Journal of Agriculture, Forestry & Environment, 2022, 6(1): 65 - 72

Variability in selected genotypes of fluted pumpkin (*Telfairia occidentalis* Hook F.) in Calabar, Cross River State

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Abstract

Fluted pumpkin remains an important vegetable in Nigeria.Assessing genetic variability in this crop provides a basis for selection and breeding purposes. This investigation was carried out to assess genetic variability in selected genotypes of fluted pumpkin in Calabar. The field experiment was laid out in a randomized complete block design (RCBD) with three replications. A total number of seven genotypes was used for this study.The results showed that genotypes varied significantly for some traits under consideration. Among some morphological traits evaluated, significant differences were observed only in leaf area and leaf area index. The heritability values ranged from 79 – 81%. Leaf area and Leaf area index at 6 weeks after planting (WAP) had the highest heritability value of 81%. Similarly, genetic advance as percent of mean (GAM) ranged from 11.29 – 13.63. The highest GAM was recorded in leaf area at 6 WAP.The high heritability and genetic advance observed in leaf area and leaf area index at 6 WAP, suggests that these characters have additive gene effects and can be further evaluated for the improvement of this crop.

Keywords: Variability, Fluted pumpkin, Heritability, Genetic advance

Introduction

Fluted pumpkin (*Telfairia occidentalis* Hook f.) is an important vegetable in West Africa. It is indigenous to south eastern Nigeria from where it is distributed to other parts of the country and other West African nations. It is cultivated as an important nutritional and commercial vegetable (Dahunsi *et al*., 2016). In the Northern Nigeria, it has gained acceptability and there is increase in its cultivation by small holder farmers as a source of income (Ndor *et al.*, 2013). Alphaagrobiz (2020) reported that fresh shoot yield of fluted pumpkin can be as high as 500-1000 kg/ha depending on the management system.Fluted pumpkin leaves apart from being used as vegetables are extensively used in African traditional herbal medicine for the treatment of anemia in view of high ferrous content and in the treatment of cough, diarrhea, tuberculosis and other bacterial infections (Ezenwata *et al.*, 2019). It has a creeping growth habit that spreads across the ground to produce an efficient cover on the ground against soil erosion (Nwangburuka *et al.*, 2014).

Genetic variability provides knowledge of relationship among breeding population and helps in selecting desirable parents for new breeding programmes. A rewarding success can be achieved through genetic variability, genetic advance, character association, which includes direct and indirect effects on yield and its attributes. The value of heritability estimates together with genetic advance clearly shows traits that are likely transmissible from parents to offspring (Abu and Asember, 2011). The genetic advance depends on the extent of genetic variability, the magnitude of masking effect of genetic expression and the intensity of selection. Information on the amount and direction of association between yield and related characters as well as variability studies is important for rapid progress in selection and genetic improvement of a crop (Enete and Okon, 2010). This will provide suitable means for indirect selection since yield is a polygenic character. Genetic variability and heritability studies have been conducted on various vegetable crops such as okra, cucumber, lettuce and other crops. Nwangburuka *et al.*(2012)in their study on okra recorded sufficient variability in the genotypes studied. They also observed high genotypic coefficient of variability, broad-sense heritability and genetic advance for plant height, fresh pod length, fresh pod width and pod weight per plant, suggesting the effect of additive genes and reliability of selection based on phenotype of these traits for crop improvement. Ahirwar and Singh (2018) in their study on cucumber reported that the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) and the difference between PCV and GCV was narrow for most of the characters revealing little influence of the environment in the expression of the traits. Similar report by (Oliya *et al.*,2022) on lettuce showed heritability estimate ranging from 45.85 to 98.59% for vegetative characters and the need to continually assess variability for the improvement of vegetable crops.

