



Original Research Paper

Broad-sense heritability estimation and correlation among sugarcane (*Saccharum* spp. hybrids) yield and some agronomic traits in western Kenya

Accepted 27 November, 2013

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Genetic improvement of sugarcane (*Saccharum* spp. hybrids) yield is crucial in the improvement of crop productivity. The objectives of this study were to estimate broad sense heritability and phenotypic and genetic correlations among sugarcane yield components. Thirteen sugarcane clones and one cultivar were evaluated in randomized block design in three locations in western Kenya. The study was conducted in plant and first ratoon crops. Significant ($p \leq 0.05$) differences among the genotypes for all the traits were observed. Genotype \times location (G \times L) interactions were significant ($p \leq 0.01$) for stalk height, stalk weight and cane yield. High broad sense heritability (h^2) was detected for stalk diameter (0.928), number of millable cane (0.912), single stalk weight (0.907) and number of internodes (0.907) indicating that these traits could be selected for easily. Highest expected genetic gains were recorded in stalk weight (34%) and number of millable cane (26.7%). Except number of internodes, all traits had low to moderate genetic correlations ($r_g = -0.299$ to 0.586) with cane yield. On average genetic correlations were higher than phenotypic correlations. The study suggests that evaluation of sugarcane clones in many locations as opposed to crop years would be satisfactory. In view of their high GCV, broad sense heritability and expected genetic advance, a selection strategy based on single stalk weight and number of millable cane could lead to improvement in cane yield.

Key words: Heritability, genetic correlation, genetic advance, sugarcane.

INTRODUCTION

Sugarcane (*Saccharum* spp. hybrids) is an important agro industrial crop and knowledge of heritability of agronomic traits is important in breeding programmes worldwide. In Kenya, it is mainly grown commercially in the western region. Genetic improvement in cane yield may be achieved by targeting traits closely associated with cane yield. A number of characteristics have been proposed as indirect selection criteria for genetic improvement of yield in plant breeding programmes (Skinner et al., 1987; Rebetzke et al., 2002).

Understanding the associations between traits is of great importance in breeding and selection studies especially for

low heritability or difficult to measure traits (Bakhsh et al., 2006; Silva et al., 2007). Consideration of genetic relationships between important attributes in exploiting genetic populations through breeding and directed selection is essential, primarily to understand how changes made by selecting one character may cause changes in others (Jackson, 1994; Tyagi and Khan, 2010). This knowledge can be used when devising appropriate selection strategies for particular traits in a sugarcane breeding programme (de Sousa-Vieira and Milligan, 2005). Number of millable stalks, stalk height and stalk diameter were reported to be positively associated with cane yield

(Milligan et al., 1990; Gravois et al., 1991b). Tyagi and Lal (2007) studied phenotypic associations between yield and its components in sugarcane and concluded that selecting for stalk number, diameter and length should be emphasised in sugarcane variety development programmes where high cane yield is the primary goal.

The breeder also requires information on the nature and magnitude of genetic variability in the material available. Heritability estimates, together with expected genetic gain, are more useful than the heritability values alone in predicting the effects of selecting the best genotypes. Chaudhary (2001) reported high heritability and genetic gain for single cane weight followed by number of millable cane in a study of 36 clones indicating substantial scope for cane yield improvement. On the other hand, sucrose content recorded low heritability and genetic gain suggesting little scope for improvement in this character (Pandey, 1989). Patil et al., (2008) also reported high heritability estimates for single cane weight, number of internodes, tiller number, hand refractometer brix, cane diameter and millable cane length, which were associated with moderate to high (23-190%) genetic advance. The results indicated that the characters could be improved through selection. Chavanne and Mariotti (1989) found moderate heritability estimates for length of stalk (0.41), diameter of stalk (0.51) and number of millable stalks (0.53) and significant positive genetic correlations between yield and the three traits in their programme. However, it should be remembered that the magnitude of heritability and association among traits is peculiar to the type of population and environments in which they are evaluated (Pires and da Costa, 1980).

Genotypic coefficient of variation (GCV) is another measure of relative genetic variation of a trait in a population (Ram and Hemaprabha, 1992). Traits exhibiting relatively high GCV estimates may respond favourably to selection. Chaudhary (2001) reported high GCV for single stalk weight and millable cane.

