The Use of Proximate Composition Analysis in the Identification of Superior Progenies for Selection in a Segregating Population of Sweetpotato (Ipomoea Batatas. (L) (Lam)

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ABSTRACT

A research was conducted to carry out an evaluation analysis of the proximate composition of sweetpotao genotypes from both half and full-sib families in the identification of superior progenies in a segregation population of sweetpotato. From the results obtained, a highly significant relationship (p<0.050) was observed among the proximate components analysed. The results revealed high moisture content in most of the progenies having 71.73% for A095 as against 55.27% for A176.The starch content (% carbohydrate) showed highest in A095 (62.40%) as against A0037 which had the lowest starch content (carbohydrate) value (1.92%). This trend is also the case observed in percentage composition of crude protein, fat, crude fibre and ash in the sweetpotato root samples. A negative and very highly significant association was also observed between the dry matter and carbohydrate (r = - 996**). A negative association was observed between crude fibre and carbohydrate (r = - 0.410**), as well as between ash and carbohydrate (r= -0.287*). The association between crude protein and ether extract was positive but not significant. Crude fibre had a negative and significant relationship with moisture content (r = -0546*). Ether extract had a positive and significant association with moisture content (r = 0.502*).

Key Words: Progenies, Sweetpotato, Half-Sib, Full-Sib, Proximate composition.

Introduction

Sweet potato (Ipomoea batatas (L) Lam) Is a widely grown food crop which serves as a major staple food in many parts of the world and Africa very inclusive. Sweet potato is actually a tropical crop which is grown widely in major tropical regions (Woolfe, 1992). Apart from being a tropical crop, Sweet potato have also been found to grow and perform well in different agro-ecological zones, while maintaining the growth production of between three to five month (Afuape et al, 2011). Woolfe (1992), observed that sweetpotato can also thrive in soil that are not too rich in nutrients as compared to the nutrient requirement of other crops. Sweetpotatos provide a wide range of usefulness as it is a major source of food to man, use for animal feed production and also serves as industrial raw material for different products and also used for biofuel production (Aregheore,2004) Leobenstein and Thottappily (2009). Apart from the tubers, the leave of potato which is very rich in vitamins and minerals, are consumed as vegetable among many communities around sub-Saharan Africa (Low et al. 2007; Ma et al. 2009) Lin et al (2007) and County et al (2008). Have observed that due to the high level of yield of sweet potato, it has contributed immensely to the reduction of food scarcity and malnutrition among the people. In crop improvement, there is need to identify and characterize superior genotypes which has the desired traits needed for sustainable production (Tseng et al. 2002; Elameen et al. 2011). Understanding the genetic variability and genetic interrelationship present among germplasm collection is valuable to avoid redundancy and allows plant breeders to select potential parents with desirable traits for cultivation and development (Chaudhary and Singh 1982;Yoshide 2004).

In the identification of superior genotypes of sweet potato, proximate composition analysis plays a major role. Therefore breeders have taken into cognizance the result of proximate composition analysis in their breeding decisions. Some cultivars which are orange/yellow fleshed are very rich in carotenoids and good dietary sources of B- carotene from which the human body synthesis the vitamins A (Low and Var Jaarsveld, 2008).These cultivars have at different times formed major areas of research in sweetpotato.

This research work aims at the identification of superior progenies for selection through the use of proximate composition analysis for further breeding of sweetpotato.

Related work/Literature

Nweke. O.L (2019) worked on the variation in proximate composition among cultivars sweetpotatoes. The result obtained from the study showed that the values of moisture and dry matter were low when compared to the value obtained by other researchers. The result obtained from the study showed that sweet potato showed variations in the composition of crude protein, carbohydrate, ash, moisture, fat, crude-fibre among the eight variation worked on. Zulkifi N.A et al (2021) worked on the proximate composition of Malaysian local sweetpotato. From the results, the five local varieties of sweetpoto used in the experiment revealed that the composition and the potential of the varieties performing well in a wide range of industries. From the result of the proximate analysis of 26 accessions of sweetpotato carried out by Afolabi M.S et al (2020), sweetpotato accessions were observed to have high moisture, carbohydrate and crude-fibre content. The research work concluded by emphasizing on the need for breeders to consider proximate result on sweet potato breeding. In the work of O.M Makanjuola et al (2017) in their study of the effect of variety on proximate composition of potato flour, the result showed that sweetpotato has more carbohydrate content as when compared to other red potatoes considered in the research. Anha and Baruch (2016) carried out an evaluation experiment on proximate composition of sweet potato for better utilization through agro- food proceeding chain. The result supported the use of proximate analysis in making decisions on the sweetpotato breeding.

