Original Article

Evaluation of Inter Family Variations in Sweet Potato (Ipomoea Batatas L.Lam) Using Root Descriptors

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Abstract - *The result obtained from a field experiment conducted in 2014 showed that full-sib progenies like ZB002(22.46), F002(24.86), F009(18.43) and G004(10.72) all had better performance in terms of total number of roots, low virus incidence and severity. Half-sib progenies like C082(19.01) and B050^b(9.00) had a high total number of roots per plot but lower than that obtained from full-sib progenies. When compared with check varieties in terms of total number of roots, total root weight and yield in tons per hectare, the check variety TIS87/0087^{BLK1} gave a high total number of roots(28.19), total root weight (7.34kg/plot) and yield in turns per hectare (8.86t/h) as compared to progenies of both and full-sib families considered. A highly significant relationship (P<0.05) was observed among the root descriptor traits measured between the half and full-sib families. From the result obtained from the half-sib progenies, the number of marketable roots had a strong positive correlation with the number of unmarketable roots (r=0.402**), marketable roots weight (r=0.316*), total number of roots (r=0.757**) and total root weight (r=0.750**). Also, from the result obtained from the full-sib families, the number of marketable roots had a strong positive association with the marketable roots weight (r=0.756), total number of roots (r=0.625**) and total roots weight (r=0.426**).*

Keywords - *Half-Sib, Full-Sib, Phenotypic variation, Progenies, Root Descriptors.*

1. Introduction

Sweet potato, which is majorly grown in Africa as a staple food, is thought to have originated from the Central American region. Sweet potato is said to have entered into Africa around the 19th century [7]. Sweet potato is an herbaceous plant whose root forms the major edible parts and contains large quantities of starch. Sweet potato belongs to the family Convulvulaceae and is also a tropical crop [12]. The sweet potato remains the fifth most consumed and most important food crop in developing countries, followed by rice, wheat, maize and cassava [13]. Sweet potato is a dicotyledonous plant with a family of about 45genera and 100 species, but only *Ipomoea batatas* are of economic importance as food. Sweet potato is a perennial plant, but it is normally grown as an annual crop. Under cultivation, it is usually propagated from vine. A very large number of sweet potato cultivars exist. The number is larger than that of yam, cassava, or cocoyam. Many of these cultivars have arisen through systematic breeding efforts, but an appreciable member of them has also arisen through natural hybridization and mutations [12]. Sweet potato production runs into millions of tons (124 million tons) per year, with a greater majority of the production coming from China [17].

Varietal differences that exist in sweet potatoes have led to myriad research work on sweet potatoes. Through the use of characterization, the variation that exists in accessions or lines based on their morphology and phenology can be estimated. One of the aims of characterization is to clearly differentiate and distinguish between individual genotypes and germplasms [15]. In sweet potato characterization, the use of standard descriptor lists provides an international format that allows for a universally understood language for plant genetic resource data (CIP et al. 1991). The morphological characterization of sweet potatoes using root descriptors is very important in the identification of progenies and finding out their characters, and also knowing the nature of the population of the genotype to be conserved, which makes the selection process by plant breeders easier [8].

In addition to identifying duplicates, it has been applied to research genetic diversity patterns and their relationship to agronomically significant traits [15]. Sweet potato cultivars vary greatly in their botanical qualities and are typically identified by their physical traits. It is imperative to include adjectives when characterizing sweet potatoes. Descriptors are the qualities that allow germplasm to be identified and its possible applications assessed. Distinguishing between phenotypes is made reasonably simple by characterization descriptors. The majority of those pertaining to phenotypic traits match the plant's morphological description and

architectural design [17]. Standard descriptor lists provide a worldwide format. Morphological characterization is an important first step in assessing sweet potato diversity. However, it has limitations because of morphological plasticity [9], the tendency of a species to physically change appearance in response to the environment. Morphological characterization produces a universally understood language for plant genetic resource data (CIP et al., 1991). Diseases are one environmental component that has been frequently mentioned as being crucial to the preservation of genetic diversity in plant populations. Pathogens such as viruses can have a significant impact on the composition, variety, and functionality of plant populations [11].

According to [1], the high physical diversity among sweet potato accessions may not be a reliable indicator of genetic diversity because environmental conditions can vary. If morphological characterization is repeated in time and location, variables including soil types and fertility levels, light, temperature, and moisture regimes could still lead to varied outcomes [2]. As such, their role is to supplement rather than replace phenotypic characterization and morpho-agronomic evaluation. Due to the importance of characterizing new genotypes of sweet potatoes, root descriptors of the genotypes must be properly analyzed in order to establish well-characterized individual traits of the genotypes. This research has looked into the gaps in sweet potato research. It aims to use root descriptors to ascertain the level of inter-family variations in the sweet potato genotype.