Genotype \times environment (G \times E) interactions are a serious concern in breeding programmes as they affect selection decisions. When the rank of a genotype changes across environments it necessitates evaluation of genotypes across the environments to determine their real value (Kimbeng et al., 2002). Studies in various sugarcane breeding programmes have reported significant G \times E interactions for cane and sugar yield (Parfitt 2000; Kimbeng et al., 2002; Glaz and Kang, 2008)

Yield is one of the key selection objectives in the Kenyan sugarcane breeding programme. Although breeding of sugarcane has been in progress in Kenya since 1967, information on genetic parameters and the relationships among cane yield and its components, for the crop which is commercially grown for at least 18 months at high altitude is lacking. The study was therefore conducted to estimate heritability of sugarcane yield and some of its components, and to determine phenotypic and genetic correlations

among sugarcane yield components such as stalk number, weight, length, number of internodes and diameter.

MATERIALS AND METHODS

Experimental sites and genetic materials

The study was carried out at three sites: the Kenya Sugar Research Foundation (KESREF) research farm is situated at Kibos (34° 48'E, 0° 04'N) 1184m above sea level on clay loam soil with long term mean annual rainfall of 1490 mm. The temperatures range from 15.3°C to 30°C; Mumias Sugar Company Ltd estate (34° 30'E, 0° 21'N) at 1314m above sea level, receives 2194 mm annual rainfall with a temperature range of 16.4-30.9°C and has free draining loam soils; and Nzoia Sugar Company Ltd estate (34° 40'E, 0° 35'N) situated at 1445 m above sea level, receives average annual rainfall of 1650 mm with a temperature range of 13-32°C and has sandy clay loam soils. These locations were deemed to be representative of areas where commercial cane is grown in Kenya.

Thirteen sugarcane clones selected from the routine breeding programme in Kenya and a commercial control N14 were used in this study. The experimental clones, selected on the basis of brix (an indicator of sucrose content) and cane yield per plot in the multiplication and preliminary observation trial (Stage 3) at the KESREF research farm in Kibos were KEN01-24, KEN01-26, KEN01-41, KEN01-279, KEN01-345, KEN01-592, KEN01-819, KEN01-848, KEN01-1009, KEN01-1104, KEN01-1108, KEN01-1139 and KEN01-1294.

Planting procedure and experimental design

The plots were mechanically ploughed using a mould board plough in the heavy clay loam soils at Kibos, and disc plough in light soils at Mumias and Nzoia to depths of 25-30cm. The plots were then disc harrowed to depths of 20-25cm to produce a good tilth for dry-season cultivation. Furrows were made 25cm deep and spaced at 1.2 m, 1.5 m and 1.6 m at Kibos, Mumias and Nzoia respectively.

The crop was planted by hand during the long rainy season in August 2007 at all the locations. For each clone the seed rate was 40 three-budded setts or 120 buds per row in all the sites with setts placed end-to-end or slightly over-lapping, within the rows. Setts were then covered with soil by breaking the banks using hoes. The randomized complete block design (RCBD) with 3 replications was used at all the three locations. Each variety was grown in a gross experimental unit comprising four 8m-rows. The net plot for data collection and harvest was two rows. In all sites phosphate as diammonium phosphate (46% P₂O₅ and 18% N) was applied at the rate of 35.12 kg P ha⁻¹ at planting. Nitrogen as urea (46% N) was top-dressed in two equal slits of 26 kg N ha⁻¹ when the crop was 3 and 6 months old

in both plant and ratoon crops at all locations. Plots were hand weeded several times to control weeds. The crop was manually harvested and plot cane yield measured and used to compute tonnes cane yield per ha (TCH). Data was collected in both the plant and first ratoon crops. The plant crop was harvested in January and February 2009 at 18 months' age while the first ratoon crop was harvested in June 2010 at 16 months.

Data collection and statistical analysis

The total number of millable stalks in the net plot was counted and expressed as stalks per ha. During harvest all millable stalks were cut by hand at ground level, stripped of all leaves and topped at the topmost visible dewlap. Stalk height was estimated from the mean of the 5 stalks taken randomly in the net plot and measured from ground level to the top visible dewlap or auricle using a marked mast in each plot. Similarly the diameter of the stalks was measured at the mid-stalk internode using a varnier calliper and averaged. The number of internodes from the base of the stalk to the last visible node at the top of the stalk was determined. A 10-stalk sample taken randomly from each plot at harvest was weighed to obtain average stalk weight. After topping and removing the stalks of trash the weight of millable stalks in the net plot was obtained and used to calculate tonnes cane per ha.

