



MODELLING FOR YIELD PARAMETERS INFLATED PUMPKIN (*Telfairia occidentalis* Hook F.) COLLECTIONS

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ABSTRACT

This study assessed the genetic diversity among fluted pumpkin (*Telfairia occidentalis*) collections for their breeding values. Seeds were collected from five (5) different markets each with three sub-locations per market within Makurdi metropolis. A total of sixty (60) accessions were planted in a Randomized Complete Block Design (RCBD) structure in the field. Evaluation was done using twenty (20) characters comprising eleven (11) quantitative and nine (9) qualitative characters. Data were subjected to statistical analysis using Minitab (Version 16.0). Seedlings showed excellent vigour indices ranging from 69 to 159. Mean plant spread was 24.42±2.2. Number of branches at day 30 recorded the widest CV value of 81.87% among the quantitative characters. Plant length at day 30 was 89cm maximum in RWM3A and 200cm highest at day 60 in the same accession. Mean plant length was 93.39±7.61. Based on CV ranking with >50%, high variability was recorded in number of branching, plant length and spread. Correlation matrix showed a very high coefficient r between NB@30 and NB@60 (+0.912), and high correlations among PG and VI (+0.816), PH@60 and LL (+0.830) as well as PH@60 and LW (+0.788). Multiple regression analysis revealed three significant predictors of yield in a fit model ($F= 28.6$, $P<0.05$) with high coefficient of determination R^2 of 83.1%. Clustering of accessions was not based on locations of seed collection but on characters. Dendrogram revealed more convergence of accessions than divergence, an indication of low genetic diversity. The most divergent of all the accessions was RWM3A representing seeds collected from Railway market at station 3. This report is useful in the bioconservation of genetic resources and biotechnological improvement of *T. occidentalis* in the quest for food security.

Keywords: Biotechnology, Genetic diversity, *Telfairia*, Crop Improvement, Food security

1. INTRODUCTION

Fluted pumpkin (*Telfairia occidentalis*) is an important species in the family Cucurbitaceae. It is a leafy vegetable crop commonly cultivated in South-Eastern part of Nigeria (Odiaka *et al.*, 2008) but it has also gained prominence in the South-Western part of the country (Schippers, 2002). The fluted pumpkin is a very important vegetable crop well known for its high nutritional, medicinal and economic values (Ehiagbonare, 2008). It ranks among the three most widely consumed vegetables at homes and in restaurant across Nigeria (Ajayi *et al.*, 2006). The vegetable crop is indigenous to Nigeria and is widely propagated in tropical wet coastal areas of West-African countries. The wild type are fast disappearing due to over exploitation and are now replaced by cultivated forms (Uboh *et al.*, 2013).

The fluted pumpkin is a very important vegetable crop well known for its high nutritional values, (Ehiagbonare, 2008). Studies reveal that the plant possesses antibacterial properties that make it capable of inhibiting the growth of intestinal pathogens such as *Escherichia coli*, *Pseudomonas aeruginosa*, *Salmonella typhi* (Oyewole and Abalaka, 2012).

The success of any crop breeding program largely depends on the availability of huge genetic variability, genetic advances and character association, direct and indirect effect on yield and its attributes (Uboh *et al.*, 2013). Determination of heritability estimates will provide information on the proportion of phenotypic variance that is due to genetic factor for different trait (Odiaka 2008). This will indicate the inter-relationship between two or more plant characters and yield providing suitable means for indirect selection for yield. The narrowness of genetic diversity has been a challenge in the improvement of fluted pumpkin (Uboh *et al.*, 2013), thus a challenge to growers and breeders. This work aimed at assessing the genetic diversity among fluted pumpkin (*Telfairia occidentalis* Hook.f) collections using morphological markers in order to explore their breeding values.

2 MATERIALS AND METHODS

Seed Collection and Identification

Fluted pumpkin seeds (*Telfairia occidentalis*) were collected from five (5) different markets, three (3) locations per markets. A total of 15 locations were sampled as given in Table 1 with appropriate codes. Seeds were authenticated in the Department, Botany Federal University of Agriculture, Makurdi, Benue State.

Experimental Design and Planting

Five (5) seeds from the 15 sampled locations were planted, each location replicated 4 times. A total of sixty (60) accessions were planted in a Randomized Complete Block Design (RCBD) structure in field layout measured 40 by 50 meter with 40cm x 40cm ridges for planting. The experimental field was irrigated up to seedling establishment after which there was no further irrigation. Seeds were planted in wet season followed by post planting activities such as inorganic manure application and manual weeding.

Table 1: Market Locations, Replicate and the Accession symbols.

