
US17	28.73 ± 1,23g	40.10 ± 1,36ab	1.39 ± 0.06bcd	59.60 ± 0,34b
55–437	21.90 ± 0,65bcd	46.00 ± 1,17ef	1.26 ± 0.10ab	55.16 ± 0,51a
SP2B	19.80 ± 0,75ab	50.60 ± 1,20g	1.16 ± 0.07a	56.33 ± 0,64a
Means	23.62 ± 2,18	44.88 ± 3,23	1.43 ± 0.17	67.05 ± 6,58
CV(%)	9.23	7.20	11.89	9.81

NPP: Number of pods per plant; NSP: Number of seeds per plant; W100P: Weight of 100 pods; PY: Pod yield in kilograms per hectare; %L: Lipid content; %P: Protein content; PPT: Total polyphenol content; AOA: Antioxidant activity; CV: Coefficient of variation.

3.3 Correlations between yield and biochemical parameters

The weight of 100 pods (W100P) was strongly and positively correlated with yield (PY) (r = 0.97); total polyphenol content (PPT) and antioxidant activity (AOA) with r = 0.91; and the number of pods (NPP) and the number of seeds (NSP) with r = 0.77. The weight of 100 pods (W100P) was positively and moderately correlated with the lipid content (%L) (r = 0.50) and negatively correlated with protein content (%P) (r=-0.49) (Table 4).

Similarly, the Pod yield per hectare was positively and moderately related to the total polyphenol content (PPT): r = 0.30, positively correlated with the antioxidant activity (AOA) of peanut seeds. Lipid content (%L) was strongly and negatively correlated with the protein content (%P) (r = 0.90). It was also negatively correlated with polyphenol content and antioxidant activity.

Table 4
Correlation matrix between agronomic and biochemical parameters

Variables	NPP	NSP	W100P	PY	%L	%P	PPT	AOA
NPP	1							
NSP	0.77*	1						
W100P	-0.34	-0.24ns	1					
PY	-0.29	-0.18	0.97**	1				
%L	-0.09	-0.11	0.50	0.40	1			
%P	0.11	0.13	-0.49	-0.43	-0.90**	1		
PPT	-0.06	0.08	0.29	0.30	-0.13	0.18ns	1	
AOA	-0.20	0.02	0.21	0.21	-0.19	0.19	0.91**	1

NPP: Number of pods per plant; NSP: Number of seeds per plant; W100P: Weight of 100 pods; PY: Pod yield; %L: Lipid content; %P: Protein content; PPT: Total polyphenol content; AOA: Antioxidant activity; CV: Coefficient of variation.

4. Discussion

The present study revealed significant variability among the 15-exotic peanut (*Arachis hypogaea* L.) varieties grown in Northern Cameroun, particularly in pod yield, seed weight and biochemical quality traits. The strong positive correlation observed between pod weight and yield (r = 0.97) confirms that seed mass is a major determinant of productivity, consistent with earlier results by Dolinassou *et al*. (2016) and recent multi-environment analyses by Wang *et al*. (2023), who demonstrated that kernel size and weight remain the most heritable yield-related traits across diverse agro-ecological zones. Similarly, new genome wide association studies (GWAS) have identified key loci controlling pod weight and yield stability, notably on chromosomes A05 and B03 (Wang *et al*., 2024), supporting the genetic basic of these agronomic correlations.

The variability in seed protein and lipid contents among varieties aligns with previous observations from Ghana (Asibuo *et al*., 2008) and Cameroon (Noubissié *et al*., 2012). while recent genomic studies have demonstrated that oil and protein biosynthesis are inversely regulated at the molecular level (Wang *et al*., 2023; Liu *et al*., 2019). This trade-off was also evident in our study, where lipid content was negatively correlated with protein content (0.90). Recent pangenomic analyses involving 269 accessions have shown that structural variants within the *Aharf 2–2* gene regulate seed size and oil accumulation (Kunkun *et al*., 2025), providing a molecular explanation for these biochemical contrasts observed in local varieties.

The lipid content range (37.7–55.3%) obtained in this study is consistent with findings from recent evaluations in West Africa and Asia, confirming the adaptability of high oil genotypes to semi-arid conditions (Swathi *et al*.,2023). Moreover, new high protein lines developed in China between 2023 and 2025 (Li *et al*., 2025) achieved protein contents exceeding 30%, suggesting that integrating molecular makers for both traits may overcome the classical negative correlation between oil and protein concentrations.

Regarding antioxidant activity and total phenol content, our results (up to 79.33% DPPH activity and 1.73 mg GAE/100g) indicate high nutraceutical potential. This agrees with recent biochemical studies showing that phenol compounds in peanuts especially resveratrol, proanthocyanidins and flavonoids are key determinants of antioxidant defense under stress (Tavares *et al*., 2010; Devi *et al*., 2019). In 2024, transcriptomic analyses of *A. hypogaea* under *Ralstonia solanacearum* infection revealed upregulation of genes related to phenylpropanoid and flavonoid pathways (Wang *et al*., 2024), corroborating the association we found between polyphenols and antioxidant activity (r = 0.91). These results suggest that biochemical traits could serve as indicators of both nutritional value and stress tolerance.