2. Related Literatures

[3]investigated root yield and root flesh color separation of sweet potato seedlings. The results showed that there was a significant difference between the genotypes used for the experiment. In the phenotypic characterization of sweet potato genotypes for selection dual purpose traits, [5] discovered that there exists a highly significant difference among the progenies eternals of literature, root size, root weight and marketable root number. This goes to prove the importance of the use of root descriptors in sweet potato breeding. [6] worked on the evaluation of root yield performance of the newly bred orange-fleshed sweet potatoes genotype in Ethiopia. From their research, significant variations were identified in all root descriptor indices measured in the research. [4] Research was done on genotypes by environment interaction and the measurement of stability in eight orange-fleshed sweet potatoes in Ethiopia. The result obtained showed that root descriptor indices were greatly affected by the interaction of environmental factors with the genotypes. Root descriptors have also been measured among exotic orange-fleshed sweet potatoes using morphological characters. The result also showed a high level of significance among the progenies [10].

3. Material and Methods

Newly released genetic materials developed from poly crosses (half-sib) and controlled crosses (full-sib) were used for this experiment. The materials were obtained from CIP Mozambique, where the crosses were carried out. Because the families have different numbers of seeds, half-sib families with up to twenty progenies and full-sib families with up to ten progenies were included in the study. Below is the list of the genotypes used and the families to which they belong:

Full-Sib Families (Controlled Crosses)
MUSG 0619 -16 x MUSG 1101 – 34 –F
LOC 193AL x107031 – 18 –G
MUUSG 0621 – 07 x 105193 – 4-H
LOCAL x 105268 –7-1
LOAL x107007 – 12-J
LOCAL x105193 -4-K
LOCAL x MUSG 11018-34-L
LOCAL x105419-3
MUSG 0621-07 x MUSG 1103-1-N
MUSG 0621 – 07 x MUSG 11006-3-0
LOCAL x 105268 -10
MUSG 0621 -07 x 105097 -72-Q
MUSG 0621 – 07 x 107038 -3-R
MUSG 06121 – 07 x MUSG 11002 – 26 –S
LOCAL x MUSG 111003 –1-T
LOCAL x 105097-12-U
MUSG 0621-07 x10193 -4-V
LOCAL x MUSG 11005 -14
LOCAL x 105413-14-X
MUSG 0621 -07 x MUSG 11007-36-Y
LOCAL x107031 -18-Z
MUSG 0621-07x 105141 -8-ZA
LOCAL x 105199 -29-ZB
MUSG 0621 – 07 x 105268-5
MUSG 0621 – 07 x MUSG 11002 -26
LOCAL x 105053-3-ZE
HALF-SIB FAMILIES (POLYCROSS)
MUSG 0606 – 15-A
MUSG 0614-22-B
MUSG 0608 -61-C
NC 995573 – 50-07 -02 –D
MUSG 11006 –E

3.1. Data Collection and Analysis

Because the families have different numbers of seeds, data were collected from half-sib families that had up to twenty (20) progenies and full-sib families that had up to ten (10) progenies. Data were collected at 6 weeks and 12 weeks after planting (6&12WAP). The data were collected on the following attributes:
A Yield and Yield Components
Number of marketable roots
Number of unmarketable roots
Total number of roots
Weight of marketable roots

Weight of unmarketable roots
Total weight of roots
Variability of storage root shape
Variability of storage root size
Storage root formation
Total yield (tons/hectare)
B. Biotic Stress
- Virus Disease Incidence (VDI
-virus severity.

3.2. Experimental Design

The design used for the experiment was an Incomplete Block Design (IBD) or Augmented Block Design with a check variety planted in every block, and there were fourteen (14) blocks on the whole. This is because of the number of progenies involved in the experiment, which will not be easy to replicate.

3.2.1. Data Analysis

The data collected were subjected to Analysis of Variance (ANOVA) using the Genstat Discovery Edition 3. The Least Significant Difference(LSD) was used for separation of means. Correlation analyses (step-wise) were carried out to examine the variations between the progenies of both families (half and full-sib) (Yan, 2001).

4. Results and Discussion

Table 4.1 shows the performance of progenies of both half and full-sib families. The number of marketable roots ranged from 19.01kg/ha – to 6.34kg/ha. The virus incidence ranges between 1.80 and 0.20. The virus severity score showed a range of 1.46 – 0.25. C082 gave the highest value of the number of marketable roots (19.01) among the half-sib progenies considered, while A176 gave the lowest value (6.34) among the half-sib progenies.

