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Original Paper

Morphological Characterization of Peanut (*Arachis Hypogaea L.*) Genotypes

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***Abstract*— The current study was done on peanut genotypes including one check. The aim of this study was to characterize the morphological variance of genotypes using Shannon-Weaver diversity index. The experiment was laid out in a simple lattice design. Among the genotypes about (46.94%) had erect growth habits, followed by (34.69%) decumbent-3, while decumbent-2 (12.24%), procumbent-1 (4.02%) and decumbent-1 was the least (2.04%). The genotypes revealed three different branching patterns such as alternate, sequential, and irregular with flowers on the main stem accounted (14.29%), (53.06%), and (32.65%) respectively. The majority genotypes had red (46.96%) seed coat color followed by purple-red (22.45%). Purple, pink, and tan seed colors accounted for (12.24%), (10.20%), and (6.12%) respectively. The white seed coat color was observed for check. Among the studied trait the seed coat color (H'=1.44) had the highest diversity index, followed by leaf color (H'=1.29), pod beak (H'=1.20) and growth habit (H'=1.19), indicating that the presence of high diversity among genotypes for these traits. The diversity in qualitative traits might be good for varietal preference and its marketability. This genetic variability can be useful for improvement programs.**

***Keywords*— diversity, peanut, phenotypic, Shannon-diversity**

I. INTRODUCTION

Peanut (Arachis hypogaea L.) is an important oilseed legume crop. It is an unpredictable crop due to its underground pods' development. Its ranks 5th among oilseed crops after oil palm, soybean, rapeseed, and sunflower in terms of volume of production globally and widely grown in more than 110 countries of tropical, subtropical, and warm temperate regions [1]. It is a multi-purpose crop largely cultivated in tropical and sub-tropical parts of the world [2]. Globally, China, India, Nigeria, USA and Sudan are the leading peanut-growing countries [3]. The annual peanut production was estimated about 536,389.32 metric ton from 31.6 million hectares of production area. Similarly, Nigeria, Sudan, Chad, Cameroon, Senegal, Guinea, Burkina Faso and Niger are the leading peanut producing countries in Africa.

It is a rich source of protein, oil, minerals and vitamin [4]. Peanut plants need well-drained sandy loam or clay loam soil and the pH of the soil is around 5.5 to 7 with a high fertility [5]. It needs optimum temperature for growth and development ranges from 25 to 30 ºC, and the crop requires about 500-600 mm of well distributed rainfall [6].

The degree of genotypic diversity in a population for a trait determines the development of an improved cultivar that can yield more under different agroclimatic. The observed variability is a combined measure of genetic and environmental causes. Recording traits that are highly heritable, easily observable with the naked eye, and expressive in all settings is the process of characterization [7]. Morphological Variability is the total amount of genetic traits present in the genetic make-up of species. The success of any breeding program depends on the amount of variability present for different characters in a population. Plant breeders attempt to make their genetic material broader through many programs such as germplasm introduction, landraces exploration, hybridization, artificial mutation, etc.

The presence of genetic Variability is an important part of any breeding program in meeting the diversified goals of plant breeders such as breeding to increase yield, wider adaptation, desirable quality, drought, and pest resistance. Morphological characters and physiological traits have been extensively used for grouping peanut varieties into classes [8]. Estimating the extent of genetic variability existing in the population is a key step in determining the genetic potential of the crop for future improvement [9]. Several research have done on the existence of genetic variation concerning qualitative and quantitative characteristics in peanut [8]. Improving the genetic potential of peanut for qualitative and quantitative traits is one of the major objectives in most peanut breeding programs. Commonly, the use of only few elite germplasm lines and/or cultivars in breeding programs reduces the genetic variation, leading to a narrow genetic base in the peanut gene pool[10]. Sustainable peanut improvement programs, therefore, need to discover and incorporate genes from germplasm with high genetic variability for desired traits. Furthermore, the seed coat color and size influence the quality and appeal of processed grain, it is a crucial breeding criterion for legume crops. Evaluating morphological variability and defining genetic resources is very important for the improvement of peanut in the future breeding program. Therefore, the present study was conducted to evaluate peanut genotypes on the basis of different qualitative traits and analyze the variability exist among genotypes.

II. MATERIALS AND METHODS

A. *Description of the Study Site*

Yaoundé 1 University in Cameroon was the site of the field trial. Geographically, the experiment location is located at a height of 750 meters above sea level and has latitude 3°52'30"N and longitude 11°30'00"E. The experimental site experiences 24°C, 79% relative humidity, and 1600 mm of rainfall annually [11].

