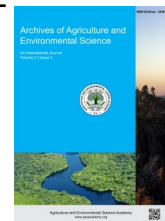This content is available online at AESA

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ORIGINAL RESEARCH ARTICLE

Genotypic variability and genetic parameters for root yield, dry matter and related traits of cassava in the Guinea Savannah ecological zone of Ghana

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ABSTRACT

The aim of this study was to assess the agronomic performance and genetic parameters governing storage root yield and related traits in cassava genotypes in order to identify superior genotypes. The study involved 18 elite cassava genotypes which were arranged in a randomized complete block design with three replications and assessed for storage root yield and yield components (12 months after planting) in the Guinea savannah ecology of Ghana for three seasons. Analysis of variance indicated significant ($p < 0.05$) genotype and year main effects for fresh and dry root yields, dry matter content, starch yield and harvest index. Genotype × year effect was significant ($p < 0.05$) for fresh root yield, dry root yield and starch yield. Estimates of the variance components revealed greater genotypic influence for starch yield, fresh and dry root yields implying the potential for genetic gain with selection for these traits among the genotypes. Relatively high (69 %) broad sense heritability estimate was observed for dry storage root yield indicating the depth of genetic influence. Path coefficient analysis revealed a direct positive effect of dry matter content on dry storage root yield whilst dry storage root yield had direct positive effect on starch yield suggesting the possibility of indirect selection for starch yield through dry storage root yield. The study revealed ample genotypic variability among the cassava genotypes to warrant selection. Four genotypes, IBA 070134, IBA 419, IBA 950289 and IBA 980581 were identified for high and stable fresh and dry root yields for multilocational testing.

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INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a perennial shrub belonging to the *Euphorbiaceae* family and widely cultivated in the tropics particularly South America, Africa and the Pacific for its starchy roots (Lopez-Diago *et al.*, 2018). Due to its high productivity under adverse conditions, all year-round availability and compatibility with different farming systems, it is consid-

ered an ideal food security crop (Okeleye *et al.*, 2001). The crop possesses different adaptive morphological and physiological attributes that make it resilient in dry ecologies where most crops grown for food and feed would fail (Adjebeng-Danquah *et al.*, 2020; Okogbenin *et al.*, 2013; El-Sharkawy and Cadavid, 2002; El-Sharkawy, 2007; Lenis *et al.*, 2006) It is therefore an ideal feed and food security crop in such ecologies (El-Sharkawy, 2004; Hillocks, 2002). Despite the high potential

of cassava as an industrial raw material particularly starch and animal feed industry (Ceballos *et al.*, 2004; Ceballos *et al.*, 2012), past breeding efforts in the Guinea savannah ecology have focused on developing early bulking varieties and varieties with good food quality with adaptation to the short growing season of the Guinea Savannah agroecological zone of Ghana (Adjebeng-Danquah *et al.*, 2012; Adu-Gyamfi *et al.*, 2016; Osei *et al.*, 2002). Genotypes that fail to meet these objectives are discarded at an earlier stage of the breeding programme. This has thus limited the broad scale utilization of the crop to only food uses and minor processing. However, certain cassava varieties have high dry matter content which makes them ideal for industrial processing. Dry matter content is highly polygenic trait in cassava and is very useful for the acceptance or rejection of cassava varieties by most end-users including processors (Prasannakumari *et al.*, 2021). High dry matter cassava varieties have been useful in starch production since high dry matter content has been found to be positively associated with high starch content (Maraphum *et al.*, 2021; Teye *et al.*, 2011). Starch from cassava is one of the most preferred and cheapest sources of starch and has relatively better pasting properties, good texture, good stability and swelling power (Amelework and Bairu, 2022). This makes it ideal as raw material for a number of industries. The starch also has numerous applications in the paper, textile, pharmaceutical (as excipient), adhesives, food (as thickener), water treatment (as coagulant), and polymer industries (Hernández-Carmona *et al.*, 2017; Koopmans, 2005) as well as in the production of biopolymeric materials and food packaging film (Tumwesigye *et al.*, 2017).

