GENETIC VARIABILITY AND PATH ANALYSIS FOR IMPORTANT TRAITS IN ORANGE FLESHED SWEET POTATO

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Abstract: Estimation of genetic variability, genotypic and phenotypic correlation and inheritance of among agronomic traits is fundamental to improvement of any crop. Ten (10) OFSP genotypes were evaluated at the National Root Crop Research Institute, Umudike, Abia State , Nigeria, during 2014, 2015 and 2016 cropping seasons.The experiment was laid out in Randomized Complete Block Design with four replications to estimate correlations, genetic variability, heritability and genetic advance of root yield and its component characters in Orange-fleshed sweetpotato. There were significant differences among the genotypes ($p < 0.05$) and in genotype by year interaction for total number of roots per plant, total root weight per plant and root yield. Correlation analysis revealed that significant positive correlation ($p < 0.05$) coefficient (r) values involving root yield were 0.71 ($p < 0.05$), 0.70 ($p < 0.05$), and 0.50 ($p < 0.05$), for root girth, total number of root per plant and root weight per plant respectively. Correlations between root yield and and root girth and between root yield and total number of root per plant were very high (r = 0.71 and 0.70 respectively). Path coefficient analysis for root yield (RY) showed that traits like, root girth (RG), total root weight per plant (TRWPP) and starch (SCH) had high positive direct contribution on RY (4.26, 2.65, and 2.25 respectively). Phenotypic (PCV) and genotypic coefficient of variations (GCV) were highest for beta carotene (98 and 97% respectively) and vine length at 18WAP (248 and 38.96% respectively) across the years. High heritability accompanied by low genetic advance for B-Carotene and vine length at 18WAP was indicative of predominance of non-additive gene actions which could be exploited through crossbreeding to take advantage of heterosis for these traits. Highest heritability was obtained for B-Carotene, dry matter and Starch with each having 1. This was followed by vine length at 18wap (0.93) and internode length at 18WAP (0.81) across the years. This implied the presence of more additive gene effect and a potential for improvement in orange-fleshed sweet potato through selection. The genetic advance for dry matter (128.7), Starch(161.84), day to 50% flowering(22842.3), vine length at 18wap (175993.8) and root yield (665.08) were also high.

Keywords: Correlations, Genetic variability, heritability, OFSP, Path Analysis.

INTRODUCTION

Vitamin A deficiency (VAD) is a serious public health problem in many developing countries, including most countries of Africa (WHO, 1995). It mainly affects poor, young children (6 months to six years of age) and pregnant women. The clinical form of VAD (or xerophthalmia), results when the eye is adversely affected, and is expressed as night blindness or, at its most severe, as total, irreversible blindness. Xerophthalmia affected an estimated 3.1 million children world-wide in 2009 (IVACG, 2009). Sub-clinical VAD affects many more people – an estimated 227.6 million in 2009 (IVACG, 2009) – and results in increased sickness and death rates due to diseases such as diarrhea and measles among those affected. Public health efforts aimed at combating VAD call for a combined approach, including dietary diversification and food fortification. Dietary diversification involves consumption of β- carotene-rich crops like orange fleshed sweetpotato (OFSP). The β- carotene pigment (a dietary precursor of vitamin A) is known to be responsible for the yellow to orange colouration of the flesh of tuberous roots of

some sweetpotato varieties (Degras, 2003; Rodriguez-Amaya and Kimura, 2004).

Sweetpotato (*Ipomoea batatas* [L.] Lam.); 2n=6x=90) is one of the valuable crops producing the highest root dry matter content for human consumption. It provides comparatively high calorie at 152 MJ ha^{-1} day^{-1} and regarded as an important staple food crop in Nigeria (Ukpabi, 2009). These genotypes, especially those of orange fleshed sweet potato (OFSP), were bred as a tool for the global fight against VAD in areas that lack vitamin A rich food materials (Degras, 2003). Thus, it can be used to develop composite flour and added to several products viz., bread, cake, doughnuts, etc thereby increasing the β-carotene intake among the populace. One way to increase the consumption of β-carotene in OFSP is through improvement in in root yield as well as quality of the root produced(Tyagi and Khan, 2008).

