



# Quantitative variation and interrelationship between factors influencing cassava yield

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## ABSTRACT

*Objective:* Cassava is a crop with largely unexplored and unexplained potentially valuable genetic variability. This study aimed to investigate interrelationship between factors that control cassava yield.

*Methodology and results:* Fourteen quantitative characteristics were assessed in ten cassava genotypes at three locations (Namulonge, Bulisa and Kapchorwa) during two seasons in Uganda. Highly significant ( $P < 0.001$ ) influence of the environment and genotype by environment interactions were observed in most of the plant traits evaluated. Broad sense heritability was relatively moderate for storage roots and dry matter content ( $h^2 = 0.39$  and  $0.56$ , respectively) while it was high for petiole length ( $h^2 = 0.82$ ). The most productive in storage root yield was clone Migyera at all locations during the first season. Storage root performance decreased during the second season and clones SS4, TMS 82/01635 and TMS I 91/0057 led at Namulonge, Bulisa and Kapchorwa, respectively. Dry yield production per clone was high at Bulisa in season one while it was high at Namulonge during second season. Phenotypic correlations were significant between dry root yield with storage root number ( $r = 0.53$ ,  $p < 0.001$ ), storage root size ( $r = 0.37$ ,  $p < 0.001$ ), storage root girth ( $r = 0.54$ ,  $p < 0.001$ ), stem girth ( $r = 0.38$ ,  $p < 0.05$ ), leaves and stems biomass ( $r = 0.38$  and  $0.58$ ,  $p < 0.05$ , respectively). The leaf area, petiole length, storage root number, root size, root girth, stem weight, and starch content gave the best equation for yield prediction ( $R^2 = 0.69$ ,  $C(P) = 5.6$ ).

*Conclusion and application of findings:* Indirect path analysis revealed that selection of high potential clones could be achieved based on storage root number, storage root size and storage root diameter as the main yield components contributing factors to yield enhancement in cassava, and could be used as selection criteria for higher storage root yield potential. Results from multiple regression and path analysis suggested, however, that the model does not fully explain the complex interrelationship of factors determining cassava yield and this will need additional research to understand better yield factors.

**Keys words:** Cassava, yield components, heritability, phenotypic correlation, path analysis

## INTRODUCTION

Cassava (*Manihot esculenta* Crantz) belongs to the genus *Manihot* that represents a yet unexplored reservoir of potentially valuable genetic variability (Rogers, 1965). The early growth and development of cassava depends on genetic and

environmental factors, implying that a better understanding of the relationship between environmental factors and growth / development processes is of great use.



Dry weight yield accumulation and distribution among different plant organs changes sharply during the growth cycle and partitioning of dry matter to their storage root tends to be more important, determining how other factors influence the growth of the plant as a whole (Homes & Nilson, 1977). High storage root yield is one of the main goals in cassava improvement. However, it is difficult to assess storage root yield in large populations compared to other plant traits that are phenotypically observable.

Different studies have reported that storage root yield is genetically related to the number of storage roots per plant, root size, harvest index, stem girth, canopy width and total number of branches (Magoon *et al.*, 1970; Mahungu, 1983 ; Cock, 1987; Mahungu, 1993, Ntawuruhunga *et al.* 1998). Tai (1975) found that cassava yield components comprise of the number

of storage roots, average storage root weight and percentage of dry matter while Ntawuruhunga *et al.* (2001) reported storage root number, storage root weight, storage root girth and total leaf area as yield components explaining 72% of storage root yield.

These components are determined at different stages in the ontogeny of the plant and are differentially affected by variation in the environment. The formation of yield components in sequence results then in a different relationship between a component trait and other traits as affected by environment resources.

The aim of this paper is to report the findings of a study conducted to determine the extent of variation in quantitative continuous characteristics and discuss the interrelationship in cassava clones for identification of factors determining yield in cassava.