The full economic potential of cassava for industrial use can be exploited if high yielding productive and industry-preferred cassava varieties could be identified for cultivation. The productivity of cassava and suitability for different products depends on several factors including variety and environmental factors at the time of production (Amelework *et al.*, 2023; Amelework and Bairu, 2022). Several studies have reported significant genetic variation among cassava genotypes in terms of dry matter content and starch properties which can be influenced by the environment and genotype × environment interaction (Agunbiade and Ighodaro, 2010; Ayetigbo *et al.*, 2018; Eke *et al.*, 2007; Nuwamanya *et al.*, 2009; Omodamiro *et al.*, 2007). Dry matter content as well as the quality and quantity of starch obtained depend on the genotype, environmental conditions and the interaction between a number of factors (Adjebeng-Danquah *et al.*, 2016; Eke *et al.*, 2007). It has thus become important to evaluate and select cassava varieties not only for their food quality and uses, but also as an industrial commodity. Since most traits of economic importance in cassava are subject to influence by genotype, environment and genotype × environment interaction (Amelework *et al.*, 2023; Aghogho *et al.*, 2022; Bakare *et al.*, 2022; Uchendu *et al.*, 2022), it is difficult to predict genotypic performance in different years or environments. As a result, genotypes have to be evaluated for several years or across several environments to assess their stability for these traits (Haldavankar *et al.*, 2009). Genotypes that exhibit less

variation in performance relative to a check variety across years and/or environments, are considered to be stable (Olivoto, *et al.*, 2019). After these multi-year or multi-environment evaluations, the successful genotypes that show superior performance are considered as suitable candidates that have the potential to thrive under the different environmental conditions on farmers' fields and across years. The objective of this study was to assess the genotypic variability for agronomic performance, genetic parameters and stability for storage root yield, dry matter content, root starch content and related traits among 18 elite cassava genotypes in the Guinea Savannah ecology of Ghana.

MATERIALS AND METHODS

Description of the study site
The study was carried out at the CSIR-Savanna Agricultural Research Institute research fields, Nyankpala from 2016 to 2018. The study area is located in the Guinea savannah agroecological zone which is characterized by a single rainy season which normally begins in April and ends in October or November. Intermittent dry spells often lasting two to three weeks occur within the growing season (Alua *et al.*, 2018). Average annual rainfall is estimated to be about 1033 mm. Average annual temperature is 28.1 °C and relative humidity of 61 % also occurs in the area. Average potential evapotranspiration (1720 mm) normally exceeds annual rainfall (Agyemang and Abdul-korah, 2014; EPA, 2003). The soil of the study areas was a well-drained ferric luvisol, locally known as the Tingoli series (FAO-UNESCO, 1977).

Germplasm and planting materials used for the study
Eighteen cassava genotypes were used for the study. These genotypes comprised 16 elite genotypes obtained from the breeding programme of the International Institute of Tropical Agriculture (IITA). They were evaluated alongside two farmer preferred varieties, "Biabasse" and "Eskamaye". Biabasse is a landrace widely cultivated in cassava growing communities in northern Ghana whilst Eskamaye was formally released as a variety in 2002 by the Savannah Agricultural Research Institute of the Council for Scientific and Industrial Research, Nyankpala, Ghana and has a yield potential of 16-23 t ha^{-1} (Osei *et al.*, 2002).

Land preparation, experimental design and planting
The land was ploughed and harrowed after which ridges were manually raised with hoes using inter-row spacing of one meter. The cassava genotypes representing the treatments were arranged in a randomized complete block design (RCBD) with three replications. Each plot consisted of four rows with five stands within a row giving a total of 20 stands in a plot resulting in an estimated population of 10,000 plants per hectare. Cassava stakes measuring approximately 25 – 30 cm were planted on top of the ridges using intra row of one meter. Manual weed control was carried out as and when necessary. Reshaping of ridges was carried out after each weeding to avoid exposing the roots.

Data collection

Harvesting was done at 12 months after planting on the two middle rows. Data were recorded on fresh root weight (kg) and fresh shoot weight (kg). Fresh root yield (t ha^{-1}), harvest index and dry matter content (%) were computed according to the procedure described in Adjebeng-Danquah *et al.* (2016). Dry root yield (t ha^{-1}) was obtained by multiplying the fresh root yield by the dry matter content (%). Starch content was estimated using the specific gravity method as described by Fukuda *et al.* (2010). Starch yield (t ha^{-1}) was computed as the product of starch content and fresh storage root yield (t ha^{-1}).

Data analysis

The data was subjected to analysis of variance using Genstat Statistical package version 12.1 (Payne *et al.*, 2009). Treatment means were separated using the standard error of the difference (*p < 0.05*). Genotypes were considered as fixed factors whilst years were considered as random factors. Estimates of variance components were obtained from the observed mean squares by equating with their respective expected mean squares (Ewa *et al.*, 2017; Ntawuruhunga and Dixon, 2010). Genotypic coefficient of variation (CV_g), environmental coefficient of variation (CV_e), and relative coefficient of variation (CV_r) and broad sense heritability were then estimated (Adjebeng-Danquah *et al.*, 2017; Oliveira *et al.*, 2021).