Variability plays an important role in crop breeding. An insight into the magnitude of variability present in crop species is of utmost importance as it provides the basis for selection. Yield improvements have been achieved through directional selections for yield and yield contributing traits (Akbar and Kamran, 2006) using correlation and other statistical tools. Correlation is the degree to which two or more variables are related and change together. According to Hallauer and Miranda report (1988) correlation measures the degree of association between two or more characters and is measured by a correlation coefficient. However, under a complex situation, the estimates of correlation alone may be often misleading due to mutual cancellation of component traits, so it becomes necessary to study the path coefficient analysis simultaneously which takes in to account the casual relationship in addition to the degree of relationship. Path coefficient analysis also suggests the selection criterion, and reduces the time taken by a breeder during the selection process (Qaizar *et al.*, 1991). For example, the breeder focuses only on the traits with a large direct effect on a dependent trait such as maturity and yield, thus selection is only restricted to a few essential traits (Vijayabharathi *et al.*, 2009). Path coefficient analysis gives information about the direct and indirect effects of different traits on a complex trait. Genetic variability for agronomic characters is a key component of breeding programmes for broadening the gene pool of crops (Ahmad *et al.,* 2005). However, the success of any crop improvement programme is not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Sumathi *et al*., 2005; Wang *et al*., 2011). Again, the assessment of performance of parental lines based on the yield components could aid in the selection of superior parents for the production of better yielding hybrids (Bocanski *et al*., 2009). This can successfully be achieved if the genetic parameters which govern inheritance of important agronomic traits are established (Mahiboobsa *et al.,* 2012).

Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Waqar *et al*., 2008; Laghari *et al.,* 2010). The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay 1996). Characters with high heritability can easily be fixed with simple selection resulting in quick progress. Apart from heritability, genotypic and phenotypic variances, genetic advance and correlations are some of the key parameters which determine the efficiency of a breeding programme. The genotypic variance explains the proportion of phenotypic variance attributable to the failure of homogeneity among genotypes in different environments (Sujiprihati *et al.,* 2003; Bello *et al.*, 2012) while the phenotypic variance explicates the total variance among phenotypes tested in different environments of interest to the plant breeder. Genetic advance is the difference between the mean of the selected plants in

the original population and the mean of the progeny raised from the selected plants in the next generation. The correlations give reliable and useful information on nature, extent, and direction of selection (Zeeshan *et al*., 2 013). Considering the importance of OFSP and its potential for future Nigerian economy, it is imperative to increase its productivity and other important traits through genetic manipulation. Therefore; the present study was proposed to estimate the extent of variability, heritability and genetic advance in OFSP genotypes and to study the associations among yields and yield related traits in OFSP.

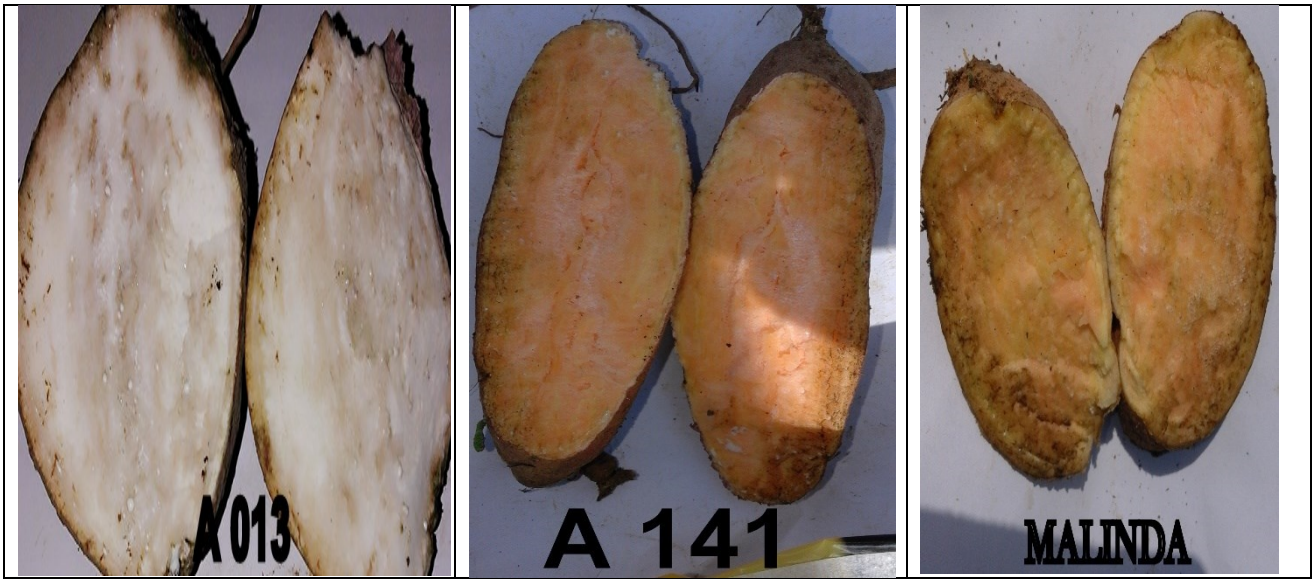
MATERIALS AND METHODS

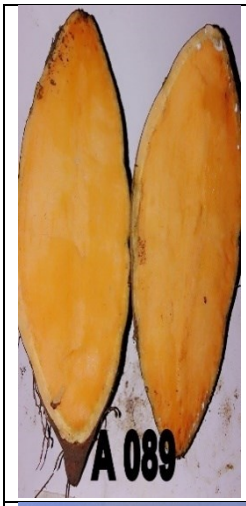
Experimental Site: The experiment was conducted in the National Root Crops Research Institute (NRCRI), Umudike which is situated at Latitude 05°29' N, Longitude 07°33'E and at an altitude of 122m above sea level. Umudike has a total rainfall of about 2000-2500mm per annum with annual average temperature of about 26^{0}C.

