Research Article

Assessment of Morphological Variation of Peanut (*Arachis hypogaea L.*) in Ghana

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Abstract

Genetic diversity in crops is critical for advanced crop improvement as it provides alternatives for breeders to develop improved cultivars. Traditionally, morphological traits are used to evaluate genetic divergence and classify existing germplasm. Morphological characterization relies on plants possessing different phenotypic traits to identify the individual. Information on the diversity of peanut grown in Ghana is limited. This study was conducted to determine variation in peanut cultivars in Ghana through morphological characterization. Ninety-five accessions of peanut were collected from three sources across five administrative regions of the country that included farmers, open markets, and research institutes. Morphological characterization comprised 31 characters including 11 quantitative and 20 qualitative traits. Seventy-five percent of the accessions belonged to the fastigiata subspecies. The study revealed through cluster analysis that the accessions were only 30% diverse. Principal Component Analysis of the traits showed that yield attributing traits were the main factor that influences dispersion and superior accessions. These traits included seed length, growth habit, pod length, pod width, plant width, and main stem height. This study demonstrates that phenotypic diversity of peanut cultivars in Ghana is limited.

Introduction

Peanut *(Arachis hypogaea L.)* is an annual legume crop native to the South America where most of the *Arachis* species exist [1]. On the basis of differences in branching pattern and distribution of reproductive axes, peanut is classified under two major sub-species; *hypogaea* and *fastigiata* [2,3]. However, commercially grown peanut fall under four main groups; virginia (*hypogaea*), runner (*hypogaea*), Valencia (*fastigiata*), and Spanish (*vulgaris*) [4]. Peanut is a major food and cash crop playing a significant role in food security and financial income in Ghana. According to Owusu-Adjei et al. [5], peanut is the most widely sold crop in all five Northern regions of the Ghana. This crop is ranked seventh in total production and fifth in area planted in the country [6] making it the largest cereal legume cultivated. Peanut production is highly concentrated in the Northern region of the country and in parts of the Bono East and Ashanti Regions.

The informal system plays a crucial role in the supply of peanut seed to farmers in Ghana and is estimated to supply more than half of peanut seed demand [5,7]. It is not uncommon for farmers to replace their own saved seeds with seeds of the same cultivar from a different source over a period of years. Generally, their initial preferred source of seed replacement is often from a relative, neighbor, or the local market. Farmers may not exercise choice of seed supply if there is no information about differences between cultivars [8]. Therefore, the need to determine the level of similarity or diversity that exists between peanut cultivars from different seed sources (e.g., farmer-saved, local markets, and research institutions). This information is critical for developing strategies to ensure that farmers have access to seeds that more effectively meets their needs.

According to Govindaraj et al. [9], diversity in plant genetic resources offers plant breeders the chance to develop new and improved cultivars that meet both farmer-preferred traits and traits preferred by the breeding and genetics community. Traditionally, morphological traits were used to evaluate genetic divergence and classify existing germplasm materials [10]. Neya et al. [11] indicated that morphological characterization allows identification of varieties or accessions from a collection and contributes to increased understanding of genetic diversity. Also, assessment of genetic diversity using morphological traits allows for determining variability in the presence of differences in environmental conditions which cannot be disregarded from the genotypic variation [9]. Identification and classification of peanut cultivars available to farmers are important in determining the variation of peanut varieties grown by farmers. Additionally, it is essential for farmers as information on varietal attributes is key to their adoption and farm management decisions. According to Van Etten et al. [8], information is an important part of seed delivery as farmers may not exert choice from the different options of cultivars available if information about differences between varieties is not available or is incomplete.

Characterization is the determination of highly heritable traits ranging from morphological or agronomical features to seed proteins or molecular markers. Morphological characterization relies on plants possessing different phenotypic traits to identify the individual. Peanut cultivars have been characterized using morphological traits [12,13]. However, information on the diversity of peanut grown in Ghana is limited. Frimpong [14] reported considerable genetic variability based on morphological traits among twenty-three peanut cultivars collected from four ecological zones in Ghana. The objective of our research was to determine natural variations that exists in peanut cultivars in Ghana through morphological characterization.

