

EVALUATION OF ADVANCED CASSAVA GENOTYPES IN UGANDA

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ABSTRACT

In a bid to increase the number of genotypes reaching farmers, on-farm trials were conducted in 2001/2002 with the aim of increasing the number of genotypes available to farmers to be evaluated for performance, adaptation and acceptability. Twenty improved genotypes were planted in Lira, Nakasongola, Gulu, Kumi and Katakwi districts using augmented design. The results indicated that cassava mosaic disease (CMD) varied from location to location but was more influenced by the genotype than the environment. The highest CMD severity (>4) was recorded among the farmers' local varieties across all environments, followed by Alice local (3.8 ± 0.4) in Nakasongola and Lira (2.8 ± 0.2) districts and I 60142 (3.0 ± 0.0) in Kumi and Lira (2.8 ± 0.2) districts. Six clones (MM96/0245, MM96/0561, I92/2324, MM96/3585, MM96/4589 and MM96/0264) showed resistance (score 1 for CMD) while the rest had severity scores below the average (2.5). At harvest, the highest yield (60.8 ± 3.7 t ha⁻¹) was obtained from Alice local followed by clone MM 96/0561 (59.5 ± 6.6 t ha⁻¹) in Nakasongola district and clone MM 96/4614 (52.5 ± 13.2 t ha⁻¹) in Lira district. The lowest yield was from clone MM 96/3585 (10.3 ± 4.2 t ha⁻¹) followed by Oko Iyawo (1) 99 (14.2 ± 4.2 t ha⁻¹) in Kumi district. All the varieties tested were either sweet or slightly bitter with the scores of 1 or 2, respectively. Genotype MH97/2961 was the most preferred in Kumi and Lira districts, while it was third in Nakasongola district. All these genotypes also had a sweet taste for cooking. The most preferred genotypes in Nakasongola were TME 5 and MM96/5312 and had a sweet taste for cooking. The genotype by environment analysis indicated that genotypes TME 5, MM96/1419, I92/0427, and MH97/044 (2) UG were the most stable and adapted across all environments while MM96/4614 and Alice local were more specific for Lira and Nakasongola, respectively. These findings provide a basis for recommendations with regard to cultivation and preference of cassava genotypes in different environments.

Key Words: Cassava mosaic virus disease, resistant genotypes, tuber quality, Uganda

RÉSUMÉ

En vue d'augmenter le nombre de génotypes disponibles aux agriculteurs, des tests de terrain étaient effectués en 2001/2002 dans le but d'accroître la quantité de génotypes disponibles aux cultivateurs et qui seraient évalués pour leur performance, leur adaptation et leur acceptabilité. Vingt génotypes améliorés étaient plantés dans les districts de Lira, Nakasongola, Gulu, Kumi et Katakwi en utilisant la disposition augmentée. Les résultats ont indiqué que la maladie de la mosaïque du manioc (CMD) variait en fonction des localisations mais était plus influencée par le génotype que par l'environnement. La sévérité de CMD la plus élevée (>4) était enregistrée au sein des variétés locales des cultivateurs à travers tous les environnements, suivi de Alice locale (3.8 ± 0.4) à Nakasongola et (2.8 ± 0.2) à Lira ; et de I 60142 (3.0 ± 0.0) à Kumi et (2.8 ± 0.2) à Lira. Six clones (MM96/0245, MM96/0561, I92/2324, MM96/3585, MM96/4589 et MM96/0264) ont montré une résistance (Degré 1 pour CMD) pendant que le