Although some research works have been carried out on fluted pumpkin as one of the most important and extensively cultivated food and income generating crop in many parts of Africa (Adebisi-Adelani *et al*., 2011), numerous studies have focused on the profit efficiency for small-scale farmers (Nwauwa and Omonona, 2010; Abu and Asember, 2011)and the effects of climate change (Onyeke, 2022) on its production. Other studies too have focused more on the vegetative and yield characters (Fayeun *et al.*, 2012; Nwonuala and Obiefuna, 2015). In spite of the desirable attributes exhibited by fluted pumkin, information on variability and heritability for this crop is sparse hence the need to continually improve the crop. Improvement could be possible if there is sufficient genetic variability in traits of economic interest. The understanding of variability in fluted pumpkin of various accessions will therefore enhance our exploitation of these benefits. Therefore, this study was carried out to assess the variability of some selected genotypes of fluted pumpkin in Calabar.

Materials and Methods

The experiment was conducted from May to August 2021 at the University of Calabar Crop

Science Teaching and Research farm, Calabar Nigeria. Calabar lies between Latitude: 4° 57' 32.15" N Longitude: 8° 19' 37.02" E. Calabar has a bimodal annual rainfall of 1250mm / 3306 mm, humidity ranging from 65% - 90% and an ambient temperature of 27°C to 38°C(NIMET, 2016). The experimental site was cleared and tilled manually and then divided into three blocks each containing 7 beds (plots). Each bed size was 2m x 1.5m with a pathway of 1 m between replications and 0.5m between plots.The experimental design was randomized complete block design (RCBD) with three replications.The treatments involved seven genotypes of *Telfairia occidentalis* namely; Cordata, Queen, Field, Curcubita, Fig leaf, Eden and Bush obtained from East West seed farm Akpabuyo, Cross River State. Two seeds were sown per hole at a spacing of 0.5 m x 0.5 m and later thinned to one per hole, five days after emergence giving a plant population of 40,000plants/ha. NPK 20:10:10 fertilizer was applied at the rate of 60 kg/ha two weeks after planting (WAP) by band placement.Weeds were controlled manually by hand hoeing at 4 and 8 weeks after planting (WAP). Data was collected from four plants in each plot beginning at 4WAP. Data was collected on the following attributes at two weeklyintervals for four sampling periods: vine length, number of leaves, fresh weight in grams at 4 and 8 WAP, leaf area (LA)and leaf area index (LAI) was calculated using the formula by Akoroda (1993):LA=0.9467 +0.275lw + 0.972lwn

Where,LA= leaf area; l= length of central leaflet; w= maximum width of central leaflet

n= number of leaflets per leaf; while

leaf area index was determined using the formular:

LAI = LA/ plant spacing

Data collected was subjected to analysis of variance (ANOVA)to estimate the level of variability among the genotypes. The phenotypic variation for each trait was partitioned into genetic and non-genetic factors and estimated according to Uguru (2005):

$$Vp = MSg/r$$

$$Vg = (MSg-MSe)/r$$

$$Ve = MSe/r$$

Where Vp, Vg and Ve are phenotypic, genotypic and environmental variance respectively

MSg, MSe and r are mean squares of genotypes, error and number of replications respectively.

To compare the variations among traits, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV) were computed according to the method suggested by Allard (1960):

$$PCV = (\sqrt{Vp/x})\ 100$$

$$GCV = (\sqrt{Vg/x})\ 100$$

Where Vp, Vg and x are phenotypic, genotypic variance and grand mean respectively for each of the studied traits. Broad sense heritability (h^2B)

was calculated according to Allard (1960) as the ratio of the genotypic variance (Vg) to the phenotypic variance (Pp).

