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Genotype X environment interaction, stability and agronomic performance of carotenoid-rich cassava clones

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Cassava is widely consumed in Africa where malnutrition is rampant; there is, therefore, a major effort to produce micronutrient biofortified cassava. Adoption of such cassava genotypes will largely depend on their agronomic performance, resistance to biotic stresses, and the stability of these traits. The objectives of this study were to (i) evaluate the influence of genotype (G) environment (E), and G x E interaction on fresh root yield (FRY), dry root yield (DRY), dry matter content (DM), cassava mosaic disease (CMD), bacterial blight (CBB), cassava anthracnose diseases (CAD), and cassava green mite (CGM) in carotenoid-rich cassava, (ii) evaluate performance of the selected clones for the traits and establish any linear relationships between them, and (iii) determine the most stable clones for FRY, DRY, and DM. Genotypes were evaluated over two years (2004/2005, 2005/2006) at five locations in Nigeria. All clones expressed mild CBB and CAD symptoms; eleven clones did not have CMD symptoms, while CGM was the most severe biotic stress. There were significant negative correlations between CMD and CBB, CBB and CAD, CBB and FRY, CBB and DRY, CAD and CGM, and CGM and FRY. This implies that selecting for one trait in a pair may be indirectly selecting against the other. There were significant positive correlations between CMD and CAD, CMD and FRY, CMD and DRY, CBB and CGM, CAD and FRY, and CAD and DRY. This implies that improving one trait in a pair may indirectly improve the other. G effects had the largest impact on CMD, CGM, and DM; location effect (L) had largest impact on CBB, CAD, FRY and DRY. Effects of L, G x L and G x year x L interaction were significant for all traits. The high influence of E on FRY, DRY, CBB, and CAD, will limit progress in breeding and selection for these traits in carotenoid-rich cassava. The substantial E and G x E effects on CMD, CGM, and DM, albeit with high G effects, suggest prospects for advance in breeding for these traits though the extent may be limited by the failure of some genotypes to respond. Clones 01/1235, 94/0006, 01/1206, 01/1412 and 91/2324 (check) were stable with relatively high FRY; 01/1380, 94/0006, and 30572 were stable with high DRY; 94/0330, 01/1646, 01/1277, and 95/0379 were stable with relatively high DM.

Key words: Yellow-fleshed cassava, carotenoids, agronomic performance, stability.

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a major source of calories for roughly two out of every five Africans (Nweke et al., 2002). Though the crop is relatively tolerant to many biotic and abiotic stresses, it suffers heavy yield losses in some areas caused by pest and disease infes-

tations. The most important diseases of cassava in Africa are the African cassava mosaic (ACMD), cassava bacterial blight (CBB), and cassava anthracnose (CAD) (Geddes, 1990); the cassava green mite (CGM) is the most economically important pest. Host plant resistance has proved to be the most suitable control strategy against these biotic constraints.

The expression of a phenotype of an individual is determined by both the genotype and the environment. These

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Table 1. Carotenoid concentration (µg/g) of 25 yellow-fleshed and 3 white-fleshed check cassava clones used in the study.

Clone	Total Carotenoid Concentration	Clone	Total Carotenoid Concentration
01/1115	5.2	01/1610	5.6
01/1206	3.7	01/1646	4.0
01/1224	6.0	01/1649	5.7
01/1235	5.7	01/1663	7.1
01/1273	5.5	90/01554	3.3
01/1277	5.7	94/0006	3.1
01/1331	5.8	94/0330	3.7
01/1335	5.6	95/0379	4.3
01/1368	7.3	98/2132	4.8
01/1371	6.9	96/1089A	3.1
01/1380	3.5	TME1 (white)	0.9
01/1404	5.7	30572 (white)	0.9
01/1412	6.6	91/02324 (white)	0.9
01/1413	6.4	**Mean**	**4.732**
01/1442	5.5	**SE (±)**	**0.342**

two effects are not always additive because of the interaction between genotype and the environment (GEI).GEI is a result of inconsistent performances of genotypes across environments. A significant GEI results from changes in the magnitude of differences between geno-types in different environments or from changes in the relative ranking of the genotypes (Fernandez, 1991). A significant G x E interaction presents limitations in the selection of superior genotypes, and thus, reduces the usefulness of the subsequent analysis of means and the inferences that would otherwise be valid (Shaffi et al., 1992). Breeders face the GEI challenge by evaluating genotypes in several environments to ensure that they select genotypes with high and stable performance. Genotypes whose GEI is insignificant are said to be stable.