## MATERIALS AND METHODS

The study was conducted at 3 different locations with varying altitudes, i.e. Bulisa (650 m asl), Namulonge (1250 m asl) and Kapchorwa (1750 m asl). Ten cassava clones selected for adaptation to 5 different agro-ecologies (Table 1).were used in a completely randomized block design with 3 replications at each location. The block size was 5m wide and 17m long planted using cutting of 25 cm long with a space of 1 m x 1 m, giving a population of 10,000 plants ha<sup>-1</sup>. No

fertilizer or herbicide was applied during the course of the experiment. Hands weeding were done whenever necessary. The experiments were conducted for 2 growing seasons, 1997/98 and 1998/99. The first season lasted 15 months while the second season lasted only 9 months and the data presented were for plants harvested at 9 months after planting.

**Table 1:** Identity and origin of 10 cassava genotypes studied for variation and yield parameters in Uganda.

Source	Location	Clone name
S1 Low land altitude	Bulisa-Masindi (Uganda) (650m)	1.Nyarukuhi 2.Nyarubekane
S2 Mid land altitude	Namulonge (Uganda) ( 1250m)	3.Migyera 4.SS4
S3 High land altitude	Rubona (Rwanda) (1650m) Rubona (Rwanda) (1650m)/ Kapchorwa (Uganda) (1750)	5.Eala 07 6.Kiryumukwe/ Serere
S4 Low land-Ibadan	Ibadan (Nigeria) (210m) Ibadan (Nigeria) (210m)	7.TMS 81/01635 8.TMS I 92/067
S5 Wide adaptation	Jos (Nigeria) (1280m) Jos (Nigeria) (1280m)	9.TMS I 92/0057 10.TMS I 91/0397

Data were recorded on the two middle rows harvested, leaving two lines on each side of the plot as borders. For leaf area estimation, samples were taken among the youngest expanded and fully developed leaves

because they are photosensitive. Lualadio's equation (1985) was used to estimate leaf area and means computed for the analysis of variance. Two components, internode length and diameter were

measured using a vernier caliper and a ruler for determining stem development. Measurements were taken on 6 stems per stand of the two middle rows harvested, and the means were calculated before analysis. Where a plant stand had more than one stem, the more developed stem was used. Diseases and pests, particularly cassava mosaic virus and green mites were observed and scored. Cassava mosaic virus disease, which was predominant on some genotypes, was used as covariant in data analysis to adjust the severity means. Dry matter content was estimated using oven method at 105°C for 24 hours.

The following parameters: plant height, leaf area, petiole length, height at first branching, stem

$$Y_{ijkn} = U + G_i + S_j + L_k + LS_{jk} + R_n(jk) + (GS)_{ij} + (GL)_{ik} + (GSL)_{ijk} + E_{ijkn}$$

where

$Y_{ijkn}$  = the value of the character for the  $i$ th genotype in the  $n$ th replicate in the  $j$ th season in the  $k$ th location;

$U$  = the population mean;

$G_i$  = the effect of the  $i$ th genotype;

$S_j$  = the effect of the  $j$ th season;

$L_k$  = the effect of the  $k$ th location;

$LS_{jk}$  = the effect of the interaction between the  $k$ th location and the  $j$ th season;

$R_n(jk)$  = the effect of the  $n$ th replicate in the  $j$ th season and  $k$ th location;

$(GS)_{ij}$  = the effect of the interaction between the  $i$ th genotype and the  $j$ th season;

$(GL)_{ik}$  = the effect of the interaction between the  $i$ th genotype and the  $k$ th location;

$(GSL)_{ijk}$  = the effect of interaction between  $i$ th genotype,  $j$ th season and  $k$ th location;

$E_{ijkn}$  = the error term associated with the  $i$ th genotype in the  $n$ th replicate in the  $j$ th season in the  $k$ th location; and where  $l=1$  to  $g$  ( $g$  =number of genotypes),  $n=1$  to 3 replicates,  $j = 1$  to 2 seasons, and  $k =1$  to 3 locations.