B. *Experimental Design and Crop Management*

The experiment was laid out in a simple lattice design. A total of 49 peanut genotypes were used in this study. Each entry was planted in a plot having one row of 2 meters length. blocks, plots, and plants were spaced 1m, 0.8m, and 0.2m respectively. Each row had ten plants and two seeds were planted per hole and thinned to one after emergence. Hand weeding was carried out occasionally to ensure plant health. NPK Fertilizer was applied with the rate of 100 kg per ha at sowing time and all other agronomic management practices were applied properly as per recommendations.

C. *Data Collected*

Qualitative data was taken using morphological and phenological descriptors based on the international board for plant genetic resources descriptor for peanut qualitative traits [7]. Some of these data were taken during the pod setting period and after harvest.

1. Growth habit, Stem branching pattern, and Leaf color were recorded at pods setting stage using the code
2. Pod beak, and pod constriction recorded when pods had dried after harvesting
3. Major seed coat color recorded after complete drying

TABLE I. DESCRIPTIONS AND CODES OF QUALITATIVE TRAITS OF PEANUT

Qualitative traits	Characters code
Growth habit	Procumbent-1
	Procumbent-2
	Decumbent-1
	Decumbent-2
	Decumbent-3
	Erect
Stem branching pattern	Alternate
	Sequential
	Irregular with flowers on the main stem
	Irregular without flowers on the main stem
	Other
Leaf color	Yellow/yellow-green
	Light green
	Green
	Dark green
	Bluish-green
Pod beak	Absent
	Slight
	Moderate
	Prominent
	Very prominent
Pod constriction	None
	Slight
	Moderate
	Deep
	Very deep
See coat color	White
	Off white
	Yellow
	Very pale tan
	Pale tan
	Light tan
	Tan
	Dark tan
	Greyed orange
	Rose
	Salmon
	Light red
	Red
	Dark red
	Purplish red
	Light purple
	Purple
	Dark purple
	Very dark purple
	other

D. *Data Analysis*

1) *Shannon Weaver Diversity Index*

Shannon Weaver Diversity Index was estimated based on the phenotypic frequency data. It was computed to assess the phenotypic diversity for each character; entire genotype. H' was calculated using Microsoft Excel 2016 [12] ; [13] . The index used as a measure of the phenotypic diversity of each qualitative trait is determined as follows.

$$H' = -\sum_{i=1}^{s} pi(\ln pi) \quad \text{......} (1)$$

Where:

S is the number of phenotypic classes for a trait

pi is the proportion of genotypes in the ith class ln = natural logarithm.

III. RESULTS AND DUSCUSSION

A. *Qualitative Traits Analysis*

Genetic diversity analysis based on qualitative traits is an important approach toward identification and improvement of peanut crop [14]. In the present study, observations on five qualitative traits were recorded for all the 49 peanut genotypes in Table 2. Shannon-weaver diversity index accounted for growth habit (1.19), branching pattern (0.98), leaf color (1.29), pod beak (1.20), pod constriction (1.07), and seed color (1.44). Accordingly, there was the diversity for all traits under study. Shannon diversity indexes can be classified into three categories, according to [15] high (> 0.67), moderate (0.66 - 0.34), and low (0.33- 0.01). [16] Reported that Shannon diversity indexes for seed coat color, growth habit, and stem pigmentation. Similarly, [17] also reported that in peanut collection, 75% of the accessions presented an irregular branching pattern without flowers on the main stem and 25% had irregular branching patterns with flowers on the main stem with 50% of erect, and 50% creeping growth habit accessions.

TABLE II. THE GENETIC DIVERSITY INDICES OF 49 PEANUT GENOTYPES

Traits		Shannon diversity	
	No of genotypes	index (H')	Equitability
Growth habit	49	1.19	0.73
Branching pattern	49	0.98	0.89
Leaf color	49	1.29	0.92
Pod beak	49	1.2	0.86
Pod constriction	49	1.07	0.77
Seed coat color	49	1.44	0.8

B. *Phenotypic Variation*

In the present study about twenty-three (46.94%) peanut genotypes had erect growth habits, followed by seventeen (34.69%) decumbent-3, while decumbent-2 six (12.24%), procumbent-1 two (4.02%) and decumbent-1 one (2.04%). Similar result was reported by [16] about 58.2% of total peanut collection revealed erect growth. The genotypes revealed three different branching patterns such as alternate, sequential, and irregular with flowers on the main stem accounted 7(14.29%), 26(53.06%), and 16(32.65%) of genotypes respectively. Current research was disagree with the report of [17] who reported that 75% of total peanut accessions showed irregular branching pattern without flower on the main stem and 25% irregular branching pattern with flower on the main stem. Leaf color showed that there was diversity among tested peanut genotypes that observed yellow/yellow-green 7(14.29%), light green 16(32.65%), green 19(38.77%), and dark green 7(14.29%). Considering pod beak, 32.65% of genotypes had no pod beak, 38.77% slight, 22.45% moderate, and three of the genotypes had been prominent 6.12%. Out of the total tested genotypes, 7 genotypes showed no pod constriction, 17 genotypes had slight, 24 genotypes had moderate, and only one genotype had deep constriction pod.[18] has been reported Fifty percent (50%) and thirty-three percent (33.34%) of the accessions have moderate and prominent pods constriction, respectively. The seed coat color of tested peanut genotypes was presented in Figure1. The majority of seed coat color that was observed in the genotype is red (46.96%), followed by purple-red (22.45%). Purple, pink, and tan seed colors accounted for (12.24%), (10.20%), and (6.12%) respectively. White seed coat color was seen only in one local cultivar. Wide diversity of seed coat colors with desirable agronomic traits for commercial usage and breeding studies. Generally, there was adequate variability among the peanut genotypes studied in one local cultivar. Generally, there was adequate variability among the tested peanut genotypes which used in the selection program.

