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ARTICLES

- Genetic variation for corm yield and other traits in Ethiopian enset (*Ensete ventricosum* (Welw.) Cheesman) 150**
Zerihun Yemataw, Kassahun Tesfaye, Tesfaye Taddese, Tesfaye Dejene, Sadik Muzemil, Zeritu Shashego and Daniel Ambachew
- Stability, agronomic performance and genetic variability of 10 cassava genotypes in Ghana 157**
Bright B. Peprah, Adelaide Agyeman, Elizabeth Parkes, Ofori Kwadwo, Asante K. Isaac, Okogbenin Emmanuel and Maryke T. Labuschagne
- Heritability analysis to screen elite sugarcane (*Saccharum* spp.) soma clones under field condition 168**
Sardar Khatoon Solangi, Sadaf Tabasum Qureshi, Nusrat Solangi, Mukhtiar Khatoon Solangi, Imtiaz Ahmed Khan and Asma Parveen, Asma Parveen Channar and Altaf Hussain Solangi

Full Length Research Paper

Genetic variation for corm yield and other traits in Ethiopian enset (*Ensete ventricosum* (Welw.) Cheesman)

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Enset (*Ensete ventricosum* (Welw.) Cheesman) is a multipurpose crop used for food, fuel, housing materials, fencing and livestock feed. The major food types obtained from enset are kocho, bulla and amicho. Kocho is fermented starch obtained from decorticated (scraped) leaf sheaths and grated corms. Bulla is obtained by squeezing out the liquid containing starch from scraped leaf sheathes and grated corm and allowing the resultant starch to concentrate into white powder. Amicho is boiled enset corm pieces that are prepared and consumed in a similar manner to other root and tuber crops. Thirty-five cultivars of *Ensete ventricosum* were grown in RCBD (two replications) to study the different quantitative morpho-agronomic characters contributing to the diversity analysis at Areka and Chichu during 2012 to 2013 cropping season. Data on 10 quantitative traits were collected and exposed to statistical analysis. Analysis of variance revealed that there was significant difference between the two locations in all tested phenotypic characters. The mean squares due to cultivars, locations and cultivars x locations interaction were highly significant ($P \leq 0.001$) for all the quantitative traits. The highest corm yields were recorded for varieties Chohot, Ashakit, Bose and Gazner. Farmers in the two locations ranked cultivar Ashakit first and Kataniya took second place whereas the first best performing cultivars (*Chohot*) was among the least preferred genotypes with low score (3). Among the studied character, phenotypic and genotypic coefficient of variation was highest for corm weight (36.17 and 27.28 $\text{tha}^{-1} \text{y}^{-1}$). High heritability was estimate for plant height (77%). The phenotypic and genotypic coefficients of correlation indicated that corm yield $\text{ha}^{-1} \text{y}^{-1}$ was positively correlated with most of the characters. The present study indicated a considerable amount of variability for the majority of the characters of interest in *Ensete* for exploitation.

Key words: Corm, enset, genotype-by-environment interaction, quantitative traits.

INTRODUCTION

Enset (*Ensete ventricosum*) is well-established, sustainable, and environmentally resilient plant with farming system that contributes to food security of farmers in densely populated areas of the south and south-western part of Ethiopia (Bacha and Taboge, 2003).

The major foods obtained from Enset are *kocho*, *bulla* and *amicho*. *Kocho* is fermented starch obtained from decorticated (scraped) leaf sheaths and grated corms. *Bulla* is a liquid that is obtained when leaf sheaths and corm are pulverized, the liquid containing starch is

squeezed out from scraped leaf sheathes and grated corm and the resultant starch are allowed to concentrate into white powder. *Amicho* is boiled enset corm pieces (usually from young enset plant) that are prepared and consumed in a similar manner with other root and tuber crops (Brandt et al., 1997).

Based on quality and characteristics in terms of harvesting, softness and hardness, palatability when immature and resistance to disease and pest, enset clones can also be categorized into male and female (Yemataw et al., 2014). Female enset are seen as early maturing, more palatable (sweet or tasty in other ways, especially when the corm is boiled), more easily scraped, less fibrous and generally delicious.

The yielding ability of a genotype is the ultimate result of favorable interaction of genotype (G) with the environment (E). Environmental factors differ across years and locations, having significant influence at different developmental stages of crop growth (Bull et al., 1992). Sprague (1966) indicated that G x E interactions constitutes an important limiting factor in the estimation of variance components and in the efficiency of selection programs. The presence of significant G x E interactions for quantitative traits such as seed yield can reduce the usefulness of subsequent analysis, restrict the significance of inferences that would otherwise be valid, and seriously limit the feasibility of selecting superior genotypes (Flores et al., 1998).

Among many tools morphological characterization based on the traits are commonly used to analyze genetic diversity since they provide a simple way of quantifying genetic variation while assessing genotypic performance under normal growing environments (Revilla and Tracy, 1995).

Furthermore, the effectiveness of selection also depends on the amount of variability existing in the material, the extent to which a character is heritable and the association/correlation between traits (Pandey and Gritton, 1975). Assessment of both nature and extent of variability as well as genetic association between characters helps in identifying the most important character to be considered in the improvement program.

Thus, since a remarkable phenotypic variation among *E. ventricosum* collection have been observed (Tabogie, 1997; Tsegaye, 2002), phenotypic variability of the crop based on different use value is essential to identify and categorize different accessions grown in different area of the country to establish a bench mark for further improvement or documentation.

Hence, information on the extent and pattern of G x E interactions on enset is scarce. Therefore, this study was proposed with the following objectives: (i) to determine the magnitude of G x E interaction for corm yield of enset cultivars under Ethiopian conditions, (ii) to determine the

value and magnitude of genetic variability among 35 enset cultivars from morphological and agronomic variables that might guide the choice of parents for future breeding works in enset.

MATERIALS AND METHODS

Description of the research area

The experiment was conducted in two locations of Southern Ethiopia at Areka and Chichu in 2012-2013 enset cropping season. Areka is located at 7° 09' N and 37° 47' E and at an elevation ranging from 1,750 to 1,800 m above sea level (m.a.sl). Areka has an average rainfall of 1,539 mm and a minimum and maximum mean temperature of 14.5 and 25.8°C, respectively. The soil is silty loam with a pH of 4.8 to 5.6 and low to medium organic matter content (2.65-5.67%) (Esayas, 2003). Chichu is one of the kebele in Dilla Zuria woreda of the Gedee Zone, Southern Nations Nationalities and People's Regional State (SNNPRS), Ethiopia. It is situated at 6° 21'-6°24' N latitude and 38° 17'-38° 20' E longitude. It is warm humid temperate with an altitude of 1600 m.a.sl. and annual temperature ranging from 22-29°C. The soil is sandy clay loam.

Treatments and design

A total of 35 cultivars collected from different parts of the country by Areka Agricultural Research Centre were included for this experiment (Table 1). The experiment was laid out in a randomized complete block design and each accession was replicated two times. The respective spacing between plants and rows were 1.5m and 2m (a plot size of 12 m²).

Crop management and data collection

Equal sized suckers were directly planted in holes on the prepared experimental units on May 12, 2012 at Areka and on May 15, 202012 at Chichu. The experiment was conducted under rain-fed condition. Four plants per plot were considered for characters measured on individual plant basis. The whole plant was harvested two years after transplanting to the main plot. A total of 10 quantitative characters were recorded for evaluation. These are Plant Height, Pseudo stem Height, Pseudo stem Circumference, Leaf length, Leaf Width, Leaf Number, Corm Yield Per Hectare Per Year, Corm circumference, Corm length, Corm Yield Per Hectare Per Year.

$$\text{Corm yield (tonsha - 1 yr - 1)} = \frac{\text{Corm Yield per plant} \times 10000 \text{m}^2}{\text{No of years to maturity} \times \text{plot area (m}^2\text{)}}$$

Statistical analysis

The analysis of corm yield and other quantitative traits was performed using SAS computer software packages (SAS, 2002). Corm yield data was subjected to analysis of variance separately

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Table 1. List of enset cultivars, with their collection site.

S/N	Cultivar name	Locality/origin of collection	S/N	Cultivar name	Locality/origin of collection
1	Sebera	Kembata-Tembaro	19	Astara	Gurage
2	Switea	Kembata-Tembaro	20	Chohot	Gurage
3	Tessa	Kembata-Tembaro	21	Qibnar	Gurage
4	Qoyina	Kembata-Tembaro	22	Ashakit	Gurage
5	Guariye	Kembata-Tembaro	23	Gazner	Gurage
6	Bose	Kembata-Tembaro	24	Fenqo	Gurage
7	Leqaqa	Kembata-Tembaro	25	Agade	Gurage
8	Bino	Kembata-Tembaro	26	Diqa	Dawro
9	Sirareia	Wolaita	27	Musula	Dawro
10	Neqaqa	Wolaita	28	Bukuniya	Dawro
11	Shelequmia	Wolaita	29	Neqaqa	Dawro
12	Silqantia	Wolaiya	30	Switea	Dawro
13	Haleko	GamoGoffa	31	Argema	Dawro
14	Matiya	GamoGoffa	32	Arkiya	Dawro
15	Keteniya	GamoGoffa	33	Niffo	Gededo
16	Gena	GamoGoffa	34	Addo	Sidama
17	Tuffa	GamoGoffa	35	Gedeme	Sidama
18	Zinka	GamoGoffa			

Where, Y_{ijk} = observed value of cultivars i in block k of environment (location) j , \bar{y} = grand mean, G_i = effect of cultivar i , E_j = environment or location effect, GE_{ij} = the interaction effect of cultivar i with location (environment) j , $B_k(j)$ = the effect of block k in location (environment) j , ϵ_{ijk} = error (residual) effect of cultivar i in block k of location (environment) j .

Mean separation was conducted using least significant difference (LSD) test to discriminate the genotypes and identify superior ones based on the trait of interest.

Estimation of phenotypic and genotypic variances

The genotypic and phenotypic coefficients of variation (GCV and PCV) for each trait were calculated using the following formula:

Genotypic coefficients of variation (GCV) = $(\sigma^2_g / \text{grand mean of character}) \times 100$

Phenotypic coefficients of variation (PCV) = $(\sigma^2_p / \text{grand mean of character}) \times 100$

Estimation of heritability and expected genetic advance

Broad sense heritability and expected genetic advance (gain) with one cycle of selection were estimated for each character using variance components as described by Allard (1960):

$$\text{Heritability, } H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Genetic advance as percent of mean, $GAM = (GA/\bar{Y}) \times 100$, where GA = genetic advance and \bar{Y} = mean of the trait for all cultivars.