reste avait un degré de sévérité en dessous de la moyenne (2.5). A la récolte, le rendement le plus élevé (60.8 ± 3.7 t/ha) était obtenu à partir de Alice locale suivi du clone MM 96/056 (59.5 ± 6.6 t ha⁻¹) dans le district de Nakasongola et du clone MM 96/4614 (52.5 ± 13.2 t ha⁻¹) dans le district de Lira. Le rendement le plus bas provenait du clone MM 96/3585 (10.3 ± 4.2 t ha⁻¹) suivi de Oko Iyawo (1) 99 (14.2 ± 4.2) dans le district de Kumi. Toutes les variétés testées étaient soit sucrées soit légèrement amères avec des degrés de 1 et 2 respectivement. Le génotype MH97/2961 était le plus préféré dans le district de Lira et de Kumi tandis qu'il était troisième dans le district de Nakasongola. Tous ces génotypes avaient également un goût sucré à la cuisson. Les génotypes les plus préférés dans le district de Nakasongola étaient TME 5 et MM96/5312 et avaient un goût sucré à la cuisson. Le génotype par analyse environnemental indiquait que les génotypes TME 5, MM96/1419, 192/0427 et MH97/044 (2) UG étaient les plus stables et se sont adaptés à travers tous les environnements pendant que MM96/4614 et Alice locale étaient les plus spécifiques pour Lira et Nakasongola respectivement. Ces résultats apportent une base de recommandations relatives à la culture et la préférence de génotypes du manioc dans différents environnements.

Mots Clés: La maladie du virus de la mosaïque du manioc, génotypes résistants, qualité de tubercule, Ouganda

INTRODUCTION

Cassava is an important crop in Africa where it serves as a famine reserve crop, rural and urban food staple, industrial raw material and livestock feed (Nweke *et al.*, 2002). In sub-Saharan Africa, it is the major source of carbohydrates for over 70 million people, who obtain more than 500 calories per day from cassava (Kawano, 2003; Aerni, 2004). With its productivity on marginal soils, ability to withstand disease, drought, and pests, and flexible harvest dates, cassava is a remarkably adaptable crop which is consumed where drought and poverty are often prevalent.

In Uganda, cassava is recognised as the second most important food crop after bananas in terms of area cultivated, production and consumption per capita (Ssemakula *et al.*, 2002). Despite its increasing importance in sub-Saharan Africa, and in Uganda in particular, cassava production is being constrained by a number of biological constraints such as diseases especially cassava mosaic disease (CMD) and cassava bacterial blight (CBB), and of recent cassava brown streak virus disease (CBSD) while the major pests are the green mite and the mealy bug. Of these however, CMD is the most serious and it almost wiped out the cassava sub-sector in the early 1990s (Semakula *et al.*, 2004).

Following the development of the severe epidemic of CMD in Uganda (IITA, 1990), the Cassava Program of the National Agricultural Research Organisation (NARO) together with International Institute of Tropical Agriculture (IITA) and the East Africa Root Crops Research

Network (EARRNET) put extensive effort on development, release, multiplication and dissemination of resistant cassava germplasm as a strategy to curb the progress of the disease. As a result, up to 12 resistant varieties have been released by NARO since the outbreak of the epidemic and many other promising genotypes are due for release. However, despite the many resistant/tolerant genotypes generated annually, few reach the farmers and those that reach the farmers are not grown largely, possibly due to lack of access to planting materials and/ or preference of their local materials to the improved ones. In a bid to evaluate their adaptability and preferences hence increase the number of genotypes available to the farmers, the Cassava Program in collaboration with IITA/EARRNET conducted on-farm trials in five districts of Uganda in 2001/2002. The objective of the study was to evaluate the performance of improved genotypes under farmer field conditions and management as well as acceptability of those clones by the farmers.

MATERIALS AND METHODS

Study locations and farmer selection. The trials were conducted in five districts of Uganda i.e. Nakasongola (Central), Lira and Gulu (Northern), Katakwi and Kumi (Eastern Uganda) between July, 2001-July, 2002. From each district, twenty (20) willing farmers were selected by the research team in collaboration with the district agricultural offices and local Non Government Organisations (NGOs), forming clusters within the study.

Materials used in the study. Twenty (20) cassava varieties used in the study were selected from the Advanced Yield Trial (AYT) and Uniform Yield Trial (UYT) materials. The genotypes included TME 12, I 60142, Oko Iyawo (1) 99, I 92/0427, Oko Iyawo (2) 247, Abbey Ife, MM96/4614, MM96/0245, MH 97/2961, TME 5, Alice local, MM96/5312, MM96/1419, MM96/0561, I 91/2324, MM96/3585, MH 97/044 (2) UG, MM96/4004, MM96/4589 and MM96/0264. Along the 20 new genotypes, an improved check (SS4=Nase 4) and a local provided by each of the farmers were planted at each farm giving a total of twenty two clones.