Location	Replicates and Accession symbol
Railway market – 1	RWM 1A, RWM 1B, RWM 1C, RWM 1D
Railway market – 2	RWM 2A, RWM 2B, RWM 2C, RWM 2D
Railway market – 3	RWM 3A, RWM 3B, RWM 3C, RWM 3D
North bank market – 1	NBM 1A, NBM 1B, NBM 1C, NBM 1D
North bank market – 2	NBM 2A, NBM 2B, NBM 2C, NBM 2D
North bank market – 3	NBM 3A, NBM 3B, NBM 3C, NBM 3D
Wurukum market – 1	WKM 1A, WKM 1B, WKM 1C, WKM 1D
Wurukum market – 2	WKM 2A, WKM 2B, WKM 2C, WKM 2D
Wurukum market – 3	WKM 3A, WKM 3B, WKM 3C, WKM 3D
Wadata market – 1	WAM 1A, WAM 1B, WAM 1C, WAM 1D
Wadata market – 2	WAM 2A, WAM 2B, WAM 2C, WAM 2D
Wadata market – 3	WAM 3A, WAM 3B, WAM 3C, WAM 3D
Modern market – 1	MM 1A, MM 1B, MM 1C, MM 1D
Modern market – 2	MM 2A, MM 2B, MM 2C, MM 2D
Modern market – 3	MM 3A, MM 3B, MM 3C, MM 3D

Tables 2: Evaluated Characters and their codes

S/N	Characters		Type
1	Percentage germination (%)	PG	Quantitative
2	Vigor index	VI	Quantitative
3	Internodes length (cm)	IL	Quantitative
4	Number of branches at day 30	NB@30	Quantitative
5	Number of branches at day 60	NB@60	Quantitative
6	Plant height at day 30 (cm)	PH@30	Quantitative
7	Plant height at day 60 (cm)	PH@60	Quantitative
8	Leaf length (cm)	LL	Quantitative
9	Leaf width (cm)	LW	Quantitative
10	Leaf petiole length (cm)	LPL	Quantitative
11	Stem circumference (cm)	SC	Quantitative
12	Plant spread (cm)	PS	Qualitative
13	Plant habit	Ph	Qualitative
14	Phyllotaxy	Pt	Qualitative
15	Leaf shape	Ls	Qualitative
16	Leaf margin	Lm	Qualitative
17	Stem pigmentation	Sp	Qualitative
18	Stem hairiness	Sh	Qualitative
19	Leaf hairiness	Lh	Qualitative
20	Leaflet texture	Lt	Qualitative

Data collection and Statistical Analysis

Accessions were evaluated using a total of twenty (20) characters comprising eleven (11) quantitative and nine (9) qualitative characters as given in Table 2. Vigour index was calculated based on standard procedure (Olasanet al., 2018a). Data were subjected to statistical analysis using Minitab (Version 16.0). Descriptive statistics performed were the mean and its standard error, coefficient of variation (CV), the range, minimum and maximum values. Other statistical operations performed were: Correlation, multiple regression and cluster analysis. Dendrogram was constructed using the Single Linkage method measured on Euclidean distance. Level of significance was flagged at 0.05 for all test statistics.

3 RESULTS AND DISCUSSION

Table 3 gives the description of quantitative evaluation of *T. occidentalis* accessions. All seeds recorded 100% germination. Seedlings showed excellent vigour with indices ranging from 69 to 159. Accessions had different germination, spread and growth rates. Mean plant spread was 24.42 ± 2.2 ranging between 7cm and 50cm in RWM2C. Number of branches at day 30 recorded the widest CV value of 81.87% among the quantitative characters and it was between 0 and 4 branches per plant. Maximum branching at day 60 was observed in WKM3E with 9 branches per plant. Plant length at day 30 was 89cm maximum in RWM3A and 200cm highest at day 60 in the same accession. Mean plant length was 93.39 ± 7.61 . The longest leaf was 13cm as observed in NBM1D bearing petiole of 3cm long. Mean stem circumference was 1.89 ± 0.14 but stem was widest in MM3C by 3cm. Based on CV ranking with 50% cut off point, NB@30 > NB@60 > PL@30 > PS. Thus, high variability was recorded in number of branching, plant length and spread. Correlation matrix (table 4) showed a very high coefficient r between NB@30 and NB@60 (+0.912), and high correlations among PG and VI (+0.816), PH@60 and LL (+0.830) as well as PH@60 and LW (+0.788). Other associations were either weak or moderate but all in positive direction.