Analysis of phenotypic and genotypic correlation coefficients

Genotypic and phenotypic correlation coefficients for corm yield and

its components were estimated by calculating the variance and covariance at phenotypic and genotypic levels by using the formula suggested by Singh and Chaudhury (1985).

Farmers' preferences

In this study, group discussion was used for evaluation and data collection with farmers. Through focus group discussions with key informants in the two locations, a total of 4 (color, test, texture, overall acceptance) different criteria were used for selection purpose. After harvested, the cultivars are tested by farmers and gave its ranking of selected cultivars based on the evaluation criteria. The pair-wise ranking (Russell, 1997) method was used to analyze the position of each of cultivar in tested areas by farmers evaluation criteria. A matrix table of cultivars in the two locations was constructed. Farmers were asked to compare each cultivar to the other ones with regards to the values of each criteria and the priority each farmer gives to the cultivar. Each cultivar was compared in turn with each of the other cultivars.

RESULTS

The combined analysis of variance over locations showed ensete corm yield was significantly ($P < 0.001$) affected by location, which is a proxy for environment (E), cultivar, which is a proxy for genotypes (G) and cultivar x location interactions (Table 2). The significance of the interaction indicated the best cultivars in one locations (and hence environment) are not necessarily, the best in another.

The highly significant genotype x environment (G x E) interaction may be either a crossover G x E interaction or a non-crossover nature. In crossover nature, the GXE interaction a significant change in ranks occurs from one environment to another. In non-cross over, GXE

Table 2. Pooled analysis of variance, coefficient of variation (CV), and coefficient of determination (R^2) for 10 traits assessed in 35 Enset cultivars across three environments.

Source of variation	Mean Squares									
	DF	PH	PSH	PSC	LL	LW	LN	COM CI	COMLEN	CORTON
Treatment	34	3.59***	0.24***	0.35***	2.15***	0.07***	28.52***	0.04***	0.01**	187.34***
Location	1	109.32***	0.55***	1.72***	53.82***	0.93***	10.76NS	1.29***	0.002 NS	6349.17***
Treatment x Location	34	1.48***	0.10***	0.15***	0.87***	0.03***	16.49***	0.03***	0.013**	123.77***
Error	210	0.58***	0.16***	0.20***	0.45***	0.09***	2.16***	0.12***	0.08***	5.15***
CV		20.88	24.84	23.15	23.76	16.34	17.64	18.47	31.95	43.24
R^2		0.79	0.70	0.68	0.76	0.75	0.61	0.57	0.39	0.75

***, **, *, ns= significant at 0.1, 1, 5%, and non-significant, respectively. CV= coefficient of variation, R^2 = Coefficient of determination, ***, **, *, ns= significant at 0.1, 1, 5%, and non-significant, respectively. SV= source of variation, CV= coefficient of variation, R^2 = Coefficient of determination, PH=Plant Height, PSH=Pseudo stem Height, PSC=Pseudo stem Circumference, LL=Leaf length, LW=Leaf Width, LN=Leaf Number, CORTON = corm Yield Per Hectare Per Year, COMCI= Corm circumference, COMLEN= corm length, CORTON = corm Yield Per Hectare Per Year.

interaction, ranking of genotypes remains constant across environments and the interaction is significant because of changes in the magnitude of response (Matus et al., 1997).

Genotypes differ significantly in their mean yield performance. The G x E interaction of genotypes in this study was of crossover nature. Cultivars' performances across the two locations differ significantly in their mean yield performances (Table 3). The genotypes 'Chohot, Ashakit, Bose and Gazner had the highest values for corm yield $ha^{-1} year^{-1}$ (Table 3). Hence, cultivars which were grouped in high and medium yielding were found to be promising for corm yield. These highest yielding cultivars should be released as varieties for wide adaptation.

Sensory evaluation

For selection, good performance is not sufficient; the cultivar must also have desirable sensory and utilization characteristics. *Ashakit* and *kataniya* were the most preferred cultivars with all test attributes having good scores (2.0), whereas the first best performing cultivar (*Chohot*) was among

the least preferred genotypes with low score (5) (Table 4).

Variability components

A wide variation was observed between maximum and minimum values for most of the characters (Table 5). The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the assessed traits (Table 5). The PCV ranged from 12.74 for corm circumference to 36.17 for corm weight $tha^{-1} y^{-1}$ and the genotypic coefficient of variation ranged from 5.54 for corm circumference to 27.28 for corm weight $tha^{-1} y^{-1}$.

The heritability estimates obtained for the traits studied ranged between 19 (corm circumference) and 77% (plant height) (Table 6). High to medium broad sense heritability was observed for plant height, leaf width, pseudostem height, leaf length, leaf number, pseudostem circumference, corm weight in tone per hectares per year and corm weight per plot. The low broad sense heritability observed for corm length (39%) and corm circumference (19%). High to medium heritability

and genetic advance as percent of the mean were recorded for corm weight in tone per hectares per year, corm weight per plot, plant height, pseudostem height and leaf length. High heritability estimates with low genetic advance observed for leaf number, leaf width and pseudostem circumference.

Genotypic coefficients of correlation, in general, were higher than the corresponding phenotypic coefficients of correlation (Table 5, above and below diagonal, respectively) indicating relatively little influence of environment on any inherent association among the traits studied. The phenotypic and genotypic coefficients of correlation indicated that corm yield $ha^{-1} y^{-1}$ was positively correlated with most of the characters. This suggests that selection for corm yield can be done through selection of those traits with which it is strongly correlated (Table 6).

DISCUSSION

Information on phenotypic variation and its geographical distribution is important for genetic

Table 3. Average values for plant growth and yield traits of highly performing enset cultivars evaluated across two locations.

Cultivar name	PH	PSH	PSC	LL	LW	LN	COM CI	COMLEN	CORTON
Chohot	4.07	1	1.21	2.97	0.61	15.37	0.71	0.34	23.29
Ashakit	3.1	0.71	1.17	2.26	0.58	15.87	0.75	0.32	20.13
Bose	3.78	0.85	1.22	2.79	0.67	12.37	0.74	0.27	19.66
Gazner	3.04	0.7	0.96	2.21	0.56	12.87	0.69	0.25	18.53
Neqaqa	4.17	0.9	1.32	3.12	0.68	10.5	0.64	0.22	17.29
Sebera	2.84	0.74	1.2	2.12	0.62	13.25	0.6	0.31	16.92
Musula	2.83	0.74	1.01	2.37	0.5	13.12	0.66	0.26	16.6
Fenqo	3.14	0.68	0.98	2.41	0.5	12.62	0.72	0.24	16.55
Keteniya	3.38	0.83	1.01	2.56	0.61	13.12	0.77	0.26	15.94
Tessa	3.23	0.7	1.07	3.06	0.52	14.62	0.66	0.21	15.42

PH=Plant Height, PSH=Pseudo stem Height, PSC=Pseudo stem Circumference, LL=Leaf length, LW=Leaf Width, LN=Leaf Number, CORTON = corm Yield per Hectare per Year, COMCI= Corm circumference, COMLEN= corm length, CORTON = corm Yield Per Hectare Per Year.

Table 4. Over all preference ranking of high yielder cultivars.

Cultivar	Scores				
	Color	Texture	Test	Over all acceptance	Pair-wise rank
Bose	3	3	2	3	2
Chohot	5	5	5	5	3
Keteniya	2	2	2	2	1
Ashakit	2*	2	2	2	1

*Note: 1=Excellent, 2=Very good, 3=good, 4=not bad, 5=bad

conservation, plant breeding and efficient utilization of plant genetic resources (Bekele, 1996).

Highly significant difference between the (cultivars) of enset under study may be due to differences in their genetic background and diverse nature of origin. The highly significant differences between locations indicated an existence of variation in the prevailing environment during the growth and developmental stages of the experiments. The highly significant genotype x environment (G x E) interaction may be either a crossover G x E interaction or a non-cross over nature.

The G x E interaction of genotypes in this study was of crossover nature. In crossover, significant change in ranks occurs from one environment to another (Matus et al., 1997). Genotypes (cultivars) differ significantly in their mean yield performance. Tabogie (1997), Tsegaye (2002) and Yemataw et al. (2014) reported a wide phenotypic variation among enset cultivars across a broad set of agro-ecological zones in southern Ethiopia.

Cultivar *Chohot*, *Ashakit* *Bose* and *Gazner* had superior corm yields. For selection, good performance is not sufficient; the cultivar must also have desirable sensory and utilization characteristics. Cultivars *Ashakit* and *katania*, which had the second and the ninth corm yield, were moderately liked by taste panelists. This implies that

taste attributes may be as important as agronomic traits when farmers are making decision on which cultivars to adopt or reject. This is in agreement with Kapinga et al. (2009) who reported that sweet potato varieties adoption highly dependent on farmers' main criteria such as high yield, early maturity, disease and pest tolerance, sweetness, root firmness, low fiber content and extended ground storability. Moreover, Faye (2002) reported similar results on cowpea in Senegal and found that buyers are willing to pay a premium for grain size and white skin color but discount price for other color and number of bruchid holes on the grain.

The wide variation in observed traits may point to opportunities for selecting enset cultivars with desirable characters. The wide range in each of the traits studied offers broad opportunities for selecting parents of interest in breeding programs to develop varieties suitable for different agro-ecologies of the country. Similar results were obtained by Yemataw et al. (2012), who studied the variability of 240 ensete cultivars for *kocho* yield.

The authors reported a wide variability in *kocho* yield ranging from 1.29 to 25.32 t ha⁻¹ y⁻¹. Nevertheless, there was a close relationship between phenotypic and genotypic coefficients of variation for all traits. Closeness of the two coefficients of variation indicates the

Table 5. Estimates of ranges, means, PCV, GCV, heritability (%) in broad sense (h^2b) and genetic advance as percent of the mean (GAM) for 10 quantitative morphological characters in 35 Enset cultivars.

