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GROUPING LOCATIONS FOR EFFICIENT CASSAVA EVALUATION IN MALAWI

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SUMMARY

Cassava, a crop widely adapted in the tropics, has the important attribute of withstanding adverse environmental conditions better than do many other staple crops. The performance of an individual genotype, however, is influenced by the environment in which it grows. In Malawi, the heterogeneity of agro-ecologies requires the cumbersome and costly assessment of new cassava genotypes at many sites. This study was conducted, therefore, to test the feasibility of selecting only a few locations for cassava evaluation that would be representative of all the agro-ecologies in which cassava is grown in Malawi. Enormous environmental effects, largely contributed by the interaction between season and location, were manifested. Genotype × environment interaction, due largely to a third level interaction (genotype × season × location), was highly significant for all the traits studied. A principal component analysis scatter plot showed no particular grouping of environments, but a pair-wise comparison showed that some of the locations had limited genotype × environment interaction, indicating that it would be sufficient to use one of these sites for evaluating these traits. The value of the residual was often large, probably as an effect of environmental heterogeneity in the test sites. The authors conclude that cassava genetic improvement will continue to be slow if Malawi is used as a single breeding zone. They recommend a much finer grouping of the locations and the use of smaller plot sizes to allow more clones to be tested at more sites for the same cost. Locations may be selected for intensive cassava breeding work from those that give the best discrimination between genotypes while having insignificant genotype × environment interactions in a relatively large number of environments.

INTRODUCTION

The tuberous roots of cassava (*Manihot esculenta* Crantz) are the most important root-crop source of starch, and one of the main staple foods, in Africa as well as in many other tropical regions. For the purposes of this document and unless specified otherwise, the term 'root' applies to the edible tuberous roots of cassava as opposed to its finer feeder roots. The crop's most important attribute is that it withstands adverse environmental conditions better than do many other staple crops. Cassava grows and yields well, therefore, in a wide range of environments within the tropics.

Despite this wide adaptation, however, the environment in which cassava is grown influences the performance of individual genotypes (Bokanga *et al*., 1994). Significant genotype × environment (G × E) interactions have been reported for

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various important traits of cassava. For example, Dixon and Nukenine (2000) reported significant effects of G × E interactions on all cassava yield traits. In Malaysia, Tan and Mak (1995) found significant effects of environment, G × E and location × season (L × S) on fresh root yield, marketable root number, harvest index, root starch, cyanide content and root dry matter. Otoo *et al*. (1994) documented a highly significant G × E interaction for fresh root yield, and for a number of cassava diseases and pests. They found that the root yield variance due to the G × E interaction exceeded that due to genotypes and was large enough to confuse differences among genotypes and to complicate selection.

In Malawi, small-scale farmers grow cassava without the application of chemical fertilizers. The diverse agro-ecologies and farmers' socio-economic status result in large differences in the agricultural systems practised. Variations in crop species, varieties and cultural practices occur over short distances and over seasons. Consequently, it is important to assess the performance of new cassava genotypes in a number of locations over a number of seasons in order to quantify their relative performances in all the main agro-ecological areas where cassava is grown. Being a vegetatively propagated crop with a long growing cycle (9–24 months), it is costly, cumbersome and difficult to manage extensive multi-locational trials for cassava. With the rising cost of conducting field research and the scarcity of resources, prudent use of these limited resources is necessary. Thus, a review of the popular cassava-breeding scheme (Figure 1) is required. This is also timely considering the recent interest in farmer participatory plant breeding (Joshi and Witcombe, 1996; Sperling *et al*., 1993; 2001). This approach is especially appropriate for small-scale subsistence farming in diverse agro-ecologies.

This paper reports the results of G × E interaction studies that were conducted in order to group locations for efficient cassava evaluation in Malawi.

MATERIALS AND METHODS

Genotypes

In total, eight cassava clones were evaluated over three seasons at eight locations in Malawi. The clones included: six local genotypes, Mbundumali, Gomani, Nyasungwi, Chitembwere, Thipula, and Kanonono; one breeding line, MH 108; and one elite clone, TMS91934, introduced from the International Institute of Tropical Agriculture (IITA) in Nigeria. Mbundumali, Chitembwere and MH 108 are sweet genotypes while the rest are bitter.

Locations

The locations chosen were Meru, Baka, Mbawa, Mkondezi, Chitala, Chitedze, Makoka, and Thutchila, areas where most crop research in Malawi is conducted. They were selected to cover the major agro-ecological zones where cassava is grown (Table 1 and Figure 2). Baka, Mkondezi and Chitala are low-lying locations along the shores of Lake Malawi, and the other five are in the mid-altitude plains.