Areas in Africa where cassava is widely consumed are characterized by rampant malnutrition because the tuberous root is low in micronutrients. There is, therefore, a major effort to produce biofortified cassava. Biofortification is the process of breeding food crops that are rich in bio-available micronutrients. Yellow-fleshed (YF) cassava genotypes have featured prominently in biofortification because they have higher levels of micronutrients, such as carotenoids (Iglesias et al., 1997; Chávez et al., 2005) than the white-fleshed (WF) genotypes. Adoption of micronutrient biofortified genotypes will largely depend on their agronomic performance, including fresh and dry root yield, resistance to major pests and diseases, and the stability of these traits over time and space. Though cassava is widely adapted to a variety of environmental conditions, usually the adaptability of most WF varieties is narrow and shows large GEI effects (Dixon et al., 1994; Dixon and Nukenine, 1997). Through a breeding program at the International Institute of Tropical Agriculture (IITA), Nigeria, a number of YF cassava genotypes were identi-

fied with relatively high levels of carotenoids (Table 1). Though studies have shown that β-carotene concentration is a stable trait in cassava (Ssemakula et al., 2007) there is hardly any published information on the agronomic performance of YF cassava. This study was, therefore, designed with the following objectives: i) to evaluate the influence of genotype (G) environment (E), and G x E interaction on fresh root yield (FRY), dry root yield (DRY), dry matter content (DM), cassava mosaic disease (CMD), bacterial blight (CBB), cassava anthracnose diseases (CAD), and cassava green mite (CGM) in carotenoid-rich cassava, ii) to evaluate performance of the clones for the traits and establish any linear relation-ships among the traits, and iii) to determine which clones are the most stable for FRY, DRY and DM.

MATERIALS AND METHODS

Twenty-five YF and three WF check clones of cassava (Table 1) were planted in Nigeria at five locations during 2004/2005 and 2005/2006. Table 2 gives a brief description of the locations, Onne, Ubiaja, Ibadan, Mokwa, and Zaria, which represent the major cassava growing agroecologies in the country. Planting in both years was done during the months of May - June, coinciding with the onset of rains. The clones were grown under rain-fed conditions in randomized complete block design with four replications. Each plot consisted of 40 plants in four rows (ridges 0.3 m high and 10 m long) spaced 1 m apart. No fertilizers or herbicides were applied during the course of the experiment; weeding was done as deemed necessary. The genotypes were evaluated at monthly intervals (starting at 1 month after planting (MAP) to 9 MAP) for their reaction to CMD, CBB, CAD, and CGM. Damage symptoms were scored on a scale of 1 - 5, where 1= no symptoms and 5=very severe symptoms (IITA, 1990). Only the score of the most severely affected plant/s was recorded in a plot. Harvesting in both years was done in May - June, at approximately 12 MAP. Only the inner

Table 2. Brief descriptions of the locations where the trials were planted

Location	Eco-zone	Altitude (metres)	Minimum/Maximum temperature	Mean Annual Rainfall (mm)	Wet season	Soil type
Ibadan	Forest-savanna transistion	215	12-34 ^{o}C	1300	March-August	Ferric- luvisols
Onne	Humid forest	17	12-32 ^{o}C	2960	February-December	Thionic - fluvisals
Ubiaja	Sub-humid forest	310	12-32 ^{o}C	1670	March-December	Dystric- nitosols
Zaria	Moist northern- Guinea savanna	630	15-36 ^{o}C	1060	May-September	Lixisol - luvisol
Mokwa	Sub-humid southern- Guinea savanna	161	13-36 ^{o}C	1150	April-November	Ferric- luvisols

Table 3. Mean cassava mosaic disease severity (CMD), cassava bacterial disease severity (CBB), Cassava anthracnose disease severity (CAD)' cassava green mite severity (CGM) fresh yield (t ha^{-1}), dry yield (t ha^{-1}), and dry matter (DM) content of 28 clones evaluated at five locations in Nigeria, 2004/05-2005/06