## RESULTS AND DISCUSSION:

Figure 1 summarizes results of storage root number produced by each genotype in each location. The results showed that at Namulonge, the genotypes (with high storage root number) were Migyera with a mean of 11.9 and TMS 82/01635 with an average of 11.6. The genotypes with low storage root number were Nyarubekane and Eala 07. On the same basis, the best genotypes at Bulisa were Myigyera and Nyarubekane with an average of 11 and 10, respectively. In the high altitude location, the best genotypes were Migyera followed by TMS I 92/0397 and TMS I 91/0057 with

diameter, internode length, plant biomass (stem, leaves, storage root fresh weight), tuberous root number, tuber diameter, fresh yield, dry matter content, sugar content, starch content and cyanogenic potential in storage roots were evaluated. Data were subjected to combined analysis of variance using the General Linear Model (GLM) (SAS, 1988) to test the significance of variation due to genotypes, genotype x location, replication x years and genotype x location x year interactions. The following mixed model, with genotypes and locations as fixed effects and seasons as random effect was assumed:

The cassava mosaic disease scores were used as covariant to adjust yield in each plot to a common level of disease scores. The estimates of variance components were computed, and their significance tested using the appropriate error term. Variance components were used to compute phenotypic and genotypic variance, broad heritability for yield, yield components and some important traits in the genotypes studied. Broad heritability (H) and phenotypic (PCV) and genotypic (GCV) coefficient were estimated according to Singh and Chaudhary (1979) as follows:

$$H = \sigma^2_g / \sigma^2_p \text{ and}$$

$$\sigma^2_p = \sigma^2_e / rly + \sigma^2_{gly} + \sigma^2_{gy/y} + \sigma^2_{gl/l} + \sigma^2_g;$$

Equations and parameters in annex 1, 2 and 3 were generated to enable calculation of these values.

Indirect path analysis was performed using a program written within SAS (1988) to determine the magnitude and directions of multiple effects on storage root yield complex in cassava.

average storage root number of 7.2, 7.2 and 4.2, respectively.

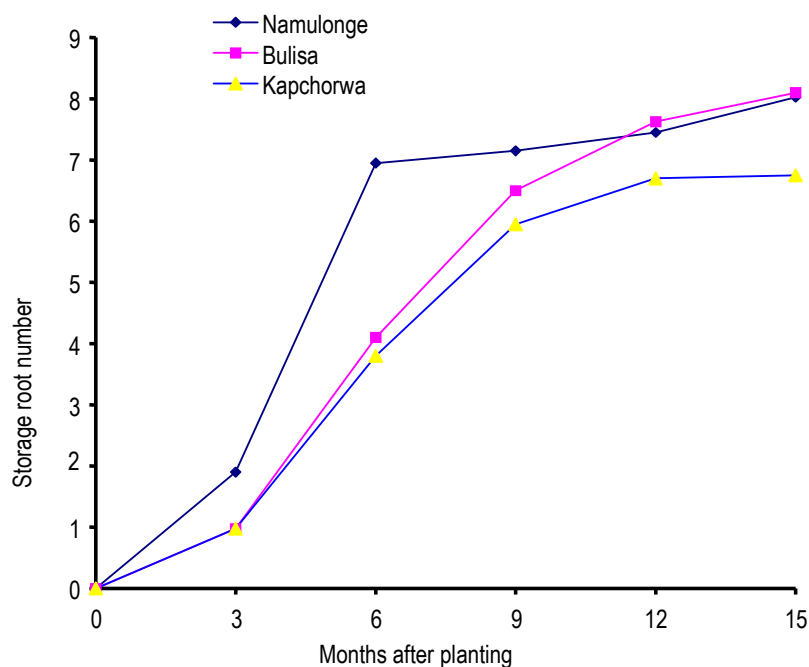
During the second season (1998/1999), the performance in terms of storage root number was poor. At Namulonge, SS4 and TMS I 91/0057 were the best with an average of only 8.3 and 8.2, respectively. At Bulisa, it was clones TMS 82/01635 and SS4 that performed best with an average of 5.7 and 4.5 storage roots, respectively, while it was TMS I 91/0057 and TMS I 91/0067 producing 5.1 and 4.8 average storage roots. The change in genotypes behavior in storage

root number formation between the two seasons could have been due to rainfall, which was generally low in the second season but also to bad distribution at the beginning after planting during the second season. Though results are not presented here, the rains delayed in the second season and particularly at Bulisa site. Differences existing in the environment can induce noteworthy changes in the general pattern of growth and development of cassava (De Vries, 1985). Many authors have reported that highest cassava storage root yields were obtained under high rainfall. According to Rojanaridpched (1978), crop growth rate appeared to depend on rainfall.