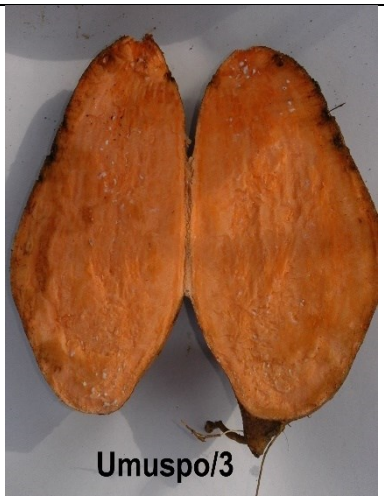
Table 1. Meteorological data of the experimental area at Umudike in 2014, 2015 and 2016

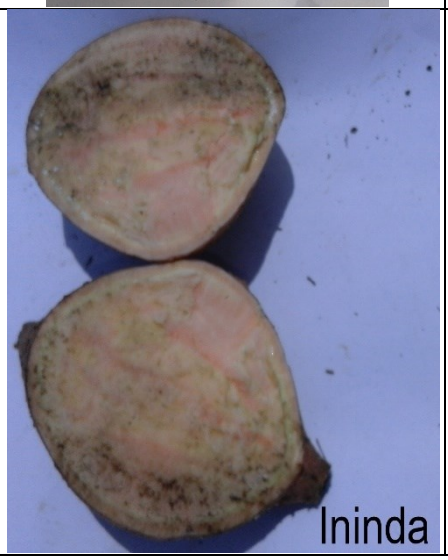
Meteorological Factor	Jan	Feb	March	April	May	June	July	Aug.	Sept.	Oct.	Nov.	Dec.	Mean
2014													
Min. Temp. (^{0}C)	25	25	24	23	23	22	22	23	22	23	23	24	23.3
Max. Temp. (^{0}C)	32	32	31	29	29	28	28	30	28	30	31	31	29.9
Sunshine (Hrs)	6.6	6.7	6.6	4.8	5.8	2.7	2.5	6.3	2.6	6.2	6.4	6.5	5.3
Solar Radiation(ml)	5.5	5.6	4.9	5.0	5.2	2.6	1.8	2.9	1.9	3.0	5.3	5.4	4.1
Monthly Rainfall(mm)	74.8	0.0	13.0	89.7	310.9	361.2	302.7	176.3	361.6	206.1	0.6	15.9	159.4
Number of rainy days	1	0	4	6	18	20	24	16	22	14	3	2	10.8
Relative Humidity (%)	58	56	67	70	72	74	78	68	76	66	62	60	67.3
2015													
Min. Temp. (^{0}C)	23	23	23	22	22	20	20	21	21	20	21	22	258.0
Max. Temp. (^{0}C)	35	35	33	32	32	32	31	33	31	32	33	34	393.0
Sunshine (Hrs)	6.7	6.8	6.5	4.9	5.9	2.8	2.6	6.2	2.7	6.3	6.5	6.6	64.5
Solar Radiation(ml)	5.3	5.4	5.0	4.8	4.6	3.2	1.6	3.8	1.8	2.8	5.2	5.1	48.6
Monthly Rainfall(mm)	18.2	0.0	88.3	169.9	202.8	164.2	232.1	282.5	304.0	205.8	150.2	5.4	1823.4
Number of rainy days	1	0	5	8	20	22	26	18	24	16	4	2	146.0
Relative Humidity (%)	60	58	67	70	76	78	80	68	79	66	64	62	828.0
2016													
Min. Temp. (^{0}C)	24	24	23	22	22	21	21	23	21	22	22	23	268.0
Max. Temp. (^{0}C)	33	33	32	31	30	30	29	31	29	30	31	32	371.0
Sunshine (Hrs)	6.8	6.9	6.7	4.9	6.0	2.9	2.7	3.0	2.8	6.3	6.5	6.6	62.1
Solar Radiation(ml)	5.1	5.2	5.0	4.8	4.9	1.6	1.4	2.8	1.5	3.1	4.7	4.6	44.7
Monthly Rainfall(mm)	4.1	0.0	12.2	88.8	316.8	368.0	402.6	264.1	392.4	277.0	62.1	11.2	2199.3
Number of rainy days	1	0	5	8	19	22	25	16	23	17	5	1	142.0
Relative Humidity (%)	62	59	69	70	71	80	80	85	82	70	65	63	856.0

Source: Meteorological station of the National Root Crops Research Institute (NRCRI), Umudike.