Broad sense variance and covariance components were estimated using the linear model (Gravois et al., 1991):

$$T_{ijkm} = \mu + L_i + G_j + Y_l + R_{k(i)} + GL_{ij} + GY_{il} + GLY_{ijl} + \epsilon_{ijkl} \dots \dots \dots \text{combined over locations and crop-years}$$

Where, T_{ijkl} = observation on j^{th} genotype in the k^{th} replicate and i^{th} location and l^{th} crop year; μ = overall mean; L_i = effect due to i^{th} location; G_j = effect due to j^{th} genotype in k^{th} replicate; Y_l = effect of the l^{th} crop-year in the i^{th} location; $R_{k(i)}$ = effect of the k^{th} replicate within the i^{th} location; GL_{ij} = effect of the j^{th} genotype in the i^{th} location; GY_{il} = effect of the j^{th} genotype in the l^{th} crop-year; GLY_{ijl} = effect of the j^{th} genotype in the i^{th} location and l^{th} crop-year and ϵ_{ijkl} = the residual.

Analysis of variance and covariance was conducted considering genotypic and location effects as random components because they were considered representative (Bouzerzour and Dekhili, 1995; Chang, 1996; Brown and Glaz, 2001). Combined analysis over three locations and two crop-years was conducted using the general linear model (GLM) procedure of the Statistical Analysis System (SAS Institute, 2001). Estimates of genetic, genotype by environment ($G \times L$, $G \times Y$, and $G \times L \times Y$) and error variance components were computed using the VARCOMP procedure of SAS using the restricted maximum likelihood (REML) method. These components were used to estimate broad-sense heritability (Falconer and Mackay 1996; Holland, 2003) on genotype-mean basis as follows:

Heritability on genotype mean basis (3 replicates, 3 locations and 2 crop years):

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gi}^2}{l} + \frac{\sigma_{gy}^2}{y} + \frac{\sigma_{gily}^2}{ly} + \frac{\sigma_e^2}{rly}}$$

where, σ_g^2 = genotype, σ_{gi}^2 = genotype \times location, σ_{gy}^2 = genotype \times crop year, σ_{gily}^2 = genotype \times location \times crop year, σ_e^2 = error, σ_p^2 = total phenotypic variances, r = number of replications, l = number of locations and y = crop years respectively.

All variance components were converted to their respective coefficients of variation to allow direct comparisons between traits. Genetic coefficients of variation provide a unit less measure of a trait's genetic variance relative to its mean and permit comparisons among traits with different units and scales and give perspective to available variability to be potentially exploited for genetic gain (Milligan et al., 1990). The phenotypic coefficient of variation (%) was calculated as $PCV = 100\sigma_p/\text{phenotypic mean of a trait}$, and genotypic coefficient of variation as $GCV = 100\sigma_g/\text{phenotypic mean of a trait}$.

Expected genetic advance (GA) for each trait was calculated as a proportion of the general mean to allow comparison among traits for potential improvement through selection (Milligan et al. 1990; Gravois and Milligan, 1992) thus:

$$GA = \frac{i\sigma_p h^2}{\text{phenotypic mean of trait}}$$

where, i = selection intensity, σ_p = phenotypic standard deviation of trait, h^2 = heritability.

Genetic (r_g) and phenotypic (r_p) correlation coefficients and their standard errors were obtained among all the traits by estimating genetic, genotype by environment and error covariances in a combined RCBD across locations using version 8.2 of SAS Proc Mixed and the REML analysis method (Holland, 2006) based on the variance and covariance components according to Falconer (1989) as:

$$r_{ij} = \frac{\sigma_{ij}}{\sigma_i \sigma_j}$$

where, σ_{ij} = genetic or phenotypic covariances between trait i and trait j ; σ_i and σ_j are phenotypic or genetic standard deviations of trait i and trait j respectively. Genetic and phenotypic correlations were considered significant if their absolute value was higher than 1.96 times their standard deviation (Holland, 2006; Cardinal and Burton, 2007).