Materials and Method

The study was conducted in 2019 from December through April at the Crops Research Institute (CRI) at Fumesua in Kumasi of the Ashanti Region of Ghana in the transitional forest zone with an elevation of approximately 250 m above sea level. Soil was a dark brown, moderately drained sandy loam [15].

Ninety-five accessions of peanut were collected from three sources across five administrative regions of the country including:
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a) farmers
b) local open markets
c) research institutes

Each accession was planted on a 4-m long row on a ridge at a rate of one seed per hill and spaced at 75cm between rows and 30 cm within rows. Peanut was irrigated to maintain optimum growth. Weeds were controlled by hand.

For all 95 accessions, five plants were randomly selected to characterize morphological features including 11 quantitative and 20 qualitative traits. Quantitative traits included height of main stems, plant width, leaflet length, leaflet width, pod length, pod width, seed length, seed width, and seed weight. Qualitative traits recorded included growth habit, branching pattern, stem pigmentation, stem surface, type of inflorescence, standard petal color, color of standard petal markings, peg pigmentation, leaf color, leaflet shape, leaflet surface, leaflet margin, leaflet tip, pod beak, pod constriction, pod reticulation, seed color, primary seed color, and secondary seed color. These data were recorded based on a published peanut descriptor [16].

The experimental design was a randomized complete block with each accession replicated four times. Data for quantitative morphological traits were subjected to analysis of variance. Means were separated using Fisher's Protected LSD test at p < 0.05. Minimum and maximum values for all quantitative morphological were calculated. All qualitative morphological plant data collected were subjected to basic descriptive statistics where frequencies and percentages were computed. Morphological plant data were also subjected to cluster analysis and a dendrogram was generated using the Unweighted Pair-Group Method with Arithmetic Average (UPGMA) based on the Euclidean Distance Matrix [17]. Both qualitative and quantitative variables were subjected to cluster analysis. Quantitative data were standardized to ensure uniformity. Principal Component Analysis (PCA) was performed to determine the morphological traits that contribute to the total variation among the accessions. Statistical analysis was performed using GenStat (edition 12) and R-statistical package (version 4.0.3).

Results and Discussion

Analysis of variance showed significant differences (p < 0.05) among the 95 accessions for all the quantitative traits (Table 1). The variation for primary branches was 2 to 13 while that of secondary branches was 0 to 38 (Table 1). Main stem height varied from 11 to 38 cm. There was considerable variation in plant width with some accessions with a width as low as 34 cm. Mean width was 58 cm. Also, days to 50% flowering varied from 28 to 42 days. The highest seed length recorded was 21 mm with a mean of 13 mm. The average seed width was 8 mm while some accessions had the highest seed width of 10mm.

Table 1: Minimum and maximum value, standard error, coefficient of variation, F statistic, and P > F for 95 peanut accessions.

Traits	Minimum	Maximum	Mean	Standard Error	Coefficient of Variation (%)	F-ratio	P > F
Primary branches	2	13	4.8	1.07	22.3	5.2	<0.001
Secondary branches	4	61	26.1	2.29	8.8	71.3	<0.001
Tertiary branches	0	38	6.5	2.14	32.7	32.3	<0.001
Main stem height (cm)	11.4	38	25.1	3.6	14.5	3.3	<0.001
Plant width (cm)	34.4	84.4	58.3	7.9	13.7	1.9	<0.001
Leaflet length (mm)	37	86	65	4.5	6.9	5.2	<0.001
Leaflet width (mm)	22	39	32	1.9	5.8	6.6	<0.001
Pod length (mm)	21	45	29	1.4	5	20.2	<0.001
Pod Width (mm)	8	14	11	1	5	5.2	<0.001
Seed Length (mm)	2	21	13	1	8	5.7	<0.001
Seed Width (mm)	6	10	8	1	5	5.6	<0.001
Days to 50% Flowering	28	42	35	3.2	9.2	1.9	<0.001

The frequency distribution for qualitative traits for all 95 accessions is presented in table 2. Three main distinct forms of growth habits were observed among the accessions which comprised erect, semi-erect (decumbent-2 and decumbent-3), and spreading (procumbent-1, procumbent-2 and decumbent-1). However, most plants (54%) possessed an erect growth habit. Variation for branching pattern among the accessions was noted with 76% sequential, 16% alternate, 8% irregular without flowers on main stem, and 2% irregular with flowers on main stem.

