INFLUENCE OF GENOTYPE X ENVIRONMENT INTERACTION ON THE PRODUCTIVITY AND STABILITY OF IMPROVED CASSAVA GENOTYPES IN HUMID ECOZONES OF NIGERIA

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ABSTRACT

Sixteen Cassava Genotypes - TMS 30001, TMS 30555, TMS 30572, TMS 4 (2) 1425 TMS 50395, TMS 63397, TMS 81/00110, TMS 81/01635. TMS 82/0058, TMS 82/00661. TMS 82/00942, TMS 82/00959, TMS 90059. TME, TME 2 and NR/41044 were evaluated for yield, resistance to diseases and yield stability in five locations in the humid ecozones of Nigeria for two years (1991 and 1992). The responses of the 16 Genotypes to the five locations differed in relation to yield, disease severity and yield stability. Combined analysis of variance for yield, yield components and diseases severity showed highly significant mean square for location, genotype and GxE interaction. Location, genotype and GxE interaction accounted for 16.4%, 26.2% and 13.8% respectively of the variations recorded in African Cassava Mosaic Disease (ACMD) incidence. Location, genotype and GxE interaction accounted for 52.6%, 5.1% and 5.0% of the variations recorded in Cassava Bacterial Blight (CBB) severity. Location had the greatest influence (33%) on root number generated followed by genotype (17.1%). The highest variation in root yield was accounted for by genotype (17%) followed by location (11.2%). Fresh root yields were highest in Genotype TMS 82/0058 and in Ubiaia location. African Cassava Mosaic Disease (ACMD) and Cassava Bacterial Blight (CBB) were mild in most locations. Six genotypes (TMS 82/00959, TMS 30572, TMS 81/00110, TMS 50395, TMS 82/00942 and TMS 82/00661) showed outstanding stability across the locations with TMS 82/00959 being most stable.

INTRODUCTION

Cassava (Manihot esulenta, Crantz) is one of the major principal root crops grown and eaten by Nigerians. Apart from being major source the carbohydrate for most Nigerians, it has other diverse used in pharmaceutical, confectionary and livestock industries in Nigeria. Nigeria is the largest producer of cassava in the world with an annual production of 33 million tones (APMEU, 1996).

Performance evaluation of cassava genotypes in new different ecologies is a routine breeding practice for selection and nomination of best cassava genotype to the varietal release mechanism (VRM) in Nigeria. Naturally, cassava is adapted to diverse range of environments. Therefore, the response individual genotype to different environments (GXE interaction) follow a diverse pattern due to the influence of the climate and soil variations. It is on this pattern that

selection for high root yield, pest and disease resistance and stable root yield are based. This paper presents the results of the disease resistance, yield and yield components and stability performance of sixteen improved cassava genotypes evaluated in five different locations in humid ecologies of Nigeria.

MATERIALS AND METHODS

Sixteen improved cassava genotype (TMS 30001, TMS 30555, TMS 30572. TMS: 4 (2)1425, **TMS** TMS 63397, 50395. **TMS** 81/00110, TMS 81/021635, TMS 82/00058, TMS 82/00661, TMS 821/00942, TMS 82/00959, TMS 90059 TME 1, TME 2 and NR/41044 bred for Nigerian ecologies by International Institute of Tropical Agriculture (IITA) and National Root Crops Research Institute (NRCRI) in Nigeria, were evaluated for disease resistance, yield and yield stability in five locations (Agba, Calabar, Onne. Ibadan and Ubiaja). Details of the trial sites are show in Table 1.

Table 1: Description of Trial State.

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Location	Agroccozone	Coordinate	Altitude	Rainfall	Soil Type
Agba	Swamp Forest	5°31'N	6m	3024.8mm	Alluvial soils
Calabar	Coastal Swamp	4°58'N	60.9m	2457mm	Ferrasols (Deep porous soils)
1badan	Derived	7º17'N	214m	1740mm	Altisol (moderately deep soils on
	Coastal	3°30E			unsulating landscape)
Onne	Coastal Swamp	4°43'N	15m	Over 2500	Ultisol (Deep porous brown soils
	-	7°05E			derived from coarse and deposits)
Ubia ja	Humid forest	6"39'N	150m	1840.5mm	Reddish brown soil from sandstone.