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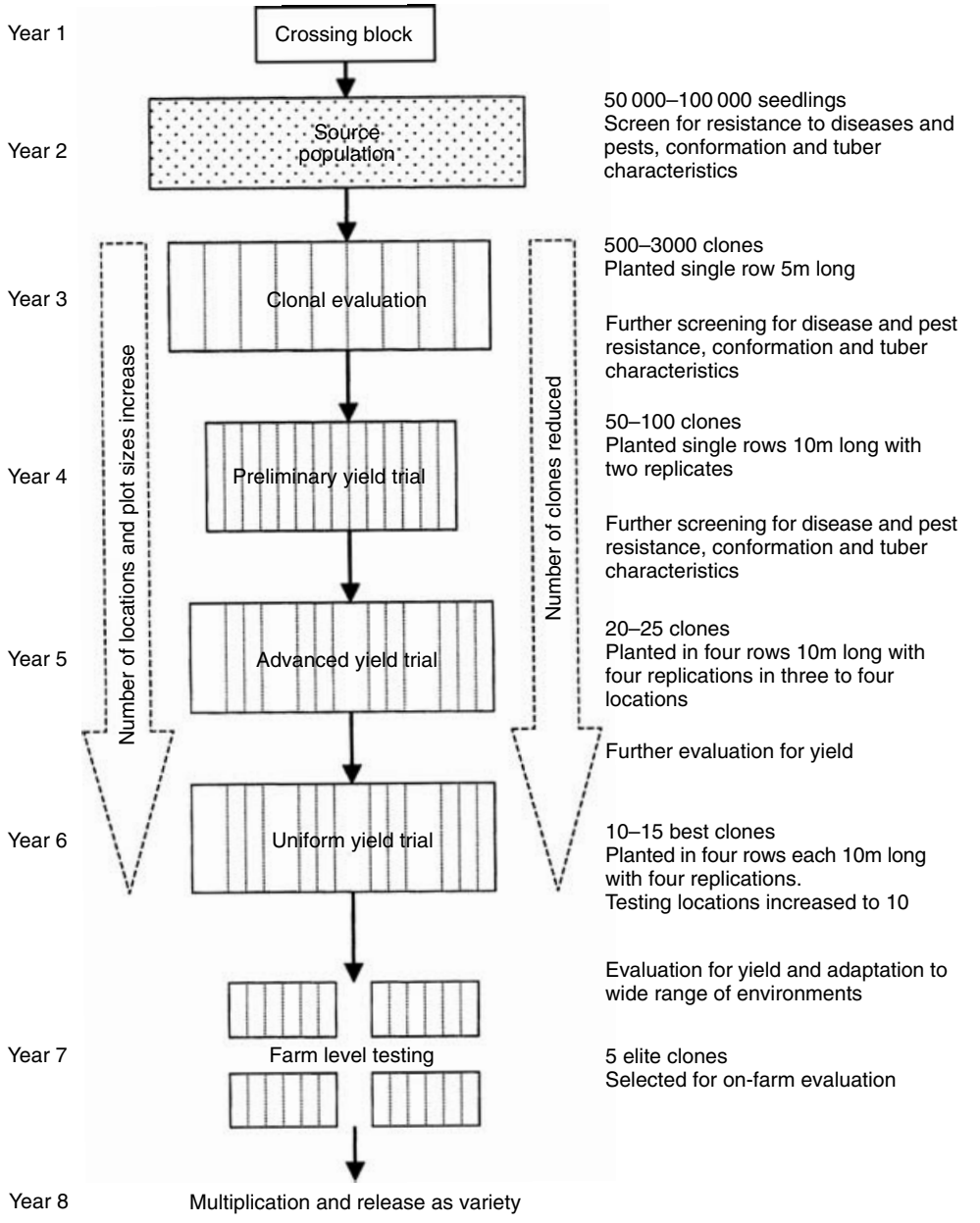


Figure 1. Conventional cassava breeding scheme used in Malawi.

Trial

A randomized complete blocks design, replicated four times, was used for each trial. The recommended spacing for cassava in Malawi (0.90 m between ridges and plants) was used. Cuttings (0.25 m) from mature woody stems were planted in the ridge tops at an angle of approximately 45°. The plot sizes were 9 × 3.6 m, i.e. 40 plants per

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Table 1. Descriptions of the experimental locations where trials were conducted in Malawi.