Citation: Abogoom J, Akromah R, Aidoo R, Awuah E, Jordan DL (2023) Assessment of Morphological Variation of Peanut (*Arachis hypogaea L.*) in Ghana. Arch Agri Res Technol 4: 1056

Table 2: Frequency distribution for qualitative traits associated with branching pattern and growth habit.

Trait	Description	Frequency	Percentage
Branching pattern	Alternate	13	13.7
	Sequential	72	75.8
	Irregular with flowers on main stem	2	2.1
	Irregular without flowers on main stem	8	8.4
Growth habit	Procumbent-1	1	1.1
	Procumbent-2	1	1.1
	Decumbent-1	5	5.3
	Decumbent-2	18	18.9
	Decumbent-3	19	20.0
	Erect	51	53.7
Inflorescence type	Simple	24	25.3
	Compound	71	74.7
Leaf color	Light green	12	12.6
	Green	58	61.1
	Dark green	21	22.1
	Bluish green	4	4.2
Leaflet margin	Entire	31	32.6
	Hairy	64	67.4
Leaflet shape	Cuneate	4	4.2
	Elliptic	1	1.1
	Oblong-elliptic	56	58.9
	Narrow-elliptic	13	13.7
	Wide-elliptic	10	10.5
	Ovate	7	7.4
	Obovate	2	2.1
	Lanceolate	2	2.1
Leaflet surface	Almost glabrous on both faces	83	87.4
	Almost glabrous above, hairs below	12	12.6
Leaflet tip	Obtuse	15	15.8
	Acute	80	84.2
Peg pigmentation	Absent	0	0.00
	Present	95	100.0
Petal color	Orange yellow/yellow-orange	95	100.0
Petal markings color	Dark orange	95	100.0

Trait	Description	Frequency	Percentage
Pod beak	Absent	1	1.1
	Slight	21	22.1
	Moderate	48	50.5
	Prominent	17	17.9
	Very Prominent	8	8.4
Pod constriction	Absent	15	15.8
	Slight	31	32.6
	Moderate	30	31.6
	Deep	13	13.7
	Very deep	6	6.3
Pod reticulation	Absent	15	15.8
	Slight	12	12.6
	Moderate	32	33.7
	Prominent	15	15.8
	Very Prominent	21	22.1
Primary seed color	Off-white	3	3.2
	Very pale tan	15	15.8
	Pale tan	29	30.5
	Light tan	6	6.3
	Tan	1	1.1
	Dark tan	1	1.1
	Greyed orange	3	3.2
	Salmon	15	15.8
	Light red	4	4.2
	Red	1	1.1
	Dark red	8	8.4
	Purplish red/red purplish	1	1.1
	Light purple	8	8.4
Secondary seed color	Blotched	79	83.2
	Flecks of color	8	8.4
	Striped	2	2.1
	Tipped at the embryo end	6	6.3
Seed color	One color	79	83.2
	Variegated	16	16.8
Seeds per pod	1-Feb	59	62.1
	2-3-1/2-1-3	30	31.6
	2-3-4-1/2-4-1-3/3-2-4-1/3-2-1-4	1	1.1
	3-4-2-1/3-4-1-2	5	5.3

Stem pigmentation	Absent	42	44.2
	Present	53	55.8
Stem surface	Glabrous	34	35.8
	Sub-glabrous, hairs in one or two rows along the main stem	38	40.0
	Moderately, three or four rows along the main stem	18	18.9
	Hairy, most of the stem surface covered with hairs	5	5.3

Similarly, a wide variation was observed with regards to primary seed color and leaflet shape, with pale tan seeds (31%) and oblong-elliptic leaflets (59%), respectively. However, there was no variation in peg pigmentation, petal color, and petal markings color among the accessions. However, narrow variation was observed in leaflet surface, number of seeds per pod, and secondary seed color table 3.