Character	Mean	Range		GCV	PCV	h^2b	GAM
	\pm SE	Minimum	Maximum				
PH(m)	2.79 \pm 0.07	0.37	5.12	19.51	28.64	77	32.94
PSH(m)	0.63 \pm 0.01	0.07	1.40	21.53	32.84	74	35.64
PSC(m)	0.65 \pm 0.02	0.10	1.81	19.17	29.02	65	27.43
LL (m)	2.06 \pm 0.05	0.36	7.96	20.10	29.00	72	32.1
LW (m)	0.53 \pm 0.01	0.14	1.30	13.76	20.89	75	22.51
LN	12.27 \pm 0.18	3.00	20.00	15.07	20.14	69	21.83
Comci (m)	0.65 \pm 0.01	0.23	1.10	10.21	12.74	19	4.96
ComLe (m)	0.26 \pm 0.005	0.10	0.44	11.51	14.95	39	12.26
ComW (Kg)	5.77 \pm 0.24	0.20	18.5	32.78	35.04	54	39.09
CORTON (tha ⁻¹ yr ⁻¹)	11.91 \pm 0.54	0.43	41.71	26.39	36.17	57	42.39

***, **, *, ns= significant at 0.1, 1, 5%, and non-significant, respectively. SV= source of variation, CV= coefficient of variation, R^2 = Coefficient of determination, PH=plant height, PSH=pseudostem height, PSC=pseudostem circumference, LL=leaf length, LW=leaf width, LN=leaf number, Comci= Corm circumference, Comle= corm length, ComW= corm yield per plant, CORTON= corm yield per hectare per year.

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient for selected traits of enset cultivars for Amicho trial at Areka.

Characters	PH (m)	PSH (m)	PSC (m)	LL (m)	LW (m)	LN	Comci (m)	ComLe (m)	ComW (Kg)	CORTON (tha ⁻¹ yr ⁻¹)
PH (m)	1.0	0.95***	0.81***	0.94***	0.79***	0.33	0.76***	0.33	0.82***	0.69**
PSH (m)	0.92***	1.0	0.79***	0.92***	0.77***	0.38	0.64	0.34	0.76***	0.65
PSC (m)	0.78	0.75	1.0	0.89***	0.62***	0.52**	0.77***	0.28	0.91***	0.89***
LL (m)	0.93***	0.86***	0.79***	1.0	0.75***	0.40	0.81***	0.18	0.87***	0.74**
LW (m)	0.74	0.69**	0.62	0.68**	1.0	0.27	0.85***	0.53	0.63**	0.53
LN	0.40	0.41	0.59**	0.43	0.34	1.0	0.06	0.44	0.69**	0.74***
Comci (m)	0.54	0.52	0.47	0.55**	0.40	0.50	1.0	0.24	0.86***	0.86***
ComLe (m)	0.26	0.26	0.18	0.16 ns	0.22	0.25 ns	0.42	1.0	0.25 ns	0.21 ns
ComW (Kg)	0.68	0.69**	0.76**	0.71**	0.49	0.53	0.72	0.28 ns	1.0	1.00
CORTON (tha ⁻¹ yr ⁻¹)	0.60	0.62**	0.72	0.64	0.41	0.54	0.71**	0.26	0.95***	1.0

***, **, *, ns= significant at 0.1, 1, 5%, and non-significant, respectively. SV= source of variation, CV= coefficient of variation, R^2 = Coefficient of determination, PH=plant height, PSH=pseudostem height, PSC=pseudostem circumference, LL=leaf length, LW=Leaf Width, LN=leaf number, Comci= Corm circumference, Comle= corm length, ComW= corm yield per plant, CORTON= corm yield per hectare per year.

importance of the genotype/genetic makeup in determining the phenotypic traits. In general, enset cultivars used in this study were phenotypically as well as genotypically diverse, which points to the existence of a large diversity in enset for quantitative characters.

The broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and it is used as a predictive role in selection procedures (Allard, 1960). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation. The low broad sense heritability observed for corm length and corm circumference indicates the influence of the environment on these traits. The low heritability recorded for these traits indicates that direct selection for these traits will be ineffective. Since high

heritability does not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties (Ali et al., 2002). High to medium heritability and genetic advance as percent of the mean suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance. High heritability estimates with low genetic advance for those traits indicates non additive type of gene action and that G x E interaction plays a significant role in the expression of the traits.

Correlations between characters are of interest to determine whether selection for one trait will have an effect on another (De Araujo and Columan, 2002). The

association between vegetative traits such as plant height, pseudostem height, pseudostem circumference, leaf length and corm weight has positive correlation (Tabogé et al., 1996). This is in agreement with Yemataw et al. (2012) who reported that *kocho* yield was positively and significantly correlated with plant height, pseudostem circumference, leaf sheath number and leaf sheath weight. Therefore, it is logical to examine the correlation between various yield components and measure the intensity of the association. These relationships may reveal the yield components or agronomic traits that are useful indicators of ensete corm yield.

Conclusion

Cultivars *Chohot*, *Ashakit*, *Bose* and *Gazner* had superior corm yield. For selection, possession of good performance was not good enough; it must also have desirable sensory and utilization characteristics. Cultivars *Ashakit* and *katania*, were moderately liked by taste panelists. Taste attributes may be as important as agronomic traits when farmers are making decision on which cultivars to adopt or reject. The broad sense heritability, genetic advance as percent of the mean and correlation analysis of the study revealed that plant height, pseudostem height, leaf width and corm weight were the most important yield components. Therefore, the results suggest that these four traits are important yield contributing traits and selection based on these traits would be most effective.

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Conflict of interests

The authors declare that they have no competing interest.

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Full Length Research Paper

Stability, agronomic performance and genetic variability of 10 cassava genotypes in Ghana

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Genetic enhancement of cassava aimed at increasing productivity through the provision of broad-based which improved germplasm and is also a major goal for cassava breeders. 10 genotypes (4 landraces and 6 developed lines) were evaluated at Fumesua, Ejura and Pokuase in 2 growing seasons in a randomized complete block design in 3 replicates to determine variability among genotypes for fresh root yield (FRY), root number (RTN), plant stands harvested (PSH), top weight (TW), harvest index (HI) and dry matter content (DMC) and their adaptation to different environments. Genotype main effect was significant ($P < 0.001$) for all the traits, GEI effect was significant ($P < 0.001$) for DMC, ($P < 0.01$) for TW and HI ($P < 0.05$). Environment main effect was significant ($P < 0.001$) for FRY, RTN and TW. The most stable and high yielding genotype for dry matter content was LA07/012. Genotypes AW07/001 and AW07/015 were adjudged as the most productive genotypes in terms of FRY, DMC, HI and stability. The high genotype and low environmental effects, and the relatively low interaction on DMC imply that evaluation and selection can be effectively done in fewer environments to select clones with high performance while FRY requires multiple environments to identify clones with broad and specific adaptation. The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted for 84.1 and 9.2% of GGE sum of squares respectively for dry matter content, explaining a total of 93.3% variation. Fum-2, Eju-2 and Pok-2 were the most discriminating and least representative environments while Fum-1 and Eju-1 environments were the most representative environments.

Key words: Cassava, additive main effects and multiplicative interactions (AMMI), genotype by environment interaction (GGE) biplot, dry matter content.

INTRODUCTION

Cassava is an important crop in Africa where it serves as a famine reserve crop, rural and urban food staple,

industrial raw material and livestock feed (Nweke et al., 2002). About 70 million people derive more than 500 cal/

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day from food based on its roots (Chavez et al., 2005). Breeding efforts are focusing on the improvement on storage root yield potential and storage root quality traits through development of many new cassava genotypes. One major way of realizing this objective is by harnessing valuable genetic resources including landraces that could constitute useful genetic materials for variety development. The maintenance and conservation of local germplasm is therefore, crucial in cassava improvement (Aina et al., 2009). A number of Africa's cassava landraces have been reported to possess useful agronomic and food quality characteristics that could be potentially utilized for further quality and productivity improvement (Raji, 2004). Despite this, the use of African genetic resources for cassava improvement has been very limited compared to breeding initiatives in Latin America and Asia where cassava genetic resources have been highly introgressed into elite gene pools.

Genetic resources have been widely explored globally in the improvement of crops. Landraces of white lupin have been identified as important source of alleles for shortening the vegetative period, reducing plant height, as well as improving yield components (Raza and Msgsrd, 2005). Rubio et al. (2004) observed wide variation among landraces for trait phenology, plant structure, and yield characters, indicating the possibility of improving yield components and increasing yield among locally adapted landraces of lupins. Evidence of drought tolerance has also been identified among landraces of chickpea (Kashiwagi et al., 2005). The findings of Brocke et al. (2003) also confirmed higher variations within landraces populations' of pearl millet than for other populations. Sharma et al. (2000) discovered that traditional landraces of durum wheat were low yielding but generally stable and suggested the need to enhance landraces cultivation with modern varieties to improve competitiveness in yield. Landraces were useful in the incorporation of diseases and pests resistant genes into *Musa* sp. in International Institute of Tropical Agriculture (IITA) (Herzberg et al., 2004). The improved new rice for Africa rice (NERICA) was as a result of crosses between the African landrace *Oryza glaberrima* and the Asian rice *Oryza sativa*, which produced combined positive characters of high grain yield and resistance to pests and diseases (Futakuchi et al., 2003). Selection rapidly advances crop breeding. However, the advancement in crop improvement will depend on the nature and the extent of heritable variations in the populations and the trait of interest (Sapey et al., 2015). Information on genetic variability can be positively explored to enhance genetic gains through the efficient selection of parents for breeding activities. Genetic dissection based on the efficient partitioning of the overall trait variability into its heritable and non-heritable components with the use of suitable genetic parameters such as genotypic coefficient of variation, heritability estimates, genetic advance and phenotypic

variances will be crucial in genetic improvement of productivity traits in cassava. Studies have revealed strong and significant genotype \times environment interaction (G \times E) effect for storage root yield in cassava (Kvitschal et al., 2007). The magnitude and dimension of environmental effect may vary from genotype to genotype, thus, necessitating the need to assess G \times E interaction for genotypes under evaluation for selection (Okoye et al., 2008). In developing superior materials for commercial use, assessment and selection of cultivars with higher yield and stability is very important (Carneiro, 1998). Stable yields play a major role in developing countries, where small-scale farmers, particularly those cultivating in marginal areas, are working towards risk-minimization (Adugna and Labuschagne, 2002).

The objective of this study was to evaluate six cassava genotypes developed from bi-parental crosses involving cassava landraces to explore heterosis for fresh root yield and yield related characters as well as wider adaptation to environments.