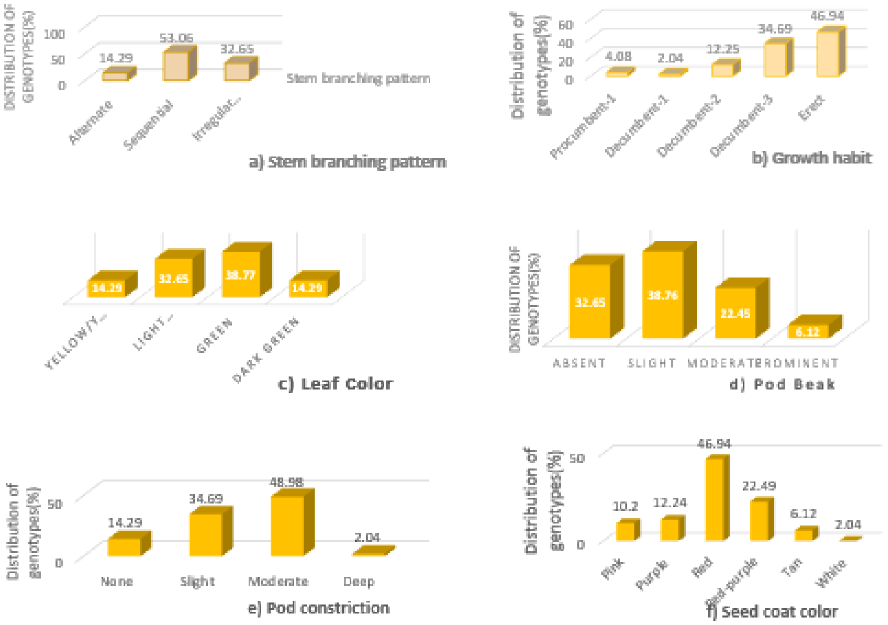

Fig. 1. Frequency distribution percentage of 49 peanut genotypes for a) growth habit, b) stem branching pattern, c) leaf color, d) pod beak, e) pod constriction and f) seed coat color.

Fig. 2. Seed coat color and size of peanut genotypes

TABLE III. FREQUENCY DISTRIBUTION OF 49 PEANUT GENOTYPES AND PERCENTAGE VALUE OF GROWTH HABIT, BRANCHING PATTER, LEAF COLOR, POD BEAK, POD CONSTRICTION, AND SEED COAT COLOR TRAITS

Traits	Variation	No. of genotypes	Percentage (%)
Growth habit	Procumbent-1	2	4.02
	Decumbent-1	1	2.04
	Decumbent-2	6	12.24
	Decumbent-3	17	34.69
	Erect	23	46.94
Branching pattern	Alternate	7	14.29
	Sequential	26	53.06
	Irregular with flowers on the main stem	16	32.65
Leaf color	Yellow/yellow-green	7	14.29
	Light green	16	32.65
	Green	19	38.77
	Dark green	7	14.29
Pod beak	Absent	16	32.65
	Slight	19	38.77
	Moderate	11	22.45
	Prominent	3	6.12
Pod constriction	None	7	14.29
	Slight	17	34.69
	Moderate	24	48.98
	Deep	1	2.04
Seed coat color	White	1	2.02
	Tan	3	6.12
	Purple	6	12.24
	Red	23	46.95
	Purple -red	11	22.45
	Pink	5	10.2

IV. CONCLUSION

The present result showed that most of morphological traits showed high variability. Shannon-weaver diversity index accounted for growth habit (1.19), branching pattern (0.98), leaf color (1.29), pod beak (1.20), pod constriction (1.07), and seed color (1.44). This indicating that peanut genotypes under study were widely diversified for these characters. The results should be prioritized for breeding programs to improve the good criteria found in peanut which provides opportunity for the breeders to develop new varieties. It will also be helpful for farmers in selecting market preferable varieties. However, the present result based on morphological traits alone can't make definite conclusion. As a result, it is recommended that molecular studies have to be carried out to make reliable conclusion.

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