Experimental design. Given the high number of genotypes that were to be evaluated, the research team adopted the augmented design for setting up the trials. Each farmer planted five of the new clones, the improved check plus a local check thus new genotype is replicated five times within a cluster of 20 farmers. The local check varied from one farmer to another depending on what was available. Each genotype was planted to five rows of ten metres with a spacing of 1 m x 1 m between and with rows giving a total plot area of 50 m² per clone.

Data collection and analysis. Data collection for biotic constraints was carried out at 1 month after planting (MAP), 3, 6 and 9 MAP. The biotic parameters examined included vigour, CMV, CBB, cassava green mite (CGM) incidence and severity, cassava anthracnose (CA) and the cassava mealy bug (CM). The severity of CMV, CBB, CGM and CA severity were scored using a scale of 1-5 where 1= resistant and 5= highly susceptible (IITA, 1990). Plant vigour was also evaluated using a scale of 1-5, where 1 was the least vigorous and 5 the most vigorous. Cassava mealybug was reported as either present (+) or absent (-). At harvest (12 MAP), three middle rows were harvested. Data were collected on number of marketable tubers, non marketable tubers, total yield and mealiness and taste. After evaluation at harvest, farmers were asked to rank the different genotypes depending on their preference. All data were collected by the research team together with the farmers. However, management of the plots

throughout the trial period was carried out exclusively by the farmers. All data collected were analysed by Statistical Analysis System (SAS) using the mixed model (SAS, 1990) while G x E interaction was analysed by GGEbiplot analysis, using model 1 which generates biplots based on singular value decomposition of tester centered data (Weikai, 2001). The GGE (genotype main effect (G) plus genotype by environment interaction (GE)), is the source of variation that is relevant to genotype evaluation. Tangibly, GGE is the total variation of the environment-centered or standardised data (Zobel *et al.*, 1988). In this model, all the testers used the same unit i.e. GxE table of a single trait, yield and CMD, separately for this case.

RESULTS AND DISCUSSION

Genotype vigour. Most of the genotypes had growth vigour above the average of 2.5 in all the districts, data from Gulu and Katakwi districts are not presented (Table 1). Overall, Kumi district had the lowest growth rates when compared with the rest of the locations. The highest growth vigour recorded in Kumi was on genotype MM96/1419 with a score of 3.8 ± 0.6 , followed by MM96/4004 (3.7 ± 0.9) and I 92/0427 (3.4 ± 0.4) while the lowest were recorded from I 60142, MM96/0561, MM96/3585, MM96/4589 and SS4 with scores of 2.3 each. While clone MM96/4589 performed poorly in Kumi and Nakasongola, it was one of the best performers in Lira together with MM96/4614 and MH97/044 with average vigour scores of 4.0. The least vigour score in Lira was 2.6 recorded in clone MM96/5312. For Nakasongola, the most vigorous genotypes were MM96/0561 (4.0), I 92/0427 (3.7), MM96/4614 and MM96/4004 (3.5) while the least was the farmers' local variety with a score of 2.4. These results demonstrate the fact that while some genotypes such as MM96/4614 and MM96/4004 maintain high vigour across all districts, some of the most genotypes are more vigorous in one or two of the districts. Genotype I 92/0427 performed well in Nakasongola and Kumi districts but was among the least vigorous in Lira district, while MM96/0561 and MM96/4589 were more vigorous at Nakasongola and Lira, respectively.