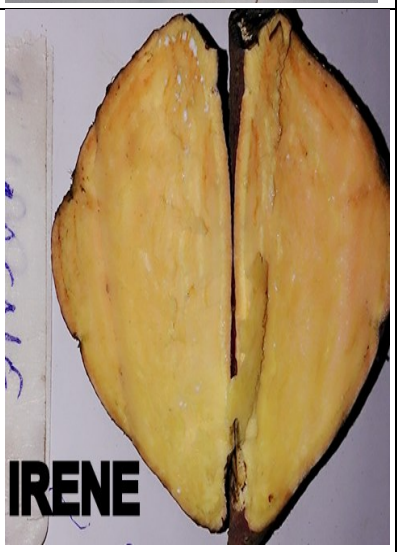


Plate 1. Flesh characteristics of the 10 evaluated OFSP genotypes.

The predominant vegetative type is rain forest (NEST, 1991). However, the soil type is classified as sandy loam ultisol (Agboola, 1979). The ten (10) genotypes (Plate 1) obtained from the (NRCRI) Umudike were grown in a plot size of 1 × 3m ($3m^2$) with a spacing of 1 seedling per stand, with inter and intra row spacing of 1.0 and 0.3m respectively giving a plant density of 33,333 plants per hectare. The experiment was replicated 4 times using a randomized complete block design.

Data collection and analyses: Data was collected on vine length (cm),vine internode length (cm), vine internode diameter (mm), number of secondary stem per plant, number of days to 50% flowering, weight of saleable roots per plant (kg), storage root length (cm), storage root diameter (cm), weight of roots per plant(kg), storage root fresh yield per hectare (t/ha), storage root dry matter content (%),total starch content (mg/100g) and beta-carotene content(mg/100g). The data collected were subjected to uni- and multi-variate analyses; including analysis of variance and Spearman Correlation Coefficient (Ofori, 1996; Hailegebrial, *et al*.,2015). GenStat (2012) and Statistical Package for Social Sciences (SPSS) were the software used for the analysis. Significant means were separated by Fisher's Least Significant Difference Test (LSD), at 5% level of significance. Percentage of each of β-carotene, dry matter, starch and moisture were determined according to standard methods described by FAO (1980).

The genotypic and phenotypic coefficient of variation were calculated by Kwon and Torrie (1964) technique. The genetic advance in percentage of mean was calculated by using Falconer (1989) formula.

Genetic Variance (V_g)

$$= \frac{Genotype\ Mean\ Square - Error\ Mean\ Square\ ((\text{MSG} - \text{MSE}/\text{r})}{Number\ of\ replications\ (r)}$$

Environmental Variance = Error Mean Square (EMS)

Phenotypic Variance (Vp) = Vg + Vg/ r OR (MSG / r)

Genotypic and Phenotypic coefficient of Variation was calculated as

$GCV(\%) = \{(\sqrt{\delta^2_p}/X) \times 100/1\}$,

$PCV = \{(\sqrt{\delta^2_p}/\overline{X}) \times 100/1\}$.

Where, δ_p = phenotypic standard deviation, δ_g = genotypic standard deviation, and X = Grand mean for the characteristic x; PCV and GCV= phenotypic and genotypic coefficient of variation, respectively.

Heritability (H^2) on Entry Mean Basis was calculated as

$$H^2 = \frac{Vp}{Vg}$$

The expected Genetic Advance for each trait was calculated as

$$GA = K\sqrt{VP}\ H^2$$

Where, K = 1.40 at 20% selection intensity for trait;
Vp = Phenotypic variance for trait;
H^2 = Broad Sense Heritability of the trait;

Genetic Advance as percentage of mean is calculated as,

$$GA = \frac{GA}{X} \times 100\%$$

RESULTS AND DISCUSSION

Combined analysis of variance indicated that the effect of year was significant (P< 0.05) for all the characters (Table 2). Rainfall amount and distribution that was higher and favourable in the year 2016 compared to 2014 and 2015 may be responsible for the differences observed between the years for these traits (Table 1). Mean squares due to genotypes, year and genotype x year interaction were significant (P< 0.05) for total number of root per plant, total root weight per plant, dry matter and root yield indicating presence of genetic variability for these traits in the germplasm material studied and which also varied with the differences in yearly conditions. This offers way for further improvement through simple selection. However, the interaction of the year with genotypes is very important in this study. The significant effect of genotype by year interaction indicates the diversity of the genotypes and their differences in environmental responses across the three years for these traits. The mean performances across the three years for culinary qualities, root yield and yield related characters of the OFSP are presented in Tables 2 and 3. The results showed significant differences among the genotypes for culinary qualities, root yield and yield components. The most outstanding genotypes for root yield are Umuspo/3, A

089, and Delvia in descending order with yield ranging from 24.23 to 21.11t/ha, while Malinda had the lowest value for root yield (10.64 t/ha) over the three years. Total root weight per plant varied from 0.47 to 3.38 in the three years with A 089 having the highest (3.38).