Location	Altitude (m asl)	Agro-ecology	Annual rainfall (mm)			Dry season		
			1996/97	1997/98	1998/99	1996/97	1997/98	1998/99
Baka	460	Lake-shore lowland	956	952	1208	June–Oct	June–Oct	June–Oct
Chitala	600	Lake-shore lowland	834	618	1036	May–Oct	April–Oct	June–Oct
Chitedze	1097	Lilongwe plain	633	598	896	June–Oct	May–Oct	June–Oct
Makoka	1029	Phalombe plain	1028	578	975	July–Oct	June–Oct	July–Oct
Mbawa	1137	Mzimba plain	591	776	651	May–Oct	May–Oct	May–Oct
Meru	1027	Chitipa plain	740	802	859	June–Nov	June–Oct	June–Nov
Mkondezi	600	Lake-shore lowland	2002	1119	1612	–	July–Oct	Sep–Oct
Thutchila	800	Phalombe plain	977	557	937	Aug–Oct	Aug–Oct	Oct

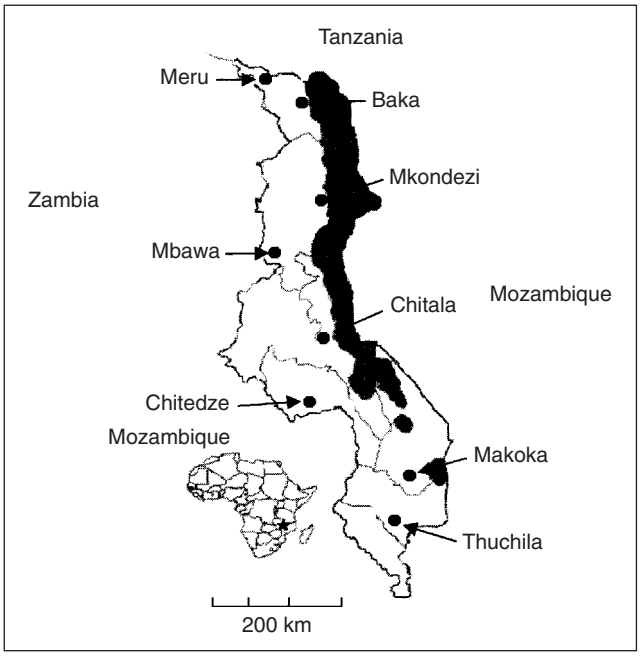


Figure 2. Locations where G × E trial was conducted in Malawi.

plot, and data were collected from a net plot area of 7.2 × 1.8 m, i.e. 16 plants. The fields were weeded twice and no fertilizer (organic or inorganic) was applied. In each of the eight locations, the trial was run for three consecutive seasons from 1996 to 1999. Subsequent trials were planted on a different patch of land following a pre-set crop rotation plan for each location.

Data collection

Data were collected on cassava green spider mite (CGM), cassava mosaic disease (CMD), number of roots, root weight and rainfall. Pest and disease incidence was assessed four times, at three-months intervals on two middle rows per plot using a

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one-to-five qualitative scale, where one indicated no visible symptoms of diseases or pests and five, severe infection or infestation (Hahn *et al*., 1980). The trials were harvested 12 months after planting (MAP), and the roots were counted and weighed. Rainfall data were collected from the nearest meteorological station to each location.

Data analysis

The average score per plot was computed for CGM and CMD. Yield data were converted to the number of roots and tonnes (fresh weight) per hectare. These data were subjected to analysis of variance (ANOVA) using models 1 and 2.

$$Y_{ijkn} = \mu + S_i + L_j + SL_{ij} + R_{n(ij)} + G_k + GS_{ki} + GL_{kj} + GSL_{kij} + e_{ijkn} \quad (1)$$

Where Y_{ijkn} = the value of the character for the kth genotype in the nth replicate in the j th location in the ith season; μ = the population mean; S_i = the effect of the ith season; L_j = the effect of the jth location; SL_{ij} = the effect of the interaction between the ith season and the jth location; $R_{n(ij)}$ = the effect of the nth replicate in the ith season and jth location; G_k = the effect of the kth genotype; GS_{ki} = the effect of the interaction between the kth genotype and the ith season; GL_{kj} = the effect of the interaction between the kth genotype and the jth location; GSL_{kij} = the effect of the interaction between the kth genotype, the ith season and the jth location; e_{ijkn} = the error associated with the kth genotype in the nth replicate in the ith season in the jth location; and where $k = 1$ to g ($g = 8$ genotypes), $n = 1$ to r ($r = 4$ replicates), $i = 1$ to s ($s = 3$ seasons), $j = 1$ to l ($l = 8$ locations).

$$Y_{jkn} = \mu + E_j + R_{n(j)} + G_k + GE_{kj} + e_{jkn} \quad (2)$$

Where Y_{ijkn} = the value of the character for the kth genotype in the nth replicate in the jth environment; μ = the population mean; E_j = the effect of the jth environment; G_k = the effect of the kth genotype; GE_{kj} = the effect of the interaction between the kth genotype and the jth environment; e_{jkn} = the residual associated with the kth genotype in the nth replicate in the jth environment; and where $k = 1$ to g ($g = 8$ genotypes), $n = 1$ to r ($r = 4$ replicates), $j = 1$ to l ($l = 24$ environments).