Clone	CMD	CBB	CAD	CGM	Fresh yield	Dry yield	DM (%)
01/1115	1.0	2.0	1.5	2.7	13.8	4.3	27.7
01/1206	1.1	2.1	1.8	3.1	22.9	7.6	30.8
01/1224	1.7	1.9	1.7	2.8	15.4	5.1	31.5
01/1235	1.6	2.1	1.8	2.8	18.7	5.6	27.5
01/1273	1.0	2.0	1.7	2.6	11.0	3.2	25.8
01/1277	1.0	2.1	1.4	3.0	14.2	4.6	29.7
01/1331	2.5	1.8	1.6	3.3	10.0	3.1	25.7
01/1335	2.3	2.0	1.7	3.2	16.5	4.7	25.0
01/1368	2.3	2.0	1.5	2.5	19.0	6.1	29.3
01/1371	1.4	2.1	1.5	2.9	14.1	4.2	27.7
01/1380	1.1	2.1	1.8	3.2	17.9	5.9	29.3
01/1404	1.0	2.0	1.5	3.0	14.9	5.0	29.9
01/1412	1.0	2.1	1.6	3.2	22.3	5.8	26.2
01/1413	1.0	2.0	1.3	3.1	16.4	4.6	26.6
01/1442	1.3	2.1	1.4	2.8	15.5	4.3	25.0
01/1610	2.5	2.1	1.5	2.6	16.4	4.7	25.2
01/1646	1.2	2.0	1.7	2.5	17.4	6.0	31.2
01/1649	1.0	2.2	1.4	3.1	15.0	4.5	26.6
01/1663	1.0	2.1	1.8	2.0	16.6	4.5	26.2
90/01554	1.7	2.1	1.8	3.2	17.0	6.2	32.7
94/0006	1.0	2.4	2.2	2.5	19.4	6.9	32.5
94/0330	1.0	2.0	1.5	2.6	12.9	4.5	32.4
95/0379	1.2	2.1	1.8	2.6	19.3	5.9	29.4
96/1089A	1.1	2.3	1.6	3.2	22.9	8.9	32.6
98/2132	1.0	2.2	1.8	3.1	26.9	7.8	28.1
TME 1 (check)	2.3	2.2	2.4	1.8	17.4	5.9	34.7
30572 (check)	2.0	2.3	2.1	3.6	15.8	6.0	34.1
91/02324 (check)	1.0	2.4	2.3	2.6	25.4	8.7	33.3

Table 3. contd.

Mean	1.40	2.10	1.69	2.85	17.31	5.51	29.17
Se	0.10	0.02	0.05	0.07	0.75	0.28	0.57
CV (%)	24.5	17.8	28.6	13.9	29.4	34.5	14.8
Environment means:							
Ibadan05	1.7	1.2	1.7	2.6	23.3	6.4	27.6
Ibadan06	1.5	1.6	2.4	2.8	23.4	6.2	26.7
Mokwa05	1.1	2.4	-	2.6	12.2	3.7	29.7
Mokwa06	1.2	2.7	-	2.6	21.9	6.0	27.5
Onne05	1.8	-	-	-	29.7	8.5	28.8
Onne06	1.6	1.5	2.1	-	18.2	5.7	30.7
Ubiaja05	1.4	2.4	1.1	3.1	11.2	4.3	33.6
Ubiaja06	1.4	3.0	1.2	3.3	13.9	4.2	28.5
Zaria05	1.1	1.1	-	-	7.5	2.7	31.6
Zaria06	1.1	2.8	-	-	9.1	2.8	29.4
Means	1.39	2.07	1.69	2.84	17.05	5.04	29.40
Se	0.08	0.24	0.24	0.12	2.32	0.58	0.67
CV (%)	24.5	17.8	28.6	13.9	29.4	34.5	14.8

Disease and pest damage scored on a scale of 1 - 5, where 1 = no symptoma and 5 = very severe symptoms.

plants in a plot were harvested (excluding the border); equating to a maximum of 16 plants, and the fresh tuberous root yield per plot was recorded. Root DM percentage of storage root cortex was determined from a random bulk sample of four plants selected from the inner two rows of only two replicates. The roots were washed and shredded after which one hundred grams of fresh cassava root chips was sampled and dried at $70^{\circ}C$ for 48 h in a forced air oven. The dried sample was weighed and the DM percentage was calculated as: (Dry weight / Fresh weight) x 100. DRY was derived as a product of DM percentage and FRY.