Variance components:

$$CV_g\ (\%) = \left(\frac{\sqrt{\sigma_g^2}}{x}\right) * 100$$

$$CV_p\ (\%) = \left(\frac{\sqrt{\sigma_p^2}}{x}\right) * 100$$

$$CV_r = \frac{CV_g}{CV_e}$$

Where: CV_g = Genotypic coefficient of variation; CV_e = environmental coefficient of variation; CV_r = relative coefficient of variation; X = grand mean

σ^2_g = genotypic variance: $\quad \sigma_g^2 = MSg - {MSe}/{r}$

σ^2_p = phenotypic variance: $\quad \sigma_p^2 = \sigma_g^2 + \frac{\sigma_{gxy}^2}{Y} + \frac{\sigma_e^2}{YxR}$

Where: MSg = Genotypic mean square; MSe = Error mean square; σ^2_{gxy} = Genotype × year variance; σ^2_y = Year variance; *Y* = number of years; *R* = number of replications.

Broad sense heritability : $\quad H^2 = \frac{\sigma_g^2}{\sigma_p^2} X100$

Estimation of the AMMI stability value

To assess the different genotypes for stable performances over the years of evaluation, the additive main effect multiplicative interaction (AMMI) analysis was performed using Genstat 12.1 (Payne *et al.*, 2009). Subsequently, AMMI stability value and genotype stability index were estimated (Purchase *et al.*, 2000). The AMMI stability value (ASV) was calculated as follows:

$$ASV = \sqrt{\left[\frac{IPCA1_{Sum\ of\ squares}}{IPCA2_{Sum\ of\ squares}}(IPCA1_{Score})\right]^2 + (IPCA2_{Score})^2}$$

Where: $\frac{IPCA1_{Sum\ of\ squares}}{IPCA2_{Sum\ of\ squares}}$ = the weight given to the IPCA1-value by dividing the IPCA1 sum of squares (from the AMMI analysis of variance table) by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive, the more adapted a genotype is to a certain environment. Smaller ASV scores indicate a more stable genotype across environments (Farshadfar *et al.*, 2011).

Genotype stability index (GSI) was also calculated using the sum of the ranking based on yield and ranking based on the AMMI stability value.

$$GSI = RASV + RG$$

Where: RASV = the rank of the genotypes based on the AMMI stability value and RG= the rank of the genotypes based on performance across environments.

GSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Adjebeng-Danquah *et al.*, 2017; Bose *et al.*, 2014; Tumuhimbise *et al.*, 2014).

Correlation and path analysis

The information on the interrelationships between traits is important in the selection of key secondary traits for crop improvement. Both phenotypic and genotypic correlation analyses were carried out to determine the relationship between the different traits based on sequential stepwise multiple regressions (Adu *et al.*, 2016). For the path analysis, storage root yield, starch content and the other agronomic traits measured were examined based on stepwise multiple analysis and illustrated using path diagram.

RESULTS AND DISCUSSION

Combined analysis of variance for storage root yield and yield components

Recent demand for cassava as an industrial crop has moved the crop from a staple food security crop to industrial raw material (Ceballos *et al.*, 2020). This has necessitated the development of new varieties not only with good cooking quality but with industry-preferred attributes such as high dry matter and high starch content which are preferred by most cassava industries (Dankwa and Peprah, 2019). This study sought to evaluate and identify cassava genotypes with high storage root yield and high dry matter content for industrial processing.

Table 1. Mean squares for six traits measured on 18 cassava genotypes evaluated at Nyankpala from 2016 – 2018.

Source of variation	d.f.	FSRY (t ha⁻¹)	DM (%)	DSRY (t ha⁻¹)	Stch (%)	Stchyld (t ha⁻¹)	HI
Replication	2	135.06	16.10	13.96	12.39	5.67	375.42
Genotype	17	130.75***	66.58***	22.77***	32.55***	7.57***	189.02*
Year	2	955.08***	278.93***	51.64***	15.05ns	48.95***	857.57***
Genotype × Year	34	42.82*	15.16ns	5.11*	10.11ns	2.35*	130.84ns
Error	106	29.47	13.40	3.03	7.82	1.27	89.28
Total	161						

*,**,*** = significant at *P <0.05*, *P <0.01* and *P <0.001* respectively, ns = not significant (*P >0.05*). FSRY = fresh storage root yield (t ha⁻¹), DM% = dry matter content, DSRY = dry storage root yield, Stch% = starch content of storage roots, Stchyld (t ha⁻¹) = starch yield (t ha⁻¹), HI = Harvest index.

Table 2. Mean (±), estimates of variance components, heritability, phenotypic and genotypic coefficient of variation for five traits from 18 cassava genotypes evaluated from 2016-2018.

