Food and Agriculture Research Journal
ISSN: 1234-5678 (Print), 1234-5678 (Online)

OPEN ACCESS

Research Article

Genetic variability Analysis for various Yield Contributing Traits in Orange-Fleshed Sweetpotato Genotypes

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Article History
Received: June 12, 2022
Accepted: August 12, 2022
Published: September 15, 2022

Abstract

An experiment was conducted to estimate genetic variability of 47 orange-fleshed sweetpotato (OFSP) genotypes. It was established in two locations (Umudike and Igbariam) in a RCBD fashion with three replications. Data collected were subjected to ANOVA using the software; AGD-R. The results showed that all the characters studied were highly significant ($p<0.01$) for genotypes. All the traits were significant for location except the vine length, days to 50% flowering and root yield. Most of the characters were also significant for genotypes-location interaction. Significant differences observed among genotypes for most traits indicated the presence of genetic variation among the materials. The genotypic coefficient of variation (GCV) was very high for beta carotene (73.8%) and vitamin A (70.0%). Phenotypic coefficient of variation (PCV) was very high for beta carotene(183.5%), root yield per hectare(151.6%), total root weight per plant(150.6%) and total number of roots per plant(113.5%). The PCV was higher than their corresponding GCV for all the characters studies, indicating that the expression of these characters was influenced by environment. The GCV was consistently higher than PCV in all the traits. The genotypic variance was high for days to 50% flowering (373.16), dry matter (220.30), root girth (140.73), root length (68.10) and root yield per hectare (349.66). The magnitude of VA was consistently larger than that of VD for all the traits suggesting that the additive genetic variance was more important than the dominance genetic variance in the inheritance of most studied traits. All the characters studies had high heritability (>60%). High heritability estimates for those traits indicated a high response to selection.

Keywords: Orange-fleshed, sweetpotato genotypes, genotypic coefficient of variation, GCV, phenotypic coefficient of variation, PCV, genetic advance, GA, Heritability.

Introduction

Sweetpotato (Ipomoea batatas (L.) Lam) is a dicotyledonous plant belonging to the family Convolvulaceae (Austin, 1977). Sweetpotato ranks third among tuber and root crops worldwide (FAO, 2005). In Nigeria however, sweetpotato has been identified to be the fourth most vital root crop after Cassava, Yam, and Cocoyam (Okonkwo et al., 2009). Orange-fleshed sweetpotato (OFSP) is now becoming an important member of the tropical root crops having huge potentials as a dependable source of vitamin A (Horton, 1998). The young leaves and shoots are sometimes eaten green for its anthocyanin pigments which have anti-inflammatory and anti-carcinogenic properties (Anthony, 2013). Its starchy root contains vitamin A and some other minerals that are comparable to those of many fruits.

https://doi.org/10.55627/foodagric.01.01.0269

About 50% of sweetpotatoes grown worldwide are consumed fresh and the rest are processed into potato food products and food ingredients, feed for pigs, cattle and chickens, or converted into starch for industries. Its starch is a 100% bio-degradable substitute for polystyrene and other plastics (Kapinga, 2003). Inspite of being the cheap source of energy, the roots are high in vitamin A in the form of β-carotene. Because yield is used by African farmers to accept or reject varieties, yield and yield contributing parameters are the most widely targeted traits for orange-fleshed sweetpotato improvement programmes worldwide.

The improvement of a crop is largely dependent on the nature and magnitude of available genetic variability, heritability and the transfer of desired characters into new varieties. The success of breeding programmes can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones (Ranganatha et al., 2013; Yared and Misteru 2016). Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance (GA) are useful biometric tools for measuring genetic variability (Vimala and Hariprakash, 2011). Therefore, new genotypes development requires some knowledge about the genetic variability presents in the germplasm of the crop to build efficient breeding programme and the knowledge about genetic variability can help to know if these variations are heritable or non-heritable (Konate et al., 2016; Perera, et al., 2014). The nature and extent of genetic variation governing the inheritance of characters and association will facilitate effective genetic improvement (Yadav et al., 2010). Hence, characterizing the genetic background of orange-sweetpotato and determining breeding values should be done before carrying out any improvement programme (Agong et al., 2001). Yield is a complex polygenic character, resulting from multiple interactions between many yield contributing traits. Considering the above facts, the present research study was undertaken to estimate genetic variability, heritability and genetic advances among yield and yield contributing traits for orange-fleshed sweetpotato genotypes. This investigation provides information that could lead to the development of desirable orange-fleshed sweetpotato genotypes for root yield in future breeding programmes.

