

RESEARCH ARTICLE**BROAD-SENSE HERITABILITY, GENETIC CORRELATION AND GENETIC VARIABILITY OF SUGARCANE YIELD COMPONENTS AT FIRST SELECTION STAGE****Farrag F.B. Abu-Ellail¹, Ashraf B.A. El-Taib² and Mohamed I. Masri³****Abstract**

Sugarcane crosses exploit heterogeneity in F1 generation, indicating its potential to exploit the variability in the initial stage of clonal selection. Thirty sugarcane clones were selected from six bi-parental crosses (families) along with two check cultivars (GT54-9 and Ph8013) were evaluated in randomized complete block design trial with three replications in plant cane (PC) and first ratoon (FR), crops under Upper Egypt conditions at Shandweel Agricultural Research Station, Sohag Governorate, Egypt during 2013 and 2014 crop seasons. Estimates of broad-sense heritability, genetic correlation and genetic variance components were studied in the families. The results indicated varied significant difference between genotypes for the traits under study, Genotype×crop-year interaction had significant response in most of the studied traits except two traits (cane yield and Brix%). The genotypic correlation between cane yield and its components, viz. stalk diameter, stalk weight and number stalks/fed were highly significant in the positive direction across crop seasons. Genotypic variance, heritability, phenotypic and genotypic coefficient of variation decreased from plant cane to first ratoon for the traits, stalk diameter, cane yield and Brix%, while, they increased slightly for number of stalks/fed and purity%. The significant genotypic effects indicated existence of genetic variability among the genotypes and the possibility of utilizing them in genetic improvement.

Keywords : Sugarcane (*Saccharum* spp), plant cane, ratoon crop, genetic variance, heritability, genetic correlation

Introduction

In Egypt, sugarcane (*Saccharum* spp.) is the source of raw material to sugar industry and various agro-based industries and as well as it generates employment for many people. Sugarcane is being grown on 136.6 thousand ha with total annual production of 15.7 million tons (Annual Report of Sugar Crops Council 2017). Heritability estimates along with expected genetic gain from selection and genotypic coefficients of variation are very essential to improve traits of sugarcane and select best genotypes. (Nagarajan 1997, Tyagi and Singh 1998). The magnitude of heritability, genetic

variance estimates and relationship among traits is specific to each cross and the environment in which they are evaluated (Falconer 1989). Estimating genetic variances under a limited range of environmental conditions may lead to biased genetic variance estimates (Dudley and Moll 1969). Genetic studies in a wide range of sugarcane populations and varied environments (Hogarth et al. 1981, Kang et al. 1983, Masri et al. 2014) indicated large estimates of heritability for sugarcane yield and its components. The studies indicated least potential for selection gain for Brix% and purity%, followed by stalk length and

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stalk diameter. However, they reported that stalk weight and sucrose concentration had the largest potential for gain and amenable for improvement. Similar studies (Milligan et al. 1990) indicated that stalk number and cane yield were the important traits for exploitation. Jamoza et al. (2014) reported that high broad-sense heritability was observed for stalk diameter (0.928), number of millable cane (0.912) and single stalk weight (0.907), indicating that these traits could be selected easily and the highest expected genetic gains were recorded in stalk weight (34%) and number of millable cane (26.7%). Genotypic correlation is more important in selection as selecting one character has direct or indirect effect on the other character and this correlated response is exploited for future use (Acquaah 2007, Masri et al. 2015).

The objective of this study to estimate broad-sense heritability, genetic correlation and genetic variance components of 30 sugarcane clones at first stage of selection and identify superior crosses and clones for genetic improvement.

Materials and methods

The present study was carried out during two growing seasons, i.e. as plant cane (PC) and first ratoon (FR) during 2012/13 and 2013/14 at Shandweel Agricultural Research Station, Sohag Governorate. A total of selected 30 sugarcane genotypes and the two check cultivars; Ph 8013 and G T 54/9 were raised in 5 m × 3 rows; plot size was 15 m² with 1.0 m spacing between rows; in a randomized complete block with three replications. Planting was done by placing fifteen 3-budded cane pieces in each row. Irrigation and all other normal agronomic practices were carried out as recommended. Plant cane was ratooned

after harvested at 12 months of age. Both the plant and ratoon crops were harvested at 360 days and the following traits were measured:

Cane yield and its contributing traits: A sample of twenty stalks from each plot was harvested to measure: 1. Stalk length (cm), 2. Stalk diameter (cm), 3. Number of millable stalks/fed, 4. Stalk weight (kg) and 5. Cane yield (ton/fed).

Juice quality traits and sugar yield: Juice of twenty stalk sample from each plot was analyzed for determining the following traits:

1. Brix (%) determined with a hydrometer, 2. Sucrose (%) in clarified juice was determined using automated sacharimeter according to A.O.A.C. (1980), 3. Purity = [(Sucrose / Brix) × 100] , 4. Sugar recovery (%) = [Sucrose% - 0.4 (Brix% - Sucrose%)] × 0.73 and 5. Sugar yield (ton/fed) was estimated by multiplying net cane yield (ton/fed) by sugar recovery%.