TABLE 1. Performance (biotic and yield) of twenty new genotypes planted in an on-farm trial in three districts of Uganda in 2001

Clones	Districts									
	Kumi					Lira				
	Vigour	CMDS	Yield (t ha ⁻¹)	Taste* Rank		Vigour	CMDS	Yield (t ha ⁻¹)	Taste* Rank	
										Nakasongola
1	2.8 ± 0.6	1.3 ± 0.3	18.7 ± 3.4	1	2	3.8 ± 0.2	2.2 ± 0.2	37.1 ± 7.7	1	3
2	2.3 ± 0.3	3.0 ± 0.0	18.2 ± 7.8	1	3	3.8_0.3	2.8 ± 0.2	27.2 ± 4.6	1	4
3	2.8 ± 0.4	2.0 ± 0.3	14.2 ± 4.2	1	4	3.3 ± 0.3	2.3 ± 0.3	31.4 ± 6.2	1	2
4	3.4 ± 0.4	1.4 ± 0.2	22.5 ± 6.0	1	3	2.8 ± 0.4	2.2 ± 0.4	35.7 ± 4.1	2	4
5	2.8 ± 0.2	1.2 ± 0.2	19.4 ± 2.3	1	3	3.8 ± 0.4	2.2 ± 0.4	26.4 ± 5.2	1	2
6	3.2 ± 0.4	2.0 ± 0.3	19.0 ± 3.0	1	3	3.8 ± 0.5	2.3 ± 0.3	30.8 ± 11.5	1	3
7	3.3 ± 0.7	2.0 ± 0.6	25.8 ± 2.4	1	2	4.0 ± 0.6	2.0 ± 0.0	52.5 ± 13.2	1	2
8	3.0 ± 0.4	1.0 ± 0.0	18.8 ± 2.6	2	5	3.7 ± 0.3	1.0 ± 0.0	33.5 ± 6.1	2	5
9	3.0 ± 0.0	1.0 ± 0.0	18.2 ± 2.7	1	1	3.7 ± 0.2	1.2 ± 0.2	33.3 ± 0.5	1	1
10	2.8 ± 0.5	1.6 ± 0.2	15.0 ± 7.4	2	4	3.8 ± 0.2	2.0 ± 0.3	41.5 ± 5.2	1	4
11	2.8 ± 0.6	1.3 ± 0.3	24.8 ± 8.0	1	2	3.8 ± 0.5	2.8 ± 0.2	43.7 ± 7.9	1	2
12	2.8 ± 0.2	1.0 ± 0.0	14.5 ± 2.8	1	3	2.8 ± 0.2	1.2 ± 0.2	26.1 ± 5.8	1	2
13	3.8 ± 0.6	1.0 ± 0.0	20.5 ± 6.1	1	5	2.6 ± 0.5	1.5 ± 0.5	39.5 ± 3.0	1	4
14	2.3 ± 0.6	1.0 ± 0.0	15.3 ± 3.5	1	5	2.8 ± 0.4	1.0 ± 0.0	32.7 ± 5.3	2	4
15	2.4 ± 0.5	1.0 ± 0.0	18.8 ± 4.5	1	5	3.0 ± 0.3	1.0 ± 0.0	20.9 ± 4.0	1	5
16	2.3 ± 0.7	1.0 ± 0.0	10.3 ± 4.2	1	6	3.2 ± 0.5	1.0 ± 0.0	24.3 ± 2.2	1	4
17	3.0 ± 0.0	1.5 ± 0.5	21.3 ± 3.9	2	3	4.0 ± 0.6	1.7 ± 0.7	42.7 ± 15.5	1	4
18	3.7 ± 0.9	1.3 ± 0.3	13.0 ± 2.2	2	3	3.3 ± 0.3	1.0 ± 0.0	46.0 ± 17.6	1	5
19	2.3 ± 0.6	1.0 ± 0.0	18.6 ± 6.1	1	3	4.0 ± 0.0	1.0 ± 0.0	41.6 ± 3.6	1	4
20	3.0 ± 0.0	1.0 ± 0.0	15.9 ± 3.2	2	4	3.4 ± 0.2	1.0 ± 0.0	30.9 ± 3.3	2	4
21	2.3 ± 0.3	1.2 ± 0.1	20.2 ± 2.1	2	4	3.3 ± 0.2	1.4 ± 0.2	43.4 ± 8.3	2	5
22	3.0 ± 0.0	4.0 ± 1.0	16.1 ± 3.6	1	5	3.0 ± 0.2	4.2 ± 0.2	22.7 ± 4.9	1	5
Mean		1.5					1.8			1.2

