

Genetic analysis of root yield and agronomic traits of selected yellow root cassava across two agro-ecological zones in Nigeria

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INTRODUCTION

Cassava is one of the important staple foods in the world. The global production of cassava in 2014 was 278.7 million tons with an estimate of 281 million tons for 2015 and 288.4 million tons for 2016 (FAO, 2016). Nigeria is the leading country in cassava producing countries in the world, with 41,565,000 tons of fresh roots, while China is the least, with 15,700 tons of fresh roots (FAO, 2005). Studies by Akinwale et al. (2011), Tumuhimbise et al. (2014) and Agyeman et al. (2015) have indicated considerable variation in fresh root yield across varying environmental conditions. Vitamin A deficiency is prevalent among many developing countries. The objectives of the study were to: evaluate genetic analysis root yield and agronomic traits of selected yellow root cassava genotypes in two agro-ecological zones of Nigeria.

Table 2.Combined analysis of variance for mean fresh root yield, dry matter content and dry root yield (Kg) in 12 cassava genotypes in two locations

	Source	df	Fresh root yield(t/ha)	Dry matte content (%)	r Dry root yield (t/ ha)
-	Rep	2	155.29ns	9.79ns	20.22ns



MATERIALS AND METHOD

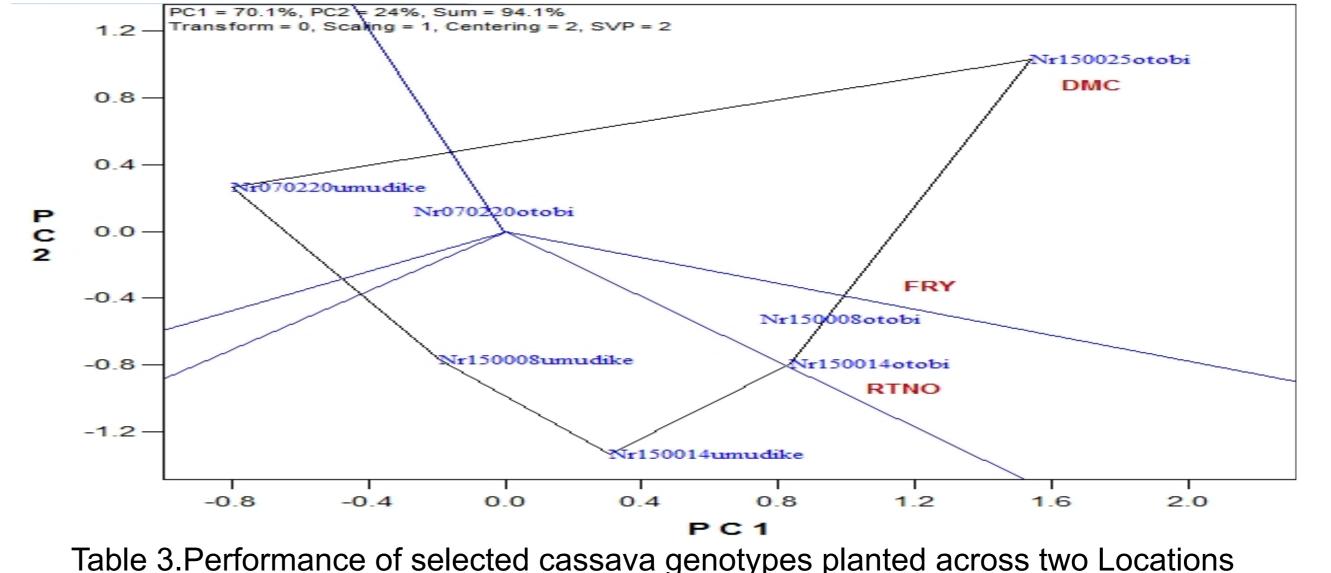
This study was conducted at the advanced multilocation yield trial breeding stage with 10 yellowfleshed cassava genotypes including two checks. The trial was run for (2017and18) cropping seasons at two locations Umudike (humid forest) and Otobi (derived savanna) representing cassava growing agro-ecological zones in Nigeria. The cassava genotypes were grown for 12-month cropping seasons under rainfed conditions in a randomized complete block design with three replications. Each plot was 4 m by 7 m consisting of 28 plants spaced 1 m x 1m. The plants were scored for resistance to major cassava disease and pests 1,3,6,9 and 12 MAP. The disease and pest were scored using a scale of 1 to 5 (1= no symptom; 5= severe symptom) according to International Institute of Tropical Agriculture (1990). DMC and FRY were determined from specific gravity method .FRY were measured by harvesting ten plants/plot at 12MAP. The data collected were collated and subjected to analysis of variance using SAS software, SAS 2002.