An additional analysis of variance was done with the environments separated into lakeshore and plain. Characterization of environments was done using principal component analysis based on the mean root yields. Mean CMD and CGM scores, root number and yield of the eight genotypes were used as variables in the analysis. Pair-wise ANOVA for the 24 environments were carried out. A total of nine comparisons were generated for each pair of locations, and three for the within-location comparisons. General linear model was used for all the ANOVA, and VARCOM for estimating the variance components (SAS software version 8.2).

RESULTS

There were considerable differences in the average root yields between genotypes within each location (Table 2). The improved genotype TMS 91934, consistently performed better in most locations. The genotypes performed best at Baka and worst

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Table 2. Means of root yield and other variables for eight cassava genotypes grown at eight locations in Malawi (1996–1999).

Genotype (G) §	Location‡ (L)									*s.e.*
	Baka	Chitala	Mkondezi	Chitedze	Makoka	Mbawa	Meru	Thutchila	Mean	*(G)*
Root yield (t ha^{-1})										
Mbundumali (s)	18.3	13.4	6.5	8.1	15.1	7.0	11.3	12.0	11.4	
Chitembwere (s)	23.0	14.5	8.2	4.4	11.5	2.6	8.3	10.3	10.4	
MH108 (s)	15.7	12.3	7.9	4.8	14.1	2.2	6.6	10.7	9.3	
Gomani (b)	19.1	12.6	8.9	6.8	10.4	5.5	11.5	12.5	10.9	
Kanonono (b)	17.4	14.7	7.5	7.0	9.6	3.5	8.8	9.3	9.7	0.484
Nyasungwi (b)	18.0	13.2	10.0	7.9	13.5	5.3	11.9	11.3	11.4	
Thipula (b)	18.7	19.3	10.0	7.5	8.4	6.1	11.1	12.4	11.7	
TMS 91934 (b)	25.0	15.1	10.3	12.4	14.8	7.9	17.3	13.4	14.5	
Mean	18.6	14.4	8.8	6.4	11.3	4.2	9.7	11.1	10.6	
s.e. (L)				1.321						
No. of roots ($\times 10^4$ ha^{-1})										
Mbundumali (s)	9.8	7.6	5.0	8.4	8.3	5.2	7.2	7.4	7.4	
Chitembwere (s)	11.0	7.7	5.2	5.1	6.4	2.1	4.7	6.0	6.0	
MH108 (s)	8.8	7.7	5.5	5.9	8.5	2.9	4.6	7.8	6.5	
Gomani (b)	6.3	5.5	4.4	5.5	6.7	4.1	6.2	5.6	5.5	
Kanonono (b)	7.5	5.9	4.6	6.5	4.7	3.3	5.2	4.1	5.2	3.824
Nyasungwi (b)	11.3	10.5	7.4	9.6	8.7	6.0	9.1	8.2	8.9	
Thipula (b)	11.9	8.7	6.3	6.3	6.0	4.6	6.7	7.5	7.3	
TMS 91934 (b)	9.7	5.8	5.2	7.2	4.9	5.8	8.0	6.1	6.6	
Mean	9.5	7.4	5.4	6.8	6.8	4.2	6.5	6.6	6.7	
s.e. (L)				4.138						
Cassava mosaic disease score (incidence scale 1–5)										
Mbundumali (s)	4.7	3.3	4.5	1.6	1.0	2.8	2.1	1.5	2.7	
Chitembwere (s)	3.8	2.3	4.0	1.4	1.5	2.3	1.8	1.7	2.3	
MH108 (s)	4.7	2.8	4.4	2.4	1.0	3.3	4.4	1.3	3.0	
Gomani (b)	4.7	2.7	4.4	1.8	1.0	3.3	3.6	1.7	2.9	
Kanonono (b)	4.3	3.0	4.0	1.9	2.6	3.4	3.6	3.3	3.3	0.149
Nyasungwi (b)	4.3	2.8	4.0	2.1	1.0	2.3	2.2	1.8	2.6	
Thipula (b)	4.3	3.5	4.5	2.8	2.9	3.5	3.8	2.9	3.5	
TMS 91934 (b)	2.9	2.2	4.0	1.3	1.0	1.9	1.2	1.7	2.0	
Mean	4.1	2.8	4.2	2.0	1.6	2.9	2.9	2.0	2.8	
s.e. (L)				0.316						
Cassava green spider mite score (incidence scale 1–5)										
Mbundumali (s)	3.7	3.7	3.6	2.6	1.9	2.8	3.5	3.1	3.1	
Chitembwere (s)	3.5	3.6	3.3	3.0	2.1	2.7	3.6	3.2	3.1	
MH108 (s)	3.7	3.2	3.6	2.9	1.5	2.5	3.6	2.3	2.9	
Gomani (b)	3.5	3.8	3.5	3.3	2.1	3.1	3.8	2.9	3.3	
Kanonono (b)	3.3	3.8	3.3	2.7	1.5	2.5	3.3	2.8	2.9	0.037
Nyasungwi (b)	3.6	3.5	3.7	2.8	1.8	3.0	3.5	2.5	3.0	
Thipula (b)	3.1	3.0	3.3	3.0	1.5	2.4	3.4	2.7	2.8	
TMS 91934 (b)	2.9	3.8	3.3	2.8	2.1	3.3	3.3	2.8	3.0	
Mean	3.4	3.5	3.4	2.9	1.8	2.8	3.5	2.7	3.0	
s.e. (L)				0.094						