Materials and Methods

The experiment was carried out at the laboratory of the National Root Crop Research Institute Umudike Nigeria. This was done by laboratory analysis of roots of the selected promising progenies. The Roots from promising genotypes and that of the check varieties were collected, peeled and washed and subjected to laboratory analysis. Standard methods of Analytical Chemistry (AOAC, 2010) were used for the proximate analysis in the determination of moisture content, dry matter content, ash content, crude protein content, crude fibre content, fat content, and carbohydrate content in percentage (%).

The genotypes used for the experiment and the families they belongs to can be found below

Full-Sib progenies

ZC002

K003

I012

Half-Sib progenies

A176

B041

A0037

A002

B049

A017

B063

A013

ZC002

A106

D077

K003

A096

A092

B069

D075

B057

A130

A079

C081

C095

A095

Check varieties

TIS87/0087

UMUSP01

UMUSP013

Data Analysis

The Least Significant Difference (LSD) was used for separation of means. Correlation analysis, (step wise) was carried out to examine the variations among and between the progenies of both families

(half and full-sib). Genotypic, phenotypic and error variances were estimated using the formulae of Wricke and Weber (1986) and Prasad et al., (1981).

The phenotypic (PCV) and genotype (GCV) coefficients of variation were estimated by the methods of Burton (1952) and Johnson et al. (1955). Broad sense heritability (h^2_b) was expressed as the percentage of the ratio of VA to VP on genotypic mean basis as described by Allard (1991).Genetic advance was estimated using the method of Fehr (1987). GA was calculated as a percentage of the mean.

Results and Discussion

Table 4.1 shows means of the proximate composition of selected promising progenies. The results revealed high moisture content in most of the progenies having 71.73% for A095 as against 55.27% for A176.The starch content (% carbohydrate) showed highest in A095 (62.40%) as against A0037 which had the lowest starch content (carbohydrate) value (1.92%). This trend is also the case observed in percentage composition of crude protein, fat, crude fibre and ash in the sweetpotato root samples. The progeny A017 had the highest crude protein content of 4.01% as against A0037 with crude protein content of 2.41 (Table 4.18) The dry matter content was highest for A176 with a value of 44.73% with A095 having the smallest with a dry matter composition of 28.32. The crude fibre followed the same trend with the progeny B041 having the highest means and A079 having the lowest value. The EE value was highest in B057 with a value of 2.31% while A092 gave the lowest value of 0.09% the ash content for all the progenies considered was not high. It ranged between 2.29% for B069 and 0.91 for D077.

4.2: Correlation coefficients of proximate composition and dry matter of selected sweetpotato progenies.

Table 4.2 shows the correlation coefficients of the proximate composition of the selected promising progenies in 2015. From the result, dry matter had a negative relationship with crude protein (r-.309[*]) though not highly significant. A highly significant association was observed between dry matter and crude fibre (r = 0.382[**]) A negative and very highly significant association was also observed between the dry matter and carbohydrate (r = - 996[**]). A negative association was observed between crude fibre and carbohydrate (r = - 0.410[**]), as well as between ash and carbohydrate (r= -0.287[*]). The association between crude protein and ether extract was positive but not significant. Crude fibre had a negative and significant relationship with moisture content (r = -0546[*]). Ether extract had a positive and significant association with moisture content (r = 0.502[*]).

Table 4.3 Shows the analysis of variance of the attributes measured in the proximate composition of the selected promising progenies. From the result, carbohydrate (r=16.16**), dry matter (r=13.00**) and moisture contents (r=13.00***) were very highly significant. The Ash content of the progenies tested was significant but not as that of carbohydrate and dry matter. EE, crude protein and crude fibre were the least significant attributes.