The range observed for total number of root per plant was between 3.26 and 6.11. A 089, Umuspo/3 and A 141- recorded the highest number of root per plant with the values of 6.11, 6.09 and 4.58 respectively. With respect to year, 2016 and 2015 had the higher root yield per hectare compared to 2014. The variation was not significant ($p > 0.05$) across the years with respect to culinary characteristics (Table 3). However, highest beta-carotene content (11.031Mg/100gFW) was recorded for A 089, followed by Umuspo/3 (10.233Mg/100gFW) while Delvia had the lowest beta-carotene content (0.141Mg/100gFW). Dry matter content and starch estimate were highest for Delvia (44.4 and 34.0 % respectively). This was followed by Malawi/II that had dry matter content and starch estimate of 43.1 and 31.7% respectively. Umuspo/3 had the least quantity of dry matter and starch (26.0 and 15.7 % respectively). The present results suggest that the available genetic variation observed in important agronomic characters could be useful in designing better effective breeding strategies in OFSP. The variation observed in number of roots per plant, root yield per plant and root yield per t/ha may be as a result of different genetic makeup of the genotypes. The current result is in conformity with the finding of Raham *et al*. (2013).

The findings is also in good agreement with Omiat *et al*. (2005), who indicated that the varietal effect had a significant influence on the total tuberous root yield of sweetpotato. Similarly, Kathabwalika *et al*, (2013) observed significant differences in root yield per plant and root yield per t/ha among the sweetpotato varieties in their trial.

Dry matter content varies due to a number of factors such as variety, location, climate, incidence of pests and diseases, cultural practices and soil types (Shumbusha *et al*., 2010; Vimala and Hariprakash, 2011). Similarly, the variation observed in β-carotene content is attributed to their genetic constitution. According to Woolfe (1992) dark orange flesh roots are rich sources of β-carotene, while yellow/orange roots supply moderate amounts of β- carotene. Teow *et al.* (2007) reported significant variations in respect to β-carotene content among sweetpotato genotypes, and orange flesh had higher β-carotene content than white flesh.

The correlation studies revealed significant ($P < 0.05$) to highly significant ($P < 0.01$) level of probability among the traits (Table 4). The correlation coefficients were generally positive between root yield and other characters, except dry matter, starch and number of branches at 18WAP. The significant positive correlation coefficient (r) values involving root yield were 0.71 ($P < 0.05$), 0.70 ($P < 0.05$) and 0.50($P < 0.05$) for root girth, total number of root per plant and root weight per plant respectively. Positive correlation coefficient (r) of 0.19, 0.13, 0.20, 0.14 and 0.07 were found between root yield and beta carotene, days to 50% flowering, internode length at 18WAP, vine length at 18WAP and root length respectively. However, negative correlations were observed between root yield and dry matter ($r = -0.01$), starch ($r = -0.002$) and number of branches at 18 WAP ($r = -0.02$).

This study revealed that root yield was primarily influenced by root girth and total number of root per plant and secondarily by total root weight per plant as direct contribution factor. Hallauer and Miranda (1988) suggested that selection may be exerted on yield components indirectly, but however, such selection would be effective if the character used possesses high heritability compared to the primary one. In addition, the correlation between them has to be substantial. Correlations between root yield were highest between root girth and total root number per plant ($r = 0.71$ and 0.70 respectively). The high correlations indicate that any increase in root girth and total root number per plant would simultaneously increase root yield. Beta-carotene was significant and negatively correlated with dry matter ($r = -0.42$, $P < 0.01$) and starch ($r = -0.79$, $P < 0.01$) indicating that OFSP genotypes with high beta-carotene content had low dry matter and starch contents. This negative association was attributed to a competition between the dry matter, starch and the β-carotene because they are synthesised in plastids.