MATERIALS AND METHODS

Ten cassava genotypes at advanced yield stage were used for the study (Table 1). The evaluation was conducted in two planting seasons (2012/2013 and 2013/2014) at Fumesua (forest ecozone), Pokuase (coastal savanna) and Ejura (transition ecozone). The soil characteristics for the trial sites were Fumesua (Asuasi series, a ferric Acrisol with sandy loam top soil over sandy clay), Pokuase (Adam series, sandy loam) and Ejura (Amantin series, chronic Lixisol with sandy loam top soil). The genotypes were grown under rain fed conditions in a randomized complete block design with 3 replicates. Neither pesticides nor fertilizers were applied, and planting was done using disease-free stakes planted in four rows per genotype at seven plants per row making a plot size of 28 m². Weeding was done as deemed necessary. Data were collected from the 10 plants in the two middle rows for every genotype. Cassava mosaic disease severity were done at one, three and six months after planting (MAP) using a scoring scale of 1 to 5 (1 = no symptoms; 5 = severe symptoms) (IITA, 1990). At harvest (12 MAP), data were collected on fresh storage root yield, storage root number and top weight. Dry matter content of tuberous roots was determined from a random bulk sample of four plants selected from the inner rows. The roots were peeled and shredded after washing. A sample of 100 g of fresh root was taken in the form of chips and dried at 70°C for 72 h in a forced air oven. The dried samples were then reweighed to obtain the dry weights, and the dry matter content was calculated as the ratio of the dry weight over the fresh weight expressed in percentage. Storage roots were uprooted by carefully removing the top soil, and the roots were then pulled out and counted as number of roots per plot. Harvest index was calculated as the ratio of the fresh storage root weight over total plant weight. The number of plant stands harvested per plot was counted as stands harvested.

Statistical analysis

Data were subjected to combined analysis of variance using GenStat 17.0. The AMMIs statistical model (MATMODEL 2.0 (Gauch, 1993) was used to analyze the yield data to obtain mean estimates. The E and G \times E interaction biplot analysis for windows application 7.9 (Yan, 2012) was used to generate the E and G \times E

Table 1. Description of the planting materials for the study.

Genotype	Status	Source
AW07/015 (Agric × Wenchi alata)	F ₁	CRI
AW07/001 (Agric × Wenchi alata)	F ₁	CRI
DD07/001 (Debor × dabodabo)	F ₁	CRI
DL107/015 (Debor × Lagos)	F ₁	CRI
DL107/009 (Debor × Lagos)	F ₁	CRI
LA07/012 (Lagos × Agric)	F ₁	CRI
Agric	Landrace	farmer
Debor	Landrace	farmer
Lagos	Landrace	farmer
Wenchi Alata	Landrace	farmer

CRI, Crops Research Institute.

Table 2. Mean performance of 10 cassava genotypes across six environments (three locations in two years).

Genotypes	HI	RTN	FRY	STD	TW	DMC
AW07/015	0.52	51.28	26.31	7.50	23.23	30.61
Agric	0.47	51.83	24.56	8.28	28.48	30.34
AW07/001	0.57	49.83	29.27	8.28	21.86	30.99
DD07/001	0.40	33.28	16.42	7.39	22.54	30.54
Debor	0.47	57.39	24.59	9.39	29.19	31.39
DL107/015	0.30	34.83	13.97	6.39	29.41	24.57
DL107/009	0.47	51.28	20.39	6.39	22.16	27.44
LA07/012	0.41	29.72	9.27	5.80	12.51	35.74
Lagos	0.46	49.28	23.35	7.50	26.98	24.88
Wenchi alata	0.39	35.11	17.27	7.39	25.09	26.35
Grand mean	0.45	44.28	20.54	7.43	24.14	29.31
S.e.d	0.07	10.20	5.33	1.20	7.05	1.37
CV%	18.1	28.1	31.80	19.80	35.80	5.7

HI= harvest index, RTN= number of root, FRY= fresh storage root yield, STD= stands harvested and TW= top weight.

interaction biplot used to analyze the multi-environment trial (MET) data. The model used for the E and G × E interaction biplot analysis was the no-scaling and tester-centered model. Traits component and magnitude of variation responsiveness to selection was calculated based on Okwuagwu et al. (2008). Expected genetic advance of the mean for each trait was calculated according to Allard (1960).

RESULTS

Annual rainfall for the environments during the trial period was Fumesua (1605 mm), Pokuase (1250 mm) and Ejura (1350 mm). Mean performance of the 10 cassava genotypes (combined analysis) in three locations and two years are given as shown in Table 2. Fresh root yield (FRY) ranged from 9.27 to 29.27 t/ha with a mean of 20.54 t/ha. Dry matter content (DMC) ranged from 24.99 to 35.74% with a mean of 29.31%. F₁ genotype AW07/001 (29.27 t/ha and 0.57) had both the highest

FRY and harvest index (HI) respectively across location and over years; followed by AA07/015 (26.31 t/ha and 0.52) and LA07/012 (9.27 t/ha) recorded the lowest FRY but DL107/015 (0.30) had the lowest HI. The highest FRY and HI were recorded in Ejura -2012/2013 (34.27 t/ha, 0.51) and the lowest in Pokuase- 2012/2014 (7.43 t/ha, 0.38). AW07/001 and AW07/015 performed better than their parents and also the average of their parents in terms of FRY and HI. LA07/012 (f₁) recorded the highest DMC (32.74 %) with the least recorded by Lagos. There were highly significant positive correlations between HI and FRY, root number (RTN) and FRY, RTN and stands harvested (STD), FRY and STD, FRY and top weight (TW) and RTN and TW and DMC and HI (Table 3). Genotype (G), location (L), year (Y) and environment × year interaction showed high significant mean square (P <0.001) for FRY (Table 4). G × L × Y showed significant differences for the FRY. Genotype, Genotype × Location

Table 3. Phenotypic correlation coefficients for five traits measured on 10 cassava genotypes across six environments.

Trait	HI	RTN	FRY	STD	TW	DMC
HI	-					
RTN	0.21**	-				
FRY	0.53***	0.57***	-			
STD	-0.03 ^{ns}	0.63***	0.30***	-		
TW	-0.24**	0.58***	0.60***	0.35***	-	
DMC	0.25***	0.06 ^{ns}	0.02 ^{ns}	0.12 ^{ns}	-0.17*	-

*** Significant at $P < 0.001$, ** significant at $P < 0.01$, * significant at $P < 0.05$ and ns= non-significant.

Table 4. Combined analyses of 10 cassava genotypes evaluated for two years at three locations in Ghana for root yield, harvest index, stands harvested, top weight, dry matter content and root number.

Source	df	Mean square	% of total ss
Harvest index			
Genotype (G)	9	0.10***	30.24
Location (L)	2	0.02*	1.37
Year (Y)	1	0.55***	18.90
G × L	18	0.01*	7.22
G × Y	9	0.01 ^{ns}	3.78
L × Y	2	0.02*	1.37
G × L × Y	18	0.01**	8.59
Error	118		
Total	179		
Root number			
Genotype (G)	9	1777.7***	22.12
Location (L)	2	2442.3***	6.75
Year (Y)	1	140.4 ^{ns}	0.19
G × L	18	170.2 ^{ns}	4.24
G × Y	9	456.0**	5.67
L × Y	2	10608.6***	29.33
G × L × Y	18	241.2 ^{ns}	6.00
Error	118	156.0	
Total	179		
Stands harvested			
Genotype (G)	9	20.26***	23.13
Location (L)	2	8.22*	2.09
Year (Y)	1	30.99***	3.93
G × L	18	3.27 ^{ns}	7.46
G × Y	9	8.37***	9.56
L × Y	2	49.50***	12.56
G × L × Y	18	4.59**	10.46
Error	117	2.17	
Total	178		
Fresh root yield			
Genotype (G)	9	696.01***	23.66
Location (L)	2	1950.63***	14.73
Year (Y)	1	3508.60***	13.25

Table 4. Contd.

G × L	18	63.23 ^{ns}	4.30
G × Y	9	88.68*	3.01
L × Y	2	1966.87***	14.86
G × L × Y	18	103.44**	7.03
Error	118	42.68	
Total	179		
Top weight			
Genotype (G)	9	457.81***	13.98
Location (L)	2	2192.89***	14.89
Year (Y)	1	12.67 ^{ns}	0.04
G × L	18	176.73**	10.80
G × Y	9	56.38 ^{ns}	1.72
L × Y	2	3561.23***	24.17
G × L × Y	18	71.72 ^{ns}	4.38
Error	117	74.63	
Total	178		
Dry matter content			
Genotype	9	215.02***	72.01
Location	2	4.24 ^{ns}	0.31
Year	1	6.88 ^{ns}	0.26
G × L	18	7.87***	5.27
G × Y	9	22.46***	7.52
L × Y	2	7.63 ^{ns}	0.57
G × L × Y	18	1.87 ^{ns}	1.25
Error	118	2.81	12.36
Total	179		

*** significant at $P < 0.001$, ** significant at $P < 0.01$, * significant at $P < 0.05$ and ns= non-significant.

and Genotype × Year interactions showed highly significant differences for DMC. Interaction between genotype and environment was significant for harvest index but not for FRY.

The relative magnitude of the main effects and their interactions measured as a proportion of the total sum of squares showed that, G had more impact on DMC, HI, STD and FRY than other sources of variations. E × Y interaction had more impact on RTN and TW. The results show that, there were variable responses to the impact of environment on the five traits of the cassava genotypes studied. The environment was pronounced on all the traits but the magnitude was higher for FRY and TW compared to the other four traits. Partitioning of the sources of variation showed that G × L was the main contributor of Genotype × environment interaction (GEI) for harvest index indicating that the location contributed more to fluctuations in performance than years but not for DMC (Table 4).

The magnitude of phenotypic coefficient of variation

(PCV) was higher than their corresponding genotypic coefficient of variation (GCV) among all the traits studied (Table 5) but the differences were narrow for DMC, HI and FRY.

AMMI analysis

The analysis of variance of the AMMI for HI and DMC shows that the effects of G and E were significant ($P < 0.001$) and GEI was also significant but at $P < 0.01$ for HI. Genotype main effect and the interaction between Genotype and Environment were highly significant for DMC but the environment main effect was not. G accounted for 30.24 and 72.0% of total sum of squares for HI and DMC respectively, 21.65 and 1.1% were attributable to E effects for HI and DMC respectively, and GEI accounted for 19.59 and 12.6% as shown in Table 6. Two interaction principal component analysis axis (IPCA) were necessary to explain the interaction (GEI) but only

Table 5. Coefficients of variation, heritability and genetic advance for the traits.

Traits	Mean	GCV	PCV	h ² b	GAs
HI	0.45	17.56	18.00	93.94	34.83
RTN	44.38	25.51	27.53	85.68	48.60
FRY	20.54	32.96	33.93	94.44	66.02
STD	7.43	17.36	19.38	80.58	32.17
TW	24.14	19.76	23.32	71.70	34.45
DMC	29.31	12.25	12.96	89.00	23.78

GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation GAs=genetic advance as percentage of the mean, h²b=heritability in the broad sense, HI= Harvest index, RTN= number of root, FRY= Fresh storage root yield, STD= stands harvested, TW= Top weight and DMC= Dry matter content.