Data analysis

Data were subjected to combined analyses of variance using the GLM procedure of Statistical Analysis System (SAS) to determine the significance of the main effects and interactions. Because the data were unbalanced, 27 genotypes and 3 replications which were common to all the locations were subjected to the Additive Main effect and Multiplicative Interaction (AMMI) analysis using Matmodel (Gauch and Furnas, 1991). The biplots [main effect means vs first Interaction Principal Component Axis (IPCA1)] from the AMMI analysis were used to study the pattern of response of G, E and GEI. The biplots were also used and to identify genotypes with broad or specific adaptation to target agroecologies or environments for FRY, DRY and DM.

RESULTS

Mean performance of the cassava genotypes across environments is presented in Table 3. The clones had mean FRY of 17.3 t ha^{-1}. YF clone 98/2132 (26.9 t ha^{-1}) had the highest FRY across locations. Clone 96/1089A (8.9t/ha) had the highest DRY across locations; Onne-2005 environment (8.5 t ha^{-1}) had the highest DRY. The highest mean FRY were recorded in Onne-2005 (29.7 t ha^{-1}), followed by Ibadan-2006 (23.4 t ha^{-1}), and Ibadan-2005 (23.3 t ha^{-1}); Zaria-2005 (7.5 t ha^{-1}) had the lowest

FRY. All clones expressed mild CBB and CAD symptoms; 11 clones did not have CMD symptoms, CGM was the most severe biotic stress. The WF check clones (30572, 91/02324, and TME1) had relatively high DM compared to the YF clones. Clone 98/2132 had the highest FRY with high resistance to biotic stresses across locations. There were significant negative correlations between: CMD and CBB, CBB and CAD, CBB and FRY, CBB and DRY, CAD and CGM, and CGM and FRY (Table 4). There were significant positive correlations between: CMD and CAD, CMD and FRY, CBB and DRY, CBB and CGM, CGM and DRY, CAD, and FRY, DM and DRY and FRY and DRY.

Combined analyses of variance using the GLM procedure of SAS (Table 5) indicated that L and G main effects were significant ($P<0.001$) for all the traits measured. Year (Y) effect was significant for CBB ($P<0.001$), CAD ($P <0.001$), CGM ($P <0.05$), and DM ($P<0.01$). The relative magnitude of the main effects and their interactions for all traits measured as a proportion of the total sum of squares showed that G had more impact on CMD, CGM and DM than the other effects and interactions. L had more impact on FRY, CBB and CAD than the other effects and interactions. Y x L, G x L and G x L x Y interactions were significant for all the traits, but G x Y interactions were not. The largest interaction for CMD, CAD, CGM and was G x L; Y x L and G x L were the largest for CBB and FRY; G x L and G x L x Y were the largest for DM.

The analysis of variance of the AMMI (Table 6) for FRY, DRY and DM also shows that the effects of G, E, and GEI were significant *(P<0.001)*. E obtained as L x Y combination; G and GEI were highly significant (P < 0.001) for the traits. G accounted for 16.3% of total sums

Table 4. Coefficients of correlation between different parameters measured on 25 carotenoid-rich and 3 white-fleshed cassava genotypes evaluated at five locations in Nigeria, 2004/05-2005/06

	CMD	CBB	CAD	CGM	FYLD	DYLD	DM
CMD	1	-0.1217***	0.1061**	-0.0118	0.1022***	0.1031**	-0.0379
		n=965	n=554	n=662	n=1054	n=774	n=774
CBB		1	-0.3250***	0.1903***	-0.1523***	-0.1652***	0.0497
			n=554	n=662	n=953	n=673	n=673
CAD			1	-0.2324***	0.3756***	0.2634***	-0.0336
				n=442	n=552	n=443	n=443
CGM				1	-0.1395***	-0.0976*	0.0316
					n=658	n=466	n=466
FYLD					1	0.9175***	-0.0475
						n=775	n=775
DYLD						1	0.3050**
							n=775
DM							1

CMD-cassava mosaic disease severity; CBB- cassava bacterial disease severity; CAD- cassava anthracnose disease severity. CGM- cassava green mite damage severity; Disease and pest severity scored on a scale of 1-5 where 1 = no symptoms and 5 = very severe symptoms; FYLD- fresh yield; DM-Dry matter content; *** Significant at $P<0.001$, ** significant at $P<0.01$, * significant at $P<0.05$.

Table 5. Combined analyses of 25 yellow-fleshed and 3 white-fleshed cassava clones evaluated for two years (2005 and 2006) at five locations in Nigeria for yield, dry matter content, and reaction to biotic stresses.