Even rainfall distribution is favorable for highest storage root yield of which storage number is one of the major root yield components. Ntawuruhunga

(2000) reported that that selection through storage root number trait could be effective in identifying a genotype with high storage root yield. The positive influence of rainfall on root yield of many cassava varieties, particularly during the first 4-6 months of growth, is demonstrated by the positive effect of the earlier planting time in the first few months of the rains season (de Vries, 1985). Variety effect does also have genetic effect on storage root number formation which can vary due to environmental factors because of G X E interaction which is well known in cassava (Dixon and Nukene, 2000; Ntawuruhunga . 2000).

In overall the best genotypes producing high number of storage roots were Migyera, SS4 and TMS I 91/0057. The combined analysis results are presented in Table 2.



**Figure 1:** Effects of altitude on formation of storage roots by different cassava genotypes grown at low altitude (Bulisa), mid altitude ( Namulonge) and high altitudes ( Kapchorwa).

**ANOVA G X E:** The precise genetic variance estimates and heritability are presented in Table 3. Broad-sense heritability estimates were generally low and moderate for storage root number, root diameter, fresh storage root yield per plant, dry yield, and plant height. Heritability estimates were high for dry matter content, fresh storage root yield and leaf area while it was very

high for the petiole length. The results indicate also that the petiole length had phenotypic and phenotypic coefficient of heritability, which were close suggesting that the petiole length could be easily improved by simple phenotypic selection among genotypes, although it does not have any direct link with the yield.

**Table 2:** Means squares for storage root yield, yield components and some cassava plant traits, analyzed over 3 locations and 2 years.

Source of variation	DF	Means squares						
		RTN (+)	RTSIZE	DMC	FYLD(+)	RTGIRTH	DRYLD	PTHT
Rep (Location)	4		0.069	2.034ns	22.094ns	24.479ns	20.224ns	627.916ns
Location	2	0.296NS	0.503**	616.073***	200.175*	658.398**	250.707***	113561.020***
Rep (Season)	2	49.552***	0.022	33.597*	26.776ns	21.294ns	21.790ns	905.955ns
Season	1	0.158NS	0.255**	50.263ns	553.780*	2045.629*	791.263***	16565.582**
Genotype	10	8.926**	0.051*	32.508ns	55.095*	131.397ns	87.714***	2452.215***
Genotype*Location	12	2.751***	0.049**	14.822ns	31.359***	150.910***	51.066**	1033.545ns
Genotype*Season	9	2.935**	0.069**	82.497*	9.518ns	208.044***	11.289ns	1433.722**
Genotype*Location*Season	12	1.859***	0.096***	18.317**	22.117**	1028.362***	18.327ns	1151.426*
ACMD	1	6.099**	-	-	-	178.870*	-	3006.036**
Pooled error	80	-0.711	0.023	8.214	9.518	36.015	15.723	586.188

(+) : Square root transformation

Where RTN: Number of storage root, RTSIZE= Storage root size; DMC: Dry matter content; FLYD: Fresh storage root yield ; RTGIRTH: Storage root girth DRYLD: Dry storage rooy yield; PTHT: Plant height

Table 2 continued:

Source of variation	DF	Means squares						
		La	Petiolog	Internode	Stemdia	cnp	sugar(#)	starch(#)
Rep (Location)	4	1916.636***	9.070ns	45.169ns	32.68ns	6670.187ns	0.022ns	0.397ns
Location	2	15167.277*	32.918ns	583.643**	480.456***	14632.891ns	3.632***	0.346ns
Rep (Season)	2	1639.699***	10.689ns	56.751ns	6.173ns	1742.666ns	0.007ns	0.183ns
Season	1	7768.967NS	233.192*	146.724ns	1108.711**	72537.066*	1.221***	4.157*
Genotype	10	2446.703NS	191.517***	174.661ns	33.567ns	13818.087*	0.164ns	2.832***
Genotype*Location	12	302.218***	134.609*	143.069***	24.291*	23548.865*	0.174ns	4.295**
Genotype*Season	9	1404.162*	16.609***	212.123*	50.977***	9083.942**	0.259*	3.979***
Genotype*Location*Season	12	1648.222**	35.849**	140.259*	86.496**	3083.104ns	0.274**	10.320***
Pooled error	80	-	8.093	67.564	11.857	4002.584	0.117	0.078
		172.538						