Table 3: Percentages of the component of traits contributing to the phenotypic variations observed in the peanut samples.

Dimensions of Principal Components	Percentage of Explained Variance
Dim. 1	18.4
Dim. 2	11.6
Dim. 3	9.4
Dim. 4	6.9
Dim. 5	5.8
Dim. 6	5.3
Dim. 7	4.3
Dim. 8	4.0
Dim. 9	3.7
Dim. 10	3.6

Cluster analysis using all the 31 morphological traits grouped the 95 accessions into two main clusters at 30% dissimilarity (Figure 1). Between the two clusters, cluster I was the largest containing 74 accessions while cluster II contained 21 accessions. At 25% dissimilarity, Cluster I is furthered grouped into two clusters (Cluster IA and IB) making Sub-Cluster IA containing the least number of accessions (11 accessions) (Figure 1). Sub-Cluster IA comprised 3 improved accessions (Obolo, Oboshie, and Sarinut 2), 2 and 3 accessions obtained from farmers in Northern region (NRF-15 and NRF-9), and Ashanti region (ASF-4, ASF-5, and ASF-2), respectively. One genotype obtained from the market in Ashanti region (ASM-4) was also present. Sub-Cluster IB comprised mostly of accessions from markets in Upper East (UEM-10, UEM-9, UEM-4, UEM-7, UEM-1, UEM-2, UEM-6, UEM -5, UEM-3, and UEM-8) followed by equal number (8) of accessions from markets in the Upper West (UWM-10, UWM-5, UWM-9, UWM-1, UWM-7, UWM-8, UWM-2, and UWM-6), farmers in Upper West (UWF-7, UWF-1, UWF-10, UWF-11, UWF-4, UWF-2, UWF-6, and UWF-5), and Northern regions (NRF-4, NRF-13, NRF-10, NRF-11, NRF-5, NRF-8, NRF-14, and NRF-12). Accessions from the research institutes (Yenyawoso-S, Yenyawoso-C, and CRI-Dehye) and markets in the Bono East region (BEM-3, BEM-5, and BEM-1) were the least in number (3 each) in the cluster. Cluster II, however, comprised 7 and 5 accessions from markets (NRM-12, NRM-2, NRM-6, NRM-14, NRM-7, NRM-4, and NRM-8) and farmers (NRF-1, NRF-6, NRF-7, NRF-2, and NRF-3), respectively, in the Northern region. Three accessions from the