Table 2: Mean values of three yield traits of orange fleshed sweetpotato genotypes evaluated for three years in Umudike

Genotype	Total No. of root Per plant				Total root Weight per plant (kg)				Root yield (t/ha)			
	2014	**2015**	**2016**	**Mean**	**2014**	**2015**	**2016**	**Mean**	**2014**	**2015**	**2016**	**Mean**
A 013	5.2	5.63	2.33	**4.39**	0.36	0.66	0.38	0.47	11.92	20.33	12.56	**14.94**
A 089	5.6	8.73	4	**6.11**	0.75	8.73	0.66	3.38	25.11	17.89	22	**21.67**
A 097 a	3.77	6.73	3	**4.5**	0.25	4.84	0.48	1.86	8.26	26.22	16.11	**16.86**
A 141	7.8	3.27	2.67	**4.58**	0.51	3.27	0.35	1.38	17.14	5.22	11.67	**11.34**
Delvia	3.33	5.83	4.33	**4.5**	0.25	2.52	0.86	1.21	8.33	26.33	28.66	**21.11**
Ininda	6.87	1.63	1.33	**3.28**	0.72	1.43	0.23	0.79	23.91	10.27	7.78	**13.99**
Irene	5.33	1.63	3	**3.32**	0.38	1.43	0.38	0.73	12.73	10.27	12.56	**11.85**
Malawi II	6.87	2.1	4	**4.32**	0.68	2.1	0.55	1.11	22.51	8.0	18.33	**16.28**
Malinda	3.4	3.37	3	**3.26**	0.29	2.8	0.46	1.18	9.58	7.11	15.22	**10.64**
Umuspo/3	6.27	6.67	5.33	**6.09**	0.57	1.62	0.74	1.31	19.02	28.89	24.78	**24.23**
Mean	**5.44**	**4.56**	**3.3**		**0.48**	**0.5**	**0.51**		**15.85**	**16.05**	**16.97**	
$LSD_{(0.05)}$ for Genotype	1.78				1.153				7.18			
$LSD_{(0.05)}$ for Year	0.98				0.631				NS			
$LSD_{(0.05)}$ for interaction	3.09				1.996				12.43			
CV (%)	5.9				23.5				8.0			

Table 3. Mean values of three culinary traits of orange fleshed sweetpotato genotypes evaluated for three years in Umudike in three years combined

Genotype	B-Carotene (Mg/100g FW)				Dry matter (%)				Starch (%)			
	2014	2015	2016	Mean	2014	2015	2016	Mean	2014	2015	2016	Mean
A 013	0.187	0.22	0.22	**0.209**	40.3	40.2	40	**40.2**	30.5	30.5	29.8	**30.3**
A 089	11.02	11.02	11.053	**11.031**	28.2	27.8	28.5	**28.2**	18.6	18.0	18.1	**18.2**
A 097 a	0.167	0.167	0.157	**0.163**	34.8	34.8	35.3	**35**	26.4	26.4	25.7	**26.1**
A 141	7.167	7.167	7.167	**7.167**	26	26.3	26.3	**26.2**	16.0	16.7	16.7	**16.4**
Delvia	0.123	0.147	0.153	**0.141**	44.5	44.7	44.1	**44.4**	34.7	33.7	33.7	**34.0**
Ininda	4.613	4.63	4.64	**4.628**	33.6	34	33.7	**33.8**	20.0	20.0	19.7	**19.9**
Irene	1.69	1.667	1.667	**1.674**	38.3	38.6	37.9	**38.3**	30.6	30.5	30.5	**30.6**
Malawi II	3.02	3.087	3.03	**3.046**	43.3	43.6	42.8	**43.1**	31.4	31.8	31.8	**31.7**
Malinda	3.653	3.653	3.653	**3.653**	29.3	29.4	29.4	**29.0**	17.7	17.2	17.5	**17.4**
Umuspo/3	10.233	10.233	10.233	**10.233**	15.2	15.3	48.7	**26.0**	15.4	16.1	15.7	**15.7**
Mean	**4.187**	**4.199**	**4.197**		**33.4**	**33.5**	**36.7**		24.1	24.1	23.9	
$LSD_{(0.05)}$ for Genotype	0.132				10.06				0.7			
$LSD_{(0.05)}$ for Year	NS				5.51				NS			
$LSD_{(0.05)}$ for interaction	NS				17.42				NS			
CV	0.74				5.6				0.5			

Table 4: Simple correlation coefficients among traits measured on 10 OFSP genotypes evaluated in three years combined