Source	DF	Type III SS	Mean Square	F Value	% of total sum of squares
Cassava mosaic disease					
Rep (Year*Location)	30	5.33	0.18	1.52*	
Year (Y)	1	0.70	0.70	3.93	0.1
Location (L)	4	45.33	11.33	63.8***	7.9
Genotype (G)	27	259.78	9.62	32.14***	45.5
Y*L	4	5.16	1.29	7.26***	0.9
Y* G	27	8.08	0.30	1.15	1.4
L* G	108	99.75	0.92	7.89***	17.5
Y*L* G	102	26.60	0.26	2.23***	4.7
Error	762	89.18	0.12	4.17***	11.0
Total	1065	571.22	0.26	2.23***	4.7
Cassava bacterial blight					
Rep (Year*Location)	27	11.76	0.44	3.11***	
Year (Y)	1	83.22	83.22	191.11***	13.8
Location (L)	4	308.71	77.18	177.24***	51.4
Genotype (G)	27	11.51	0.43	2.12*	1.9
Y*L	3	34.86	11.62	26.69***	5.8
Y* G	27	5.42	0.20	0.92	0.9
L* G	108	28.01	0.26	1.85***	4.7
Y*L* G	77	16.85	0.22	1.56***	2.8
Error	690	96.53	0.14		
Total	964	601.05			
Cassava anthracnose disease					
Rep (Year*Location)	15	7.90	0.53	2.25**	
Year (Y)	1	16.21	16.21	30.79***	5.2
Location (L)	2	83.81	41.91	79.6***	27.0
Genotype (G)	27	37.31	1.38	4.1***	12.0

Table 5. contd.

Y*L	1	11.28	11.28	21.42***	3.6
Y* G	27	9.10	0.34	0.91	2.9
L* G	54	20.08	0.37	1.59**	6.5
Y*L* G	26	9.68	0.37	1.59	3.1
Error	400	93.42	0.23		
Total	553	310.66			
Cassava green mite					
Rep (Year*Location)	18	5.05	0.28	1.8*	
Year (Y)	1	1.61	1.61	5.75*	0.5
Location (L)	2	41.03	20.51	73.17***	13.7
Genotype (G)	27	98.22	3.64	9.63***	32.8
Y*L	2	2.44	1.22	4.36*	0.8
Y* G	27	10.20	0.38	0.72	3.4
G* L	54	36.65	0.68	4.35***	12.2
G*Y* L	52	27.19	0.52	3.35***	9.1
Error	478	74.52	0.16		
Total	661	299.64			
Fresh yield					
Rep (Year*Location)	30	2343.32	78.11	3.03***	
Year (Y)	1	56.70	56.70	0.73	0.1
Location (L)	4	29975.39	7493.85	95.94***	28.4
Genotype (G)	27	16561.86	613.40	24.44***	15.7
Y*L	4	12990.61	3247.65	41.58***	12.3
Y* G	27	677.63	25.10	0.52	0.6
G*L	108	11629.41	107.68	4.17***	11.0
G*Y*L	102	4952.30	48.55	1.88***	4.7
Error	751	19374.37	25.80		
Total	1054	105559.76			
Dry yield					
Rep (Year*Location)	19	119.79	6.30	1.77*	
Year (Y)	1	13.70	13.70	2.17	0.19
Location (L)	4	1755.89	438.97	69.63***	23.90
Genotype (G)	27	1381.34	51.16	17.31***	18.80
Y*L	4	604.38	151.09	23.97***	8.23
Y*G	27	79.81	2.96	0.83	1.09
G*L	107	998.46	9.33	2.62***	13.59
G*Y*L	101	460.40	4.56	1.28*	6.27
Error	484	1721.51	3.56		
Total	774	7346.22			
Dry matter content					
Rep (Year*Location)	19	931.61	49.03	2.64***	
Year (Y)	1	366.67	366.67	7.48**	1.4
Location (L)	4	1490.66	372.66	7.60***	5.8
Genotype (G)	27	5921.40	219.31	9.54***	22.9
Y*L	4	966.90	241.73	4.93**	3.7
Y* G	27	620.89	23.00	0.77	2.4
G*L	107	2879.77	26.91**	1.45**	11.1
G*Y*L	101	3008.70	29.79	1.60***	11.6
Error	484	9003.39	18.60		
Total	774	25847.35			

Table 6. Analysis of variance (Matmodel) for fresh yield and dry matter content of 24 yellow and 3 white-fleshed cassava genotypes evaluated at five locations in Nigeria, 2004/05-2005/06.