Parameters	Fresh root yield (t ha⁻¹)	Dry matter content (%)	Dry root yield (t ha⁻¹)	Starch content (%)	Starch yield (t ha⁻¹)	Harvest index (%)
Mean (±STDEV)	19.90±7.47	32.91±4.81	6.50±1.70	19.30±3.33	3.86±1.68	59.91±11.03
σ^2_g	16.01	7.59	2.76	3.87	0.96	25.62
$\sigma^2_{g \times y}$	4.45	0.20	0.23	0.25	0.12	4.62
σ^2_y	9.82	4.47	1.01	2.61	0.42	29.76
σ^2_p	30.28	12.26	4.00	6.73	1.50	60.00
H^2_b	52.87	61.96	69.02	57.50	63.86	42.70
CV_p (%)	28.05	10.64	30.82	13.44	31.76	12.93
CV_g (%)	20.39	8.37	25.61	10.19	25.38	8.45
CV_e (%)	15.97	6.42	15.47	8.37	16.87	9.11
CV_r	1.28	1.30	1.65	1.22	1.50	0.93

Key: σ^2_g = genotypic variance, $\sigma^2_{g \times y}$ = genotype × environment variance, σ^2_y = Year (environmental) variance, σ^2_p = phenotypic variance, H^2_b= broad sense heritability, CV_p (%) = Phenotypic coefficient of variation, CV_g (%) = Genotypic coefficient of variation, CV_e (%) = environmental coefficient of variation, CV_r = relative coefficient of variation.

Analysis of the results indicated highly significant (*p < 0.001*) variability among the cassava genotypes for storage root yield, dry matter content and harvest index over the three years of study. Genotype × year interaction effect was also significant (*p < 0.05*) for fresh root yield, dry root yield and starch yield (Table 1). The effect of year was also highly significant (*p < 0.001*) for all the traits except for starch content which was not significant (*p > 0.05*). Several studies have suggested that the success of any plant breeding programme depends on the extent of genotypic variability present in the germplasm assembled (Salgotra and Chauhan, 2023; Swarup *et al.*, 2021; Varshney *et al.*, 2021; Cobb *et al.*, 2019). The observed significant genotype effect for the different traits suggests the presence of ample genotypic variability for these traits indicating the chance of success in terms selection for best genotypes for these traits (Oliveira *et al.*, 2021).

Estimates of genetic parameters and broad sense heritability
Estimates of variance components indicated that genotypic variances (σ^2_g) for all the traits were greater than their corresponding variances due to year (σ^2_y) and genotype × year interaction ($\sigma^2_{g \times y}$) except for harvest index (Table 2). Harvest index had a greater year variance than the genotype and genotype × year variances. These results though similar to the observations of Oliveira *et al.* (2021), are contrary to the findings of Silva *et al.* (2019) who recorded higher error or environmental variance than variance due to genotype in 49 cassava accessions

evaluated under drought conditions. This implies that these parameters vary with the specific population used. Harvest index had a greater year variance than the genotype and genotype × year variances suggesting that, the conditions in a particular year had a greater influence on the amount of dry matter partitioned into the storage roots relative to the above ground biomass. It also suggests that the performance of genotype(s) could vary with different years. Therefore, multilocational trials need to be considered within the target region to understand, exploit and/or minimize the adverse effect of years and genotype × environment interaction when selecting for selecting for genotypes based on harvest index. Earlier studies have reported strong influence of years or environments on harvest index and such influence tends to increase under unfavorable environmental conditions (Adjebeng-Danquah *et al.*, 2020; Baafi and Safo-Kantanka, 2008). For a clonally propagated crop like cassava, desirable traits to be considered for selection must have higher genotypic influence which ensures more reliability than traits with higher environmental influences for simple direct selection to be possible (Tuberosa, 2012). Broad sense heritability estimates ranged from low (43 %) to medium (69 %) for harvest index and dry root yield respectively (Table 2). In the case of traits with low broad sense heritability estimates, direct selection within this population may not be effective and will result in slow progress (Li *et al.*, 2020; Diniz and Oliveira, 2019). It will thus require the use of secondary traits that are strongly linked to these traits of interest.

Table 3. Phenotypic correlation (below diagonal) and genetic correlation (above diagonal) among traits for 18 cassava genotypes evaluated over three years at Nyankpala.

Traits	FSRY (t ha⁻¹)	DM (%)	DSRY (t ha⁻¹)	Stch (%)	Stchyld (t ha⁻¹)	HI
			Genotypic correlation			
FSRY (t ha⁻¹)	-	-0.15ns	0.93***	0.09ns	0.91***	0.28***
DM (%)	0.58**	-	0.21**	0.81***	0.17*	0.13ns
DSRY (t ha⁻¹)	0.98***	0.74***	-	0.37***	0.97***	0.33***
Stch (%)	0.35ns	0.99***	0.56*	-	0.47***	0.04ns
Stchyld (t ha⁻¹)	0.94***	0.84***	0.98***	0.76***	-	0.26***
HI	0.93***	0.61**	0.86***	0.49*	0.89***	-
			Phenotypic correlation			

Key: *,**,*** = significant at *P <0.05*, *P <0.01* and *P <0.001* respectively, ns = not significant (*P >0.05*), FSRY = Fresh storage root yield (t ha⁻¹), DM = Dry matter content (%), DSRY = dry storage root yield (t ha⁻¹), Stch = starch content of storage roots (%), Stchyld = starch yield (t ha⁻¹), HI = Harvest index.