TRAITS	1	2	3	4	5	6	7	8	9	10	11	12
B-CaroteneMg100gFW	1											
Dry matter	-0.42**	1										
Starch	-0.79**	0.52**	1									
Days to 50% flowering	0.21*	0.05	-0.10	1								
Internodelength@18WAP	0.26*	-0.24*	-0.22*	0.55**	1							
Vinelength@18WAP	0.18	-0.15	-0.18	0.61**	0.66**	1						
No. of braches@18WAP	-0.09	0.04	0.03	0.63**	0.42**	0.62**	1					
Root length (cm)	0.11	-0.04	-0.17	0.05	0.12	0.11	0.074	1				
Root girth (cm)	0.08	-0.13	-0.03	-0.23*	-0.03	-0.27*	-0.40**	0.23*	1			
Total root No. per plant	0.26*	-0.12	-0.12	-0.21	-0.04	-0.12	-0.31**	-0.18	0.35**	1		
Total root Wt per plant(kg)	0.22*	-0.12	-0.15	-0.15	-0.20	-.220*	-0.21**	-0.18	-0.01	0.37**	1	
Root yield(t/ha)	0.19	-0.01	-0.002	0.13	0.20	0.14	-0.02	0.07	0.71**	0.70**	0.50*	1

* Correlation is significant at the 0.05 level (2-tailed), ** Correlation is significant at the 0.01 level (2-tailed).

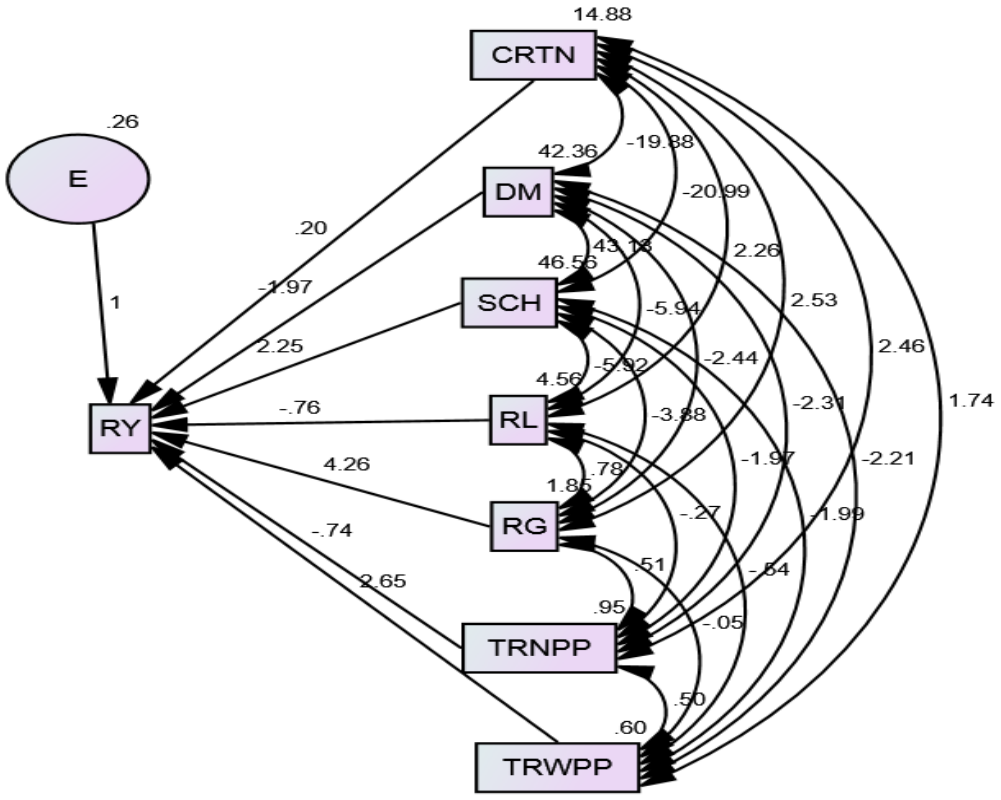


Fig. 1: Path diagram and correlation coefficient of seven characters. Single headed arrow denotes direct effect on root yield, double headed arrow denotes the correlation coefficients between traits

This finding is supported by (Cervantes-Flores *et al.*(2008) who observed negative correlation between dry matter and beta carotene. Knowledge of inter-character relationship is very important in plant breeding for indirect selection of the characters that are not easily measured and for those that exhibit low heritability. CRTN = beta carotene, DM = dry matter, SCH = starch, RL = root length, RG = root girth, TRNPP = total number of root per plant, TRWPP = total root weight per plant, E1 = residual effect.