Methodology

The experiment was conducted in two locations, namely; the National Root Crops Research Institute (NRCRI), Umudike which is situated at Latitude 05o29′ N, Longitude 07o33′E and at an altitude of 122m above sea level and at Igbariam experimental farm which is located at Latitude 06o15′ N, Longitude 06o52′E and at an altitude of 81m above sea level from 2015 – 2017. Umudike has rainfall of about 2000-2500mm per annum and annual average temperature of about 260C. Igbariam temperature ranges between 21 to 32oC during the year. Vines of 47 accessions of orange fleshed sweetpotato (OFSP) obtained from the National Root Crops Research Institute, Umudike were used. The experiment was established at the on-set of the rainy season (April - May) in the two locations; Umudike and Igbariam. A Randomized Complete Block Design (RCBD) with three replicates was used. Three-month old vine cuttings of OFSP measuring between 25 – 30cm long, with 3 – 4 nodes were planted in the field with inter and intra row spacing of 1.0 and 0.3m respectively giving a plant density of 33,333 plants per hectare. The plot size was 1 × 3m (3m2). A single seedling was planted per stand. Weeding was done manually using hoe as the need arises. Vacant stands were supplied after 2 weeks from the planting date. Compound NPK 15:15:15 fertilizer was applied at 1 month after planting at the rate of 400kg/ha. The field was sprayed regularly, especially against sweetpotato weevils, leaf scab, and caterpillars that feed inside the flowers. Other crop management practices such as weeding once per month was applied following research recommendations for the site.

https://doi.org/10.55627/foodagric.01.01.0269

The plants were harvested when the leaves began to senesce.

Statistical Analysis

The recorded data for different parameters were assembled and organized properly for statistical analysis. The estimate of genetic components and heritability for each trait was calculated according to Feher (1987).

Heritability(bs) = $\delta 2g / \delta 2p$. Where:

Genotypic variance ($\delta 2g$) = MSG – MSE/r

Phenotypic variance ($\delta 2p$) = MSE/r

MSG = Genotypic mean squares from the analysis of variance (ANOVA)

MSE = Error mean squares of ANOVA

r = number of replications

The broad sense heritability estimates were classified as low, moderate and high as follows: 0 - 30 % = Low; 31 - 60 % = Moderate, and > 60 % = High (Lu and Sheng, 1990).

Broad sense heritability= $Vg/Vp = (Va+Vd+Vi)/(Va+Vd+Vi+Ve)$

Where Va = additive variance, Vd = dominance genetic variance, Vi = epistasis, Ve = environmental variance, Vp = phenotypic variance. Similarly, the coefficients of variation at phenotypic and genotypic levels were estimated using the formula adopted by Johnson et al. (1955) as: GCV (%) = $\{(\sqrt{\delta 2g}/X) \times 100/1\}$,

PCV ◎ $\{(\sqrt{\delta 2p} / X) \times 100/1\}$. Categorization of the range of variation was affected as proposed by Sivasubramanian and Madhavamenon (1973); <10% = low, 10-20% = moderate, >20% = high; Where, δp = phenotypic standard deviation, $\delta 2g$ = genotypic standard deviation, and X = Grand mean for the characteristic x; PCV and GCV= phenotypic and genotypic coefficient of variation, respectively. This was analysed using the software; Analysis of Genetic Designs (AGD-R) written by Francisco et al. (2015). The expected Genetic Advance (GA) for each trait was calculated as; GA = $K\sqrt{(Vp)}\,H2$; Where, K = 2.06 at 5.0% selection intensity for trait; Vp = Phenotypic variance for trait; H2 = Broad Sense Heritability of the trait.

Result

Analysis of Variance

The analysis of variance showed (Table 1) that the difference among genotypes for all the characters under study were highly significant for genotypes. Similarly, all the traits were significant for location except the vine length, days to 50% flowering and root yield that were non-significantly different. Most of the characters were also significant for genotypes-location interaction except traits like vine length, root length, marketable roots per plant, total number of roots per plant and root yield.

Estimate of Genetic Parameters

Estimates of environmental ($\delta 2e$), additive ($\delta 2A$), dominant ($\delta 2D$) and genotypic variances ($\delta 2g$), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), heritability (%), and genetic advance (GA) are shown in Table 2.