Separate and combined analyses of variance for collected data were performed according to Gomez and Gomez (1984). The comparison among means was done using the least significant difference test (LSD) at 5% level of probability. Variance components were calculated by equating appropriate mean squares for the differences among genotypes to their expectations and solving for the components. Broad-sense heritability (H%) on genotype mean basis was estimated using variance components following the formula according to Johnson et al. (1955): $H = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e / r + \sigma^2_{gc} / rc}$,

where, (σ^2_g) and (σ^2_e) refers to genotypic and error variance, respectively. The divisor (r) refers to number of replications, σ^2_{gc} refers to genotype

by crop interaction variance. The divisor *c* refers to number crops. Genetic coefficients of variance (GCV) provide measure of traits genetic variation relative to its mean estimated according to Burton and Devance (1953). The GCV facilitates comparisons among traits with different units and scales, and gives perspective to the variation as: $GCV\% = (\sigma^2g/\text{general mean}) \times 100$.

Expected genetic gains as % of mean (GA %) from the individual selection were calculated according to Falconer (1981): $GA = K \times H \times \sigma_p$ (GA as % of mean) = (GA / general mean) $\times 100$,

where, $K = 1.756$ for 10% selection intensity in standard deviation units, σ_g is within family genetic variances and σ_p is the phenotypic standard deviation. The genotypic correlation coefficient was tested with the following formula given by Robertson (1959), equation (1) and equation (2):

$$t = \frac{r_{gxy}}{SE_{rgxy}} \quad (1)$$

$$SE_{rgxy} = \sqrt{\frac{1 - r^2_{gxy}}{2h^2_x h^2_y}} \quad (2)$$

where, r_{gxy} is the genotypic correlation coefficient between character *x* and *y*, SE_{rgxy} is the standard error of genotypic correlation coefficient between character *x* and *y*, h^2_x is the heritability for character *x* and h^2_y is the heritability for character *y*.

The calculated absolute t-value was tested against the tabulated t-value at *g*-2 d.f. for genotypic correlation coefficients where *g* is the number of genotypes. The thirty sugarcane clones used in this study listed in Table 1.

Results and discussion

The combined analysis of variance across two seasons (Table 2) revealed that all studied traits were highly significant under Shandawel conditions. Furthermore, the mean squares due to

Table 1. Sugarcane hybrid populations and their clones

Clones	Parents			Clones	Parents		
	Female Origin	Male	Origin		Female	Origin	Male Origin
G.2009-1 G.2009-2 G.2009-3 G.2009-4 G.2009-5	E H 9 4 - 181-1 Egypt	E H 9 4 - 119-72	Egypt	G.2009-16 G.2009-17 G.2009-18 G.2009-19 G.2009-20	F153	Taiwan	BO3 Indonesia
G.2009-6 G.2009-7 G.2009-8 G.2009-9 G.2009-10	MIX58- 1866 Mexico	PH8013	Philippine	G.2009-21 G.2009-22 G.2009-23 G.2009-24 G.2009-25	CO622	India	G85-37 Egypt
G.2009-11 G.2009-12 G.2009-13 G.2009-14 G.2009-15	79D1 Egypt	PH8013	Philippine	G.2009-26 G.2009-27 G.2009-28 G.2009-29 G.2009-30	CO1075	India	CP31- 294 USA

Table 2. Mean square of some agronomic traits in sugar cane across plant cane and first ratoon crops

S.O.V	d.f	Stalk diameter (cm)	Stalk weight (kg)	Number of stalks/ fed	Cane yield (ton/fed)	Brix (%)	Sucrose (%)	Purity (%)	Sugar yield (ton/fed)
Crop-year (C)	1	0.600*	1.592**	6485.24**	6.98	40.77**	0.049	759.02**	0.375
Rep/year	4	0.032	0.009	56.38	13.05**	0.336	1.209	27.06	0.891
Genotypes (G)	31	0.18**	0.32**	1221.94**	973.20**	27.08**	19.43**	352.66**	22.51**
G×C	31	0.096**	0.091**	173.64**	240.99	0.370	2.49**	90.369**	4.95**
Error	124	0.022	0.002	5.269	3.803	0.358	0.204	11.510	0.156

* and ** denote significance at 0.05 and 0.01 levels of probability, respectively

crop-year were highly significant for all studied traits, except for cane yield, sucrose% and sugar yield and genotype × crop-year interaction was highly significant for all traits, except cane yield

Table 3. Variance components, mean, heritability in broad-sense (H%), phenotypic coefficient of variation (PCV%), genetic coefficient of variation (GCV%) and genetic advance as % of mean (GA%) for cane yield and its components for plant cane (PC), first ratoon (FR) and across crops during 2012 - 2014 seasons