Table 3: Descriptive Statistics for quantitative Characters

Characters	Mean	S.E Mean	CV	Minimum	Maximum
%G	100.00	0.000	0.00	100.00	100.00
PS	24.42	2.20	51.75	7.00	50.00
VI	95.03	2.85	17.21	69.00	159.00
IL	11.424	0.805	40.47	2.0000	25.000
NB@30	1.212	0.173	81.87	0.000	4.000
NB@60	3.303	0.363	63.09	1.000	9.000
PL@30	46.76	4.38	53.77	10.00	89.00
PL@60	93.39	7.61	46.83	20.00	200.00
LL	9.030	0.438	27.89	5.000	13.000
LW	4.758	0.272	32.83	3.000	10.000
LP	1.3939	0.0967	39.86	1.0000	3.0000
SC	1.89	0.136	41.57	1.000	3.000

Legend: S.E= Standard error, CV= coefficient of variation, DG=day to germination, NG=number of germination, %G=percentage germination, PS=plant spread, I=vigor index, PH=plant habit IL=internodes length, NB@30=number of branches at 30 days, NB@60=number of branches at 60 days, PL@30=plant length at 30 days, PL@60=Plant length at 60 days, LL=leaf length, LW= leaf width, LP=leaf petiole length, SC=stem circumference

Table 4: Pearson's Correlation Matrix among Quantitative Characters

	PG	VI	NB@30	NB@60	PH@60	LL	LW	LP	SC
PG	1	0.816	0.254	0.359	0.460	0.657	0.595	0.520	0.504
VI		1	0.270	0.291	0.375	0.597	0.459	0.356	0.501
NB@30			1	0.912	0.538	0.555	0.382	0.113	0.372
NB@60				1	0.695	0.679	0.483	0.231	0.509
PH@60					1	0.830	0.788	0.617	0.555
LL						1	0.634	0.480	0.643
LW							1	0.634	0.389
LP								1	0.181
SC									1

Legend: S.E= PG=percentage germination, PS=plant spread, VI= vigor index, PH=plant habit IL=internodes length,

NB@30=number of branches at 30 days, NB@60=number of branches at 60 days, PL@30=plant length at 30 days, PL@60=Plant length at 60 days, LL=leaf length, LW= leaf width, LP=leaf petiole length, SC=stem circumference

Weak r =0.00-0.39, Moderate r=0.4-0.69, High r=0.70-0.89, Very high r= 0.90-1.00

Multiple regression analysis among five regressors showed that NB@60 (T=3.05), LL (T=2.56) and IL (T=3.36) were good predictors as $P < 0.05$ (table 5). Hence, plant length at maturity (yield) could be predicted in a regression equation $PL @ 60 = 0.8 - 0.830 DG - 0.166 VI + 7.73 NB @ 60 + 6.23 LL + 3.63 IL$ with a high coefficient of determination (R^2) of 83.1%. This predictive model was fit with a large F value of 28.6 ($P < 0.05$) as given in Table 6.

Variability was observed in some qualitative characters, each having 2-3 character states especially in stem pigmentation and leaf properties including texture and hairiness. Characters that did not vary were plant habit, phyllotaxy, leaf margin and its shape (Table 7). Among the qualitative characters, stem pigmentation and leaf texture were the most important traits that contributed to the observed variability.

Cluster analysis combined both qualitative and quantitative data that produced a dendrogram (Figure 1). It revealed some levels of differences and similarities among the accessions based on shared characteristics. Clustering of accessions was not based on locations of seed collection but on characters. The most divergent of all the accessions was RWM3A representing seeds collected from Railway market at station 3. This accession was not included in any cluster. Other notable divergent accessions but within clusters were NBM2A and RWM3C representing seeds collected from North bank market at station 2 and Railway market at station 3 respectively. Some accessions with good yield attributes formed a cluster while other groupings were based on similarities in qualitative traits of accessions.

Table 5: Predictive Model for Yield

Predictor	Coef	SECoef	T	P
Constant	0.82	13.54	0.06	0.952
DG	-0.8302	0.9072	-0.92	0.368
VI	-0.1665	0.2129	-0.78	0.441
NB@60	7.730	2.531	3.05	0.005
LL	6.231	2.434	2.56	0.016
IL	3.627	1.080	3.36	0.002

S = 21.2489 R-Sq = 83.1% R-Sq(adj) = 80.2%

The regression equation is $PH @ 60 = 0.8 - 0.830 DG - 0.166 VI + 7.73 NB @ 60 + 6.23 LL + 3.63 IL$

Legend: DG=day of germination, VI= vigor index, NB@60=number of branches, LL=leaf length, IL= internodes length.