Table 6. Analysis of variance (AMMI) for harvest index and dry matter content of 10 cassava genotypes planted at three locations in Ghana for two years.

Source	df	Sum of square	Mean square	% of total ss
HI				
Total	179	2.91	0.02	
Trt	59	2.08	0.04***	71.48
Genotype	9	0.88	0.10***	30.24
Environments	5	0.63	0.13***	21.65
Block	12	0.11	0.01 ^{ns}	3.78
Interaction	45	0.57	0.01**	19.59
IPCA 1	13	0.30	0.02***	
IPCA 2	11	0.15	0.01*	
Residual	21	0.13	0.01 ^{ns}	
Error	108	0.72	0.01	
DMC				
Total	179	2683.3	15.01	
Trt	59	2343.2	39.71***	87.2
Genotype	9	1935.2	215.02***	72
Environments	5	30.5	6.11 ^{ns}	1.1
Block	12	55.9	4.65 ^{ns}	2.1
Interaction	45	337.4	8.39***	12.6
IPCA1	13	209.8	16.14***	
IPCA2	11	100.5	9.14***	
Residual	21	67.1	3.20 ^{ns}	
Error	108	288.2		

the first PCA was extremely important in explaining the interactions for HI. IPCA 1 explained 52.63% of variation in the interaction with 28.89% interaction degrees of freedom (df). The first two IPCA axes jointly accounted for 78.95% of the GEI sum of squares, leaving 21.05% of the variation in the interaction (within 46.67% of the interaction df) in the residual. The residual accounted for only 4.47% of the total sum of squares. For dry matter content, two interaction principal component analysis axis (IPCA) were necessary to explain the interaction (GEI) and both were extremely important in explaining the interactions. IPCA 1 explained 62.2% of variation in the

interaction with 28.89% interaction degrees of freedom (df). The first two IPCA axes jointly accounted for 92% of the GEI sum of squares. The residual accounted for only 2.5 % of the total sum of squares.

AMMI biplot analysis for DMC

The AMMI biplot analysis (Figure 1) for dry matter content shows the main effects in the x- axis and IPCA 1 in the y- axis. The total treatment sum of squares accounted for 83.51%, leaving 16.49% in the residual

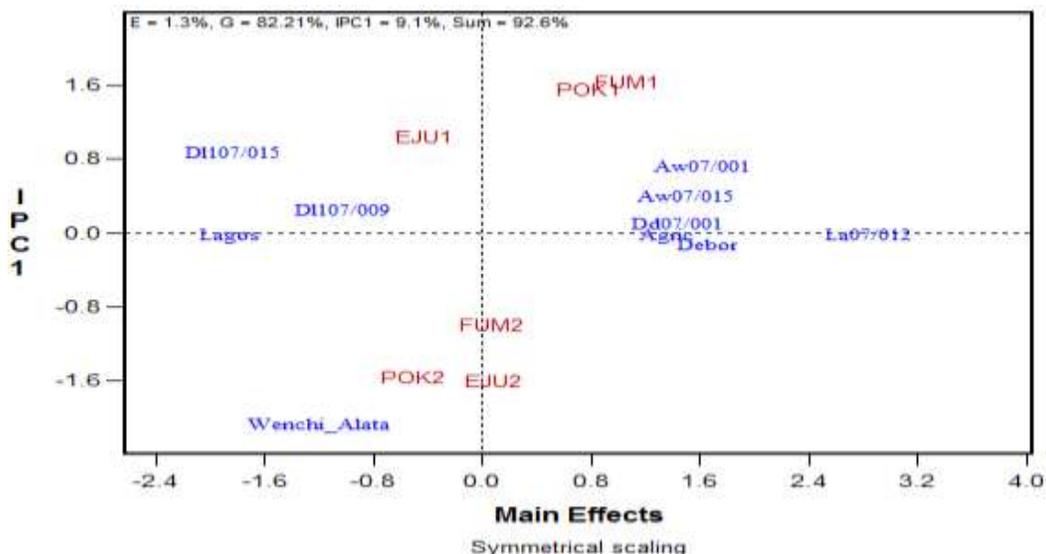


Figure 1. AMMI biplot for dry matter content of 10 cassava genotypes in 6 environments (Eju= Ejura, Fum= Fumesua and Pok= Pokuase) for two years.

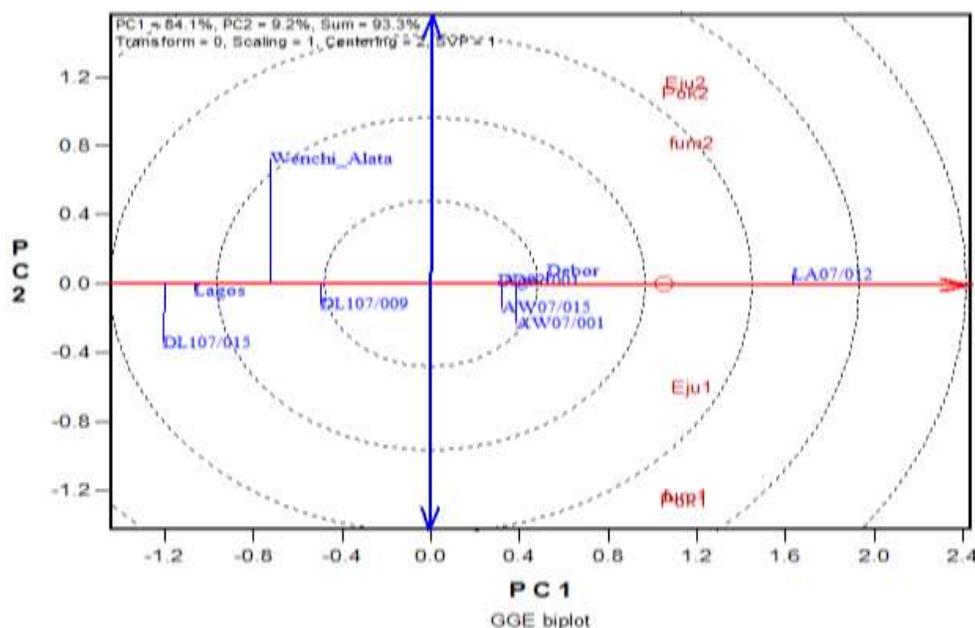


Figure 2. GGE biplot showing mean performance and stability of different cassava genotypes.

and revealed differential response of genotypes to the tested environments. Genotype LA07/012 was the least interactive with the environment (low IPCA 1 score) but had the highest dry matter content. Genotypes Lagos, Agric, LA07/012, DD07/001 and Debor were considered as stable genotypes being closer to the zero line from the Y-axis. DL107/015 had the highest positive interaction score (1.05) while Wenchi Alata (-2.51) had the highest negative score.

GGE biplot analysis

GGE biplot for average DMC and stability of genotypes

In Figure 2, the mean dry matter and stability performance of the cassava genotypes were shown. The genotypes were ranked along the average environment co-ordinate (AEC) x-axis with an arrow indicating the

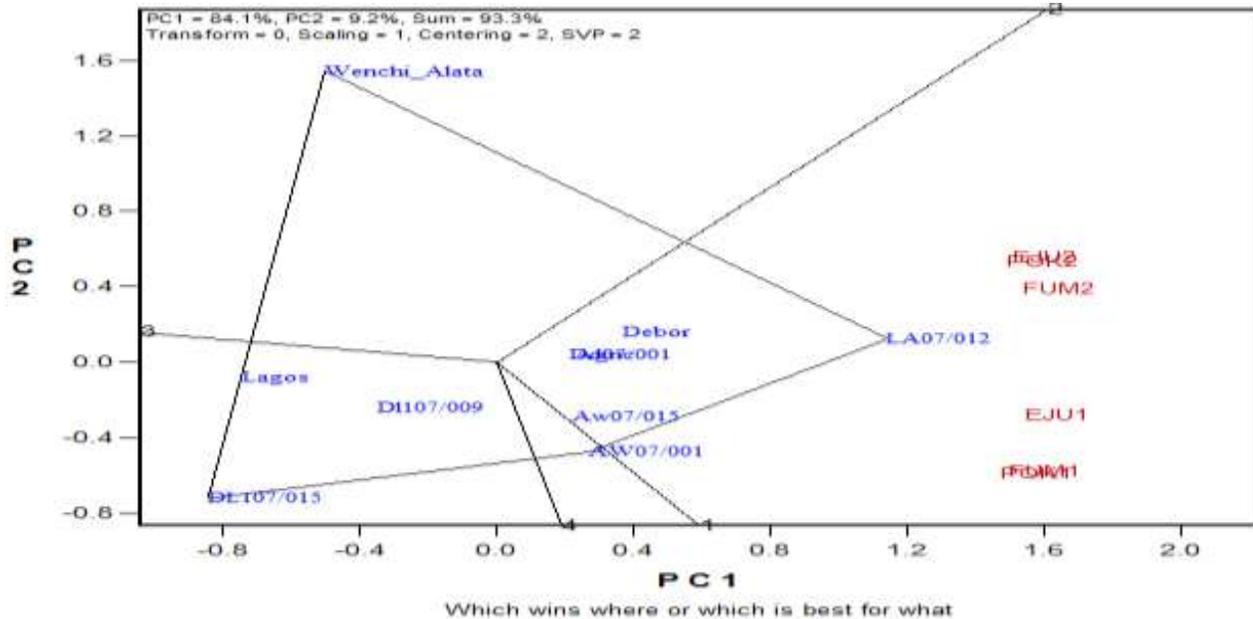


Figure 3. GGE biplot for best cultivars in different environments.

highest dry matter content. Thus, genotype LA07/012 which was closer to the AEC x-axis had the highest mean value while genotypes DL107/015 and Lagos had the lowest values because they were further away from the AEC x-axis. Wenchi Alata with the longest projection from the AEC x-axis was adjudged as an highly unstable genotype and also with DMC lower than the mean while genotypes DD07/001 and LA07/012 with small projection from the AEC x-axis were selected as being the most stable. AW07/001 (most productive genotype) recorded the highest fresh root yield (Table 2), quite stable and DMC higher than the mean. Although, LA07/012 recorded the highest DMC, the fresh root yield was the lowest as compare to the other genotypes.