Estimates of Phenotypic and Genotypic Coefficients of Variation

The range of genotypic coefficient of variation was high for most of the traits considered and ranged from 14.3% (days to 50% flowering) to 73.8% (beta carotene). The genotypic coefficient of variation was very high for beta carotene (73.8%) and vitamin A (70.0%). However, root yield per hectare (56.4%), total root weight per plant (56.2%), total number of roots per plant (41.0%) and vine length (34.7%) had moderate genotypic coefficient of variation. The genotypic coefficient of variation for days to 50% flowering (14.3%), root girth (25.2%), root length (21.0%) and dry matter (17.8%) were low. Similarly, the phenotypic coefficient of variation was high for most of the traits considered, but it was very high for beta carotene (183.5%), vitamin A (174.7%), root yield per hectare (151.6%), total root weight per plant (150.6%), total number of roots per plant(113.5%), vine length (85.5%). However, root girth (68.8%) was high, while root length (58.4%), dry matter (44.6%) and days to 50% flowering (38.13%), were moderate.

Estimates of genetic variance, environmental variance, additive and dominance genetic variances: The overall mean of genotypic variance was high for some traits and moderate for others. However, it was high for vine length (12162.79), days to 50% flowering (373.16), dry matter (220.30), root girth (140.73), root length (68.10), root yield per hectare (349.66) and vitamin A (316313.49), while root length (68.10) and Beta carotene content (57.85), were moderate.

Table 1. Analysis of variance for different morphological plant traits of 47 orange-fleshed sweetpotato genotypes.

TRAITS	d.f.	Vine Length (cm)	Days to 50% Flowering	Root Girth (cm)	Root Length (cm)	No. of marketable Roots Per plant	Weight of marketable Roots Per plant(kg)	Total no. of roots Per plant	Total root Weight per Plant (kg)	Root Yield (t/ha)	B-carotene Content (Mg/100g_FW)	Dry Matter (%)
Replication	2	8159.0	1.17	7.50	5.69	1.99	2.07	1.10	1.26	193.70	0.01	0.067
Genotypes (A)	46	13083.0 **	2204.69**	165.44**	84.13**	18.97 **	3.77 **	37.91**	7.54 **	362.19**	80.25**	200.10**
Location (B)	1	3212.0ns	203.58 ns	205.96**	111.60**	7.05 *	129.11 **	12.97 *	338.47 **	46.31ns	14.75**	1600.1**
A X B	46	619.0ns	162.36 **	18.24*	5.34 ns	0.67 ns	2.59 **	2.48 ns	6.37 **	14.68ns	0.2643**	128.0**
Residual	186	1549.0	77.89	9.38	5.19	0.89	0.44	2.23	1.16	20.55	0.0026	0.089

** Indicates significant at 0.01 probability level and * indicates significant at 0.05 probability level.

The overall mean of additive genetic variation was high for vitamin A (191440.40), days to 50% flowering (295.12), root girth (111.97), root yield per hectare (271.75), dry matter content (135.72), while root length (54.48), total number of root per plant (30.75) and beta carotene content (34.56) were moderate. However, total root weight per plant (5.44) was low. The overall mean of dominance genetic variance was high for vitamin A (79078.37), while vine length (3040.70), days to 50% flowering (78.04), dry matter (55.08) and root yield per hectare (77.91) were moderate. However, root girth (28.76), beta carotene content (14.46), total number of root per plant (7.82), root length (13.62), and total root weight per plant (1.56) had low dominance genetic variance (Table 2).

Broad Sense Heritability Estimates

In general, the values of heritability in broad sense were high for all the traits considered in the experiment with total number of roots and dry matter content having the highest with the value of 99.6%, each.

Estimates of Genetic Advance

In the present study, high value of GA was recorded for such characters as vine length (1533.1), days to 50% flowering (268.84), root girth (165.49), root length (114.87), root yield per hectare (260.98), beta carotene content (106.09), dry matter (207.29), total number of roots per plant (87.08) and vitamin A (7854.1). While low GA was obtained for total root weight per plant (36.82).

Discussion

The significant results from the ANOVA recorded from the genotype indicated that the genotypes were possessing inherent genetic variances among themselves with respect to the characters studied. Similar result was reported by Bekele et al. (2013). According to Dagne et al. (2007), significant differences observed among genotypes for most traits studied, indicated the presence of genetic variation among the materials, which makes