Recent progress in peanut breeding further reinforces these findings. Quantitative trait locus (QTL) mapping and GWAS have identified genomic regions linked to disease resistance, including *PSWDR-1* for Tomato Spotted Wilt Virus (Dongliang *et al*., 2025) and several loci conferring resistance to stem rot (Veerendrakumar *et al*, 2025). These discoveries support marker assisted selection for high-yield and high-quality genotypes. Furthermore, the application of tissue culture free genome editing approaches such as CRISPR is accelerating improvement of traits like oil composition, drought tolerance and allergen reduction (Alam, 2025).

The strong phenotypic associations found in this study may reflect coordinated metabolic networks regulating lipid and protein biosynthesis (Wang *et al*., 2019). Environmental stresses, particularly temperature and water deficit, are also know to influence these processes (Zhao *et al.*, 2011). Integrating such physiological and molecular understanding into local breeding programs could enhance the development of peanut cultivars adapted to the semi-arid zones of Northern Cameroon.

Grouping of varieties into three biochemical clusters (protein, polyphenol, lipid) is consistent with current global strategies for peanut value-chain diversification (Li *et al*, 2025). Similar approaches combining rhizobial inoculation and mycorrhizal symbiosis have been reported to improve both yield and nutritional composition under West and central African conditions (Igiehon *et al.*, 2021; Mpongwana *et al.*, 2023; Ajayi *et al.*, 2024).

Overall, the integration of agronomic and biochemical traits in this study offers a comprehensive framework for the genetic improvement of *Arachis hypogaea*. The correlations observed mirror recent global findings and confirm that the concurrent enhancement of yield, oil content and antioxidant potential is feasible through combined molecular breeding and agronomic practices.

5. Grouping of varieties

With a view to improving agro-nutritional qualities, the quality of the harvested product and the availability of varieties for peanut production in semi-arid areas, the adoption of relatively more plastic and more suitable varieties that require less intensive technical inputs. In addition, genetic variability is the basic condition for crop improvement, as it provides a wider germplasm for varietal selection. Confectionery and oilseed varieties could be distinguished from food varieties in order to enhance the peanut sector both nutritionally and commercially in this Northern Zone of Cameroon.

The Ascending Hierarchical Classification (AHC) (Fig. 1) allowed the fifteen varieties studied to be classified into three classes:

Class 1: Varieties with protein contents between 20 and 30% are considered to have a high protein content, a finding also reported by Pinstrup Andersen *et al*. (1999) for peanuts. Varieties C5, U12-7-1, EC106965, US17, and 55–437 have the highest protein contents in this study. They can be used as "*snack peanuts*" and as part of a food supplement for infants, which would help combat severe malnutrition among children in the North Cameroon region (Brouwer *et al.*, 2004).

Class 2: The varieties RCM439, JH24, EC21164, C29 and C75 are characterized by an average protein content, high polyphenol content and high antioxidant activity (Table 3). These varieties can be recommended for confectionery and could help reduce the risk of cardiovascular disease and certain cancers (Mukuddem-Petersen *et al.*, 2005). The high polyphenol content, which is positively correlated with pods yield in kg/ha, suggests that the varieties have potential in terms of both polyphenol content and pods yield in kg/ha and could be selected for use as "*snack peanuts"*. The Virginia type is the most recommended in this case, and the C29 variety would be the most readily available in the North Cameroon region for use as snack peanuts.

Class 3: The varieties U4-4-32, 58–619, AP80-43, R4-A and SP2B are characterized by a pod yield in kg/ha and a high lipid content, a polyphenol content and average antioxidant activity. These varieties have agronomic and biochemical potential that could be part of an extension program in northern Cameroon as oilseed peanuts. In this class, varieties 58–619 and AP80-43 are more suitable for oil production (Table 3).

Conclusion

The study shows that there is significant variability among the 15 exotic peanut varieties grown in northern Cameroon. The weight of 100 pods (W100P) is strongly and positively correlated with yield (PY); Pod yield is positively correlated with lipid content, total polyphenol content and antioxidant activity, but negatively correlated with protein content. The number of pods per plants (NPP) and the number of seeds per plants (NSP) show a very high positive correlation. The identification of stable correlations between agronomic and biochemical traits offers an opportunity for breeders to combine yield and nutritional quality in the same breeding program. However, certain unfavorable correlations, such as that between yield and protein content, require compromises or the use of marker-assisted selection techniques to dissociate linked genetic traits. These results also pave the way for varietal selection that integrates both agronomic performance and biochemical quality in response to the nutritional and economic challenges of the region. Further studies, particularly in functional genomics and multi-location trials, will be necessary to validate the stability of these correlations in different agroecological environments.