The best performing genotype in each environment and mega- environments with GGE biplot for DMC

The GGE biplot (Figure 3) showed the genotypes that had the best performance in each environment. The model used to generate the biplot explained 84.1% in IPCA 1 and 9.2% in IPCA 2, both reflecting 93.3% of the DMC variation due to GGE. A convex -hull drawn on the genotypes from the origin of the biplot gave four sections with LA07/012, Wenchi Alata, DL107/015 and AW07/001 as the vertex genotypes. All the environments fell into the sector where LA07/012 was the vertex genotype. It suggests that the genotype is best in all the environments. The biplot grouped all the environments together, which is an indication of no existence of mega-environments.

GGE biplot for representativeness and discriminating ability of environments for DMC

In this study, the GGE biplot explained 93.3% of the G plus GE data (Figure 4) suggesting that the angles between the vectors of the environments might be good indicators of correlation amongst the environments.

DISCUSSION

Correlation analysis is an important tool for estimating the value and association of various characters in a crop (Edmeades et al., 1997). Correlation among traits plays a vital role in improving selection efficiency in plant breeding programs. In selection programs, yield and some yield components (Root number, number of stands harvested, top weight, dry matter content and harvest index) are some of the most economic traits usually targeted by plant breeders. The corroborative reports of significant positive correlation between fresh root yield and other yield components suggests that, any one of the traits could be used to select indirectly for fresh root yield. The relationship we observed between FRY and RTN in this study was as similarly reported by Peprah et al. (2013a), when studying genetic variability of three cassava traits in Ghana. This is in agreement with earlier findings by Parkes (2011) which efficiently selected root number indirectly for fresh root yield. The positive correlation could be explained by the fact that RTN normally has impact on the FRY. There was also significant negative correlation between HI and TW

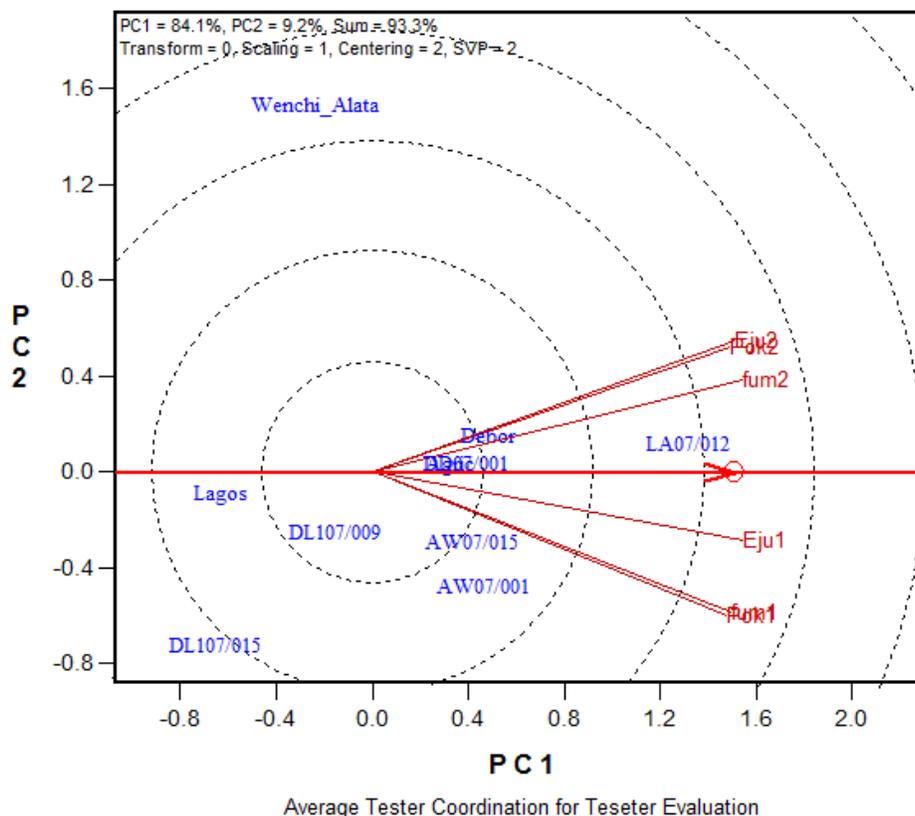


Figure 4. GGEbiplot for representativeness and discriminating ability of environments as average tester coordination for tester evaluation.

and it suggests that, selection of one trait may compromise the other trait.

The highly significant interaction between genotype and environment ($G \times E$) for DMC indicates that there is the need for multi locational testing to identify good performance for specific locations (Akinwale et al. 2011). As observed in the analysis, the non-significant GL interaction for FRY suggests that the genotypes might have similar responses across the locations in which they were evaluated and that all the genotypes can reliably be assessed under anyone of the locations used for this study in future or advance evaluation trials (Yan and Tinker, 2006). In other words, it might not be important to assess these genotypes simultaneously in the various locations used for the study in subsequent evaluations, thereby offering an opportunity to manage the limited resources available for the testing program (Tonk et al., 2011).

The high G and low E effects, and relatively low GEI for DMC, HI and FRY may necessitate evaluation over fewer environments to distinguish genotypes with high and stable performance. Peprah et al. (2013 b) also reported higher G and low E effects on DMC and FRY when working on cassava genotypes developed from landraces. This might be due to the same genotypes

(landrace) that were used to generate the hybrids in both studies and also the same locations used for the evaluation. This also suggest that improving landraces for important traits like fresh root yield and dry matter content in cassava is feasible because of the higher genotypic impact. The high significance of year effects on HI and FRY suggests the need to evaluate for more than one year for reliable inferences to be made on performance of the genotypes. The narrow differences for the three traits suggest limited environmental variation in the expression of these traits. This finding is in agreement with earlier reports by Aina (2007) and Akinwale et al. (2010). Broad sense heritability and genetic advance as percent of the mean for all the traits were high. It was suggested by Pradeepkumar et al. (2001) that, high heritability in broad sense does not always lead to better response to selection because it consists of non-additive genetic variance, therefore, genetic advance as a percentage of the mean is more of a useful response to selection combined with high heritability estimates. Selection of all the traits could be possible due to high broad sense heritability (Bhateria et al., 2006) and high genetic advance as a percentage of the mean. This may suggest that trait with significant positive correlation, high heritability estimates and

genetic advance like HI and FRY and DMC and RTN can be simultaneously improved. The large sum of squares for genotypic effects suggested that the genotypes were diverse with differences among the genotypic means for the two traits. This might be due to the diverse nature of the parental lines and probably due to where they were selected for the crosses. The highly significant ($P < 0.01$) GEI for HI and DMC suggest different performance of genotypes across environments. However, the impact of GEI was smaller than that of genotypic effects, indicating the presence of moderate variation among the genotypes over environments.

The residual mean squares for HI were not significant and even that for the IPCA 1 was twice the residual. This suggests that there were differences in performance among the 10 cassava genotypes across the six environments (3 locations and 2 years) due to the presence of high significant GEI effects (Agyeman et al., 2015). The residual mean squares were not significant and even that for the IPCA 1 was more than twice the residual. This result revealed that there was a differential performance in dry matter content among cassava genotypes across testing environments which was due to the presence of GEI. This is in conformity with the findings of Akinwale et al. (2011). This suggests that, there were differences in performance among the 10 cassava genotypes across the six environments (3 locations and 2 years) due to the presence of high significant GEI effects. The cosine of angles between vectors of all the environments were less than 90. This suggested that, there were no negative correlations among the test environments (Akinwale et al. 2011). The length of the environmental vectors (the lines that connect the test environments to the biplot origin) approximate the standard deviation within the respective environments, which is a measure of the discriminating ability of the environments (Yan, 2005). Fum-2, Eju-2 and Pok-2 environments with the longest projections from the biplot were found more discriminating of the genotypes and the least representative environments. Fum-1 and Eju-1 were found to be more representative of other test environments due to their smaller angles with the AEAs. Eju-1 was averagely discriminating and most representative environment therefore can be used for genotypes with wide adaptation. The non-representative environments such as Fum-2, Eju-2 and Pok-2 are useful for selecting specifically adapted genotypes. Dry matter content is an important cassava trait in Ghana. Processors and consumers placed more importance on the trait because of the way it's consumed, although, cassava is now becoming an industrial crop.

Conclusion

The study revealed that genotype AW07/001 (progeny) outperformed the parents (Checks) indicating that it has

the potential to increase cassava productivity in Ghana and also might be easily adopted by farmers because it is a progeny from farmers cultivars. The study also revealed some positive correlations between some important agronomic traits (FRY and RTN, RTN and TW, HI and FRY, FRY and STD, DMC and HI) of cassava which can aid indirection in the selection for cassava breeding. The biplots displayed pattern of variability of the genotypes, the locations, and their interactions. Interrelationships among agronomic characteristics allowed identification of optimal genotypes for the three locations. AW07/001 and AW07/015 were the best genotypes based on mean performance (FRY, DMC and HI) and stability. Eju-2, Fum-2 and Pok-2 were the most discriminating and least representative environments while Fum-1 and Eju-1 environments were the most representative environments.

Conflict of Interests

The authors have not declared any conflict of interests.

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Full Length Research Paper

Heritability analysis to screen elite sugarcane (*Saccharum* spp.) soma clones under field condition

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Three elite sugarcane varieties were used in this experiment to check the heritability parameters which consist of range, environmental variance, genetic variance, genetic advance and broad sense heritability. Four hundred and five soma clones were observed for phenotypic characters including number of tillers (plant⁻¹), cane height (cm), number of internode (plant⁻¹) and width of internode (cm). Variability range for different characters include number of tillers (plant⁻¹), cane height (cm), number of internode (plant⁻¹) and width of internode (cm) and were also assessed for three auxins. Highest heritability and remarkable genetic advance were recorded for the height of the cane and number of internode (plant⁻¹) was found when 2, 4-D was applied in Murashige and Skoog (MS) media, which directly affected the yield of sugarcane. High heritability and good genetic advance were observed for number of tillers (plant⁻¹) and width of internode (cm) when NAA was applied in the media. In addition to this, increasing concentration of hormones had positive effect on the heritability and genetic advance for phenotypic traits of the sugarcane soma clones. Similarly, it was observed that environmental and genetic variances have optimum effect on the heritability of the sugarcane. Application of 2, 4- D and picloram were recorded as efficient in transference of high heritability and genetic advance to them. On the basis of higher heritability selection made to develop hybrid in sugarcane, higher genetic advancement helped to develop synthetic varieties in sugarcane.

Key words: Heritability, genetic advance, sugarcane (*Saccharum* spp.), auxins, phenotypic character.