The number of marketable roots among the full-sib progenies, as shown in Table 4.9, ranged from 24.86 – 7.00. The virus incidence ranged from 2.54 – 0.95, while the virus severity ranged from 5.00 – 1.01 in the full sib progenies. The highest number of marketable roots among the full-sib families was recorded for F002 (24.86), with M005 having the lowest value(7.00). The virus incidence was highest in M005(3.05) and lowest in G004(1.01), while the severity level was highest in F002(5.00) and lowest in G004(1.01).

4.1. Storage Root Size and Unmarketable Roots Numbers

Table 4.2 shows the storage roots size and unmarketable roots number in 2014. The storage root size ranged from 4.73 – 1.25cm at twelve weeks after planting(12WAP.) ZB002 had the highest storage root size (4.73cm), while D058 had the lowest root size (4.66cm). Also, in Table 4.2, the number of unmarketable roots ranged from 6.23cm to 0.82cm. M005 produced the highest number of marketable(6.23) roots while A176 produced the lowest number of unmarketable roots (0.82)

4.2. Total Roots Number, Total Roots Weight and Yield in Tons Per Hectare of Half, Full Sib and Check Varieties

Table 4.3 shows the total number of roots, total root weight and yield in tons/hectare of selected half and fullsib progenies. The total number of roots ranged from 28.19 to 6.34. The total root's weight ranged from 7.21kg/ha to 0.60kg/ha, and yield in tons/hectare ranged from 6.23t/ha – 0.60t/ha. TIS87/0087[1] had the highest total number of roots (28.19), while A176 had the lowest(6.32). TIS87/0087[a] had the highest root weight(7.34kg/ha), while B050[b] had the lowest root weight(0.60kg/ha). The highest yield in tons/hectare was recorded for TIS87/0087[13](8.98t/ha), while the lowest yield in tons per hectare was observed in A176(0.22t/ha)

4.3. Correlation Coefficient Between Agronomic Traits of Half–Sib Progenies.

Table 4.5 shows the correlation coefficient between agronomic traits of selected half-sib progenies in 2014. From the result obtained, the number of marketable roots had a strong positive correlation with the number of unmarketable roots (r = 0.402[**]), marketable roots weight (r = 0.316[*]), total number of roots (r = 0.757**), and total roots weight (r = 0.750[**]). The number of marketable roots had a positive correlation with marketable weight (r = 0.716). There was a significant relationship between the number of marketable roots and virus incidence (r = 0.13). The relationship between the number of marketable roots and virus severity (r = -0.122), the shape of sweet potato root (r = -0.177), the size of sweet potato root (r = -0.161), and storage root formation (r = -0.142), were all negative and not significant. From the result also, the number of unmarketable roots had a highly significant relationship with the unmarketable roots weight (r = 0.789[**]), the total number of roots (r = 0.901[**]), The relationship between the number of marketable roots and virus incidence was positive but not significant. The marketable root weight had a positive and strong significant relationship with both the total number of roots (r =0.477[**]) and total root weight (r = 0.954[**]). The relationship between marketable weight and unmarketable root weight was significant and positive (r = 0.259[*]). A negative and non-significant association was observed between marketable roots weight and size of roots (r = 0.090)and storage root formation (r = -0.46), whereas the relationship between marketable roots weight and virus incidence and severity was positive but not significant (r = 0.128) and (r = 0.004). The unmarketable weight had a strong relationship with the total root number (r =0.746[**]) and total root weight (r = 0.532[**]). The relationship between unmarketable roots' weight and storage root's shape was positive and significant (r = 0.315[**]). The total number of roots had a strong significant relationship with the total root weight (r = 0.662[**]). A positive and significant relationship was observed between the total number of roots and storage root size (r = 0.219[*]). From the result also, a negative and significant relationship was observed between the total number of roots and virus

incidence (r = -0.02[**]). The result showed that most of the root descriptions were significant and had a positive correlation with each other (Table 4.12)

4.4. Correlation Coefficients Between Agronomic Traits of Full-Sib PROGENIES in 2014

Table 4.6 presents the correlation coefficient of the root descriptor performance of selected full-sib progenies in 2014. The result showed that the number of marketable roots had a strong positive association with the marketable roots weight (r = 0.756[**]), total number of roots (r = 0.426[**]) and total roots weight (r = 0.712[**]). A positive and non-significant association was also recorded between the number of marketable roots and virus incidence and virus severity. The storage shape, storage root size and storage root formation all had a negative and non-significant association with the number of marketable roots (r = 0.128, r = 0.13 and r = -0.004 r respectively).