% of source ESS	df	SS	MS	Probability	% of total SS	G x
Fresh yield						
Total	794	79642.365	100.305			
TRT	269	64423.132	239.491	0.0000000 ***	80.9	
GEN	26	12952.107	498.158	0.0000000 ***	16.3	
ENV	9	39566.945	4396.327	0.0000000 ***	49.7	
G X E	234	11904.080	50.872	0.0000001 ***	14.9	
IPCA 1	34	2986.420	87.836	0.0000001 ***		25.1
IPCA 2	32	2958.239	92.445	0.0000000 ***		24.9
IPCA 3	30	2061.578	68.719	0.0000782 ***		17.3
IPCA 4	28	1378.005	49.214	0.0150256 *		11.6
IPCA 5	26	1001.397	38.515	0.1297607		8.4
IPCA 6	24	498.408	20.767	0.8369402		4.2
IPCA 7	22	456.956	20.771	0.8244721		3.8
Residual	38	563.077	14.818	0.9937488		4.7
Error	525	15219.233	28.989			
Dry yield						
Total	658	7018.394	10.666			
TRT	269	5706.192	21.213	0.0000000 ***	81.3	
GEN	26	1612.497	62.010	0.0000000 ***	23.0	
ENV	9	2673.117	297.013	0.0000000 ***	38.1	
G X E	234	1420.578	6.071	0.0000002 ***	20.2	
IPCA 1	34	381.606	11.224	0.0000000 ***		26.9
IPCA 2	32	308.452	9.639	0.0000010 ***		21.7
IPCA 3	330	226.806	7.560	0.0002769 ***		16.0
IPCA 4	28	172.468	6.160	0.0071378 **		12.1
IPCA 5	26	149.693	5.757	0.0179563 *		10.5
IPCA 6	24	82.809	3.450	0.4349395		5.8
IPCA 7	22	56.105	2.550	0.7796124		3.9
Residual	38	42.640	1.122	0.9999490		3.0
Error	389	1312.202	3.373			
Dry matter content						
Total	658	25767.495	39.160			
TRT	269	18064.652	67.155	0.0000000 ***	70.1	
GEN	26	7100.601	273.100	0.0000000 ***	27.6	
ENV	9	3304.823	367.203	0.0000000 ***	12.8	
G X E	234	7659.228	32.732	0.0000062 ***	29.7	
IPCA 1	34	2214.735	65.139	0.0000000 ***		28.9
IPCA 2	32	1662.380	51.949	0.0000078 ***		21.7
IPCA 3	30	970.580	32.353	0.0207640 ***		12.7
IPCA 4	28	810.167	28.935	0.0636792		10.6
IPCA 5	26	757.653	29.141	0.0658526		9.9
IPCA 6	24	474.292	19.762	0.467667		6.2
IPCA 7	22	401.194	18.236	0.5671744		5.2
Residual	38	368.228	9.690	0.9957263		4.8
Error	389	7702.843	19.802			

Grand mean Fresh yield=16.9064 t/ha; Grand mean dry yield= 4.95259 t/ha; Grand mean Dry Matter Content (%)=29.2851.
***, **, * Significant at P<=0.001, P<=0.01, and P<=0.05 respectively; =Interaction principal component axis.

Figure 1. Biplot of mean fresh yield and the first Interaction principal components axis (IPCA1) scores of 24 yellow fleshed and 3 white-fleshed cassava clones planted at 6 locations in Nigeria, 2004/05 and 2005/06.

of squares for FRY; E for 49.7% and GEI for 14.9%. G accounted for 23.0% of the total sums of squares for DRY, E for 38.1% and GEI for 20.2%. G accounted for 27.6% of the total sums of squares for DM; E for 12.8%, and GEI for 29.7%. Using the main effects and the first principal component axis (IPCA1) of the GEI for the traits, able data and F-test at the 0.05 probability level, involved the inclusion of the first four interaction PCA axes in the model for FRY, the first five for DRY, and first three for DM (Table 6). However, a significant feature of multivariate models (including AMMI analysis) is that they account for a large proportion of pattern related to the treatment design in the first few dimensions. The subsequent dimensions account for a diminishing percentage of pattern and an increasing percentage of noise. Since the AMMI biplots captured a large proportion of the pattern in the data (87.72 % of the treatments sum of squares for FRY, 81.8% for DRY, and 70.67% for DM), they were accurate enough to explain the main effects and the pattern of GEI for the traits. Displacement along the x-axis of the biplots reflected differences in main effects, whereas displacement along the y-axis exhibited differences in interaction effects. Genotypes with IPCA1 scores near zero had little interaction with environments. Genotypes or environments on the same parallel line relative to the y-axis have similar mean values for the trait, and a genotype or environment on the right hand-side of the mid