INTRODUCTION

Sugarcane (*Saccharum* spp.) hybrids is an important cash crop which belongs to the Poaceae family (Sharma, 2005; Cha-um et al., 2006). Knowledge of the heritability of any phenotypic traits will be very helpful in breeding programs worldwide. So, genetic variability and heritability

are useful parameters that can help breeding during different stages of crop improvement (Ali et al., 2014ab). Genotype affected by environment was reported by many researchers (Kimbeng et al., 2002). Environment has significant relation towards genotypes that influence yield

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of sugarcane (Parfitt, 2000; Kimbeng et al., 2002; Janghir et al., 2013; Glaz and Kang, 2008; Qamar et al., 2015). The relationship between the characters is difficult to understand mostly when low heritability occurs (Bakhsh et al., 2006; Silva et al., 2007). Selection of the characters was directly made by understanding the nature of one trait affected by the other (Ali et al., 2013, 2014ab; Butt et al., 2015; Jackson, 1994; Tyagi and Khan, 2010). Phenotypic character has association with the yield components (Jamoza et al., 2013) like number of stalk (plant^{-1}), width of cane (cm), and height of cane (cm) which are helpful for the variety development (Tyagi and Khan, 2010). The function of heritability in genetics was considered to evaluate quantitative traits and qualitative traits which are valuable for economic and used for the breeding programs. Heritability estimation (Hanson et al., 1956) together with genetic advance are most important for selection of yield, and its contributing characters are useful for future selection of superior clones in sugarcane industry (Ahmed et al., 2012).

The improvement of characters will depend mostly on the extents of genetic variability in the base population and heritability. Therefore, the present study is helpful for the assessment of heritability parameters of phenotypic characters like number of tillers (plant^{-1}), number of internodes (plant^{-1}), height of cane (cm) and width of internode (cm). There are many traits which are important for the heritability enhancement, but few are optimized under field condition including those traits that are vital for the selection of character which can be utilized for further improvement of the yield of sugarcane.

MATERIALS AND METHODS

Established plants were transferred to the field from pots for further heritability analysis. Data was recorded for four hundred and five replicates (405) of sugarcane.

Assessments of phenotypic traits

Only 135 stable soma clones were finally evaluated for four phenotypic characters related to yield.

Number of tillers (plant^{-1})

Three randomly selected canes were recorded for the number of tillers from each treatment. Thereafter, their average was noted.

Height of cane (cm)

The height of each selected plant was calculated in centimeters from the surface of soil to the tip of the leaf.

Width of internode (cm)

The stem girth of each plant was recorded in centimeters by vernier

caliper, from bottom, mid and top portion and average of the three data was used for data analysis.

Number of internodes (plant^{-1})

Three randomly selected canes from each treatment were counted for number of internode. Thereafter, their average was noted.

Heritability analysis

Data was statistically analyzed by using Steel et al. (1997) analysis of variance technique. Phenotypic traits were further subjected to heritability analysis. Genetic parameters viz., heritability percentage in broad sense (h^2 b.s), environmental variance (V_e), genetic variance (V_g) and genetic advance (G.A) were calculated as suggested by Falconer and Mackay (1996):

1. Mean $\bar{x} = \frac{\sum xi}{n}$
2. Variance $S^2 = \frac{s.s}{n-1}$
3. Standard Deviation (SD) = $\sqrt{s^2}$
4. Coefficient of variability (CV) = $\frac{S.D}{Mean} \times 100$
5. Genetic variance (V_g) = $VC_3 - V_e$
6. Environmental variance (V_e) = $(VP_1 + VP_2)/2$
7. Heritability percentage in broad sense (h^2 b.s %) = $V_g / VC_3 \times 100$
8. Genetic advance (G A) = $K \times (H) \times SD$.

Where, V = variance C_3 third sub culture generation, and p = parent.

S.D = Phenotypic standard deviation

K = Constant (2.06) for selection difference at 5% Selection intensity

V_e = Environmental variance

V_g = Genetic variance

H = Heritability coefficient

VP_1 = Variance of parent one

VP_2 = Variance of parent two

VC_3 = Variance of C_3 soma clones

$h^2\%$ (b.s) = Heritability percentage in broad sense

(GA) = $K \times (H) \times SD$

N = number of replication

RESULTS

Heritability analysis in soma clones of NIA-2012

The results of parents and soma clones for heritability are presented in Tables 1, 2 and 3. Overall variations were observed among soma clones and their parents as a response of different auxins applied. Differential heritability and genetic advance was observed in tested parents and their soma clones. Number of tillers ranged from 1 to 8.5 and height of cane from 110.19 to 126.19. While number of internode ranged from 10 to 24 and width of internode ranged from 1.11 to 1.94 in 2,4-D. High heritability for height of cane (77%) with remarkable genetic advance (8.6) was observed in NIA-2012 while

Table 1. Heritability analysis of sugarcane parental genotype (NIA2012) and their soma clones affected by different concentrations of 2, 4- D.

Character	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h^2_{bs} (%)
No. of tillers	1-85	2.24	1.86	1.439	45
Height of cane	110.19-126.19	6.7335	22.681	8.602	77
No. of internode	10-24	8.41	5.59	3.076	39
Width of internode	1.11-1.94	0.0451	0.0592	0.37	56

Table 2. Heritability analysis of sugarcane parental genotype (NIA2012) and their soma clones affected by different concentrations of Picloram.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h^2_{bs} (%)
No. of tillers	1-7	1.5995	1.0405	1.319	39
Height of cane	110.11-125.12	7.569	15.259	6.563	66
No. of internode	10-19	5.5985	4.752	3.04	45
Width of internode	1.08-1.72	0.0426	0.0471	0.324	52

Table 3. Heritability analysis of sugarcane parental genotype (NIA2012) and their soma clones affected by different concentrations of NAA.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h^2_{bs} (%)
No. of tillers	1-6	1.0085	0.251	0.518	19
Height of cane	109.12-119.15	6.246	3.682	2.401	37
No. of internode	7-17	2.048	1.876	1.95	47
Width of internode	1.11-1.65	0.0118	0.0135	0.174	53

moderate heritability (56%) with less genetic advance (0.37) was recorded for width of internode. Whereas, low heritability was found for number of tillers and number of internodes exhibited with poor genetic advance, while as number of tillers ranged from 1 to 7, height of cane ranged from 110.11 to 125.12, whereas number of internode ranged from 10 to 19 and width of internode ranged from 1.08 to 1.72 in picloram. Moderate heritability for height of cane (66%) with good genetic advance (6.5) was observed in NIA-2012, while low heritability (39%) with less genetic advance for number of internode (plant^{-1}) (45%), and width of internode (cm) (52) was recorded in picloram. As number of tillers (plant^{-1}) ranged from 1 to 6, height of cane (cm) ranged from 109.12 to 119.15. Whereas, number of internode (plant^{-1}) ranged from 7 to 17 and width of internode (cm) ranged from 1.11 to 1.65 in NAA. Low heritability for number of tillers (plant^{-1}) (19%), height of cane (37%), number of internode (47%) and width of internode (cm) (53%) was recorded in NIA-2012. In case of NIA-2012 2, 4-D was the best hormone among tested auxins as it resulted in

high genetic variations for height of cane (cm), number of internode (plant^{-1}), moderate for width of internode (cm) and poor for number of tillers (plant^{-1}) followed by picloram that induced moderate genetic variations for height of cane and width of internode.

Heritability analysis in soma clones of NIA-105

The data of parents and soma clones for heritability are depicted in Tables 4, 5, 6 and 7 number of tillers (plant^{-1}) ranged from 1 to 9 and height of cane (cm) from 111.19 to 126.14. While number of internode (plant^{-1}) ranged from 10 to 28 and width of internode (cm) ranged from 1.13 to 2.34 in 2, 4-D. High heritability for number of internode (plant^{-1}) (83%) with considerable genetic advance (4.95) was observed in NIA-105 while moderate heritability (58%) with less genetic advance (0.33) was recorded for width of internode whereas, low heritability for number of tillers (plant^{-1}) and height of cane were revealed with reduced genetic advance. While as number

Table 4. Heritability analysis of sugarcane parental genotype (NIA-105) and their soma clones affected by different concentrations of 2, 4- D.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h ² bs (%)
No. of tillers	1-9	2.847	0.0885	0.1062	3
Height of cane	111.1 4-126.14	14.3	4.404	2.091	23
No. of internode	10-28	9.204	15.395	4.95	83.4
Width of internode	1.13 -2.34	0.0335	0.0465	0.335	58

Table 5. Heritability analysis of sugarcane parental genotype (NIA-105) and their soma clones affected by different concentrations of Picloram.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h ² bs (%)
No. of tillers	2-8	1.101	0.993	1.413	47
Height of cane	18.12-126.16	5.427	5.822	2.367	51
No. of internode	10-26	2.177	7.420	4.94	77
Width of internode	1.11-2.24	0.0206	0.0218	0.218	51

Table 6. Heritability analysis of sugarcane parental genotype and their (NIA-105) soma clones affected by different concentration NAA.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h ² bs (%)
No. of tillers	1-9	1.885	1.782	1.91	48
Height of cane	108.24-127.18	13.417	8.023	3.569	37
No. of internode	10-28	17.785	14.032	4.056	61
Width of internode	1.18-2.34	0.0318	0.065	0.433	67

Table 7. Heritability analysis of sugarcane parental genotype (Gulabi-95) and their soma clones affected by different concentrations of 2,4-D.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h ² bs (%)
No. of tillers	2-9	2.154	0.664	1.0671	30
Height of cane	111.23 -127.87	18.7	5.98	2.479	24
No. of internode	12-28	11.35	9.05	4.093	44
Width of internode	1.13-2.54	0.0460	0.046	0.0309	50

of tillers ranged from 1 to 9, height of cane ranged from 108.24 to 127.18. Whereas number of internode (plant⁻¹) ranged from 10 to 28 and width of internode ranged from 1.18 to 2.34 in picloram. Moderate heritability for number of internode (61%) with remarkable genetic advance (4.05) was found in NIA-105. Moderate heritability for width of internode (67%) with low genetic advance (0.433) was observed in picloram. Low heritability for number of tillers (plant⁻¹) (48%) and height of cane (37%)

was recorded in NIA-105. While as number of tillers (plant⁻¹) ranged from 2 to 8, height of cane ranged from 109.12 to 126.16. Whereas, number of internode (plant⁻¹) ranged from 10 to 26 and width of internode (cm) ranged from 1.11 to 2.24 in NAA while high heritability for number of internode (plant⁻¹) (77%) with good genetic advance was recorded in NIA-105. Low heritability for number of tillers (plant⁻¹), height of cane and width of internode was obtained in NAA. In case of NIA-105 2, 4-D

Table 8. Heritability analysis of sugarcane parental genotype (Gulabi-95) and their somaclones affected by different concentrations of Picloram.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h ² bs (%)
No. of tillers	1-9	1.885	1.782	1.91	48
Height of cane	108.24-127.18	13.417	8.023	3.569	37
No. of internode	10-28	17.785	14.032	4.056	61
Width of internode	1.18-2.34	0.0318	0.065	0.433	67

Table 9. Heritability analysis of sugarcane parental genotype (Gulabi-95) and their soma clones affected by different concentrations of NAA.