Declarations

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Authors’ contributions

Conceptualization: D. Désiré, Methodology: D. Désiré and J-B Tchiagam Noubissie. Formal Analysis: D. Désiré, O. H. Zéphirin and N. M. Antoine, writing original draft: D. Désiré, Writing-review and editing: D. Dounia, A. A. Said, K. Maygong, O. H. Zéphirin, N. M. Antoine and J-B Tchiagam Noubissie, Acquisition: D. Désiré and J-B Tchiagam Noubissie, Supervision: J-B Tchiagam Noubissie. All authors read and approved the final manuscript.

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Data Availability Statement

The datasets generated and/or analysed during the current study are available from the corresponding author on reasonable request.

Competing Interest Declaration

The authors declare that there are no competing interests.

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Figures

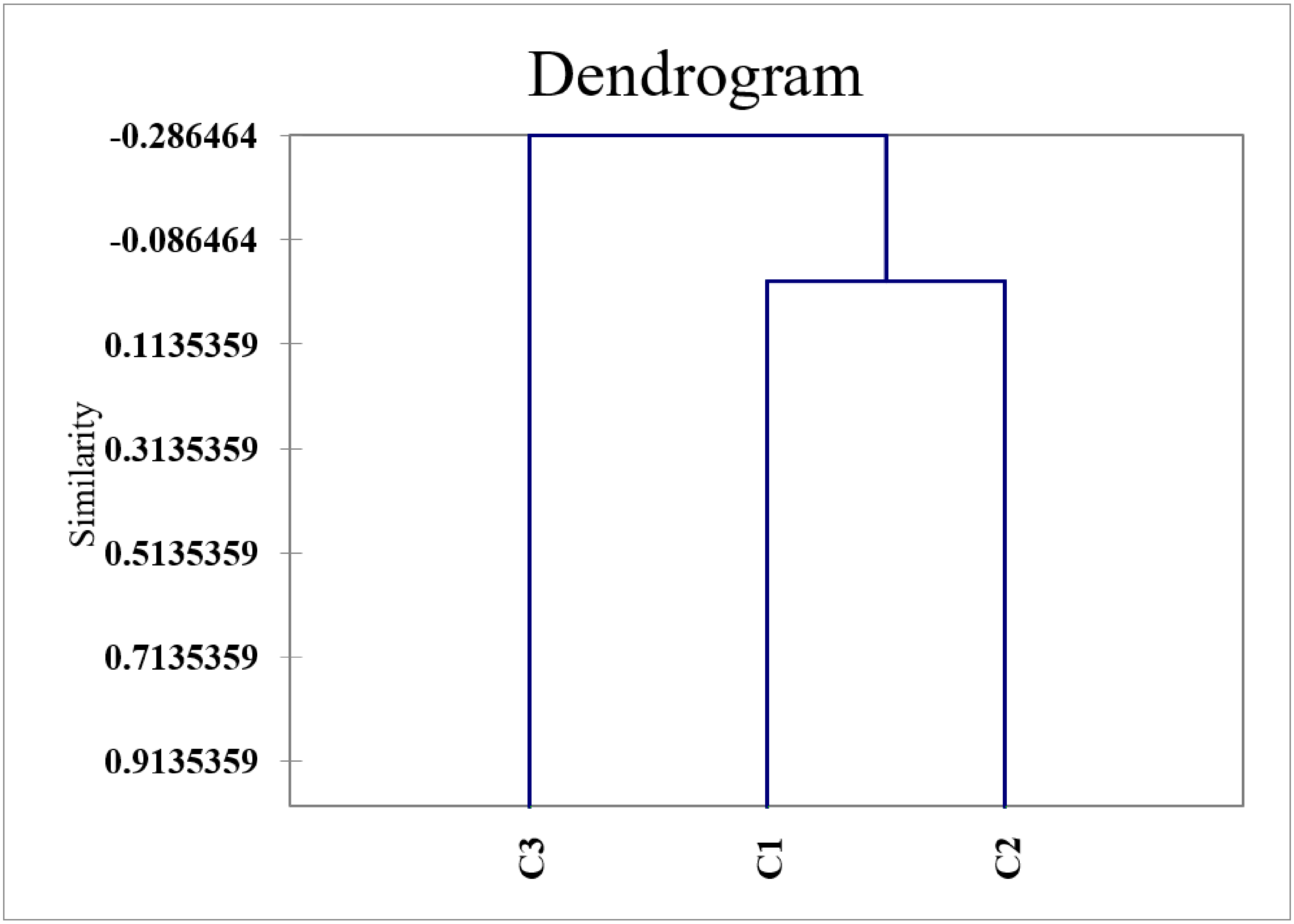

Figure 1

Dendrogram showing similarity between phenotypic class