(#): Logarithm transformation

Where La= Leaf area; Petioleng= Petiole length; Stemdia= Stem diameter; CNP= Cyanogenic potential

For these traits with high broad-sense heritability, and with phenotypic coefficient variance slightly larger than their genetic coefficient variance, it implied that it is possible to improve them by phenotypic selection with moderate time. However, it would take more time to improve the traits with moderate heritability because of their low genetic variance component and genetic coefficient of variation. The genetic variance component for petiole length was much larger than the environmental variance component. It was however, small for all other traits reported. The G x Y x L variance was much higher than the environmental variance for storage root number indicating that that trait varied considerably with environment.

Environmental variance for fresh storage root yield was higher than G x L and G x Y x L variances, implying that the trait varied strongly with the environment, due to unpredictable features of the

environment. IITA (1993) and Dixon and Nukenine (2000) reported similar results for fresh storage roots after partitioning various sources of variation into main effects due to genotypes, environments, and G x E interactions. Interaction was partitioned into the various components (Y X G, L X G and L X Y X G). The first order of interaction (Y X G) was significant ( $P < 0.01$ ) for storage root number, storage root size, fresh yield, storage root girth, dry yield, plant height, leaf area, internode, CNP, percentage of sugar and starch content indicating inconsistency in ranking among genotypes in different years.

Dixon *et al.* (1994), Tan and Mark (1995) and Dixon and Nukenine (1997) and Ntawuruhunga *et al.* (2009) also reported the existence of G X E interaction for cassava yield. This becomes more difficult because it is not possible to make an independent selection program for different years (Fehr 1982).

**Table 3:** Estimates for genotypic variance ( $\sigma^2G$ ), genotype x Season variance ( $\sigma^2gy$ ), genotype x location variance ( $\sigma^2GL$ ), genotype x location x Season variance ( $\sigma^2GLY$ ), environmental variance ( $\sigma^2e$ ), broad-sense heritability (H), phenotypic coefficient of variation (PCV) and genotypic coefficient variation (GCV) for yield and yield components and some cassava plant traits.

Variance component	Plant traits								
	RTN	RTSIZE	DMC	FYLD	FYLDPT	DRYLD	PTHT	LA	PETIOLE
$\sigma^2G$	0.225	44.49	1.31	2.03	0.01	2.42	63.13	132.70	9.79
$\sigma^2GL$	-0.527	-146.24	-0.58	1.54	0.01	5.46	-117.88	-224.33	-0.21
$\sigma^2GY$	-0.707	-136.72	-0.97	-2.10	-0.01	-1.17	47.05	-40.68	-3.21
$\sigma^2GLY$	1.796	330.78	3.37	4.20	0.03	0.87	188.41	491.89	9.25
$\sigma^2E$	0.711	36.06	8.21	9.52	0.08	15.72	586.19	172.54	8.09
$\sigma^2P$	0.564	101.62	2.33	3.75	0.02	5.23	150.13	224.26	11.96
H	39.9	43.7	56.1	53.8	43.5	46.1	41.9	59.2	81.8
PCV(%)	26.8	28.1	4.3	31.4	15.3	16.9	8.1	19.1	19.9
GCV(%)	16.9	18.6	3.2	23.1	10.1	11.5	5.3	14.7	18.1

Where RTN=storage root number; RTSIZE=storage root weight; DMC= Dry matter content; FYLD= Fresh storage root yield; FYLDPT= Fresh storage root yield per plant; DRYLD= Dry storage root yield; PTHT= Plant height; LA= Leaf area;

Phenotypic correlation results (Table 4) indicate that most of the plant traits evaluated are interrelated to one another, apart from sugar and starch content, that are not correlated with other traits. Dry matter content is positively significantly ( $P < 0.01$ ) correlated with leaf area and negatively correlated ( $P < 0.05$ ) with storage root size. Starch content is only positively and significantly ( $P < 0.01$ ) correlated with sugar content.