Table 4. Performance of genotypes for six traits of 18 cassava genotypes evaluated in Nyankpala.

Genotype	FSRY (t ha⁻¹)	DM (%)	DSRY (t ha⁻¹)	Stch (%)	Stchyld (t ha⁻¹)	HI (%)
Biabasse	15.89	36.66	5.73	21.76	3.45	60.27
Eskamaye	18.03	31.62	5.70	18.11	3.28	61.90
IBA 010034	17.15	33.72	5.77	19.68	3.39	57.99
IBA 010040	19.11	32.00	6.05	19.35	3.69	56.55
IBA 011368	17.87	30.67	5.36	17.89	3.19	57.98
IBA 011371	13.94	28.09	3.88	16.62	2.31	52.27
IBA 020431	19.89	35.72	7.01	21.75	4.33	60.99
IBA 020452	18.76	35.94	6.61	21.42	4.04	55.19
IBA 061635	17.64	29.64	5.23	16.43	2.95	53.82
IBA 070134	32.28	36.03	11.60	20.01	6.47	66.91
IBA 30572	19.35	32.74	6.13	18.88	3.61	57.90
IBA 419	23.20	35.26	8.01	21.66	5.04	65.76
IBA 9102324	21.07	32.40	7.00	19.44	4.33	65.47
IBA 950289	21.13	28.04	5.82	15.78	3.32	62.20
IBA 961089A	21.09	32.03	6.67	18.44	3.88	65.83
IBA 980505	19.20	31.57	5.87	18.42	3.47	57.82
IBA 980581	21.58	35.80	7.62	21.53	4.64	54.64
IBA 993073	20.95	34.46	6.85	20.21	4.13	64.88
Mean	19.90	32.91	6.50	19.30	3.86	59.91
SED	2.45	1.73	0.82	1.32	0.53	4.45

Key: FSRY = Fresh storage root yield (t ha⁻¹), DM = Dry matter content (%), DSRY = dry storage root yield (t ha⁻¹), Stchyld = starch yield (t ha⁻¹), HI = Harvest index.

Phenotypic coefficient of variation (CV$_p$ %) ranged from 10.64 to 31.76 % for dry matter content and starch yield respectively. Genotypic coefficient of variation (CV$_g$ %) varied between 8.37 and 25.61 % for dry matter content and dry root yield, respectively. Though phenotypic coefficients of variation were generally higher than the corresponding genotypic coefficients of variation (CV$_g$ %), the magnitude of the differences varied with the different traits. This demonstrated the extent of the effect of the environment (different years) on the different traits. The environmental coefficient of variation (CV$_e$ %) values of all the traits apart from harvest index, were lower than their corresponding genotypic coefficient of variation (CV$_g$ %). The relative coefficient of variation (CV$_r$) also known as relative variation index was greater than one for all traits except harvest index. This suggests that direct selection could be based on these traits (apart from harvest index) to select elite cassava genotypes for further improvement provided they are positively correlated with traits of economic importance (Diniz and Oliveira, 2019).

For traits with higher environmental influence, indirect selection based on secondary traits (with high heritability) could be more effective (Oliveira *et al.*, 2021).

Phenotypic and genotypic correlation analysis
Storage root yield in cassava is a complex quantitatively inherited trait which is associated with several physiological and morphological traits that are in turn highly influenced by the conditions prevailing in the growing environment (Adjebeng-Danquah *et al.*, 2020). It is therefore necessary to identify secondary traits that are positively related to the traits of interest to use them as indirect selection criteria (Rao *et al.*, 2017). The phenotypic correlation analysis showed highly significant associations (below the diagonal) between the different traits (Table 3). Fresh root yield was positively and highly correlated with dry root yield (r$_p$ = 0.93), starch yield (r$_p$ = 0.91) and harvest index (r$_p$ = 0.28) with which it had a weak association. A strong positive and highly significant correlation was found between dry root yield and starch yield (r$_p$ = 0.97).