‡ Means pooled over 12 observations (4 replicates × 3 years).

§ s = sweet genotype, b = bitter genotype.

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Table 3. Variance components of eight cassava genotypes at eight locations in Malawi based on three cropping seasons (1996–1999) data.

	Location							
Source of variance	Baka	Chitala	Chitedze	Makoka	Mbawa	Meru	Mkondezi	Thutchila
Root yield (t ha^{-1})								
Season (S)	43***	0.8	2.3**	13**	1.8***	24***	13***	32***
Genotype (G)	2.6	2.0	5***	3.0	3.7***	8**	1.4*	0
G × S	9*	3.1	1.4	3.0	0.5	5***	0	16***
Residual	44.0	22.3	6.4	33.0	4.1	7.0	14.5	12.0
Number of roots (×10^4 ha^{-1})								
Season (S)	0	7.4*	23***	18*	15***	55***	73***	21*
Genotype (G)	24*	22**	18**	15	17***	23***	7*	5
G × S	26***	13***	8*	26***	2	0	0	32***
Residual	52	23	29	26	17	43	53	40
Cassava mosaic disease scores								
Season (S)	0.3**	1.1**	0.4**	0.3	0.1	1.5***	0.1***	0
Genotype (G)	0.3**	0.1	0.1	0.1	0.2	1.0**	0.04	0.3
G × S	0.2***	0.2**	0.4***	1.0***	0.3***	0.9***	0.03	0.5***
Error	0.2	0.6	0.3	0.3	0.6	0.2	0.2	0.9
Cassava green spider mite scores								
Season (S)	0.6***	0.8***	0.2**	0.2***	1.2***	1.6***	0.4***	0.4***
Genotype (G)	0.1	0.02	0	0.1	0	0	0	0.04
G × S	0.1*	0.1**	0.1	0	0.5***	0.04*	0.05*	0
Residual	0.2	0.3	0.4	0.2	0.7	0.2	0.2	0.5

* Indicates significance at $p \leq 0.05$.
** Indicates significance at $p \leq 0.01$.
*** Indicates significance at $p \leq 0.001$.

at Mbawa. Considerable variation in the number of roots was observed between genotypes within locations. The local genotype Nyasungwi consistently had the largest numbers of roots in all the locations.

The incidence of CGM and CMD varied between locations over the three seasons, and the lakeshore sites generally had higher incidences of both than did those on the plain. The highest mean scores were recorded at Baka and Mkondezi for CMD, and at Chitala and Meru for CGM. Makoka generally had the lowest incidence for both CGM and CMD. Genotypes differed in their susceptibility to CGM and CMD between locations. Thus, TMS 91934 consistently had lower mean scores for CMD at all sites except Mkondezi, while the local genotype Thipula had relatively lower mean scores for CGM in most locations.

A summary of the analysis of variance by location shows that there was considerable seasonal variation within location for all the four traits, except at Chitala for root yield, Baka for root number and Makoka, Thutchila and Mbawa for CMD (Table 3, component S, which includes local environmental variation). Genotype performance also varied considerably in most locations with respect to root yield, number of roots and resistance to CMD, but not for CGM. The proportion of the G × S interaction within location is large except at Mkondezi for root yield, Mbawa, Meru and Mkondezi for root number, Mkondezi for CMD and Makoka and Thutchila for CGM. The

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Table 4. Variance components for combined ANOVA of eight cassava genotypes at eight locations in Malawi based on data from three cropping seasons (1996–1999).