*Taste: 1= sweet, 2= slightly bitter, 3= bitter; Clones 1= TME 12, 2= I 60142, 3= Oko Iyawa (1) 99, 4= I 92/0427, 5= Oko Iyawa (2) 247, 6= Abbey life, 7= MM 96/4614, 8= MM 96/0245, 9= MH 97/2961, 10= TME 5, 11= Alice local, 12= MM 96/5312, 13= MM 96/1419, 14= MM 96/0561, 15= I 91/2324, 16= MM 96/3585, 17= MH 97/044 (2) UG, 18= MM 96/4004, 19= MM 96/4589, 20= MM 96/0264, 21= Nase 4, 22= Local ; where Yld= Fresh Storage yield and CMDS= Cassava mosaic disease severity

CMD disease severity. The only disease observed on the genotypes during the trial period was Cassava Mosaic Virus Disease (CMD) that generally occurred across all environments, though to varying severities and on different genotypes, especially the farmers' local varieties (Table 1).

The highest CMD severity (>4) was recorded in the farmers' local varieties in across all environments, followed by Alice local (3.8 ± 0.4) in Lira and Kumi (2.8 ± 0.2) districts and I 60142 (3.0 ± 0.0) in Kumi and Lira (2.8 ± 0.2) districts. Six genotypes; MM96/0245, MM96/0561, I92/2324, MM96/3585, MM96/4589 and MM96/0264 did not show any CMD symptoms while the rest showed susceptibility depending on location. Overall, CMD pressure was high in Lira, then Kumi and least was Nakasongola. The good reaction of the genotypes to CMD was expected as they were developed initially for resistance to CMD. Since the outbreak of the cassava mosaic epidemic, breeding efforts have been focussed on development of mosaic resistant cassava genotypes. These resistant materials have been responsible for the restoration of cassava production as evidenced by the increase in production and yield since 1997 (Ssemakula *et al.*, 2002).

Performance of the genotypes at harvest. The results of yield performance are shown in Table 1. Overall, Kumi district registered the lowest yields across all genotypes, followed by Lira district while Nakasongola had the highest yields. The highest yielding clone in Kumi district was MM96/4614 (25.8 ± 6.0 t ha⁻¹) followed by Alice local (24.8 ± 8.0 t ha⁻¹), I92/0427 (22.5 ± 6.0 t/ha), MH97/044 (2) UG (21.3 ± 3.9 t ha⁻¹) and Nase 4 (20.2 ± 2.1 t ha⁻¹). The lowest yield (10.3 ± 4.2 t ha⁻¹) was obtained from MM96/3585, followed by MM96/4004 (13.0 ± 2.2 t ha⁻¹) and Oko Iyawo (1) 99 with a yield of 14.2 ± 4.2 t ha⁻¹. In Lira district, the best yielding genotype was MM96/4614 with average root yield of 52.53 ± 13.2 t ha⁻¹, followed by MM96/4004 (46.0 ± 17.6 t ha⁻¹), Alice local 43.7 ± 7.9 t ha⁻¹, Nase 4 (43.4 ± 8.3 t ha⁻¹) and MH97/044 (2) UG with average yield of 41.6 ± 3.6 t ha⁻¹. On the contrary, the lowest yielding genotypes in Lira district was I 91/2324 with a yield of 20.9 ± 4.0 t ha⁻¹ followed by the farmers' local cultivar (22.7 ± 4.9 t ha⁻¹) and then MM96/3585 that yielded

24.3 ± 2.2 t ha⁻¹. Alice local gave the highest overall yield of 60.8 ± 3.7 t ha⁻¹ of tuber yield in Nakasongola district, followed by MM96/0561 (59.5 ± 6.6 t ha⁻¹), MM96/4614 (48.0 ± 9.6 t ha⁻¹), I 92/0427 (47.3 ± 5.6 t ha⁻¹) and MM96/0245 with root tuber yield of 46.9 ± 5.6 t ha⁻¹. The lowest yield (15.0 ± 2.4 t ha⁻¹) in Nakasongola was registered from the farmers' local cultivar, followed by MM96/4589 (20.6 ± 1.2 t ha⁻¹) and MM96/3585 with average yield of 20.8 ± 12.1 t ha⁻¹.