Dry matter content was also significantly and positively correlated with starch content (r_p = 0.81) and starch yield agreeing with the findings of previous studies which also reported a significant direct positive correlation between dry matter content and starch content in cassava (Maraphum *et al.*, 2021; Diniz and Oliveira, 2019; Oliveira *et al.*, 2015). However, the correlations between harvest index and dry matter content as well as harvest index with starch content were not significant. The genotypic correlation analysis (above the diagonal) also indicated highly significant associations between the different traits. Fresh storage root yield was positively and highly correlated with harvest index (r_g = 0.93), starch yield (r_g = 0.94) and dry storage root yield (r_g = 0.98). A strong positive and highly significant correlation was found between dry matter content and starch content (r_g = 0.99), starch yield (r_g = 0.84) and dry storage root yield (r_g = 0.74). This observation agrees with agrees with the findings of Amelework and Bairu (2021) who reported strong association between dry matter content and starch content in cassava. However, there was a weak positive correlation between fresh storage root yield and starch content (r_g = 0.35), and an almost perfect correlation between starch yield and dry storage root yield (r_g = 0.98). The significant and positive associations among the different traits indicate that direct selection for any of the traits

would indirectly lead to the improvement of the associated traits simultaneously.

Path analysis

The use of secondary traits in indirect selection is one of the most effective ways of selecting traits with low heritability or traits that are difficult to measure (Li *et al.*, 2020; Diniz and Oliveira, 2019). Path analysis was used to determine the direct and indirect relationships between dry storage root yield, starch yield and the other related traits in a systematic manner. First, dry storage root yield was considered as the primary trait of interest or resultant (dependent) variable (Figure 1) whilst all the other traits including fresh storage root yield, starch content, starch yield, dry matter content and harvest index were considered as the independent or causal variables. Starch yield (0.793), fresh storage root yield (0.295) and dry matter content (0.395) all had direct positive effect on dry storage root yield whilst starch content had a direct negative effect (-0.344) on dry storage root yield. Harvest index had a positive indirect effect on dry storage root yield through fresh storage root yield (0.284) and starch yield (0.258). Strong positive correlation was found between starch yield and fresh storage root yield (0.909), dry matter content and starch content (0.809) but moderate correlation between starch yield and starch content (0.471). Though strong direct effect of fresh root yield on starch yield had been reported in an earlier study (Diniz and Oliveira, 2019), the findings from the current study rather revealed an indirect relationship between fresh storage root yield and starch yield through dry storage root yield. They further suggested that high root yield could be used as an efficient trait for targeting high starch yield. From our study, it would be important to consider dry matter content alongside storage root yield when targeting genotypes with high starch yield potential.

Secondly, starch yield was considered as the resultant (dependent) variable (Figure 2) whilst all the other traits including fresh root yield, starch content, dry matter content, dry storage root yield and harvest index were considered as the independent or causal variables. Dry storage root yield, starch content and dry matter content were classified as first order traits which had direct relationship with starch yield. Fresh root yield and harvest index had indirect effect on starch yield. Dry storage root yield had the strongest direct positive effect (0.88) on starch yield which was followed by starch content (0.436). Dry matter content (%) had a negative direct effect (-0.365) on starch yield. However, dry matter content had an indirect positive effect on starch yield through starch content (0.809). Fresh storage root yield had a strong positive indirect effect on starch yield through dry storage root yield (0.904) whilst a weak indirect relationship was observed between harvest index and starch yield through dry storage root yield.
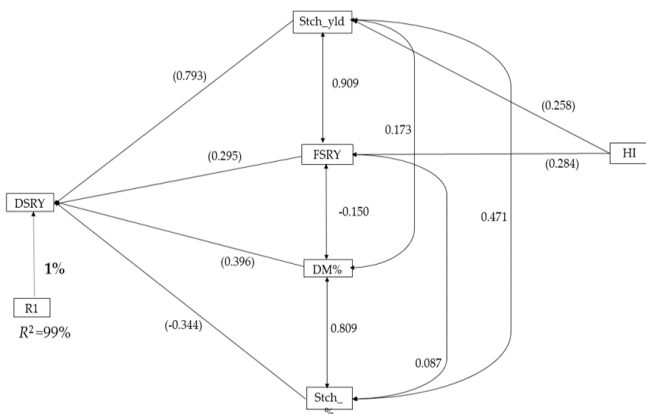
Figure 1. *Path diagram showing direct and indirect relationship between dry storage root yield and other traits. FSRY = Fresh storage root yield (t ha^{-1}), DM = Dry matter content (%), DSRY = dry storage root yield (t ha^{-1}), Stchyld = starch yield (t ha^{-1}), HI = Harvest index, R1 = Residual; R^2 = Coefficient of determination.*
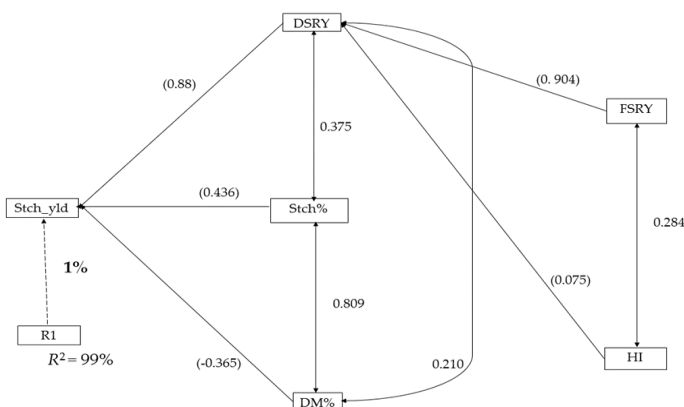
Figure 2. *Path diagram showing direct and indirect relationship between starch yield and other traits. FSRY = Fresh storage root yield (t ha^{-1}), DM = Dry matter content (%), DSRY = dry storage root yield (t ha^{-1}), Stchyld = starch yield (t ha^{-1}), HI = Harvest index, R1 = Residual; R^2 = Coefficient of determination.*