Source of variation	All locations		Lakeshore		Plain	
	Variance component	Proportion (%)	Variance component	Proportion (%)	Variance component	Proportion (%)
Root yield (t ha^{-1})						
Season (S)	0	0	0	0	0	0
Location (L)	13.9*	25	21.0	27	3.7	9
S × L	16.3***	29	22.2*	29	16.2***	40
Genotype (G)	1.8***	3	1.3	2	3.0***	7
S × G	1.0*	2	0.6	1	0.7	2
L × G	0.7	1	0.6	1	0	0
S × L × G	3.6***	7	2.9	4	4.7***	12
Residual	18.1	33	27.6	36	12.2	30
Number of roots (×10^4 ha^{-1})						
Season (S)	0	0	22	2	0	0
Location (L)	131	13	332	25	0	0
S × L	260***	25	233***	18	321***	34
Genotype (G)	110***	11	180***	14	111***	12
S × G	32**	3	4	0	38*	4
L × G	54**	5	0	0	45*	5
S × L × G	92***	9	109***	8	91***	10
Residual	361	34	424	33	325	35
Cassava mosaic disease						
Season (S)	0.2*	8	0.2	10	0.1	6
Location (L)	0.8***	32	0.5	33	0.1	6
S × L	0.3***	13	0.3***	20	0.4***	18
Genotype (G)	0.2***	7	0.1**	5	0.3***	13
S × G	0.1***	5	0.1*	5	0.2**	9
L × G	0.1*	5	0.04	3	0.1	5
S × L × G	0.3***	12	0.1***	4	0.4***	19
Residual	0.4	18	0.3	20	0.5	24
Cassava green spider mite						
Season (S)	0.39**	30	0.47	53	0.3	21
Location (L)	0.07	5	0	0	0	0
S × L	0.39***	30	0.1**	11	0.6***	41
Genotype (G)	0.01**	1	0	0	0.02**	1
S × G	0	0	0.03	3	0	0
L × G	0	0	0.02	2	0	0
S × L × G	0.11***	8	0.04**	5	0.14***	10
Residual	0.34	26	0.23	26	0.4	27

* Indicates significance at $p \leq 0.05$.
** Indicates significance at $p \leq 0.01$.
*** Indicates significance at $p \leq 0.001$.

residual was generally large for all the traits studied within location except for CMD and CGM at Meru.

The combined analysis of variance for all locations (Table 4) shows that non-genetic components (environment) contributed more to the variation observed than did genetic components in all the four traits. With the exception of CGM, the contribution of the genetic component to the variation observed in the lakeshore sites was significant. The

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Table 5. Number of environments per pair of locations with insignificant G × E based on pair-wise comparisons.

	Mkondezi	Chitala	Baka	Meru	Mbawa	Chitedze	Makoka	Thutchila
Root yield (t ha^{-1})								
Mkondezi	**3**	**7**	**7**	**6**	**7**	**6**	**6**	4
Chitala		**2**	4	3	**6**	**5**	**5**	3
Baka			**2**	**5**	4	4	4	3
Meru				0	4	**5**	4	3
Mbawa					**2**	4	**6**	3
Chitedze						**2**	**6**	**5**
Makoka							1	4
Thutchila								1
Number of roots (×10^4 ha^{-1})								
Mkondezi	**3**	**6**	**5**	**7**	**6**	**6**	4	**5**
Chitala		1	2	2	0	2	2	2
Baka			1	4	2	1	0	3
Meru				**2**	**8**	**5**	1	3
Mbawa					**3**	**5**	0	3
Chitedze						1	1	2
Makoka							0	3
Thutchila								1
Cassava mosaic virus disease								
Mkondezi	**2**	**5**	4	0	3	1	2	4
Chitala		1	3	0	4	2	1	**5**
Baka			0	1	2	0	0	2
Meru				0	1	0	0	0
Mbawa					1	1	1	3
Chitedze						0	0	3
Makoka							0	2
Thutchila								1
Cassava green spider mite								
Mkondezi	**2**	**5**	**6**	**7**	1	3	1	**5**
Chitala		1	2	4	4	3	2	**5**
Baka			1	**5**	0	3	2	**7**
Meru				**2**	0	**5**	3	**7**
Mbawa					0	3	3	**5**
Chitedze						**2**	4	**6**
Makoka							1	**5**
Thutchila								**3**

Total number of possible pair-wise comparisons per location were three within location and nine between locations. Pairs of locations with two or three within location and five or more pairs of environments with insignificant G × E interaction for each trait studied are shown in bold.

G × E interaction was highly significant for all the traits even when the environments were separated into lakeshore and plain groups. The interaction between genotypes and season × location was the largest among the G × E components for all traits.

The numbers of environments with insignificant G × E interactions, based on a pair-wise analysis of variance for the 24 environments, are presented in Table 5. Large environmental heterogeneity was observed even for environments within the same location. Pairs of locations with five or more pairs of environments with insignificant G × E interactions were considered homogeneous and are shown in bold.