research institutes (Sarinut 1, CRI-Agbeyeye, and Nkatiesari) and 2 each from markets in the Bono East (BEM-4 and BEM-2), Upper West (UWM-4 and UWM-3), and farmers in the Upper West region (UWF-9 and UWF-12) were present in Cluster II.
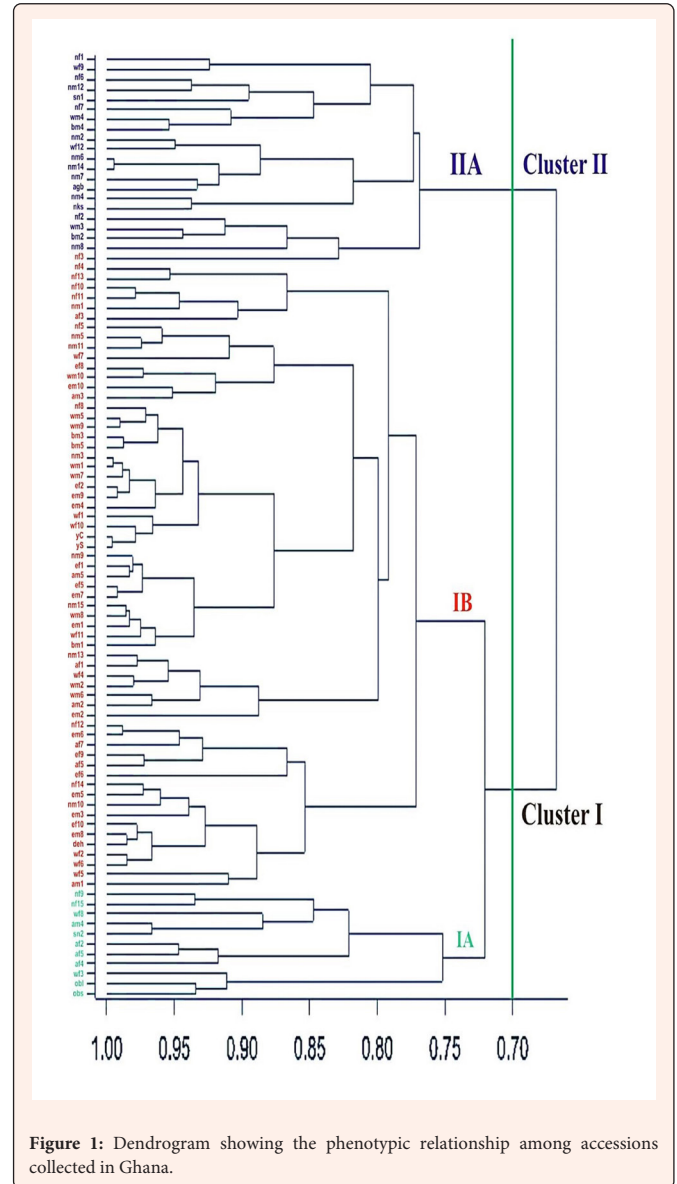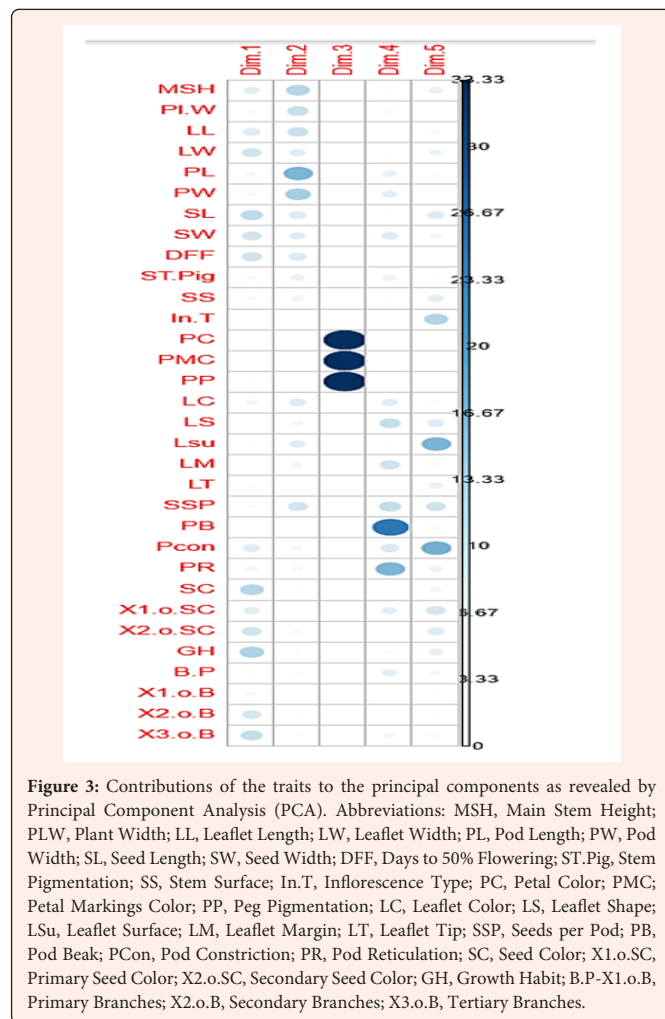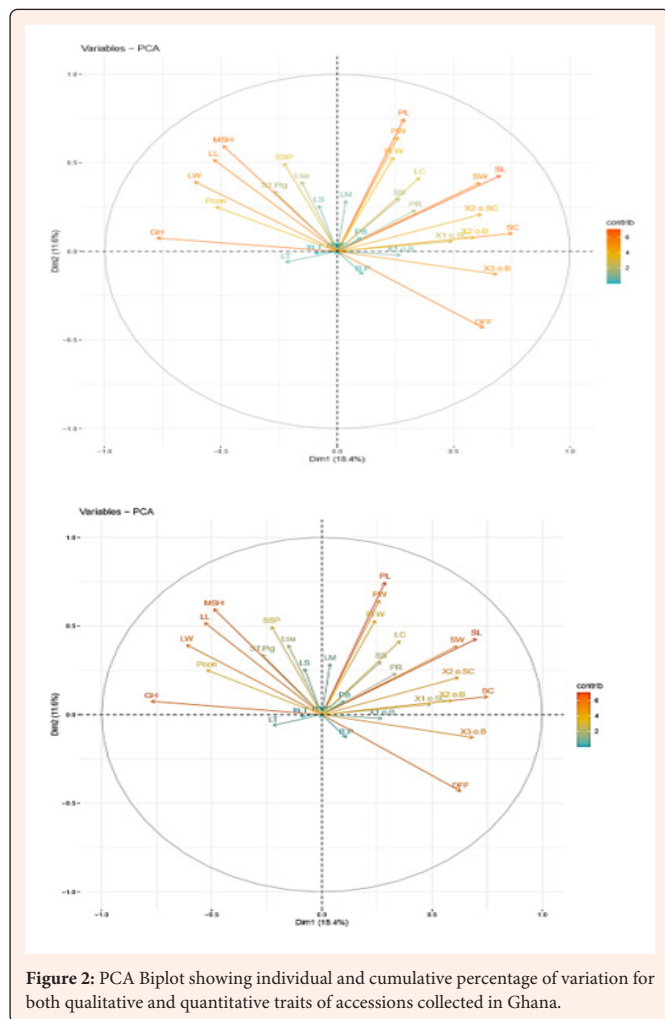