AMMI analysis provided a graphical representation (biplot) to summarize information on the main effects and the first principal component scores of the GEI of both genotypes and environments simultaneously for FRY, DRY and DM (Figures 1 - 3).

The postdictive success for AMMI, using all the available point of this axis has higher mean values for the trait than those on the left hand-side.

(Figure 1); they performed best in the Ibadan-2006 environment. Check clone 91/02324 was high yielding and moderately stable. Clones 01/1331, 01/1115, 01/-1277, and 01/1649 were stable but low yielding. Clone 98/2132 was the highest yielder but was also relatively unstable; it performed best in Ibadan-2006. Clone 01/1663 with about average FRY was the most unstable across environments; it was best adapted to Ubiaja-2006. The most stable YF clones for DRY with above average performance were 01/1380, 94/0006, and 01/1206 (Figure 2); they performed best in Ibadan-2006. Check clone 91/02324 had high DRY but was moderately un-stable. Clones 01/1335, 01/1277 and 01/1273 were stable but with low DRY. Of the YF clones, 98/2132 had the highest DRY but it was also relatively unstable; it per-formed best in Ibadan-2005. Clone 01/1663 was the most unstable across environments; it was best adapted to Ubiaja-2005. The most stable clones for DM with above average per-formance were 94/0330, 01/1277, 01/1646 and 95/0379
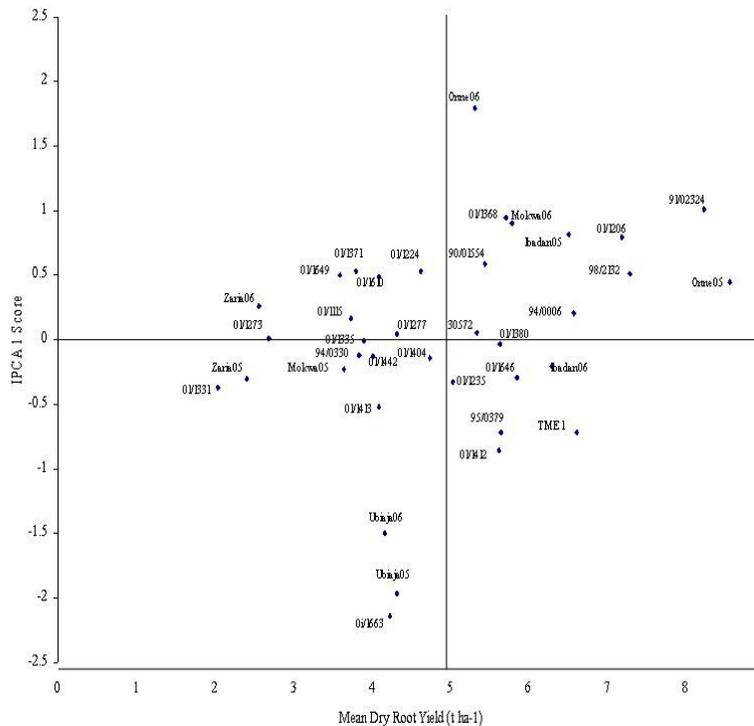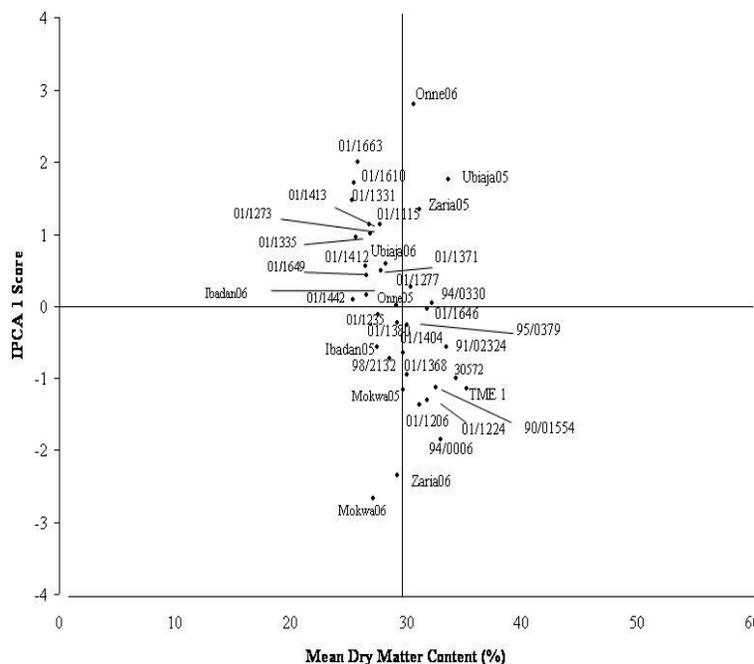
Figure 2. Biplot of mean dry matter yield and the first Interaction principal components axis (IPCA1) scores of 24 yellow fleshed and 3 white-fleshed cassava clones planted at 6 locations in Nigeria, 2004/05 and 2005/06.