A highly significant correlation was recorded between the unmarketable root number, unmarketable root weight (r = 0.809[**]) and total number of roots (r = 0.818[**]). The result also showed that most of the root descriptor traits had negative and non-significant relationships with the number of unmarketable roots. The marketable weight had a strong positive relationship with the total roots weight and a positive but non-significant relationship with unmarketable roots weight (r = 0.217), total number of roots (r = 0.35) and storage root formation (r = 0.53).

The unmarketable root weight had a high positive correlation with the total root number (r = 0.759[**]) and total root weight (r = 0.450[**]). The total number of roots had a highly positive significant association with the total roots weight (r = 0.524[**]) but had negative and non–significant association with the rest of the root descriptor traits. A positive and significant association was also recorded between virus incidence, virus severity and storage root size (Table 4.13)

5. Conclusion

The performance of the progenies revealed that most of the progenies with high marketable roots weight, yield in tons/hectare and high marketable weight all had low cases of virus severity and incidence. From the half-sib families, B053[a] performed better in terms of the number of marketable roots, total number of roots, and total root weight, with a very low rate of virus incidence and severity. C082 also followed the same trend. E034 had very high virus incidence and severity values. These may have accounted for their low mean values in the root descriptor attributes measured. Also, similar trends were observed in full-sib progenies. F002 produced the highest number of marketable roots with a very low level of virus incidence and severity. The highest virus incidence and severity values were seen in I013 and may have accounted for its poor performance in the number of marketable roots, the total number of roots and root weight. The check varieties used in different blocks during the experiment showed good performance but not better than most of the progenies from both half and full-sib families. TIS87/0087 produced the highest number of market roots, while the highest number of marketable roots was observed in ZA002. UMUSP03 gave the lowest number of marketable roots, whereas the yield in tons/hectare was observed to be highest in F002. The variations between the progenies of the half and full-sib families were observed using the root descriptor attributes. C082 gave the highest value in terms of the number of marketable roots. F002 gave the highest marketable root weight but was lower when compared to that of C082. The full-sib progeny, ZB002, had the highest storage root, whereas D058 had the lowest root size. When compared with the performance of the check varieties, B050[b] had the lowest root weight but was better than the full-sib progenies when measured with the check variety, which showed very high performance in terms of number of marketable roots and weight.

The correlation analysis of root descriptors in half-sib progenies measured during the study showed that nearly all the attributes were significantly and positively correlated with each other. The number of marketable roots had a strong positive correlation with the number of unmarketable roots (r= 0.422[**]), marketable weight (r= 0.722[**]), total number of roots (r= 0.757[**]) and total roots weight. The study also revealed that the number of unmarketable roots had a highly significant relationship with the unmarketable root weight (r= 0.909[**]). The relationship between the marketable roots' weight and the total number of roots was significantly strong and positive (r= 0.532[**]).

Also, a negative and significant relationship was observed between the total number of roots and virus incidence, which suggested that virus incidence and its severity may reduce the yield of sweet potato and agree with Carroll *et al.* (2004), who reported that sweet potato yield can be reduced by as much as 30-40% due to virus infection. The correlations observed between the number of marketable roots, root weight, total number of roots and total roots weight suggested that selection for an increase in one trait will simultaneously lead to an increase in most of the other traits, as a significant and positive association between two characters under consideration indicates that the characters can be improved simultaneously in a selection programme and will give good information than each parameter considered alone.

The results obtained from this study have shown that significant differences exist between the progenies from both half- and full-sib families. The importance of these differences or variations is majorly on their usefulness in carrying out further yield trials on the progenies for characterization and naming as varieties.

Acknowledgement.