RESULTS

Significant ($p \leq 0.01$) differences were observed among the genotypes for cane yield and related traits (Table 1). Location and crop-year mean squares were also significant ($p \leq 0.01$), except for number of millable stalks (m^{-2}). Genotype \times location interactions were significant for stalk

Table 1. Mean squares for sugarcane yield and its contributing traits in 14 sugarcane genotype evaluated at Kibos, Mumias and Nzoia in plant and first ratoon crops (2007-2010)

Source of variation	df	Number of Internodes stalk ⁻¹	Stalk Diameter (cm)	Stalk height (cm)	Single stalk Weight (kg)	Number of Millable Stalks (m ⁻²)	Cane yield (t ha ⁻¹)
Location (L)	2	582.11**	2.99**	61632.62**	0.92**	40.86**	4191.04*
Rep within location(R)	6	19.02	0.13	6820.76	0.27	1.40	5732.92
Crop-year (Y)	1	638.10**	2.36**	13383.28**	3.69**	0.92	19635.63**
L × Y	2	19.82**	0.34**	24221.24**	0.99	91.57**	11547.21**
Genotype (G)	13	60.71**	0.59**	7177.93**	1.01**	53.55**	2342.91**
G × L	26	4.51	0.04	1144.64**	0.08*	2.53	1139.87*
G × Y	13	5.40	0.03	895.65	0.03	2.75	712.14
G × L × Y	26	3.08	0.02	341.29	0.07	1.39	351.17
Error	162	3.86	0.03	514.78	0.05	3.15	670.44
Mean	-	26.78	2.51	245.78	1.11	10.37	100.90
CV%	-	7.34	6.77	9.23	19.38	17.11	25.66
R ²	-	0.83	0.81	0.83	0.78	0.68	0.60

*, ** = significant at p ≤ 0.05 and p ≤ 0.01, respectively

Table 2. Combined variance components and heritability for cane yield and related traits in 14 sugarcane genotypes evaluated at Kibos, Mumias and Nzoia across plant and first ratoon crops (2007-2010)

Trait	σ_g^2	σ_{gl}^2	σ_{gy}^2	σ_{gly}^2	σ_e^2	GCV%	PCV%	h^2	GA%
Cane yield (t ha ⁻¹)	67.096	20.569	0.000	113.690	670.705	8.118	11.307	0.515	10.3
Single stalk weight (kg)	0.051	0.000	0.000	0.016	0.047	20.272	21.285	0.907	34.0
No. of internodes stalk ⁻¹	3.060	0.039	0.126	0.138	3.864	6.531	6.858	0.907	10.9
Stalk diameter (cm)	0.031	0.001	0.000	0.004	0.029	6.983	7.248	0.928	11.8
Stalk height (cm)	316.916	0.000	0.000	319.551	514.783	7.243	8.125	0.795	11.4
No. of millable canes (m ⁻²)	2.712	0.000	0.000	0.548	3.088	15.878	16.630	0.912	26.7

$\sigma_g^2, \sigma_{gl}^2, \sigma_{gy}^2, \sigma_{gly}^2, \sigma_e^2$ =genotypic, genotype × location, genotype × crop-year, genotype × location × crop-year interaction, environmental variances; GCV, PCV = genetic, phenotypic coefficients of variation, h^2 =broad sense heritability and GA% = expected genetic advance as percentage of the phenotypic mean of the trait

height (p ≤ 0.01), stalk weight and cane yield (p ≤ 0.05). For single stalk weight, stalk height and cane yield the genotype × location interactions (G×L) were 8, 16 and 49% of the genotype mean squares respectively. Genotype × crop year (G×Y) and genotype × location × crop-year (G×L×Y) interactions were not significant (p ≥0.05) for any of the traits studied. However, stalk diameter, height, weight, number and cane yield were influenced by genotype, location and crop-year. The amount of variation accounted for, ranged from moderate (R² =0.60) for cane yield to high (R² =0.83) for stalk height.