Figure 1: Dendrogram showing the phenotypic relationship among accessions collected in Ghana.

Principal Component Analysis revealed that the first five principal components accounted for 52.1% of total variation for all the morphological traits (Figure 2). The first component explained 18.4% of the total variation as defined by the following traits, seed color, growth habit, number of secondary branches, seed width, seed length, and days to 50% flowering (Figure 3). Principal component two contributed 11.6% to the total variation (Figure 2) and is positively correlated to main stem height, pod length, pod width, plant width, and leaflet length (Figure 3). The third principal component explained 9.4% of the total variation comprised of plant pigmentation, petal markings color, and petal color.

Figure 2: PCA Biplot showing individual and cumulative percentage of variation for both qualitative and quantitative traits of accessions collected in Ghana.

Figure 3: Contributions of the traits to the principal components as revealed by Principal Component Analysis (PCA). Abbreviations: MSH, Main Stem Height; PLW, Plant Width; LL, Leaflet Length; LW, Leaflet Width; PL, Pod Length; PW, Pod Width; SL, Seed Length; SW, Seed Width; DFF, Days to 50% Flowering; ST.Pig, Stem Pigmentation; SS, Stem Surface; In.T, Inflorescence Type; PC, Petal Color; PMC; Petal Markings Color; PP, Peg Pigmentation; LC, Leaflet Color; LS, Leaflet Shape; LSu, Leaflet Surface; LM, Leaflet Margin; LT, Leaflet Tip; SSP, Seeds per Pod; PB, Pod Beak; PCon, Pod Constriction; PR, Pod Reticulation; SC, Seed Color; X1.o.SC, Primary Seed Color; X2.o.SC, Secondary Seed Color; GH, Growth Habit; B.P-X1.o.B, Primary Branches; X2.o.B, Secondary Branches; X3.o.B, Tertiary Branches.

Branching is considered an essential trait that contributes greatly to seed yield. Giayetto et al. [3] reported that yield is determined by secondary branches. This study reported a higher number of secondary branches and therefore revealing the yield potential of the accessions considered in this study. Also, the high number of branches recorded in this study reveals the potential haulm yield of the accessions since the use of haulms for feeding of livestock is an important part of peanut production in Ghana [18].