Table 4.4 shows phenotypic (VP), Genotypic (VG), Error Variance (VE), Phenotypic Coefficient of Variance (PCV), Genotypic coefficient of variance (GCV), Broad Sense Heritability (H^2B) and Genetic Advance (GA) for proximate composition of the selected promising progenies. The phenotypic variance ranged from 39.82 to carbohydrate and from 0.11 for EE. The result revealed that the phenotypic variance of most of the desirable proximate attributes were high with high corresponding genotypic values. The error variance was comparatively lower than both phenotypic and genotypic variances for nearly all attributes analyzed. The phenotypic coefficients of variation (PCV) for nearly all the proximate attributes were higher than their corresponding genotypic coefficients of variation (GCV). The E.E had the highest phenotypic coefficient of variation with 27.41 whereas moisture content had the least value of 10.02. This showed a positive interaction between the composition attributes and the environment. The broad sense heritability (h^2b) of the proximate analysis was98% for crude fibre and 86% for dry matter. But on the whole the broad sense heritability have high values which were very positive. This showed that these attributes have very high tendency of being inherited. The genetic advance (GA) as percentage of the mean ranged from150.94 for dry matter and 6.96 for crude protein.

Table 4.1: Means effect of the proximate composition of selected promising progenies.

	Genotypes	Family	DM	MC	CP	CF	EE	Ash	CHO
1	A176	HS	44.73[a]	55.27[f]	3.19[gifh]	3.06[ab]	0.88[L]	1.64[hi]	46.48[efg]
2	B041	HS	44.70[a]	55.30[f]	3.22[gfh]	3.08[ab]	1.37[fcehdg]	2.35[bac]	45.27[g]
3	A0037	HS	44.64[a]	55.35[f]	2.45[n]	2.75[cd]	1.94[a]	1.9[hgf]	1.92[efgh]
4	A002	HS	44.44[a]	55.56[f]	3.16[gish]	3.05[ab]	1.04[jkkg]	2.02[edgcf]	45.98[gf]
5	TIS87/0087	CV	44.26[T]	55.74[f]	3.26[ef]	2.09[d]	1.38[bcdefg]	2.21[ebdacf]	46.78[efg]
6	B049	HS	42.49[ab]	57.51[ef]	3.83[c]	2.46[h]	1.48[bc]	2.18[ebdac]	47.41
7	A017	HS	42.04[ab]	57.95[ef]	4.01[ab]	3.05[ab]	1.35[defgh]	1.7[ebacf]	47.41[defg]
8	B063	HS	41.44[ab]	58.56[ef]	3.90[bc]	2.71[b]	1.41[bcdefgh]	2.12[ebdcf]	48.79
9	A013	HS	41.40[ab]	58.60[ef]	3.08[kish]	2.98	1.46[bcd]	2.12[ebdcf]	49.07
10	ZC002	FS	41.38[ab]	58.61[ef]	3.12[gish]	2.78[c]	1.13[D]	2.13[ebdcf]	49.45
11	A106	HS	40.98[ab]	59.01[ef]	3.33[ef]	2.56[gfh]	0.94	0.94[KL]	49.66[cdefg]
12	D077	HS	40.72[ab]	59.77[ef]	3.53[d]	2.82[c]	1.53[b]	1.91[hgf]	49.48[cdefg]
13	K003	FS	40.21[ab]	59.77[ef]	2.86[l]	3.10[a]	1.26[D]	2.13[ebdcf]	50.60[cdef]
14	A096	HS	40.21[ab]	59.78[ef]	3.16[gish]	2.64[dfe]	1.30[efgh]	1.98[ehdgf]	50.70[cdef]
15	A092	HS	39.85[ab]	60.14[ef]	3.02[kj]	3.01[ab]	0.69[m]	2.02[edgcf]	51.39[cde]
16	UMUSP01*	CV	39.83[ab]	60.17[ef]	4.05[a]	2.62[gfh]	1.21[hj]	2.42[ab]	50.42[cdefgh]
17	B069	HS	39.69[ab]	60.30[ef]	2.86[c]	3.04[ab]	1.30[efgh]	2.29[bdac]	50.81[cdef]
18	I012	FS	39.26[ab]	60.74[ef]	3.05[kj]	2.82[c]	1.32[efgh]	2.28[ebdac]	51.26[cde]
19	D075	HS	38.59[bc]	61.41[ed]	3.20[gish]	2.75[cd]	1.32[D]	1.95[ehdgf]	52.36[cd]
20	B057	HS	38.47[bc]	61.52[ed]	3.12[gish]	3.07[ab]	2.31[bdac]	2.31[bdac]	51.98[cd]
21	A130	HS	37.10[bc]	62.90[ed]	2.96[c]	2.32[I]	1.25[flhg]	2.05[edgcf]	54.22[c]
22	A079	HS	33.47[cd]	66.53[cd]	3.12[gish]	2.45[h]	1.31[fehdg]	2.01[edgcf]	58.65[b]
23	C081	HS	29.28[de]	70.26[cb]	3.20[gish]	2.45[h]	1.11[D]	2.05[edgcf]	61.48[b]
24	C095	HS	29.28[de]	70.72[cb]	3.46[ed]	2.50[h]	1.22[ihg]	1.86[hgf]	61.66[b]
25	A095	HS	22.58[f]	71.68[b]	3.47[ed]	2.53[h]	1.22[Ihg]	1.86[hgi]	62.40[b]
26	UMUSP013	CV	28.32[e]	77.42[a]	4.05[a]	2.55[gfh]	1.46[cehd]	1.50[I]	67.85[a]