The variance components were used to compute heritability estimates in Tables 2 and 3 (Butterfield and Nuss, 2002). The genetic variance component for all traits except cane yield and stalk height exceeded the genotype × location, genotype × year and genotype × location × year components (Table 3). The genotype × location and genotype × year variance components were negligible for all the traits except cane yield and number of internodes per stalk. The genotype × location × year variance component for cane yield was higher than the genetic component by 69.44%. The error variance was tenfold the

genetic variance for cane yield. Genetic and error variances were similar for stalk weight, stalk diameter and number of millable canes.

Except for cane yield, the differences between GCV and PCV were small for most traits. Broad sense heritability estimates were moderate for stalk height and cane yield and high for stalk diameter, number of millable cane, stalk weight and number of internodes. Single stalk weight recorded the highest expected genetic gain expressed as percentage of phenotypic mean followed by number of millable cane.

In plant cane (Table 3) the highest magnitude of genetic variance relative to environmental variance was exhibited by number of internodes (151.23%), millable cane (143.84%) and stalk weight (116.31%) indicating that environmental factors influenced their expression less than the other traits. Number of millable cane, number of internodes, stalk diameter, stalk weight and stalk height had high broad-sense heritability of at least 0.80 while cane yield recorded moderate heritability of 0.484. Individual stalk weight and number of millable cane recorded thrice as much GCV as cane yield. For most of the traits

Table 3. Variance components and heritability for cane yield and related traits in 14 sugarcane genotypes evaluated at Kibos, Mumias and Nzoia in plant crop (PC) (2007-2009) and first ratoon crop (FRC)

Trait	σ_g^2		σ_{gl}^2		σ_e^2		GCV%		PCV%		h^2		GA%	
	Plant crop	Ratoon crop	Plant crop	Ratoon crop	Plant crop	Ratoon crop	Plant crop	Ratoon crop	Plant crop	Ratoon crop	Plant crop	Ratoon crop	Plant crop	Ratoon crop
Cane yield (t ha ⁻¹)	69.083	105.529	26.078	11.054	584.094	788.051	7.575	11.157	10.886	15.236	0.484	0.536	9.3	14.4
Single stalk weight (kg)	0.068	0.042	0.020	0.000	0.050	0.044	19.448	20.571	21.375	21.730	0.828	0.896	31.1	34.3
No. of internodes stalk ⁻¹	2.881	3.565	0.640	0.000	1.905	4.288	6.738	6.654	7.218	7.085	0.871	0.882	11.1	11.0
Stalk diameter (cm)	0.021	0.041	0.004	0.000	0.026	0.030	5.574	8.415	6.112	8.752	0.832	0.924	8.9	14.2
Stalk height (cm)	327.467	404.494	110.402	44.719	388.425	632.144	7.151	8.433	7.976	9.278	0.804	0.826	11.3	13.5
No. of millable canes (m ⁻²)	2.651	2.983	0.000	0.000	1.843	3.754	15.790	16.557	16.388	17.676	0.928	0.877	26.8	27.3

$\sigma_g^2, \sigma_{gl}^2, \sigma_e^2$ = genotypic, genotype × location interaction, environmental variances; GCV, PCV = genetic, phenotypic coefficients of variation, h^2 = broad sense heritability and GA% = expected genetic advance as percentage of the phenotypic mean of the trait

Table 4. Genetic correlations among sugarcane yield components measured on 14 genotypes evaluated at Kibos, Mumias and Nzoia in plant and first ratoon crops (2007-2010)

Trait	Crop	Stalk diameter	Stalk height	Single stalk weight	Number of millable stalks	Cane yield
Number of internodes per stalk	P	0.777*	0.899*	0.956*	-0.847*	0.159
	FR	0.866*	0.935*	0.919*	-0.614*	0.586
	OCL	0.840*	0.929*	0.940*	-0.740*	0.372*
Stalk diameter	P		0.675*	0.949*	-0.750*	0.387
	FR		0.643	0.932*	-0.771*	0.389
	OCL		0.695*	0.943*	-0.756*	0.443
Stalk height	P			0.968*	-0.981	-0.299
	FC			0.938*	-0.613*	0.564
	OCL			0.937*	-0.775*	0.285
Single stalk weight	P				-0.928*	0.157
	FR				-0.875*	0.438
	OCL				-0.881*	0.339
Number of millable canes	P					0.279
	FR					0.027
	OCL					0.126

* = significant if |r| > at least twice its standard error (Holland, 2006)
P = plant crop, FR = first ratoon crop, OCL = over crops and locations