The phenotypic direct and indirect effects of yield-related traits on root yield are presented in figure 1. Path coefficient analysis for RY showed that traits like, RG, TRWPP and SCH showed highest positive direct effect on RY with 4.26, 2.65, and 2.25 respectively. This means that a slight increase in one of the above traits may directly increase the RY. These traits are therefore, very important components of RY and should be given high weightage in any selection process aimed at improving RY in OFSP. Similar results were reported by Mohanty *et al.*(2016). On the other hand, the maximum negative direct effect was exhibited by dry matter (-1.97) followed by root length (-0.76) and total number of roots per plant (-0.74). Indirect effects often play a more important role than direct effects. For example, the direct effect of TRNPP was negative (-0.74), but its indirect effects through CRTN was high (2.46) explaining why TRNPP was highly positively correlated with RY ($r = 0.70$, $p < 0.01$). The direct effect of RL also was negative (-0.76), but this was confounded by the larger indirect effect through CRTN (2.26) and RG (1.86), explaining why there was a positive correlation between RL and RY ($r = 0.07$). The direct effect of RG and TRWPP on RY were most closely related, indicating that plants producing larger RG and TRWPP produced highest RY in OFSP. These findings are in conformity with Yildirim *et al.*(1997) who stated that root girth and tuber weight/plant had positive and high direct effects on tuber weight/plant. He also reported that main stems/plant; plant height had positive and high direct effects on tuber yield. Conversely, the study is in

disagreement with Maris (1988) who found that number of tuber and average tuber weight had equal effects on total yield. Residual effect (26.0%) measures the role of other possible independent variables not included in the study. This could be attributed to the effect of new environment as reported in cowpea (Afuape *et al*., 2011).

Vine length at 18WAP exhibited the highest genotypic (σ^2g) and phenotypic variance (σ^2p) (2265.22 and 9173.84, respectively -Table 5). This was followed by the dry matter (81.06 and 62.40, respectively). The character with almost equal value of phenotypic and genotypic variances can be considered stable. Lower genotypic and phenotypic variance were obtained for the number of branches at 18WAP (0 and 89.40, respectively) and root length (60.03 for the respectively). A lower value of CV generally depicts low variability among the tested sample; a high proportion GCV to the PCV is desirable in breeding works. The phenotypic variance (σ^2p) and phenotypic coefficient of variation (PCV) was slightly higher than the genotypic variance (σ^2g) and genotypic coefficient of variation (GCV) for most of the traits suggesting the presence of appreciable environmental influence in the expression of these traits. The results for Phenotypic variances (σ^2p) were found to be greater than the corresponding genotypic variances (σ^2g) for most of the characters indicating that the expressions of these characters were influenced by the environmental factors. This agrees with Korkut *et al*. (2001) who obtained similar results in sweet potato. According to Deshmukh *et al.* (1992), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. With this benchmark, the GCV values obtained for B-Carotene (Mg/100g FW), vine length at 18WAP(cm), Starch (%), internode length at 18WAP(cm) and total root weight per plant (kg) can be classified as high, while medium GCV values were obtained for Root yield (t/ha) and day to 50% flowering. The GCV obtained in B-Carotene (Mg/100g FW), vine length at 18WAP, Starch, internode length at18WAP and total root weight per plant suggests selection can be applied more effectively on these traits to isolate more promising genotypes. These observations are in conformity with the findings of Kashiani *et al.* (2008) and Najeeb *et. al.* (2009).

Though genotypic coefficient of variation measures the amount of variation in character, however, the estimation of heritable variation with the help of genetic coefficient of variation alone may be misleading. Burton (1952) suggested that the genetic coefficient of variation together with heritability estimates gave a better picture of the extent of heritable variation. Similarly, the estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Thus the heritability estimates will be reliable if accompanied by a high genetic advance. So, genetic advance should be considered along with heritability in coherent selection breeding program. Dabholker, (1992) classified heritability estimates as low (5 to 10%), medium (10 to 30%) and high (30 to 60%). Considering this benchmark, heritability estimate obtained in this study was high for plant height, B-Carotene, dry matter, starch, vine length at18WAP, internode length at 18WAP, day to 50% flowering and root girth. Similarly, high heritability values coupled with high genetic advance (Table 5) were recorded for dry matter, starch, day to 50% flowering, vine length at18WAP and root yield. This indicated that additive genetic variation was important in the transmission of these traits from the parents to the progeny. Also, these traits can easily be fixed in the genotypes by selection in early generations. This finding is supported by Ahmed *et al*.(2007) and Songsri *et al.* (2008) who reported that better heritability and genetic advance values in important parameters suggest the possibility of improvement in these parameter. However, Hossain *et al*. (2000) and Choudhary *et al*. (1999) reported high estimates of both heritability and genetic advance for number of roots per plant and fresh yield of storage roots per plant in sweet potato. High heritability accompanied by high genetic advance for B-Carotene and vine length at 18WAP is indicative of predominance non-additive gene actions which could be exploited through heterosis breeding. Low heritability with low genetic advance values was

found for number of branches and root length, indicating slow progress through selection for these traits.

CONCLUSION

The mean performance of the character showed substantial amount of variability among the genotypes. Thus the experiment revealed that greater yield response could be obtained through direct selection scheme in OFSP genotypes tested.

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