Some genotypes maintained high yields in at least two of the environments while some performed well in only one of the environments. Clones MM96/4614 and Alice local performed well in all the three environments indicating possible wide adaptation. This suggests that these two clones could be promoted for planting in any of the test locations. Clone I92/0427 performed consistently well in Kumi and Nakasongola while clones MH97/044 and Nase 4 performed well in Lira and Kumi districts and could be promoted for use in the respective districts. Clone MM96/4004 performed well only in Lira district while MM96/0561, MM96/0245 performed well in Nakasongola district only. Though clone MM96/3585 exhibited considerable resistance to CMD, it had poor yield performance in all the three districts.

Preference of genotypes by farmers across the test locations. All the varieties tested were either sweet or slightly bitter with the scores of 1 or 2, respectively. Genotypes MM96/0264 and MM96/0245 had slightly bitter taste across all environments and this affected their preference by farmers. These two genotypes were, respectively, ranked 4th and 5th across all the test locations. Genotype MH92/2961 was the most preferred in Kumi and Lira districts with a rank of 1, followed by MM96/4614 and Alice local with a rank of 2. Other preferred genotypes were TME 12 for Kumi district and Oko Iyawo (2) 245 and MM96/5312 in Lira district, each with a rank of 2. All these genotypes also had a sweet taste on cooking. The most preferred genotypes in Nakasongola were TME 5 and MM96/5312 with a rank of 1 followed by Abbey Ife with a rank of 2 (Table 1).

GGE biplot analysis of reaction of genotypes to CMD across test locations. The analysis of variance for the GGE indicates that genotypes effect was the most important determinant of reaction to CMD, accounting for 75 % of the total sum of squares while the environment and interaction accounted for only 10 % and 15 %, respectively (Table 2). The first principal component for CMD reaction was the most important in explaining GGE with $\lambda= 5.5$ and accounting for 85 % of the total sum of squares, followed by PC 2 with $\lambda= 2.0$, accounting for 11 % of the total sum of squares, while PC 3 with $\lambda= 1.3$ accounted for only 4 % of the total sum of squares (Table 3). Therefore, only the first two principal components are the most important, accounting for up to 96% of all the genotype by environment interaction for reaction to CMD by the genotypes.

Reaction of the genotypes to CMD was not highly affected by G x E interaction, rather genotype effect was more important. It was observed that the farmers' local cultivar was mostly susceptible to CMD with the highest CMD severity. The genotypes with most stable response to CMD across all environments were TME 12, MM96/1419, Nase 4, and MH 97/044 (in circle) (Fig. 1). They had the smallest displacement on

the y-axis, indicating stable response to CMD according to Zobel *et al.* (1988). In addition to being stable, MM96/1419, and Nase 4 had CMD scores below average while MH 97/044 and TME 12 had average and above average response to CMD, respectively. Other genotypes with above average reaction to CMD were Oko Iyawo (1) 99, 192/0427, Oko Iyawo (2) 247, Abbey Ife, MM96/4614, TME 5, and Alice local in Kumi and Lira districts while the rest of the genotypes had below average response to CMD in Nakasongola district (Fig. 1).

GGE biplot analysis of effect of GxE on yield performance of the genotypes. The results indicated that the environment and genotypes effects accounted for 53.2 % and 25.6 % of the total sum of squares while the interaction accounted for only 21.2 % (Table 2). The environment variation for yield was most important than genotypic variation and Ntawuruhunga *et al.* (2001) reported the same confirming that cassava yield trait is most affected by environment and interaction than the genotype. The first principal component was the most important in explaining GGE with $\lambda= 56.7$ and accounting for 71 % of the total sum of squares, followed by PC 2 with $\lambda= 34.0$, accounting for 25

TABLE 2. Analysis of variance table showing the percentage of total sum of squares accounted for by each source of variation