Table 6: Analysis of Variance of Regression Model for Plant Length

Source	DF	SS	MS	F	P
Regression	5	64570	12914	28.60	0.000
Error	29	13094	452		
Total	34	77664			

Table 7: Variability in Qualitative Characters

Character States	Character	Remarks
1	Plant habit, Phyllotaxy, Leaf shape, Leaf margin	No variation
2-3	Stem pigmentation, Stem hairiness, Leaf hairiness and Leaflet texture	Variation observation

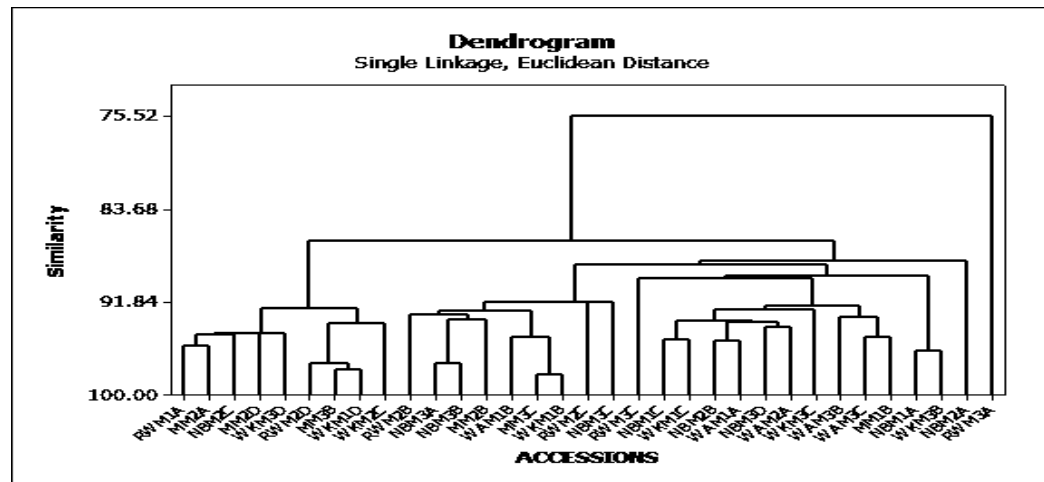


Figure 1: Dendrogram among 60 Accessions of *T. occidentalis*

The outcome of this work has yielded vital information needed for selecting best genotypes for crop improvement. Currently, fluted pumpkin farmers use landraces (local genotypes) due to lack of improved genotypes. Thus, there are unpredictable and low yields, poor quality and low tolerance to diseases and pests. The fact that the genetics of the crop has not been fully understood makes genetic improvement of the crop very difficult. Hence, there is need to exploit the genetic diversity present in the base population to breed superior and high yielding genotypes for commercial cultivation in order to meet increasing demand for the crop. In the process of genetic improvement of any crop, genetic diversity among germplasm plays a major role, since it opens the way to determine the most divergent parents based on the contribution of different qualitative and quantitative traits, for further utilization in any hybridization program (Shukla *et al.*, 2009).

Good results obtained in the plant description, correlation and regressions should be explored, especially those traits with high CV values, high positive correlations as well as those that could predict yield. Variability observed in number of branches produced, plant length and spread is noted. This outcome is consistent with previous work (Fayeunet *et al.*, 2012). In this work, plant branching was consistent from initiation to maturity. As the plants grow, so also the leaf sizes. Similar findings had been reported in other related crops. For instance, some workers reported that leaf width increased with an increase in plant height in cucumber accessions (Afangideh and Uyoh, 2007), African yam bean (Okoye and Eneobong, 1992) and groundnut (Olasanet *et al.*, 2018b). According to Fayeunet *et al.* (2012) and Olasanet *et al.* (2018b), significant correlation between characters indicates that there is the likelihood of simultaneous improvement of two or more characters. This is because it shows mutual relationships among characters and selection for one will translate to selection and improvement of the other. 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 the fluted pumpkin (Ojo and Amanze, 2001; Fayeunet *et al.*, 2012). Based on cluster analysis, there is more convergence than divergence of accessions in this work suggesting a low level of genetic variability. Except in one divergent accession in the Railway market, others recorded high similarity coefficient between 75.5- 98%. This is in agreement with the findings of Ajayiet *et al.* (2006) and in contrary that of Fayeunet *et al.* (2012) who reported wide genetic diversity among thirty-five genotypes of fluted pumpkin collected from seven States in Southern Nigeria. It thus suggests the need for a wider distribution of collection of the plant's seeds to maximize diversity studies. Nevertheless, diversity of characters recorded in this study is well noted. The assemblage of fluted pumpkin collection or germplasm that arose from this work is a huge milestone. This is a form of conservation of plant genetic resources that may also facilitate future research work on the crop. The

4 CONCLUSION

High variability was recorded in number of branching, plant length and spread. Among the qualitative characters, stem pigmentation and leaf texture were the most important traits that contributed to the observed variability. Some quantitative characters were positively associated especially plant length and leaf sizes. Yield could be accurately predicted in a fit regression model. Dendrogram revealed more convergence of accessions than divergence an indication of low genetic diversity. The most divergent of all the accessions was RWM3A representing seeds collected from Railway market at station 3. Accessions with excellent yield parameters could be selected and explored by growers. The information provided in this report is useful in the biotechnological improvement of *T. occidentalis* collections in future breeding in the quest for food security.

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