Characters	Range	Environmental variance	Genotypic variance	Genetic advance	Heritability h ² bs (%)
No. of tillers	2-8	1.101	0.993	1.413	47
Height of cane	18.12-126.16	5.427	5.822	2.367	51
No. of internode	10-26	2.177	7.420	4.94	77
Width of internode	1.11-2.24	0.0206	0.0218	0.218	51

was the best hormone among tested auxins as it results in high genetic variations for number of internode (plant⁻¹), moderate for width of internode and poor for number of tillers (plant⁻¹) followed by picloram that induced moderate genetic variations for height of cane and width of internode.

Heritability analysis in soma clones of Gulabi-95

The results of parents and soma clones for heritability are compiled in Tables 7, 8 and 9. Overall variations were observed among soma clones and their parents as a response of varying auxins applied. Number of tillers (plant⁻¹) ranged from 2 to 9, height of cane from 111.23 to 127.87. While number of internode (plant⁻¹) ranged from 12 to 28 and width of internode ranged from 1.13 to 2.54 in 2,4-D. Whereas, low heritability for number of tillers (plant⁻¹) (30%), height of cane (24%) and width of internode (50%) with less genetic advance was found in Gulabi-95. Low heritability for number of internode (plant⁻¹) (44) with remarkable genetic advance (4.09) was recorded in 2, 4-D. While as number of tillers (plant⁻¹) ranged 1 to 9, height of cane (cm) from 108.24 to 127.18. Whereas number of internode ranged from 10 to 28 and width of internode ranged from 1.18 to 2.34 in picloram. Moderate heritability for number of internode (plant⁻¹) (61%) with good genetic advance (4.05) was found in Gulabi-95. Moderate heritability for width of internode (67%) with low genetic advance (0.433) was recorded in Gulabi-95. Whereas low heritability for number of tillers (plant⁻¹) (48%), height of cane (cm) (37%) and with less genetic advance was obtained in Gulabi-95. Number of

tillers (plant⁻¹) ranged from 2 to 8, height of cane from 118.12 to 127.16. While number of internode (plant⁻¹) ranged from 10 to 26 and width of internode ranged from 1.11 to 2.24 in NAA. High heritability for number of internode (plant⁻¹) (77%) with good genetic advance (4.94) was found in Gulabi-95. Whereas low heritability for number of tillers (plant⁻¹) (47%), height of cane (51%) and width of internode (51) with less genetic advance was obtained in Gulabi-95 when NAA was applied. For Gulabi-95 x somaclones 2,4-D do not stimulate genetic variation rather Picloram and NAA generated moderate genetic variations for number and width (plant⁻¹) of internode and number of tillers (plant⁻¹) while low variations for height of cane.

DISCUSSION

Heritability exploration in NIA-2012

High heritability coupled with good genetic advance and high environmental variance in NIA- 2012 x soma clones for height is also reported earlier in some other varieties of sugarcane all around the world (Zhou et al., 2005, 2011). The results indicate existence of considerable genetic variations induced through callus culture. Moderate heritability with poor genetic advance for number of tillers (plant⁻¹) and number of internode (plant⁻¹) was consistent with the findings of Khan et al. (2009) and Raza et al. (2014). High heritability with low genetic advance and environmental effects found for thickness of cane is supported by Hoy et al. (2003) who observed smaller cane diameter in the plants regenerated from callus

culture. Generally width of internode (cm) is negatively correlated with yield of sucrose (Pandey, 1989; Butterfield and Nuss, 2002) therefore low genetic advance for this character is in favor of the present genetic improvement strategy. It can be inferred from over all heritability analysis that 2, 4-D and picloram are effective among tested auxins towards soma clonal variation as compared to NAA.

Heritability exploration in NIA-105

Good genetic advance and high heritability coupled with and low environmental variance for number of internode (plant^{-1}) is supported by the work of Bull (2000) and who also elaborated environmental effect on number of internode (plant^{-1}) directly correlated to the yield of sugarcane. It is obvious from results that this character is largely influenced by growth hormones not by environmental effects so selection for improvement of that characters must be useful. High heritability with low genetic advance was recorded for width of internode (cm) indicating non-additive effect of gene. Similar results of higher number of internodes, greater length of internodes contributing height of cane and smaller width of cane (cm) was also reported by Sood et al. (2006). Low heritability with less genetic advance and environmental variance for number of tillers is also reported by many workers dealing with same type of auxins (Sani and Mustapha, 2010; Ahmed et al., 2012; Riaz et al., 2016). It can be inferred from overall heritability analysis of NIA-105 x soma clones that more genetic changes were induced by 2,4-D followed by NAA, than Picloram.

Heritability exploration in Gulabi-95

It is evident from the result that moderate heritability with fine genetic advance and high environmental variance for number of internode (plant^{-1}) selection of that character is possible for further improvement. Low heritability coupled with less genetic advance for number of tillers (plant^{-1}) was recorded in clones of Gulabi-95 parents. Moderate heritability with low genetic advance for number of height of cane (cm) (high environmental effect) in picloram showed that this character was selected for future advancement of this phenotypic character. Similar results are consistent with Rajeswari et al. (2009). The results suggest increasing the duration and numbering of subcultures to get high genetic advance for number of internode (plant^{-1}) and number of tillers (plant^{-1}) before the selection of soma clones as a new cultivar. It can be inferred from over all heritability analysis in Gulabi-95 x soma clones that more genetic changes were induced by Picloram and NAA, respectively in spite of 2,4-D.

Conclusion

Increasing concentration of hormones in the MS (media)

has positive effect on the broad sense heritability. Genetic advance of sugarcane soma clones for phenotypic traits was improved. Although effect of each auxin on the heritability of sugarcane is variety dependent but 2, 4-D, the only general growth hormone, created remarkable genetic variation in the progeny of the sugarcane. Standardization of the type of auxin must be made for each genotype separately for heritability analysis and for better result. Besides heritability, environmental variance play important role in the phenotype character of the sugarcane varieties.

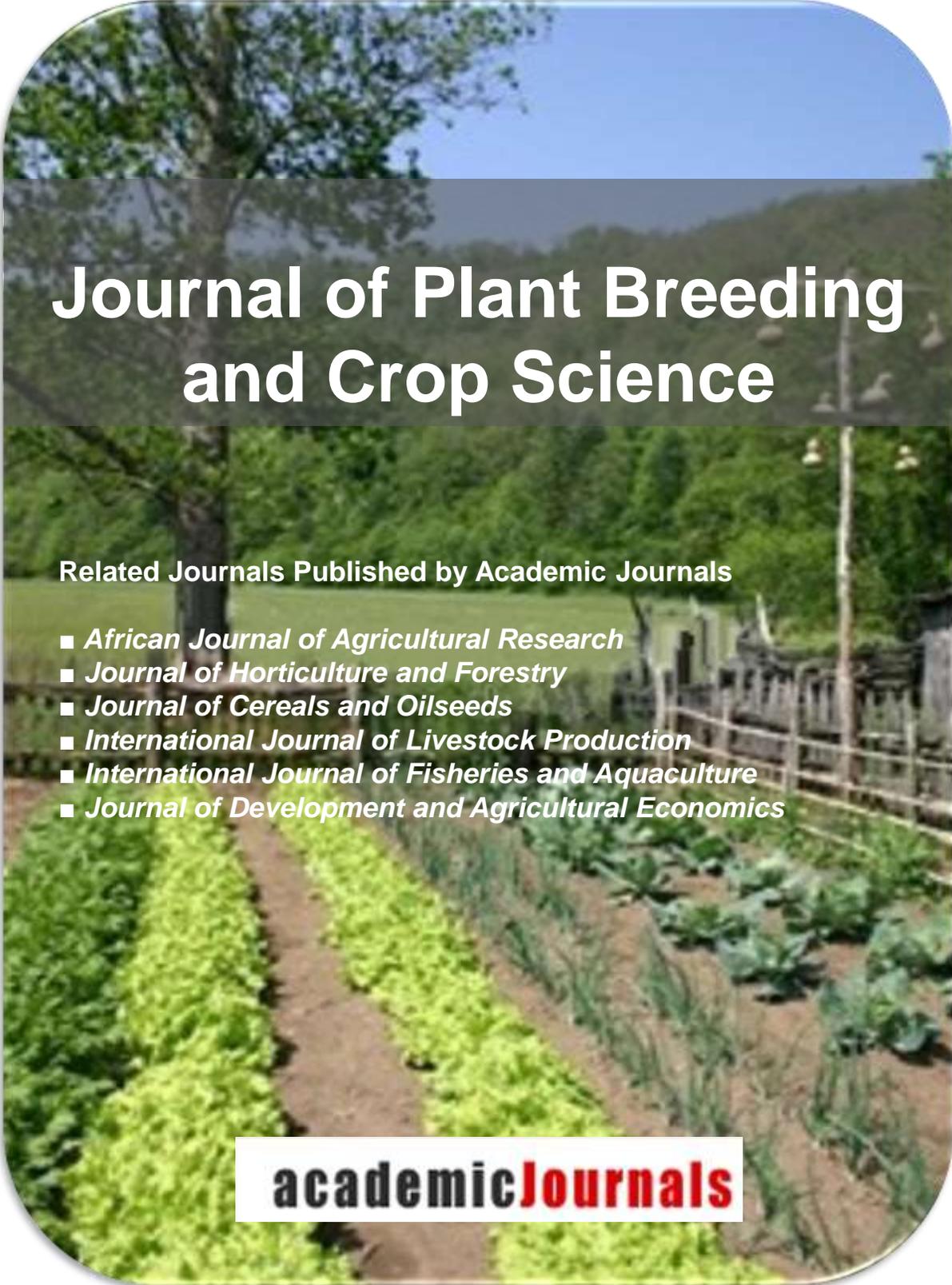
Conflict of interest

The authors have not declared any conflict of interest.

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