Storage root yield was found to be significantly and positively correlated with storage root number ( $r = 0.53$ ), storage root size ( $r = 0.37$ ), storage root girth ( $r = 0.54$ ); stem girth ( $r = 0.38$ ); and top biomass (weight of leaves and weight of stems with  $r = 0.38$  and  $0.58$  of correlation coefficient, respectively).

Multiple regression technique was used to investigate the probable predictors of storage yield and the results are presented in Table 5. The model of prediction revealed that the traits contributing most (69 % of the total variation in storage yield) by a linear function ( $R^2 = 0.69$  and  $C(P) = 5.6$ ) are leaf area, petiole length, storage root number, storage root size, storage root girth, the weight of stem, and starch content.  $C(P)$  helped to compare different prediction equations and the one that had the smallest numerical

values of  $C(P)$  among the different predictions equations was selected as the best fit and presented.

Indirect path analysis is a statistical method that helps to determine the magnitude and direction of multiple effects on a complex process. The variables used in this analysis were chosen after correlation and regression analysis, which enabled identification of the variables that are most, linked to storage root yield. Following analysis, eight independent variables were identified and used. Since the direct and indirect effects were partitions of the simple correlation coefficients, the sum of the direct and indirect effects equaled the relationship between individual yield components and final storage yield (MicGiffen *et al.*, 1994). Ntawuruhunga (2000) reported that that correlation coefficients between storage root yield and other traits when partitioned into direct and indirect effects, had four variables (storage root number, storage root weight, storage root girth and total leaf area) explaining storage root yield at 72% level. The direct effect of storage root number on yield ( $P = 0.53$ ) was equal to the correlation coefficient ( $r = 0.53$ ) suggesting that selection through this trait could be effective in identifying a genotype with high storage root yield.

**Table 4:** Phenotypic correlation (and respective level of significance) among quantitative morphological characteristics in 10 cassava genotypes.

	ptht	La	ptiol	dryd	rtn	rsize	rtdia	stmdai	wtlvs	wtstm	dmc	sugar	Starch
Ptth	1.00	-0.31 ***	0.15	0.49 ***	0.26 **	0.21 **	0.48 ***	0.44 ***	0.26 ***	0.56 ***	0.20 *	-0.10	0.05
La		1.00	-0.31 ***	0.15	0.49 ***	0.26 **	0.21 *	0.48 ***	0.44 ***	0.26 **	0.56 ***	0.20 *	-0.19
Ptiol			1.00	0.15	0.17 *	-0.04	-0.01	0.06	0.46 ***	0.34 ***	-0.01	0.12	-0.19
Dryd				1.00	0.53 ***	0.37 ***	0.54 ***	0.38 ***	0.38 ***	0.58 ***	0.09	0.06	0.02
Rtn					1.00	-0.23 **	0.30 ***	0.30 ***	0.40 ***	0.42 ***	0.01	-0.14	0.06
Rtsize						1.00	0.41 ***	0.23 **	0.05	0.31 ***	-0.25 **	-0.02	0.06
Rtdia							1.00	0.69 ***	0.13	0.36 ***	-0.08	-0.09	0.16
Stmdi								1.00	0.34 ***	0.44 ***	0.01	-0.12	-0.02
wtlvs									1.00	0.78 ***	0.15	-0.01	-0.32
wtstm										1.00	0.12	-0.10	-0.21
dmc											1.00	-0.28 ***	-0.01
sugar												1.00	0.32 ***
starch													1.00

Where:

{ptht=plant height; La= leaf area; ptiol=petiole length; rtn=storage root number; rsize=storage root weight ; rtdai=storage root girth; stmdia=stem girth; wtlvs=weight of leaves; wtstm=weight of stems; dmc=dry matter conten}.

**Table 5:** Parameter estimates, sum of squares, coefficient of determination (R<sup>2</sup>) and Mallows 'C(P) statistic between storage dry yield and other plant traits of cassava genotypes.