The trial was conducted for two years (1991 and 1992), under rainfed condition at each of the sites. The trial was laid out in a randomized complete block design with four replications. Planting was done at beginning of the rains in May each year. Cassava was planted at 1m x 1m on the crest of ridge and plot size was 4m x 10m. No fertilizer or pesticide was applied experimental the plots. Harvesting of tubers was done at twelve months after planting. Data were taken on two inner rows for each genotpe on fresh storage root number, storage root weight, and above ground biomass. Dry matter percentage of storage roots and harvest index were also determined for the genotypes on a plot basis. Disease scores of African Cassava Mosaic disease (ACMD) and cassava Bacterial Blight (CBB) were recorded by scoring for severity on the genotypes using a scale of 1 to 5 (1 = no Symptoms; 2 =Mild Symptoms; 3 = Moderate

Symptoms; 4 = Severe Symptoms and 5 = Very Severe Symptoms).

Data collected were analysed according to procedure randomized complete block design using a SAS (1985) computer programme. Mean separation of significant effect was made using the method of least significant 5% difference at level probability. Estimation of vield stability was by the models described by Shukia (1972 and Finlay and Wiklinson 1963). The rank sums for yield performance and various combinations stability parameters were obtained. All ranks were summed for each treatment and used as a parameter for stability. A low rank sum indicates high yield potential and stability (Dixon et al 1991).

RESULTS

The combined analysis of variance for disease, yields and yield components of sixteen cassava genotypes evaluated in five locations in Nigeria are shown in Table 2.

Table 2: Combined analysis of variance for yield, yield components and diseases of sixteen cassava genotypes in five locations for two years (1991 - 1992) in Nigeria.