Means in the columns followed by the same letters are not significantly different at 5% level of significance. By Duncan's multiple range test (P<0.05). Each value is a mean of double sample.

Table 4.2: Correlation coefficients of proximate composition of selected sweetpotato progenies.

Parameter(%)	DM	Crude protein	Crude Fibre	Ether Extract	MC	Ash	Carbohydrate
Dry matter		-0.309*	0.382**	0.076	0.277	0.640	-0.996**
Crude protein			0.365**	0.026	-0.632	0.040	-0.257**
Crude fibre				-0.207	-0.546*	0.740	-0.410**
Ether extract					0.502*	0.058	-0.094
Moisture content						0.660	-0.287*
Ash							-0.468
Carbohydrate-							

ns   =   not significant

*   =   P<0.05

**   =   P<0.01

Table 4.3: Grand Mean, Mean squares and variance rations of the attributes measured in the proximate analysis of the selected promising genotypes in.

Attributes	Grand Mean	Mean square Genotype	Mean Square Error	VR
DM	38.50	70.64	5.43	13.00***
CP	3.26	0.28	0.00	0.28
EE	1.26	0.11	0.00	0.11ns
MC	61.49	70.64	5.43	13.00***
CF	2.73	0.16	0.00	0.16
ASH	2.07	0.11	0.02	5.50*
CHO	35.73	75.00	4.64	16.16***

DM = Dry matter, CP = crude protein, EE = , MC = moisture content, CF = Crude fibre, A= Ash, CHO = Carbohydrate.

Table 4.4: Phenotypic (VP), genotypic (VG) and Error (VE) variances, phenotypic coefficient of variance (PCV), Genotypic coefficient of variance (GCV), broad sense heritability (h^2B) and genetic advance for proximate composition of selected promising genotypes.

S/N	Attributes	Mean	VP	VG	VE	PCV	GCV	H^2B	GA
1	Dry matter	38.50	38.04	32.60	5.4356	16.01	14.82	0.86	150.94
2	Crude protein	3.26	0.14	0.14	0.0046	10.59	11.55	0.96	6.96
3	EE	1.26	0.11	0.11	0.0046	27.41	26.87	0.96	18.03
4	Moisture content	61.49	38.04	32.60	5.4356	10.02	9.28	0.96	104.85
5	Crude fibre	2.73	0.16	0.15	0.0025	15.04	14.50	0.98	11.70
6	Ash	2.07	0.06	0.04	0.0231	12.66	10.33	0.66	3.00
7	Carbohydrate	35.178	39.82	35.17	4.6487	12.08	11.36	0.88	122.16

From the result of the analysis of variance for the attributes measured in the proximate composition of the selected promising progenies, significant differences were observed in most of the proximate composition measured. Dry matter (DM), moisture content (MC) and carbohydrate (CHO) were all highly significant in terms of their variance ratio. The ash content (A) was also significant but not as high as the other attributes mentioned above. This showed that selection can equally be based on those attributes. The phenotypic coefficient of variation was higher for all proximate composition attributes when compared to the genotypic coefficient of variation. The heritability and genetic advance were all high for all the attributes. This is considerably good as a criteria for sweetpotato selection.

In conclusion, most of the attributes considered in the proximate analysis are all the necessary culinary factors which determines the consumers behavior towards sweetpotato varieties. These behavior goes a long way to affect the level of patronage of the farmers as consumers will always buy based on preferences for certain culinary values. Consequent upon this, sweetpotato breeders can leverage on the proximate composition of these progenies or accessions in further breeding of sweetpotato. Conclusively, the result of this experiment can form the basis for further investigation on sweetpotato improvement using the same selected progenies.

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