Average performance of the cassava genotypes for six traits

Average fresh root yield across the three years ranged between 13.94 t ha^{-1} (IBA 011371) and 32.28 t ha^{-1} (IBA 070134) with a mean yield of 19.90 t ha^{-1} (Table 4).

Table 5. Ranking of 18 cassava genotypes for fresh root yield (FSRY), dry root yield (DSRY) and starch yield over three years based on AMMI stability value (ASV) and genotype stability index (GSI) at 12 months after planting.

Genotype	FSRY (t ha⁻¹)	ASV	RASV	Rank FRY	Rank sum	GSI Rank	DSRY (t ha⁻¹)	ASV	RASV	Rank DRY	Rank sum	GSI Rank	Stchyld (t ha⁻¹)	ASV	RASV	Stchyld Rank	Rank sum	GSI Rank
Biabasse	15.89	0.44	4	17	21	10	5.73	0.06	1	14	15	6	3.45	0.09	4	12	16	7
Eskamaye	18.03	1.05	8	13	21	9	5.69	0.95	14	15	29	18	3.28	0.74	11	15	26	17
IBA 010034	17.15	1.39	11	16	27	17	5.77	0.91	13	13	26	16	3.39	0.78	13	13	26	15
IBA 010040	19.11	18.42	17	11	28	18	6.05	2.53	18	10	28	17	3.69	3.70	18	9	27	18
IBA 011368	17.87	1.65	12	14	26	16	5.36	0.19	5	16	21	10	3.19	0.31	7	16	23	12
IBA 011371	13.94	0.81	7	18	25	15	3.88	0.21	6	18	24	14	2.31	0.24	6	18	24	13
IBA 020431	19.89	2.92	15	8	23	11	7.01	0.40	8	4	12	3	4.33	0.68	10	5	15	5
IBA 020452	18.76	0.36	3	12	15	6	6.61	0.85	12	8	20	9	4.04	0.87	14	7	21	10
IBA 061635	17.64	1.16	9	15	24	12	5.23	0.35	7	17	24	15	2.95	0.31	8	17	25	14
IBA 070134	32.28	0.69	6	1	7	3	11.60	0.40	9	1	10	2	6.47	0.44	9	1	10	3
IBA 30572	19.35	3.72	16	9	25	14	6.13	0.17	4	9	13	4	3.61	0.18	5	10	15	6
IBA 419	23.20	0.18	2	2	4	1	8.01	1.01	15	2	17	8	5.04	1.07	15	2	17	8
IBA 9102324	21.07	1.95	13	6	19	8	6.99	1.73	17	5	22	12	4.33	1.95	16	4	20	9
IBA 950289	21.13	0.06	1	4	5	2	5.82	0.58	11	12	23	13	3.32	0.75	12	14	26	16
IBA 961089A	21.09	2.72	14	5	19	7	6.67	0.58	10	7	17	7	3.88	0.01	1	8	9	2
IBA 980505	19.20	0.68	5	10	15	5	5.87	0.16	3	11	14	5	3.47	0.04	2	11	13	4
IBA 980581	21.58	1.26	10	3	13	4	7.62	0.09	2	3	5	1	4.64	0.05	3	3	6	1
IBA 993073	20.95	20.38	18	7	25	13	6.85	1.28	16	6	22	11	4.13	2.00	17	6	23	11

Key: FSRY = Fresh storage root yield (t ha⁻¹), DSRY = Dry storage root yield (t ha⁻¹), Stchyld = starch yield (t ha⁻¹), ASV = AMMI stability value, GSI = genotype stability index.