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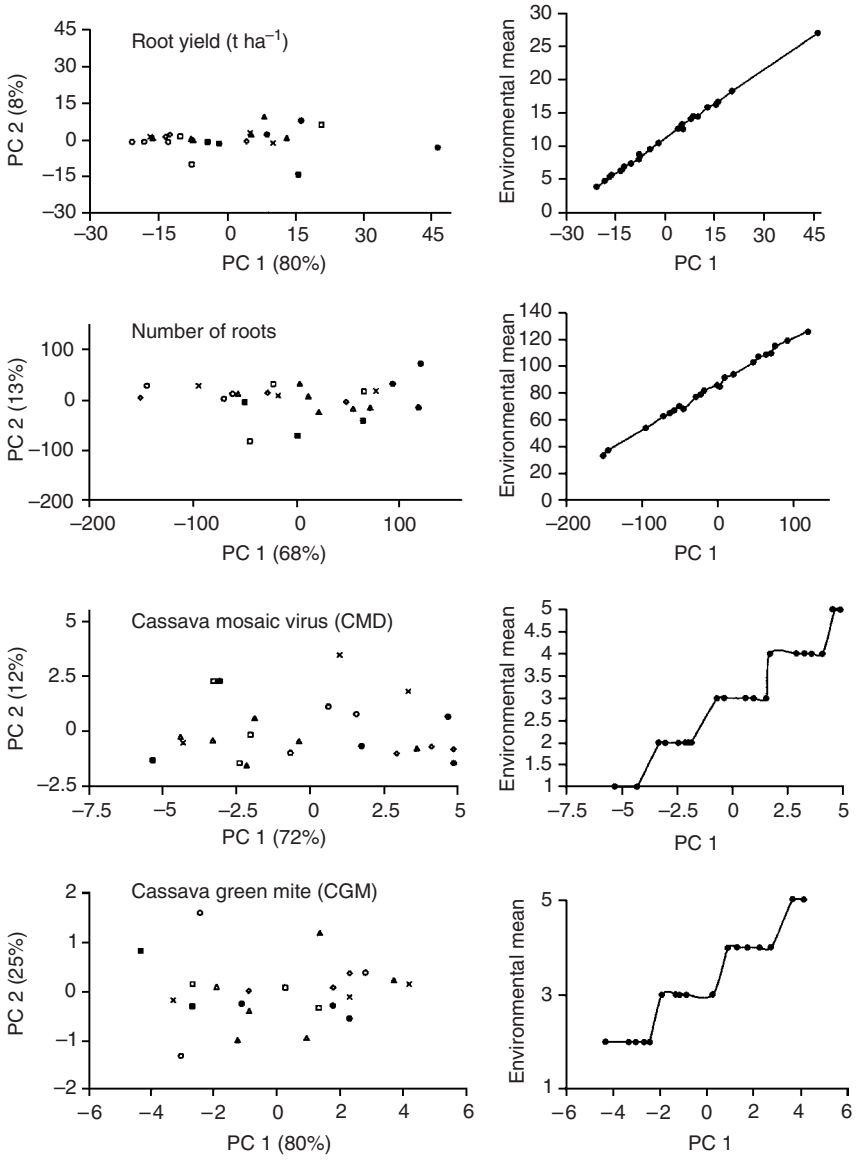


Figure 3. Plot of the 24 environments using the first two principal components and the first principal component with environmental means based on data from eight cassava genotypes grown at eight locations in Malawi for three cropping seasons (1996–1999). The eight locations are: Baka (●): Chitala (▲): Mkondezi (◇): Chitedze (△): Makoka (■): Mbawa (◯): Meru (×): and Thutchila (□).

Scatter plots made from the first two principal components, and the first principal component with environmental means, are presented in Figure 3. For all four traits, there is no particular grouping of the environments but they were clustered along principal component 1, which explained most of the variation (68–91%). Principal component 1 scores are highly correlated with the environmental means for each

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trait ($r = 0.99$). Thus, the clustering of the environments follows the gradient of the environmental means from low- (left) to high- (right) yielding environments.

DISCUSSION

In general, the results of this study indicate that the contribution of the genetic component to total variance observed is relatively low but significant for all the traits considered when all environments are analysed together (Table 4). This is due to the large and significant effect of the G × E interaction and to environmental components. Separation of lakeshore and plain environments did not change the results for root number and yield. When the analysis was done by location, a few sites had a relatively high and significant genetic component. This indicates that discrimination between genotypes for root yield and number would be much better in these environments.

The highly significant G × E interaction strongly suggests that the ranking of genotypes with respect to root number and yield varied in different environments. This is contributed largely by the second-level interaction (G × S and G × L), which indicates that the performance of the genotypes varied in different locations and seasons. When environments were analysed by location, however, the G × S interaction was significant at five and three locations respectively for root number and yield (Table 3). Thus, genotype performance will vary in different seasons even within the same location, making it difficult to compare results over seasons.