Location	1	121.68ns	201.92***	42.95***	
Genotypes	11	311.43***	2303.10***	94.26***	
Genotypes x Location	11	155.54ns	193.71***	27.93***	
Error	46	46.65	31.98	5.32	

*(P<0.05),**(P<0.01),*** (P<0.001); ns- not significant

Figure 1: Mega-environment defined by different winning cassava genotypes for fresh root yield, dry matter content root number at Umudike and Otobi



		0	71	•	
	Environment				
Umudike				Otobi	

Data were collected on many variables including fresh root weight, dry root weight and other yield component traits. The combined analysis of variance reveal that there were significant differences among the genotypes for root number (RTNO), root weight (RTWT), cassava mosaic disease severity(CMDS); across locations for cassava anthracnose disease severity (CADS) and significant genotype x environment interaction for cassava mosaic disease severity (CMDS) at P<0.001 (Table 1). Similarly, highly significant differences were also observed across locations, among genotypes for fresh root yield (FRY), dry matter content (DMC), dry root yield (DRY) and significant genotype x environment interaction for DMC and DRY; across locations for DMC and DRY at P<0.001 (Table 2). At Umudike, six genotypes with 21.53 t/ha and above FRY had DMC of 29.09% and above. Genotype NR150008 had the highest DMC of 33.73%. At Otobi, five genotypes with FRY above 22.80t/ha has DMC of 32.42% and above while genotype NR150025 had the highest DMC of 41.80%. Otobi recorded the highest mean for dry matter content and fresh root yield as well the lowest score for cassava mosaic disease severity (Table 3).NR150025 and NR150014 are the vertex and winning genotypes at Otobi(Figure 1).

Table 1.Combined analysis of variance showing the reaction of the 12 cassava genotypes to yield, disease and pest in two locations

source	DF	RTNO	RTWT (kg)	CMDS	CBBS	CADS	CGMS
rep	2	87.90ns	162.67ns	0.04ns	0.50ns	0.09ns	0.34ns
genotypes	11	786.10***	307.46***	0.33***	0.48ns	0.13ns	0.44ns
Location	1	430.20ns	110.01ns	0.01ns	1.68ns	0.01ns	26.88***
Genotypes x Location	11	370.60ns	155.47ns	0.34***	0.37ns	0.13ns	0.49ns
Error	46	175.30	46.63	0.07	0.25	0.08	0.17
CV%		30.00	33.60	25.5	32.7	28.4	16.8

Genotypes	CMDS	Yield(t/ha)	DMC (%)	CMDS	Yield(t/ha)	(%)
NR070220	2.33	14.93	27.64	1.00	15.87	33.13
NR150008	1.00	21.53	33.73	1.00	22.80	38.48
NR150014	0.66	19.67	20.65	1.00	16.87	37.62
NR150025	1.00	22.67	30.16	1.00	37.93	41.80
NR150031	1.00	23.87	32.23	1.00	30.13	37.02
NR150060	1.00	18.00	28.76	1.00	16.67	33.85
NR150085	1.00	23.93	29.09	1.00	27.20	32.42
NR150113	1.00	16.53	35.70	1.33	14.74	40.15
NR150123	1.00	33.80	31.82	1.00	18.27	34.06
TMS30572	1.00	23.80	31.89	1.33	23.33	41.04
mean	1.09	21.87	30.16	1.06	22.35	36.95
Sed	0.42	5.01	3.91	0.13	7.14	3.26
CV%	38.53	22.98	12.99	12.26	32.01	8.83
P(< 0.005)	0.600	0.113	< 0.001	0.600	0.113	< 0.001

DMC: dry matter content, CMDS: cassava mosaic disease severity, sed: standard error deviation; CV: coefficient of variation



The combined analysis of datasets reveal that there were significant differences among the genotypes for root number (RTNO), root weight (RTWT), CMDS; across locations for CADS and significant genotype x environment interaction for CMDS. Similarly, highly significant differences were also observed across locations, among genotypes for FRY, DMC, DRY and significant genotype x environment interaction for DMC and DRY; across locations for DMC and DRY.NR150025 and NR150014 are the vertex and winning genotypes at Otobi.Also, Otobi recorded the highest mean for dry matter content and fresh root yield as well the lowest score for cassava mosaic disease severity.



*(P<0.05), **(P<0.01), *** (P<0.001); ns- not significant; RTNO: root number; RTWT: root weight; CMDS: cassava mosaic disease severity; CBBS: cassava bacterial blight severity; CADS: cassava anthracnose disease; CGMS: cassava anthracnose disease severity

ACKNOWLEDGEMENT

This study was conducted with funding support from Prof. Egesi, C.N, Harvest Plus and National Root Crops Research Institute (NRCRI), Umudike, Nigeria.

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