Average dry matter content on the other hand varied from 28.04 to 36.66 % for IBA 950289 and Biabasse, respectively, with a mean of 32.91 %. Genotype IBA 070134 had the highest dry root yield (11.60 t ha⁻¹) which was superior to the local variety, Biabasse (5.73 t ha⁻¹) and the improved check, Eskamaye (5.70 t ha⁻¹). Two other genotypes, IBA 419 (8.01 t ha⁻¹) and IBA 980581 (7.62 t ha⁻¹) had significantly higher dry root yield than the checks. Average starch content ranged between 15.78 % for IBA 950289 and 21.76 % for Biabasse with a mean of 19.30 %. Average starch yield ranged from 2.31 t ha⁻¹ to 6.47 t ha⁻¹ for IBA 0110371 and IBA 070134 respectively with a mean of 3.86 t ha⁻¹. The average harvest index across years was 59.91 % and ranged between 52 % and 66.91 % for IBA 011371 and IBA 070134 respectively. Besides genotypic performance, year effect was also significant for all the traits except starch content which was not influenced by the effect of year. Additionally, genotype × year interaction effect was significant for fresh root yield, dry root yield and starch yield. This suggests the tendency of the different genotypes to produce variable performances in different years depending on the environmental conditions. Several authors have suggested that significant genotype × environment interaction arises due to differential ranking of genotypic performances in different environments or years and can confound selection (Amelework *et al.*, 2023; Aghogho *et al.*, 2022; Bakare *et al.*, 2022; Ebem *et al.*, 2021; Osei *et al.*, 2018). It could also arise from unequal variances (heterogenous variances) among genotypic means when evaluated in different environments (Amelework *et al.*, 2023; Bakare *et al.*, 2022). Therefore, multilocational testing of such genotypes is necessary to identify genotypes that would exhibit consistent performance for such traits.

Ranking of genotypes based on storage root yield and starch yield

From the study, fresh root yield, dry root yield and starch yield were highly influenced by genotype × year interaction effect suggesting high variability of these traits in the different years. This necessitated the stability analysis to identify genotypes that would remain consistent in different years in terms of performance for these traits. The AMMI stability value and genotype stability index were used to rank the performance of genotypes based on these traits. The Additive Main effect and Multiplicative Interaction (AMMI) stability value (ASV) ranked genotypes based on the least score. Low scores represent the most stable genotypes. Genotypes IBA 419 (23.2 t ha⁻¹), IBA 950289 (21.13 t ha⁻¹), IBA 070134 (32.28 t ha⁻¹) and IBA 980581 (21.58 t ha⁻¹) combined high fresh root yield with high stability and were ranked 1-4 (Table 5). Genotypes IBA 950289, IBA 419 and IBA 070134 were also found to combine good yield with stability. Other introduced genotypes (IBA 980581, IBA 9102324, IBA 993073 and IBA 961089A) combined high fresh and dry root yields with good stability. Genotypes IBA 993073 (20.95 t ha⁻¹) and IBA 020431 (19.89 t ha⁻¹) though relatively high yielding, were less stable compared to the above genotypes.

Since stability per se does not connote desirable performance unless the genotype combines it with high yield (Farshadfar *et al.*, 2011), the genotype stability index (GSI) is used to select genotypes that combine high yield with stability. Genotypes with the lowest GSI score are ranked highest and are most desired since they combine high yield with stability (Amelework *et al.*, 2023). In terms of dry root yield, genotypes IBA 980581 (7.62 t ha^{-1}), IBA 070134 (11.60 t ha^{-1}) and IBA 020431 (7.01 t ha^{-1}) also combined high dry root yield with high stability and were therefore ranked 1-3. These genotypes exhibited consistent performances over the three years of study. For starch yield, two genotypes IBA 980581 (4.64 t ha^{-1}) and IBA 070134 (6.47 t ha^{-1}) had superior starch yield compared to the farmer preferred variety, Biabasse (3.45 t ha^{-1}) and the improved variety Eskamaye (3.28 t ha^{-1}) and were also stable over the three years.

Conclusion

The study revealed significant genotypic variability for fresh root yield, dry root yield and starch yield to warrant selection among the cassava genotypes for these traits. Estimates of genetic parameters indicated strong genotypic influence for fresh root yield, dry root yield and starch yield. Genotype × year interaction effect was significant for fresh root yield, dry root yield and starch yield which necessitates multilocational testing to identify genotypes that are stable for these traits. Four genotypes, IBA 070134, IBA 419, IBA 950289 and IBA 980581 showed high and stable performance for fresh and dry root yields over the three seasons' on-station testing making them suitable candidates for multilocational testing to assess their overall adaptability across the Guinea savannah ecology of Ghana.

Conflicts of interest

The authors declare no conflict of interest.

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