Cassava green spider mite and CMD results show a similar trend to those for root number and yield. The much lower genetic component for CGM (Tables 3 and 4) may suggest (i) the equal susceptibility to CGM of the genotypes used (Table 2), or (ii) a masking effect due to the large environmental components. The high and significant genetic components at Baka and Meru for CMD indicate that genotypes would much better discriminate for this trait in these environments.

Large environmental effects, contributed mainly by the interaction between season and location, were also observed for CMD and CGM (Table 4). For the former, however, location made the largest contribution to environment. This highly significant contribution indicates that some locations have a consistently high incidence of this disease.

In addition to the grouping of locations into lakeshore and plains, an attempt was made to group similar environments together using principal component analysis. The scatter plot (Figure 3) showed no particular assemblage of environments to allow grouping of locations based on similarity. That the principal component 1 scores are highly correlated with the environmental means for each trait, indicates that environmental means alone would have been sufficient to discern this trend. Principal component 2, however, seems to explain part of the G × E interaction. Thus, the more scattered the environments along this axis indicates the presence of strong G × E interaction as the case with CMD compared to root weight plot. Similarly, results of the pair-wise ANOVA show that CMD had relatively large numbers of environments per pairs of locations with significant G × E, while root yield showed the opposite (Table 5). Thus, any groupings of locations need to be done on a trait basis.

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Based on the pair-wise and combined ANOVA results, it is possible to group some locations and select one or two for preliminary evaluation of the traits studied. Locations that discriminate best between genotypes and that have the largest number of environments with insignificant G × E interaction in pair-wise comparisons may be grouped, and one or two could be used for intensive cassava breeding work. Chitedze, though not the best discriminator between genotypes, could be considered for intensive cassava breeding work aimed at improving root yield and number of roots. Baka and Meru gave the best discrimination between genotypes for CMD but, since both locations are not similar to any of the other locations in the pair-wise comparison, they should not be considered especially for intensive breeding for this trait. Alternatively, since the results could be extrapolated to at least two other locations, namely Mkondezi and Thutchila, Chitala could be considered for intensive breeding work for CMD. Though it is the third best in discriminating for CGM, Thutchila could be used as a breeding site for this trait since the results can be extrapolated to almost all the other locations.

Although the input data for the analysis of variance are plot means, the residual shown in Table 3 is generally high, probably reflecting variation in the environmental conditions within blocks, which consequently hides genetic variation, for instance, the difference in the genetic component for CMD resistance between sites. Baka and Meru each had a high incidence of CMD with a low residual and a high genetic component for CMD-resistance. On the other hand, at Mkondezi, which also had a high incidence, the genetic differences were small, probably due to a large residual.

In general, the study results show enormous environmental effects, contributed largely by the interaction between season and location (Table 4). This is typical for most regions in Africa where the terrain varies over short distances and the environments are characterized by unpredictable variability in the frequency, timing and severity of a number of environmental stresses (Ceccarelli, 1994; Tigerstedt, 1994). Furthermore, the study results show that the highly significant G × E interaction, for all the traits studied, is contributed largely by the third level interaction (G × S × L). This is due to specific combinations of environmental effects, the recurrence of which is difficult to predict. Consequently, results of field-based research in one location or season would rarely be obtained in another setting, which poses a challenge to research on crops like cassava that have a long growing cycle (9–24 months). Cassava farmers also experience similar challenges over different seasons. Their farms are often located in marginal and unpredictable environments, and this influences their decisions, including the criteria used to adopt new cassava genotypes. With such environmental heterogeneity, opportunities for extrapolating genotype performance for all the traits studied, over space (country-wide) and time, are very limited. Thus there is a need to evaluate and select cassava genotypes in a much smaller range of target environments and in a number of seasons.

The authors envisage a two-fold need for cassava genotypes in Malawi. On the one hand, there are areas in the country where cassava is the major source of ingested calories (staple crop) and many cultivars, predominantly bitter ones, are grown. On the other hand, there are farmers within and outside these areas who produce

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predominantly a few sweet cultivars cassava for sale or famine relief. The authors propose, therefore, that breeding of genotypes for subsistence should be separate from that for the fresh-root market and for commercial processing.

The considerable G × E interaction observed in this study, and the difficulty of grouping locations, show that an economical evaluation of cassava clones will not give a precise estimate of yield performance. The authors cannot see, therefore, why large plot sizes are needed in the current cassava-breeding scheme, especially considering that the residuals were high indicating that environmental variation within blocks conceals genetic variation. In their view, it would be preferable to reduce the plot size considerably to allow for more genotypes to be tested and then sent out to farmers at a much earlier stage in the breeding scheme, preferably at the preliminary yield trial level (Figure 1). This would ensure that more genotypes, with characters above a certain minimum standard, are made available to farmers for evaluation in their fields. Consequently, the number of locations for cassava evaluation at research stations could be reduced considerably.

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