Year 1 0.560 (0.3%) 1.497** (0.6%) 20025.625** (3.6%) 1219.064** (0.9%) 12055.39** (10.6%) Location 4 3.709** (16.4%) 3.267** (52.6%) 4453.847** (33%) 3971.669** (11.2%) 4900.639** (17.2%) Loc x Yr 4 3.924** (16.4%) 3.2667** (52.6%) 4453.847** (33%) 371.669** (11.2%) 4900.639** (17.2%) Rap (Loc x Yr) 3 0.178 (2.3%) 0.134** (1.6%) 1023.420 (5.5%) 3739.930** (100%) 3916.71** (13.8%) Genotype 3 0.178 (2.3%) 0.134** (1.6%) 6358.846** (17.1%) 1598.446** (16.8%) 000.201** (12.0%) Gen x Yr 15 0.456** (3.0%) 0.306** (1.9%) 551.965** (1.5%) 184.132** (10.9%) 92.164 (1.2%) Gen x Loc 60 0.526** (1.8%) 0.200** (4.8%) 672.271** (7.2%) 183.338** (7.7%) 168.249** (8.9%) Pobled error 450 0.172 0.172 25.694 98.669 58.080		Source	DF	ACMD	СВВ	RTNC	RTWT	TPWT	=
4 3.709** (16.4%) 32.667** (32.6%) 4453.847** (33%) 3971.669*** (11.2%) 4 3.924** (6.8%) 8.193** (13.2%) 3481.589** (2.5%) 3739.930*** (100%) 5 30 0.178 (2.3%) 0.134*** (1.6%) 1023.420 (5.5%) 3739.930*** (100%) 15 0.456*** (3.0%) 0.843*** (5.1%) 6358.846*** (17.1%) 1598.446*** (16.8%) 15 0.456*** (3.0%) 0.306*** (1.9%) 551.965*** (1.5%) 184.132*** (10.9%) 60 0.526*** (13.8%) 0.291*** (5.0%) 115.885*** (12.%) 291.446*** (10.9%) 7 60 0.259*** (6.8%) 0.200*** (4.8%) 672.271*** (7.2%) 183.338*** (7.7%) 450 0.175 0.172 25.694 98.669		Year	-	0.560 (0.3%)	1.497** (0.6%)	20025.625** (3.6%)	1219.064** (0.9%)	12055.39**(10.6%)	0.518** (6.9%)
4 3.924** (6.8%) 8.193** (13.2%) 3481.589** (2.5%) 3739.930** (100%) 30 0.178 (2.3%) 0.134** (1.6%)*** 1023.420 (5.5%) 350.676** (7.4%) 15 3.996** (26.2%) 0.843** (5.1%) 6358.846** (17.1%) 1598.446** (16.8%) 15 0.456** (3.0%) 0.306** (1.9%) 551.965** (1.5%) 184.132** (10.9%) 60 0.526** (13.8%) 0.201** (5.0%) 115.885** (12.%) 291.446** (10.9%) 7 60 0.259** (6.8%) 0.200** (4.8%) 672.271** (7.2%) 183.338** (7.7%) 450 0.175 0.172 25.694 98.669		Location	4	3.709** (16.4%)	32.667** (52.6%)	4453.847** (33%)	3971.669** (11.2%)	4900.639** (17.2%)	0.509** (27.2%)
7. 30 0.178 (2.3%) 0.134** (1.6%) 4. 1023.420 (5.5%) 350.676** (7.4%) (1.5%) 15.996** (26.2%) 0.843** (5.1%) 6358.846** (17.1%) 1598.446** (16.8%) (1.5%) 15.0456** (3.0%) 0.306** (1.9%) 251.965** (1.5%) 184.132** (10.9%) (1.5%) 160 0.526** (13.8%) 0.291** (5.0%) (6.72.71** (7.2%) 183.338** (7.7%) 450 0.175 0.172 25.694 98.669		Loc x Yr	4	3.924** (6.8%)	8.193** (13.2%)	3481.589** (2.5%)	3739.930** (100%)	3916.71** (13.8%)	0.209** (11.2%)
7. 15 3.996** (26.2%) 0.843** (5.1%) 6358.846** (17.1%) 1598.446** (16.8%) 15 0.456** (3.0%) 0.306** (1.9%) 551.965** (1.5%) 184.132** (10.9%) 15 0.526** (13.8%) 0.291** (5.0%) 115.885** (1.2%) 291.446** (10.9%) 15 0.259** (6.8%) 0.200** (4.8%) 672.271** (7.2%) 183.338** (7.7%) 1450 0.175 0.172 25.694 98.669		Rep (Loc x Yr)	30	0.178 (2.3%)	0.134** (1.6%) **	1023.420 (5.5%)	350.676** (7.4%)	204.036** (5.4%)	0.209** (3.7%)
15 0.456** (3.0%) 0.306** (1.9%) 551.965** (1.5%) 184.132** (10.9%) 60 0.526** (13.8%) 0.291** (5.0%) 115.885** (1.2%) 291.446** (10.9%) r 60 0.259** (6.8%) 0.200** (4.8%) 672.271** (7.2%) 183.338** (7.7%) 450 0.175 0.172		Genotype	15	3.996** (26.2%)	0.843** (5.1%)	£ 6358.846** (17.1%)	1598.446** (16.8%)	000.201** (12.0%)	0.009** (3.7%)
60 0.526** (13.8%) 0.291** (5.0%) 115.885** (1.2%) 291.446** (10.9%) r 60 0.259** (6.8%) 0.200** (4.8%) 672.271** (7.2%) 183.338** (7.7%) 450 0.175 0.172 25.694 98.669		Gen x Yr	15	0.456** (3.0%)	0.306** (1.9%)	551.965** (1.5%)	184.132** (10.9%)	92.164 (1.2%)	0.005 (1.0%)
r 60 0.259** (6.8%) 0.200** (4.8%) 672.271** (7.2%) 183.33 8** (7.7%) 450 0.175 0.172 25.694 98.669		Gen x Loc	09	0.526** (13.8%)		115.885** (1.2%)	291.446** (10.9%)	143.708** (7.6%)	0.040** (8.2%)
450 0.175 0.172 25.694 98.669		Gen x Loc x Yr	09	0.259** (6.8%)	0.200** (4.8%)	672.271** (7.2%)	183.338** (7.7%)	168.249** (8.9%)	0.008** (6.8%)
	120	Pooled error	450	0.175	0.172	25.694	699.86	58.080	0.003

Percentage of total sum of square in parenthesis

Location genotype and GxE interaction exerted profound influence on yield and disease severity recorded in this trial. Combined analysis of variance for vield components diseases showed highly significant mean square for location, genotype and GxE interaction. Location. genotype and GxE interaction accounted for 16.4%, 26.2% and 13.8% of the variations recorded in ACMD severity. Similarly, location, and GxE interaction genotype accounted for 52.6% 5.1% and 5.0% of the variation recorded in CBB severity. Among the sources of variation listed in Table 2, location had the greatest influence (33%) on rot number generation followed by

RTNO

RTWT

TPWT

НΙ

genotype. Also variation in root weight was accounted by genotype (16.8%) followed by location (11.2%).