Table 5. Phenotypic correlations among sugarcane yield components measured on 14 genotypes evaluated in Kibos, Mumias and Nzoia in plant and first ratoon crops (2007-2010)

Trait	Crop	Stalk diameter	Stalk height	Single stalk weight	Number of millable stalks	Cane yield
Number of internodes per stalk	P	0.450*	0.563*	0.609*	-0.415*	0.107
	FR	0.525*	0.635*	0.527*	-0.191	0.214*
	OCL	0.499*	0.606*	0.550*	-0.281	0.169*
Stalk diameter	P		0.419*	0.597*	-0.359*	0.277*
	FR		0.462	0.582*	-0.428*	0.178
	OCL		0.470*	0.580*	-0.395*	0.230*
Stalk height	P			0.644*	-0.357	0.309*
	FR			0.624*	-0.149	0.398*
	OCL			0.626*	-0.244*	0.360*
Single stalk weight	P				-0.514	0.329
	FR				-0.266	0.474*
	OCL				-0.383*	0.386
Number of millable canes	P					0.293*
	FR					0.538*
	OCL					0.439*

* = significant if $|r| >$ at least twice its standard error (Holland, 2006)

P = plant crop, FR = first ratoon crop, OCL = over crops and locations

the difference between GCV and PCV was small indicating good prospects for genetic improvement of the traits. Weight of individual stalk and number of millable cane recorded three as much genetic advance (GA%) expressed as percentage of the trait mean compared with cane yield.

Stalk diameter exhibited high genetic variance (136.67%) relative to environmental variance followed by stalk weight (95.45%) in first ratoon crop (Table 3). The genetic variance component for cane yield was only 13.39% relative to the environmental variance component. Broad sense heritability was high for stalk diameter, stalk weight, number of internodes, number of millable canes and stalk height ranging from 0.924 to 0.826 but moderate for cane yield (0.536). The GCV% for stalk weight and number of millable cane were twice and one and a half times that for cane yield respectively. As in plant crop the small differences between GCV% and PCV% indicated the possibility of genetic improvement in all the traits. Greatest genetic advance is expected in stalk weight (34.3%), number of millable canes (27.3%), cane yield (14%) and stalk diameter (14%).

Except for single stalk diameter (72.41%) the genetic variance components for number of millable cane (112.52%) stalk height (123.52%), number of internodes (123.74%), cane yield (152.76%) and stalk diameter (195.74%) in the first ratoon exceeded those in the plant crop (Tables 3). In both crops heritability estimates for all traits except cane yield were high ranging from 0.484 to 0.928 in plant crop and 0.536 to 0.928 in first ratoon crop. Higher GA% (11.0 to 34.3%) was observed for all the traits in first ratoon crop than in plant crop (8.9% to 31.1%).

Stalk weight had significant positive genetic correlations with number of internodes, stalk diameter and stalk height but significant negative correlation with number of millable canes in both plant and ratoon crops (Table 4). Genetic correlation between single stalk weight and cane yield was positive and low in the plant cane and moderate in the ratoon crop. Number of millable cane had negative correlations with all the other traits except cane yield in both crops. A strong negative correlation between number of millable cane and stalk weight (-0.881) and diameter (-0.756) was recorded. All the traits, except number of internodes, had low or moderate non-significant genetic correlations with cane yield over the two crops. Generally, genetic correlation coefficients were higher than phenotypic correlations.

Phenotypic correlations between cane yield and number of internodes, stalk diameter, stalk height and number of millable canes over crops and locations were significant (Table 5). Number of millable canes was positively correlated with cane yield in both crops but negatively correlated with all the other yield components. Single stalk weight was significantly correlated with internode number, stalk diameter and height in both crops. It was also significantly correlated with cane yield in the first ratoon crop but not in the plant crop.

DISCUSSION

The significant genotypic effects indicated genetic variability among the genotypes and the possibility of

genetic improvement in most of the traits studied through selection (Punia, 1982; Khan et al., 2004). The relatively large genotypic mean squares indicated that clones differed in their potential for the traits. Significant genotype \times location interactions for stalk height, stalk weight and cane yield revealed that mean performances of the genotypes were influenced by the locations. This interaction was largely due to changes in the relative ranking of the genotypes across the locations. However, the genotype \times year interactions for all the traits were not significant indicating that the mean performance of the genotypes did not vary with environment over the year-location combinations. This suggests that at this stage evaluating sugarcane genotypes in more locations rather than one may be satisfactory (Chang, 1996; Khan et al., 2004).