Table 4.1. Half and full-sib families showing a total number of roots, virus incidence and severity

Progeny	Types of Family	No. of marketable root per plot	Virus Incidence	Virus Severity
A127	HS	8.71	0.20	0.25
A176	HS	6.34	0.60	0.76
B050[b]	HS	9.00	1.50	1.46
C082	HS	19.01	0.64	0.78
D058	HS	6.78	1.25	2.00
F002	FS	24.86	1.08	5.00
F009	FS	18.43	1.28	2.00
G004	FS	10.72	0.95	1.01
M005	FS	7.00	2.54	3.05
ZB002	FS	22.46	1.29	5.04

Table 4.2 Number of unmarketable roots and size of storage roots of selected half- and full-sib progenies

Progeny	Family/Variety	Storage Size Number (cm)	Unmarketable Root Number
A121	HS	1.27	1.22
A176	HS	2.42	0.82
B050[b]	HS	1.86	1.82
C082	HS	2.20	6.37
D058	HS	1.25	4.66
F002	FS	1.64	2.11
F009	FS	3.84	3.28
G004	FS	2.99	4.06
M005	FS	3.62	6.23
ZB002	FS	4.73	1.11

Table 4.3 Number of unmarketable roots and size of storage roots of selected half- and full-sib progenies

Progeny	Family/Variety	Storage Size Number (cm)	Unmarketable Root Number
A121	HS	1.27	1.22
A176	HS	2.42	0.82
B050[b]	HS	1.86	1.82
C082	HS	2.20	6.37
D058	HS	1.25	4.66
F002	FS	1.64	2.11
F009	FS	3.84	3.28
G004	FS	2.99	4.06
M005	FS	3.62	6.23
ZB002	FS	4.73	1.11

Table 4.4 Total number roots, Total roots weight, and yield in tons/hectare of selected Half, Full–Sib Progenies and Check varieties

Progeny	Types of Family	Total Number of Roots	Total Root Weight (kg/plot)	Yield in tons per hectare (t/ha)
A121	HS	8.71	0.90	2.42
A176	HS	6.34	2.20	0.22
B050[b]	HS	9.00	0.60	6.23
C082	HS	19.01	4.45	8.01
D058	HS	6.78	3.24	0.56
F002	FS	24.86	3.25	3.62
F009	FS	18.43	2.25	3.02
G004	FS	10.72	1.98	1.41
M005	FS	7.00	3.05	0.89

ZB002	FS	22.46	6.98	2.08
TIS 87/0087[blk1]	Check variety	28.19	7.34	8.86
UMUSP01[blk14]	Check variety	16.20	6.82	4.74
TIS87/0087[blk13]	Check variety	15.32	4.94	8.98
TIS87/0087[bl9]	Check variety	16.20	7.21	7.64
UMUSP03[blk14]	Check variety	14.30	6.33	1.06

Table 4. 5: Correlation coefficient of selected half-sib progenies.

Characters	No of unmarketable roots	No. of marketable Weight	Unmarketabler oot weight	Total no of roots	Total roots weight	Virus incidence	Virus Severity	Root Shape	Root Size	Root formation
No of marketable roots	0.402**	0.722**	0.316*	0.757**	0.750	-0.130	-0.122	0.177	-0.161	-0.142
No of Unmarketable roots	-	0.199	0.789**	0.901**	0.391	.009	-0.138	0.126	-0.221	0.012
Marketable weight roots		-	0.259*	0.477**	0.954**	0.128	0.004	0.154	-0.46	-.046
Unmarketable roots weight			-	0.746**	0.532**	-0.85	-0.215	0.35**	0.133	-0.24
Total no of roots				-	.662**	.005	-0.241*	0.219	0.165	-092
Total roots weight					-	0.003	-0.159	0.217	0.125	-097
Virus incidence						-	0.350**	0.118	0.085	0.201
Virus severity							-	0.186	0.078	0.039
Root shape								-	-0.065	0.181
Root sizes									-	0.0.64
Root formation										-

*correlation is significant at 5%, **correlation is significant at 1%

Table 4.6 Correlation Coefficients of selected full-sib progenies.

Characters	No of unmarketable roots	Marketabler oots weight	Unmarketable root wgt	Total no of roots	Total roots weight	Virus incidence	Virus Severity	Root Shape	Root Size	Root formation
No of marketable roots	- 114	0.756**	0.065	0.426**	0.712**	0.015	.054	-.12	-.016	-.004

							9		
No of Unmarketable roots		-0.76	0.809**	0.818**	0.147	-0.28	-0.192	-.029	.041	-.116
Marketable weight roots			0.217	0.235	0.878**	-0.78	-0.93	.134	-.211	.053
Unmarketable roots weight				0.759**	0.450**	-0.77	-.079	-.003	.018	.013
Total no of roots				-	0.524**	-0.38	-.034	-.013	-.015	-.068
Total roots Weight					-	-0.138	-.050	-.080	-.123	-.012
Virus incidence						-	0.307	-.165	.265*	-.178
Virus severity							-	.062	.017	-.185
Root shape								-	-1.20	.183
Root sizes									-	.093
Root formation										-

*correlation is significant at 5%, **correlation is significant at 1%

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