Sequential branching is characteristic of the fastigiata subspecies while the *hypogaea* subspecies is characterized by the alternate branching pattern. Seventy-two accessions belonged to the fastigiata subspecies. The fastigiata subspecies includes both Spanish and Valencia botanical classifications which are characterized by early maturity, a trait which is highly preferred by farmers in Ghana as a strategy to avoid drought. Spanish and Valencia botanical classifications are small seeded with mostly 2 and 3 seeds and have high oil content. They are preferred for oil extraction, roasted and boiled peanut and thus are easily marketable. These characterstics explain for their dominance in the accessions. The Shitaochi variety, which is the Spanish type, was reported by Oppong-Sekyere et al. [19] to be the variety farmers predominantly cultivate because of its early maturity and high market value. The majority of the accessions possessed an erect growth habit (54%), with pale tan seed coat (31%) and green foliage (61%). These characteristics also confirm that most accessions are fastigiata subspecies.

The cluster analysis revealed a narrow diversity among the 95 accessions both between regions and within regions (Figure 1). A similarity coefficient of 70%, indicates that accessions were only 30% dissimilar based on the 31 traits of peanut measured in this study. Accessions found in Cluster II were 70% similar to NkatieSari, Agbeyeye, and Sarinut 1 while accessions found in Cluster I were similar to Dehye, Yenyawoso, Obolo, Oboshie, and Sarinut 2 at 70% similarity index. However, at 75% similarity index, accessions found in Sub-Cluster IA were more similar to Obolo, Oboshie, and Sarinut 2 than to Dehye and Yenyawoso. The closest accessions were Yenyawoso-C and Yenyawoso-S (99% similar), NRM-6 and NRM-14 (about 98% similar), and NRM-3 and UWM-1 (99% similar) while accessions with the greatest diversity were UWF-5 and ASM-1 (91% similar). Farmer-saved seed accessions (7) and accessions from the markets (10) from Upper East were grouped in one cluster (Sub-cluster IIA) suggesting that varieties cultivated in that region are highly similar with little diversity (Figure 1). This can be explained by the fact that farmers practice exchanging seeds of newly acquired varieties with each other in the same community.

Traits that influence variation of peanut were revealed through the principal component analysis and included number of secondary branches, seed color, growth habit, pod length, pod width, and main stem height. Based on the first and second components, yield attributing traits were recognized as the main factor that influences dispersion and superior accessions (Figure 3). These included seed length, growth habit, pod length, pod width, plant width, and main stem height. Upadhyaya [20] reported that main stem height, leaflet length, leaflet width, pod length, pod width, seed length and seed width are traits that differentiate peanut varieties of the hypogaea from those of the fastigiata sub-species [21].

Results of this study revealed the narrow diversity among accessions given they were 30% dissimilar or 70% similar. Improved accessions from the research institutes were found in both two main clusters, inferring low adoption or access to improved peanut varieties among farmers. Greater access of improved varieties for farmers is needed to increase peanut production in Ghana.

Acknowledgement

References

1. Rao VR, Murty UR (1994) Botany - morphology and anatomy. In: Smartt J (Ed.), The Groundnut Crop - A Scientific Basis for Improvement. Chapman and Hall, London, UK p. 43-95.

2. Krapovickas A, Rigoni VA (1960) The nomenclature of the subspecies and varieties of *A. hypogaea* L. Revista de Investigaciones Agricoles 14: 198-228.

3. Waldron RA (1919) The peanut *(Arachis hypogaea* L.*)*, its history, histology, physiology, and utility. Contribution of the Botany Laboratory of the University of Pennsylvania 4: 302-338.

4. Desmae H, Sones K (2017) Groundnut cropping guide. Africa Soil Health Consortium. Nairobi: CAB International.

5. Owusu AE, Baah MR, Salifu B (2017) Analysis of the groundnut value chain in Ghana. World J Agric 5(3): 177-188.

6. MOFA Ministry of Food and Agriculture (2017) Agriculture in Ghana, Facts and Figures 2016. Ministry of Food and Agriculture Statistics, Research and Information Directorate.