The genotype \times location \times year interactions were not significant for any of the traits studied suggesting that mean performance of genotypes across the location and year combination of environments could be used for selecting superior genotypes (Chatwachirawong et al., 1998). In addition the genotype \times location interactions mean squares for all traits except number of millable stalks were much larger than the genotype \times location \times year interactions mean squares indicating that differential performance of the genotypes may be permanent features of the locations (Khan et al., 2004). This further indicates that genotypes with superior cane yield traits can be identified by testing at one location over crop years. However, since genotype \times location interaction exists for cane yield and its key components it is desirable to breed for cultivars with improved traits for different locations using independent selection and testing programmes (Fehr, 1987). It should be possible to assess the relative performance of sugarcane genotypes with a limited number of test environments – preferably more over locations than crop years (Yao and Mehlenbacher, 2000; Fehr et al., 2003). Jackson and Hogarth (1992) studied patterns of response of 2 sets of genotypes in 4 sites within the Herbert River in Australia and analysed cane yield, commercial cane sugar and sugar yield data from plant, first and second ratoon crops. They reported that crop-years within sites were generally more similar for genotypic responses than environments from different sites. They concluded that testing across sites was more desirable as little appeared to be gained in testing across multiple crops or years within a particular site. Similarly in this study, evaluating sugarcane clones across environments would be more desirable because the environments represent the farmers' conditions.

Genetic variance is important as it describes the amount of genetic variation present for the trait. High genetic variance relative to environmental variance for number of internodes per stalk, number of millable cane and stalk weight in the plant cane (Table 2) and for stalk diameter and stalk weight in the first ratoon across the three locations (Table 3) indicates that these traits were affected less by environmental effects. However, over locations and

crops, genetic variance for single stalk weight, stalk diameter and number of millable canes were similar to environmental variances. High genetic variance for millable cane has also been reported by other researchers (Balasundram and Bhagalakshmi, 1978; Nair et al., 1980).

Genotypic coefficient of variation (GCV) is another measure of relative genetic variation of a trait in a population (Ram and Hemaprabha, 1992). Traits exhibiting relatively high GCV estimates may respond favourably to selection. Estimates of phenotypic and genetic coefficients of variation were high for stalk weight and number of millable canes in both plant and first ratoon and over the crops in the combined analysis. Generally, the estimates of PCV were higher than the GCV for all traits suggesting that the apparent variation is not only due to genetics but also due to environmental influences. However, the differences between PCV and GCV for most of the traits were small indicating high prospects for genetic progress through selection under the conditions of this investigation (Ram, 2005).

The success of a variety improvement programme depends largely on the amount of genetic variability present in the population. Genetic coefficients of variation along with heritability estimates give a better indication of the amount of genetic variation for a trait than either parameter alone. In this study, high broad sense heritability estimates were obtained for stalk diameter (0.928), number of millable cane (0.912), single stalk weight (0.907) and number of internodes (0.907). This suggests that a large proportion of the total variance is heritable and selection of these traits would be effective. Nair et al. (1980) and Singh et al. (1994) also reported high heritability estimates for single stalk weight. Moderate heritability estimates were detected for stalk height (0.795) and cane yield (0.515) indicating that selection for these traits would not be as effective as for the other traits. These findings agree with Chaudhary (2001) who reported similar values in clonal genotypes of sugarcane. Selection for characters with low heritability (less than 0.4) can be considerably difficult or virtually impracticable because of the masking effects of environment on genotypic expression (Singh, 1993; Wunna et al., 2009). Knowledge of variability and heritability of characters is essential for identifying those amenable to genetic improvement through selection (Vidya et al., 2002). Results of the current study indicate that use of the traits with high heritability as selection criteria together with cane yield could lead to genetic improvement in cane yield. Under the conditions of this study number of millable cane and single stalk weight were reliable selection parameters.