Source of variation	DF	Reaction to CMD		Yield of genotypes	
		SS	% of total SS	SS	% of total SS
Genotype	21	30	75	2501	25.6
Environment	2	4	10	5191	53.2
G x E	42	6	15	2068	21.2

TABLE 3. Percentage of GGE explained by each principal component (PC)

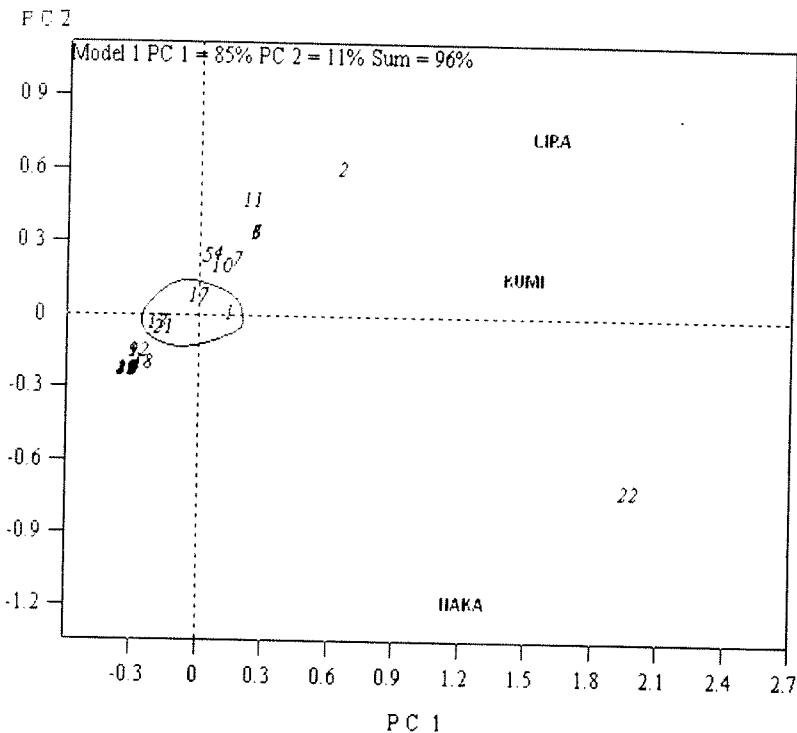
PC	Reaction to CMD		Yield of genotypes		
	Lambda (λ)	% of total SS	PC	Lambda (λ)	% of total SS
1	5.5	85	1	56.8	71
2	2.0	11	2	34.0	25
3	1.3	4	3	13.8	4

% of the total sum of squares (Table 3). These two PCs accounted for up to 96% of all the genotype by environment interaction in the data.

From the GGEbiplot, genotypes responded differently to the environment for yield. While some of the genotypes' performance was affected by G x E interaction, there are those that were more stable across the test environments. Zobel *et al.* (1988) indicated that displacement along the x-axis on a biplot reflects differences in main effects whereas displacement along y-axis exhibits differences in interaction effect. Genotype or environment close to the centroid indicate that the entry has a small interaction effect and it general response pattern across the environment

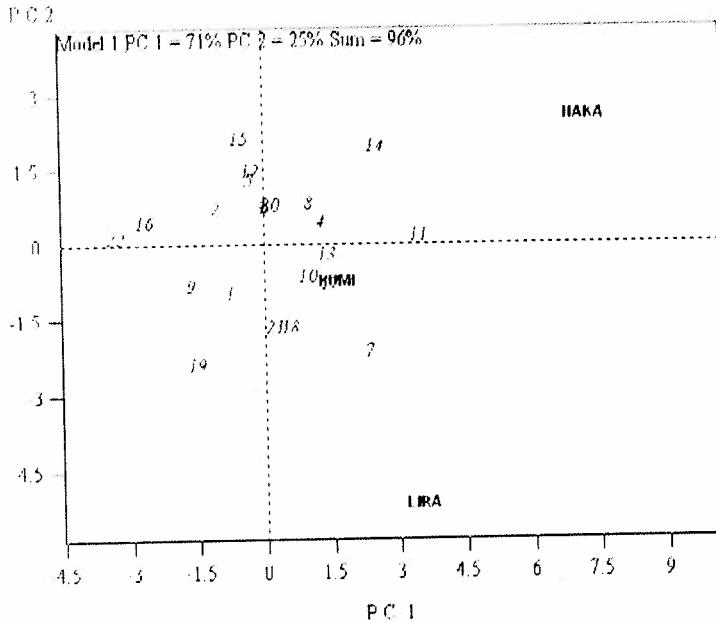
parallels the mean of all the genotypes in the trail, indicating a stable genotype or environment (Copper *et al.*, 1996).