Figure 3. Biplot of mean dry matter content and the first Interaction principal components axis (IPCA1) scores of 24 yellow fleshed and 3 white-fleshed cassava clones planted at 6 locations in Nigeria, 2004/05 and 2005/06.

(Figure 3); they performed best in the Onne-2005. Check clones 91/02324, 30572, and TME 1 had high DM with moderate stability; TME 1 had the highest DM and performed best in Zaria-2006. Clones 01/1235 and 01/1380

were stable but with low DM. Clone 01/1663 was again the most unstable for DM across environments

DISCUSSION

There were variable responses to the impact of E on FRY, DRY, DM, CMD, CBB, CAD, and CGM. The impact of L was highly significant for all the traits, justifying the need for multilocational testing to identify good performers for specific locations. The significance of Y effects on CBB, CAD, CGM and DM suggests the need to evaluate for more than one year for reliable inferences to be made on performance. Partitioning of the variance components revealed that G x L was the main source of GEI for DRY, CMD, CAD and CGM, indicating that L contributed more than Y to fluctuations in performance of the clones. This was also the case for CBB and FRY. This suggests the need to identify clones with specific adaptation for the traits. The relatively high G effect on CMD, CGM, and DM suggests prospects for the improvement of YF cassava for the traits though some genotypes may fail to respond because of the significant GEI. Benesi et al. (2004) also report higher G than E effects on DM in cassava. The high impact of E on FRY is expected, since yield is a polygenic trait (Easwari and Sheela, 1998; Cach et al., 2006) and, therefore, subject to much influence from E. The high environmental impact makes future potential genetic gain in the yield of YF cassava problematic. This may require early testing of clones in multi-environments so as to identify those with specific adaptation.

Most of the YF genotypes were below average performers for DM compared to the WF low carotenoid check varieties. This is not surprising, since low DM is a common feature in carotenoid rich cassava. However, the presence of some YF clones with DM in the same range as the WF checks is an indicator that it is possible to breed carotenoid-rich cassava with high DM.

The significant negative correlations between CMD and CBB, CBB and CAD, CBB and FRY, CAD and CGM, and CGM and FRY suggest that selection for one trait in a pair may compromise the other trait. The negative trend of the association between CBB and CMD is also evident in the local landraces (at IITA) and their progenies that are resistant to CMD but highly susceptible to CBB. However, the negative correlation between CMD and CBB in this study is contrary to earlier reports by Hahn et al. (1980) and Thresh et al. (1994). The relationship we observed between CBB and FRY is similar to that of Fokunang et al. (2000) who report a significant negative correlation between the two traits. The negative correlations between CBB and yield and CGM and yield may be explained by the negative impact of the disease-/pest on FRY. The positive correlation between CAD and FRY could be explained by the fact that CAD normally has more impact on the vigorous plants; those plants also tend to have higher FRY. However, the surprising significant positive correlation between CMD and FRY observed in this study needs to be confirmed by further studies.

Conclusion

Our results suggest that it is possible to make progress in breeding and selection of YF cassava with superior yield and resistance to the most economically important biotic stresses (CMD and CGM). However, the significant GEI for all the traits under this study may complicate selection of superior YF genotypes, thus reducing the correlation between genotype and phenotype.

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