The effectiveness of selection depends not only on heritability but also on genetic advance (Butterfield and Nuss, 2002; Shoba et al., 2009). The high genetic gain (GA %) observed for single stalk weight (34.0%) followed by number of millable cane (26.7%) and stalk diameter (11.8%) (Table 2) was the result of high broad sense

heritability and high GCV for these traits (Bakshi, 2005). The results suggest existence of considerable scope for improvement of some of the cane yield components. High genetic advance has also been reported for single stalk weight and number of millable cane (Sahi et al., 1977; Tyagi and Singh, 1998; Kamat and Singh 2001). Low genetic advance with moderate to high heritability for cane yield and number of internodes per stalk indicates little scope for improvement of these traits (Pandey, 1989; Butterfield and Nuss, 2002). The high broad sense heritability coupled with high genetic advance for single stalk weight and number of millable canes indicates these traits are under the control of additive genetic effects and highlights the usefulness of selection based on phenotypic performance (Gravois and Milligan, 1992). However, the high heritability with low genetic advance for stalk diameter and number of internodes indicate presence of non-additive gene action and therefore simple selection on phenotypic performance may not be effective.

Correlations among phenotypic traits may reflect biological processes that are of considerable evolutionary interest and can be the result of genetic, functional and physiological or developmental nature (Soomro et al., 2006; Ulloa, 2006).

In this study, all the traits had positive genetic and phenotypic association with cane yield over crops and locations (Tables 4 and 5). The strong genetic correlation between single stalk weight and other agronomic traits suggests that selection of stalk weight could simultaneously improve these traits. On the other hand, the negative genetic association between number of millable stalks and other traits except cane yield indicates that improvement in the latter could result in decrease in the other traits (number of internodes, stalk diameter, stalk height and stalk diameter). These results indicate that stalk weight, stalk diameter and stalk number are the key component characters of cane yield.

The correlations for some trait pairs were consistent over crops while others were not. Since season or year effects are usually considered as random, it is easier to recommend a trait that is less affected by change of season or year than those that vary with season. Thus association between stalk diameter and single stalk weight, stalk diameter and cane yield and stalk diameter and number of millable canes were consistent over the palnt and first ratoon crops. On the other hand, association between number of internodes and cane yield; stalk height and cane yield tended to be inconsistent suggesting that cane yield cannot be selected based on number of internodes and stalk height.

From these results, stalk weight can be increased by selecting for thick and tall stalks. Stalk weight, number of millable canes and stalk diameter had high variation, high heritability and reasonable expected genetic advance in both crop years compared to cane yield. Therefore, a selection strategy based on stalk weight and number

of millable cane could lead to improvement in cane yield (Gravois et al., 1991). Further, the correlation coefficients suggest that it is possible to identify varieties with improved cane yield, single stalk weight, number of millable canes and moderate stalk diameter. Sugarcane genotypes with high cane yield have been selected on the basis of stalk number and stalk weight (Singh et al., 2007). In the case of negative correlation, a suitable selection approach should be employed to break the negative association between numbers of millable canes and stalk traits emphasizing a compromise in stalk diameter (James, 1971, Das et al., 1997). To avoid the risk of selecting clones with few very thick canes it is suggested that a minimum millable stalk number required in the selected types may be fixed before selecting for stalk diameter and number of millable cane (Gopal et al., 1994; Gopal, 1999).

Conclusion

This study revealed that cane yield is associated with its various components genetically and phenotypically in various magnitudes. Further, the study has indicated the magnitude of the correlations among cane yield traits, their heritability, expected genetic advance and genotype \times environment interactions that could be encountered within the sugarcane breeding programme and demonstrated differential responses of different sugarcane clones to various environmental conditions.

The results suggest that evaluation of sugarcane clones for cane yield in the plant crop in many locations rather than crop-years should identify superior clones. This testing approach coupled with a selection strategy based on single stalk weight, stalk diameter and number of millable canes per unit area might result in significant genetic improvement in cane yield.

ACKNOWLEDGEMENTS

The authors are grateful to the Kenya Sugar Research Foundation for funding the project and Mr. Morris Mudeheri's assistance with data analysis.

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Cite this article as : Jamoza JE, Owuoche J, Kiplagat O, Opile W (2014). Broad-sense heritability estimation and correlation among sugarcane (*Saccharum* spp. hybrids) yield and some agronomic traits in western Kenya. *Int. J. Agric. Policy and Res.* Vol.2(1):016-025.