However, variations in top biomass and harvest index were highly influenced by location. The performance of the sixteen cassava genotype in the five locations differed in relation to yields and disease severity.

The response of the sixteen cassava genotypes in the five locations (Tables 3 and 4) to disease infection showed mild susceptibility to African Cassava Mosaic disease (ACMD) and Cassava Bacterial Blight (CBB) except TME 1 and NR 41044.

Table 3: Performance of sixteen cassava genotypes for yield, yield components and disease expression in five locations for two years (1991 and 1992(in Nigeria.

	-	•	•			
Genotype	ACMD	CBB	RTNO	RTWT (t/w)	TRWT	Н
TMS 30001	1.9	2.1	64.1	26.1	18.5	0.60
TMS 30555	2.4	2.1	54.6	30.2	32.7	0.48
TMS 30572	2.2	2.2	91.6	40.9	33.6	0.56
TMS 1425	2.3	2.1	54.8	35.0	18.0	0.68
TMS 50395	2.4	2.2	75.9	46.3	28.9	0.62
TMS 63397	2.2	2.0	84.1	36.1	22.3	0.63
TMS 81/00110	2.6	2.3	79.8	41.2	28.9	0.60
TMS 81/01635	2.6	2.2	74.1	37.9	28.4	0.59
TMS 82/00058	2.2	2.1	93.4	49.0	32.8	0.60
TMS 82/00661	2.3	2.3	77.8	44.4	26 .7	0.60
TMS 82/00942	2.4	2.2	77.8	45.5	27.7	0.62
TMS 82/00959	2.5	2.2	58.0	34.7	25.4	0.58
TMS 90059	2.4	2.2	65.9	37.6	23.1	0.62
TME I	1.9	2.4	67.4	39.5	31.6	0.57
TME 2	2.6	2.6	54.4	30.6	24.9	0.56
NR /41044	3.2	3.1	66.3	34.6	29 .0	0.56
LSD (0.05)	0.32	0.26	11.20	6.46	4.57	0.55
CV (%)	17.6	12.2	21.0	26.0	28.2	9.5
CMV	=	Cassava n	nosaic viru:	S		
CBB	= .	-Cassava b	acterial hi	ght		

Root number

Top weight (kg)

Harvest index

Root weight (kg/20m²)

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Table 4: Disease score, root yield and yield components across the five locations for two years (1991 and 1992) in Nigeria.

Location	ACMD	CBB	RTNO	RTWT	TPWT	HI
Agbarho	2.3	2.1	40.5	28.4	25.6	0.54
Calabar	2.4	1.7	84.1	39.1	22.3	0.65
Ibadan .	2.6	3.0	88.3	39.9	37.9	0.57
Onne	2.3	1.8	71.5	40.6	23.9	0.64
Ubiaja	2.2	2.3	71.9	42.6	25.4	0.63
LSD (0.05)	0.11	0.009	1.5	4.7	3.64	0.02

CMD = Cassava Mosaic Disease
CBB = Cassava Bacterial Blight
RTNO = Root Number
RTWT = Root Weight (kg/20m²)

TPWT = Top Weight (kg)

HI = Harvest Index

However there was higher severity of ACMD and CBB at Ibadan. The genotypes TMS 30001 and TMS L exhibited greatest resistance to ACMD. Cassava Bacterial Blight (CBB) severity was less in Calabar and Onne Locations.

The incidence of ACMD was genotype and location dependent while CBB incidence was location and year dependent. (Tables 3 and 4).

The performance of the sixteen cassava genotypes for yield and yield components is presented in Table 3. Root yields (root weight) of the genotypes were generally high with higher trends in TMS 82/00058; TMS 82/00942: 50395: TMS 82/00661; TMS 81/01635; and 30572 numbers TMS Root followed similar trend as in root yield, with optimum root number

in TMS 82/00058. with the exception of TMS 1425 and TMS 30001, top biomass was relatively high among the genotypes with an optimum in TMS 30572. Although the ratio of the economic yield to top biomass (HI) was relatively high among the genotype and TMS 1425 achieved the highest harvest index whereas NR/41044 gave the lowest harvest index.

The productivety of the genotypes across the five rocations with respect to root yield was high with an optimum at Ubiaja. Agba location was the poorest in root yield. The location (Ibadan) with the highest root number had the highest top biomass and the least harvest index (Table 4.)

The measure of stability of the genotypes across the locations is shown in Table 5.