Variable	Estimate	SE	SS	Probability
INTERCEP	0.369	0.607	0.287	0.5449
LA	-0.024	0.009	5.993	0.0067
PETIOLE	0.104	0.027	11.853	0.0002
RTN	0.280	0.040	37.388	0.0001
RTSIZE	2.488	0.404	29.474	0.0001
RTGIRTH	0.045	0.007	30.027	0.0001
WTSTEM	-0.221	0.058	12.138	0.0002
STARCH	-0.015	0.006	4.917	0.0137
R <sup>2</sup>	0.69			
C(P)	5.6			

## CONCLUSION

In conclusion, the study showed highly significant (P<0.001) influence of the environment and genotype

by environment interactions on most of the plant traits evaluated. Broad sense heritability was relatively

moderate for storage roots and dry matter content ( $h^2=0.39$  and  $0.56$ , respectively) while it was high for petiole length ( $h^2=0.82$ ). Storage root performance trend at the three sites of Namulonge, Bulisa and Kapchorwa was the same in both seasons. Phenotypic correlations were significant between dry root yield with storage root number ( $r=0.53$ ,  $p<0.001$ ), storage root size ( $r=0.37$ ,  $p<0.001$ ), storage root girth ( $r=0.54$ ,  $p<0.001$ ), stem girth ( $r=0.38$ ,  $p<0.05$ ), and leaves and stem weight ( $r=0.38$  and  $0.58$ ,  $p<0.05$ , respectively). The following plant traits: leaf area, petiole length,

storage root number, root size, root girth, stem weight, and starch content gave the best equation for yield prediction ( $R^2=0.69$ ,  $C(P)=5.6$ ). Indirect path analysis revealed that selection of high potential clones could be achieved based on storage root number, storage root size and storage root diameter as the main yield components. Results from multiple regression and path analysis suggested, however, that the model does not yet fully explain the complexity of interrelationship that influence cassava yield.

**Appendix 1:** Analysis of variance on plot mean basis for some traits in cassava clones over locations.

Source of variation	d.f	MS	EMS
Location (L)	l-1	M1	$\sigma^2e + g\sigma^2r(l) + r\sigma^2l$
Genotype (G)	g-1	M2	$\sigma^2e + r\sigma^2gx(l) + rl\sigma^2g$
G X E	(l-1)(g-1)	M3	$\sigma^2e + r\sigma^2gx(l)$
Rep (L)	l(r-1)	M4	$\sigma^2e + g\sigma^2r(l)$
Error	l(r-1)(g-1)	M5	$\sigma^2e$

**Appendix 2:** Analysis of variance on plot mean basis for some traits in cassava clones over locations and years.

Source of variation	d.f	Expected means squares
Location (L)	l-1	$\sigma^2e + r\sigma^2 GLY + ry \sigma^2 GL + g \sigma^2 R(LY) + rg \sigma^2 LY + rgl \sigma^2 L$
Year (Y)	y-1	$\sigma^2e + r\sigma^2 GLY + rl\sigma^2 GY + g\sigma^2 R(LY) + rg \sigma^2 LY + rgl\sigma^2 Y$
L X Y	(l-1)(y-1)	$\sigma^2e + r\sigma^2 GLY + \sigma^2 R(LY) + g r\sigma^2 LY$
Replication (LY)	(r-1)ly	$\sigma^2e + g\sigma^2 R(LY)$
Genotypes (G)	g-1	M1 $\sigma^2e + r\sigma^2 GLY + ry\sigma^2 GL + rl\sigma^2 GY + rly\sigma^2 G$
G X L	(g-1)(l-1)	M2 $\sigma^2e + r\sigma^2 GLY + ry\sigma^2 GL$
G X Y	(g-1)(y-1)	M3 $\sigma^2e + r\sigma^2 GLY + rl\sigma^2 GL$
G X L X Y	(g-1)(l-1)(y-1)	M4 $\sigma^2e + r\sigma^2 GLY$
Pooled error	(r-1)(g-1)ly	M5 $\sigma^2e$

**Appendix 3:** Computing estimates of variance components methods for various plants traits.

Variance component	Determination method
Genotype ( $\sigma^2G$ )	$(M1 + M4 - M3 - M2)/rly$
Genotype x location ( $\sigma^2GL$ )	$(M2 - M4)/ry$
Genotype x year ( $\sigma^2GY$ )	$(M3 - M4)/rl$
Genotype x year x location ( $\sigma^2GYL$ )	$(M4 - M5)/r$
Pooled error ( $\sigma^2e$ )	(M5)



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