As such, genotypes Alice local, MM96/1419, and the farmers' local cultivars showed the least interaction, indicating broad adaptability. Despite the broad adaptability, farmers' local cultivars were the lowest in yield performance, while Alice local also out yielded genotype MM96/1419 as shown by the displacement on the x-axis. Genotypes Alice local was the most stable and high yielding. Clone MM 96/4614 was found higher yielding but specifically adapted to Lira location while clone MM 96/0561 was specific to Nakasongola (Fig. 2). Other genotypes that showed



Clones 1= TME 12, 2= I 60142, 3= Oko Iyawo (1) 99, 4= I 92/0427, 5= Oko Iyawo (2) 247, 6= Abbey Ife, 7= MM 96/4614, 8= MM 96/0245, 9= MH 97/2961, 10= TME 5, 11= Alice local, 12= MM 96/5312, 13= MM 96/1419, 14= MM 96/0561, 15= I 91/2324, 16= MM 96/3585, 17= MH 97/044 (2) UG, 18= MM 96/4004, 19= MM 96/4589, 20= MM 96/0264, 21= Nase 4, 22= Local.

Figure 1 A bi-plot of GGE model 1 of the effects of genotype and environment on the response of 22 cassava genotypes to CMD in three locations of Lira, Nakasongola and Kumi districts of Uganda in 2001. PC1 and PC2 are first and second principal components, respectively.



Clones 1= TME 12, 2= I 60142, 3= Oko Iyawo (1) 99, 4= I 92/0427, 5= Oko Iyawo (2) 247, 6= Abbey Ife, 7= MM 96/4614, 8= MM 96/0245, 9= MH 97/2961, 10= TME 5, 11= Alice local, 12= MM 96/5312, 13= MM 96/1419, 14= MM 96/0561, 15= I 91/2324, 16= MM 96/3585, 17= MH 97/044 (2) UG, 18= MM 96/4004, 19= MM 96/4589, 20= MM 96/0264, 21= Nase 4, 22= Local; NAKA = Nakasongola district.

Figure 2. A bi-plot of GGE model 1 of the effects of genotype and environment on the yield of 22 cassava genotypes tested in three locations of Lira, Nakasongola and Kumi districts in 2001. PC1 and PC2 are first and second principal components, respectively.

some wide adaptation included I92/0427, MM96/0245, and TME 5. Genotypes I91/2324 and MM96/4589 were however, poor yielding compared to MM96/1419 and MM96/4614. Genotype MM 96/1419, I92/0427, MM 96/1419 and TME 5 are most suitable for growing at Kumi, while MM 96/4614 could be promoted in Lira districts. Among the three districts, Kumi district had the lowest overall yield but stable environment while Nakasongola had the highest (Fig. 1).

Based on the study findings, genotypes MM 96/1419 and Alice Local were the best yield performers and most stable across districts. They are widely adapted and could be considered for promotion. Also specific adaptations were identified with clone MM 96/4614 in Lira while

MM 96/0561 in Nakasongola. With regard to farmers preferences, genotypes MH92/2961, MM96/4614 and Alice Local were more preferred in Kumi district and Oko Iyawo (2) 245 and MM96/5312 in Lira district while genotypes TME 5, MM96/5312 and Abbey Ife were preferred in Nakasongola district. Though many genotypes that could be promoted for growing were identified, there is still a challenge to plant breeders because the most resistant genotypes were not necessary the most preferred by farmers.

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