Table 5: Estimate of two stability parameters and genotype ranks for root weights of sixteen cassava genotypes grown in five locations for two years 91991 and 1992) in Nigeria.

Genotyp	Yield (kg/m²)	Shukla Value S2	Finky and \	Vilkinson value
			bi	Ranksum
TMS 30001	26.1	252.87(9)	0.86(3)	12
TMS 30555	30.2	362.06(14)	0.77(4)	18
TMS 30572	40.9	99.70(3)	0.87(3)	6
TMS 1425	35.0	343.81(13)	0.82(3)	16
TMS 50395	46.3	93.55(2)	0.30(5)	7
TMS 63397	36.1	222.65(8)	1.14(3)	11
TMS 81/00110	41.2	115.89(4)	0.93(2)	6
TMS 81/01635	37.9	336.23(12)	1.28(3)	15
TMS 82/00058	49.0	287.45(11)	1.10(2)	13
TMS 82/00661	44.4	133.74(6)	1.16(3)	9
TMS 82/00942	45.5	131.68(5)	1.86(3)	8
TMS 82/00959	34.7	55.02(1)	0.98(1)	2
TMS 90059	37.6	467.96(16)	1.04(1)	17
TME I	39.5	375.43(15)	1.07(2)	17
TME 2	30.6	264.10(10	1.76(2)	12
NR /41044	34.9	161.40(7)	0.76(4)	11
Donk in norm	thogog	. ,	()	

Rank in parantheses

S² - Shukla 1972

bi = Finlay and Wilkinson 1963.

The two stability procedures used judged six genotypes to the highly stable (TMS 82/00959; TMS 30572; TMS 81/00110: TMS50395; TMS 82/00942; TMS 82/00661). With these methods based on the least rank sum value, TMS 82/00959 was rated as most stable

DISCUSSION

Results of the multi-locational trial clearly show that among the sixteen genotypes, TMS 82/00058 and few other genotypes (TMS30572 and TME 1) which produced the highest top biomass across the sites gave the highest root yields.

The performance of these genotypes contrasts the report of Ramanujam (1980) that profuse branching habit is considered to be undesirable as the growth of the aerial part increased more in proportion to the growth of the tubers resulting to lower harvest index. This may be true for some genotypes, such as TMS 1425 which produced the lowest top biomass but gave the highest harvest index. Even though TMS 1425 gave the highest harvest index, the performance of the evaluated genotypes is a clear indication that breeding centers are making efforts in areas of methodology to improve the

cassava crop. Among the various sources of variations enlisted in Table 2. location and genotype exerted much pressure on root number generation. The results implicated genotypes to have the greatest influence on root yield, greatly whereas location influenced biomass and top index tremendously. harvest Thus, dry matter partitioning and allocation for economic yield is location dependent. The response of the sixteen cassava genotypes to the five locations differed greatly in relation to yield and disease severity. This suggests that cassava breeders need to generation consider early selection at specific locations followed by multi-site evaluation over years thereby aiming at wider adaptation. Also, breeders need to focus on breeding genotypes for specific location in order to maximize yield and disease resistance potentials of the new lines.

The results of disease rating of the genotypes showed some measure of resistance to ACMD and CBB. There was no record of severity of ACMD and CBB across the locations. The mild severity of ACMD and CBB in most of the locations because. the was evaluated genotypes were improved materials. This also the potentials of indicates improved line over local lines. However, there was an increased

spread of CBB at Ibadan and this is reflected in the higher score of the disease observed. Combined analysis of variance for yield, yield components and diseases showed highly for significant mean square location, genotype and GxE interaction indicating that genotypes responded differently relative to each at different environments. Ranjendran et al. (1987) made similar observation in cassava. Although there was highly significant. Genotype x environment interaction for root yield, about six genotypes had good levels of yield stability across all the locations indicating that breeding cassava for improved stability across locations is possible. Also the result of the combined analysis of variance indicated that a substantial proportion of the genotypes observed environment variance for root yield could be attributed to environmental indices and traits of the genotypes. The results clearly showed that environment and genetic variations mostly accounted for the variation in root yield. The significance of interaction the GxE in productivity and stability of cassava genotypes have been confirmed in studies on cassava (Dixon et al., 1991; Otoo et al, 1991).

CONCLUSION

Breeding cassava for high productivity and stability across environments is possible as six genotypes in this study showed good level of yield and yield stability across diverse locations. Some locations gave better yield than others indicating the possibility of breeding genotype for specific locations.

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