7. Puozaa DK, Jinbaani AN, Adogoba DS, Busagri D, Rasheed MA, et al. (2021) Enhancing access to quality seed of improved groundnut varieties through multi-stakeholder platforms in Northern Ghana. In: Enhancing Smallholder Farmers' Access to Seed of Improved Legume Varieties Through Multi-stakeholder Platforms. Springer, Singapore, p. 65-79.

8. Van Etten J, Noriega IL, Fadda C, Thomas E (2016) The contribution of seed systems to crop and tree diversity in sustainable food systems. In: Bailey A (Ed.), Mainstreaming Agrobiodiversity in Sustainable Food Systems: Scientific Foundations for an Agrobiodiversity Index - Summary. Biodiversity International, Rome, Italy, p. 82-102.

9. Govindaraj M, Vetriventhan M, Srinivasan M (2015) Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. Genetics Research International.

10. Malek MA, Rafii MY, Afroz SS, Nath UK, Mondal M (2014) Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. The Scientific World Journal.

11. Neya FB, Koita K, Elise S, Zagre BMBM, Nana AT, et al. (2017) Agro-morphological diversity of six groundnut *(Arachis hypogaea* L.*)* breeding lines from three geographical areas. Journal of Experimental Agriculture International p. 1-12.

12. Wanget SA, Morales CMR, Pérez SR, Rostini N, Gómez SMA, et al. (2019) Agro-morphological and chemical characterization of traditional Indonesian groundnut *(Arachis hypogaea* L.*)* cultivars. Genetika 51(1): 179-198.

13. Yol E, Furat SH, Upadhyaya D, Uzun B (2018) Characterization of groundnut *(Arachis hypogaea* L.*)* collection using quantitative and qualitative traits in the Mediterranean Basin. Journal of Integrative Agriculture 17(1): 63-75.

14. Frimpong A (2004) Characterization of groundnut *(Arachis hypogaea* L.*)* in Northern Ghana. Pakistan. J Bio Sci 7: 838-842.

15. Oteng DP, Amponsah SK, Afful EA, Dzomeku BM (2013) Installation of Drip Irrigation at CSIR-Crops Research Institute, Ghana. International Journal of Engineering Research & Technology 2(2): 1-6.

16. IBPGR [International Board for Plant Genetic Resources (1992) Descriptors for groundnut. Rome, Italy: International Board for Plant Genetic Resources; and Patancheru, Andhra Pradesh, India. International Crops Research Institute for the Semi-Arid Tropics pp. 125.

17. Sokal RR, Michener CD (1958) A statistical method for evaluating systematic relationships. Univ Kansas Sci Bull 38: 1409–1438.

18. Martey E, Wiredu AN, Frimpong RO (2015) Baseline study of groundnut in Northern Ghana. LAP Lambert Academic Publishing.

19. Oppong SD, Akromah R, Akpalu MM, Ninfaa AD, Nyamah EY, et al. (2015) Participatory rural appraisal of constraints to groundnut *(Arachis hypogaea* L.*)* production in northern Ghana. Int J Current Res Acad Rev 3(10): 54-76.

20. Upadhyaya HD (2003) Phenotypic diversity in groundnut *(Arachis hypogaea* L.*)* core collection assessed by morphological and agronomical evaluations. Genetic Resources and Crop Evolution 50(5): 539-550.

21. Giayetto O, Morla FD, Fernandez EM, Cerioni GA, Kearney M, et al. (2013) Temporal analysis of branches pod production in groundnut *(Arachis hypogaea)* genotypes with different growth habits and branching patterns. Groundnut Science 40(1): 8-14.

Citation: Abogoom J, Akromah R, Aidoo R, Awuah E, Jordan DL (2023) Assessment of Morphological Variation of Peanut (*Arachis hypogaea L.*) in Ghana. Arch Agri Res Technol 4: 1056

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