https://doi.org/10.55627/foodagric.01.01.0269

possible for improvement of the traits. The basic idea in the study of variation is its partitioning into components attributable to different causes. The relative magnitude of these components determines the genetic properties of the population (Falconer and Mackay, 1996). The current study suggests that phenotypic coefficient variance (PCV) was higher than their corresponding genotypic coefficient of variance (GCV) for all the characters studies, indicating that the expression of these characters was influenced by environment. Similar results were reported by (Singh et al., 2014; Tuhina-Khatun et al., 2015) in rice. The traits like total root weight per plant, root yield per hectare, Beta carotene content and Vitamin A which showed higher difference between PCV and GCV indicated that environmental effect on the expression of those traits is higher. The highest genotypic and phenotypic coefficients of variation observed for the traits like vine length, total number of roots per plant, total weight of roots per plant, root yield per hectare, beta carotene, and vitamin A indicated that selection can be applied on the traits to isolate more promising lines. Similar type of observations in upland cotton was also reported by the different scientists (Amir et al., 2012; Abbas et al., 2013). Moderate PCV and GCV were observed for root girth, root length and dry matter. Abbas et al. (2013) and Amare et al. (2014) also noticed the moderate phenotypic and genotypic coefficient of variation for some traits and suggested that these characters can be improved by vigorous selection. The traits such as days to 50% flowering exhibited low PCV and GCV which indicated that the breeders should go for source of high variability for these traits to make improvement. Additionally, the magnitude of VA was consistently larger than that of VD for all the traits. This finding shows that the additive genetic variance was more important than the dominance genetic variance in the inheritance of most studied traits, indicating the effectiveness of selection in the early segregating generations for improving such traits. Sobita Devi et al. (2006) and Verma et al. (2006) also reported the predominance of additive gene action for plant height, number of productive tillers and days to 50% flowering in rice. According to them, predominance additive genetic variance was associated with homozygosity and hence it is fixable in nature and selection for these characters will be very effective.

Heritability and the genetic advance are also important selection parameters. They are more useful as selection tools when considered jointly. The estimates of genetic advance can help to understand the type of gene action of various polygenic characters. Johnson et al. (1955) suggested that high heritability estimates along with the high genetic advance is more helpful in predicting gain under selection than heritability estimates alone. Thus, the heritability estimates will be reliable if accompanied by high genetic advance. This result indicates that these characters could be easily improved by selection. The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Al-Tabbal et al., 2012). All the characters studies had high heritability (>60%). High heritability estimates for those traits indicated a high response to selection in these traits. Similar results were also reported by (Dutta et al., 2013; Raffi et al., 2014), which support the present findings.

Genetic advance (GA) under selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Wolie et al., 2013). The high value of GA was recorded with vitamin A (7854.10) and the low (36.82) with total root weight per plant. Estimates of GA for total root weight per plant was (36.82 kg) indicating that whenever we select the best, 1% high yielding genotypes as parents, average total root yield of progenies could be improved by 36.82 kg per plant. However, it was found that the PCV, δ2g, δ2e, δ2A, δ2D and GA for some traits were more than 100. In OFSP, the high estimates may be due to competition among the genotypes (Searle, 1971).

https://doi.org/10.55627/foodagric.01.01.0269

Conclusion

The results of the present study on variability, heritability and genetic advance indicated scope for improvement of root yield of orange-fleshed sweetpotato through selection, using parameters like the genetic coefficient of variation, heritability and GA which are of great importance when developing an efficient breeding program for orange-fleshed sweetpotato. This is because when there is sufficient genetic variation, breeders can exploit additive gene effects, transgressive segregation, and heterosis to improve yield.

Table 2. Beneficiaries and Non-beneficiaries Annual Income from Different Occupations (USD).

	Beneficiaries		Non-Beneficiaries	
Income source	Average annual income (USD) Beneficiaries	% Mean share of income	Average annual income (USD) Non-beneficiaries	% Mean share of income
Rice farming	1447.37	65.32	621.05	44.69
Salary	123.69	5.58	97.37	7.00
Livestock	202.63	9.14	44.74	3.21
Poultry	97.37	4.40	52.63	3.78
Fishing	13.16	0.59	81.58	5.87
Trading	294.74	13.3	450.00	32.38
Other	28.95	1.3	36.84	2.65
Total	2215.79		1389.48	

Source: Authors computation

1USD= 380 naira

Table 3. Determinants of Income Diversification.

Variables	B	Std. Error	t- statistics
Age	-117.976	58.064	2.032*
Sex	-11.661	7.774	-1.500
Family size	105.146	53.276	1.97*
Education	-25.142	10.302	2.44**
Cultivated area	298.031	8.391	35.518***
Farming Experience	-1.503	5.292	-.284
Extension contacts	2.889	5.415	.533
Credit constraints	-267.025	87.167	-3.063***
Annual income	205.23	86.32	2.38**
F-statistics	319.275***	-	-
R^2 Adjusted	.925	-	-

Source: Authors computation

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