$h^2B = Vg/Vp \times 100$

Genetic advance (GA) = k (sp) h^2B

Where K= constant 2.06 selection pressure of 5%

sp = phenotypic standard deviation

h^2B = Heritability in broad sense

Genetic advance as % of mean = GA/x

Where; x is mean

Results and discussion

The results showed that genotypes varied in leaf area at 6 and 8 WAP and leaf area index at 6 WAP (Table 1). Estimates of variance components showed that phenotypic variance (Vp) was higher than genotypic variance (Vg) for the traits studied (Table 2). Similarly, the phenotypic coefficient of variation (PCV) was also higher than genotypic coefficient of variation (GCV). GCV ranged from 6.17 to 7.33 and PCV values ranged from 6.94 to 8.12 for leaf area and leaf area index (Table 3). For leaf area at 6 WAP, GCVwas 7.33 and this was higher than the value for leaf area at 8 WAP which was 6.17 while PCV for leaf area at 6 WAP was 8.12which was also higher than leaf area at 8 WAP (6.94). The values of PCV and GCV were low for leaf area and leaf area index at 8 WAP (Table 3).Heritability values for studied traits ranged from 79 to81%. Leaf area and leaf area index at 6WAP had the highest heritability value of81%. Similarly, genetic advance as percent of mean (GAM) ranged from 11.29 to 13.63. The highest GAM was recorded in leaf area at 6 WAP, while leaf area at 8 WAP had the lowest GAM (Table 3).

The result of analysis of variance indicated non-significant differences (P> 0.05) of genotypes for all characters studied except leaf area and leaf area index at 6 and 8 WAP. This result agrees with Nwangburuka *et al.*(2012) who reported significant differences in morphological characters of okra. The observed significant variation among some of the genotypes in this study is implicative of the difference among the genotypes under study and the existence of possible genetic divergence in fluted pumpkin. The non-significant and comparably low genotypic and phenotypic variance among the genotypes for all characters except leaf area and leaf area index implies that there would not be adequate gains in selecting these characters against similar findings reported in cucumber (Afangideh and Uyoh, 2007). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values are employed for comparing the relative amount of phenotypic and genotypic variation among different characters. In this study, PCV was observed to be higher than GCV for characters such as leaf area and leaf area index at 6 WAP and this shows the environmental influence on the expression of these traits, this result agrees with

Ahirwar and Singh (2018). Therefore, greater potential could be expected in selection for these characters and further evaluation for the improvement of this crop. According to Ojo and Amanze (2001), high heritability strongly suggests that there is potential for large genetic determination for these characters which can be exploited for improvement of marketable leaf yield of fluted pumpkin. In this study, high heritability estimates were accompanied by high genetic advance for leaf area and leaf area index, an indication that the characters have high selection value with less environmental influence. Therefore, improvement by direct phenotypic selection is possible. According to reports by(Nwangburuka *et al.*, 2012; Ahirwar and Singh, 2018)if high heritability value is accompanied by high genetic advance, it may be governed by additive gene action and improvement with respect to these characters could be brought about by phenotypic selection.

Conclusion

The results showed that genotypes varied significantly for some traits studied such as leaf area and leaf area index. The high heritability and genetic advance observed in leaf area and leaf area index at 6 WAP, suggests that these characters have additive gene effects and can be further evaluated for improvement of this crop.

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Table 1: Mean squares, variance ratios and means obtained from ANOVA of fluted pumpkin genotypes.

Attributes	Genotype	Error	V. ratio	Mean
LA6WAP	1078.30	200.20	5.39**	233.40
LA8WAP	1185.00	249.20	4.76**	286.30
LAI6WAP	17250.00	3203.00	5.39**	933.75
LAI8WAP	18960.00	3987.00	4.76**	1145.00

**highly significant ($P < 0.01$)

LA: leaf area
LAI: leaf area index

Table 2: Phenotypic (Vp), genotypic (Vg) and error variances (Ve) for yield and associated traits.

Attributes	Vp	Vg	Ve
LA6WAP	359.43	292.70	66.73
LA8WAP	395.00	311.93	83.07
LAI6WAP	5750.00	4682.33	1067.67
LAI8WAP	6320.00	4991.00	1329.00

LA: leaf area
LAI: leaf area index

Table 3: Phenotypic, genotypic coefficients of variation (PCV and GCV), broad sense heritability (h^2B), genetic advance (GA) and genetic advance as percentage of mean of morphological traits of fluted pumpkin genotypes.

Attributes	**PCV**	**GCV**	**h^2bs (%)**	**GA**	**GA (%mean)**
LA 6WAP	8.12	7.33	81	31.80	13.63
LA 8WAP	6.94	6.17	79	32.33	11.29
LAI WAP	8.12	7.33	81	127.20	13.62
LAI WAP	6.94	6.17	79	129.33	11.30

LA: leaf area
LAI: leaf area index