Parameter	Stalk diameter (cm)			Stalk weight (kg)			Number of stalks/fed			Cane yield (ton/fed)		
	PC	FR	Across crop	PC	FR	Across crop	PC	FR	Across crop	PC	FR	Across crop
σ_p^2	0.05	0.04	0.03	0.09	0.05	0.05	161.78	303.42	203.66	220.47	184.26	162.20
σ_g^2	0.05	0.03	0.01	0.09	0.05	0.04	160.46	301.23	174.72	219.79	182.40	122.04
σ_{gc}^2			0.02			0.03			56.12			79.06
H%	93.51	74.62	46.67	99.25	99.32	71.56	99.18	99.28	85.79	99.69	98.99	75.24
Mean	2.40	2.32	2.36	0.98	0.82	0.90	51.05	62.4	56.73	47.59	47.99	47.79
PCV%	9.44	8.97	7.34	30.33	26.90	25.66	24.92	27.91	25.16	31.20	28.29	26.65
GCV%	9.13	7.75	5.01	30.21	26.81	21.71	24.81	27.81	23.30	31.15	28.14	23.12
GA% of mean	15.54	11.78	6.03	52.97	47.03	32.32	43.49	48.78	37.98	54.74	49.28	35.29
Range	1.80-2.90	1.70-2.70	2.00-2.68	0.58-2.19	0.46-1.42	0.56-1.81	29.71-76.10	31.24-98.76	30.48-84.19	26.60-88.12	19.97-77.37	23.50-75.17

and Brix%. These results were in accordance with those obtained by El-Hinnawy and Masri (2009) and Masri et al. (2014), who reported significant differences among genotypes and among seasons for most of traits.

Cane yield and its components

Phenotypic variance (σ^2_p) and genotypic variance (σ^2_g) increased from plant cane to first ratoon for number of stalks/fed, but they decreased for stalk diameter, stalk weight and cane yield Table 3. However, the genetic variance of crop-year interaction was lower than that of plant cane for these traits. Phenotypic coefficient of variation (PCV%) and genotypic coefficient of variation (GCV%) decreased from plant cane to first ratoon crop for stalk diameter, stalk weight and cane yield

while, they increased for number of stalks /fed. The differences between GCV% and PCV % were small for these traits; indicating the possibility of genetic improvement in these traits. Masri et al. 2014, reported that genotypic variance and GCV decreased from plant cane crop to second ratoon crop for cane yield while they increased slightly for number of stalks per fed.

Broad-sense heritability estimates were high for number of stalks/fed (85.79%) and low for stalk diameter (46.67%). Broad-sense heritability (H%) decreased for stalk diameter and cane yield with older crops, while, it increased for stalk weight and number of stalks/fed. The highest expected genetic gain was recorded in number of stalks/ fed (37.98%), while, it was low for stalk diameter

Table 4. Variance components, mean, heritability in broad-sense (H%), phenotypic coefficient of variation (PCV%), genetic coefficient of variation (GCV%) and genetic advance as % of mean (GA%) for Sugar yield juice quality traits for plant cane (PC), first ratoon (FR) and across crops during 2012 - 2014 seasons

Parameter	Brix (%)			Sucrose (%)			Purity (%)			Sugar yield (ton/fed)		
	PC	FR	Across	PC	FR	Across	PC	FR	Across	PC	FR	Across
σ^2_p	4.97	4.18	4.51	3.19	4.12	3.24	48.94	98.74	58.78	4.07	5.08	3.75
σ^2_g	4.85	4.06	4.45	3.14	4.03	2.82	46.37	93.64	43.72	4.04	5.01	2.93
σ^2_{gc}			0.004			0.76			26.29			1.60
H%	97.68	97.04	98.63	98.56	97.82	87.18	94.74	94.84	74.38	99.23	98.57	78.01
Mean	17.43	18.21	17.82	13.59	13.33	13.46	75.89	71.18	73.54	6.11	6.03	6.07
PCV%	12.79	11.23	11.92	13.14	15.23	13.37	9.22	13.96	10.43	33.03	37.38	31.91
GCV%	12.64	11.06	11.84	13.04	15.06	12.48	8.97	13.59	8.99	32.90	37.12	28.18
GA% of mean	21.99	19.18	20.70	22.79	26.22	20.51	15.37	23.30	13.65	57.69	64.85	43.81
Range	13.17- 21.50	14.50- 21.93	13.83- 21.72	10.34- 17.17	8.86- 17.13	10.15- 16.59	59.68- 91.54	52.70- 92.04	56.19- 91.79	2.68- 9.65	2.00- 9.50	2.37- 9.02

Table 5. Genotypic (r_g) correlation coefficients among the yield and its components of thirty sugarcane clones across crops

Traits	Stalk diameter (cm)	Stalk weight (kg)	Number of stalks/fed	Cane yield (ton/fe)	Brix (%)	Sucrose (%)	Purity (%)	Sugar yield (ton/fe)
Stalk diameter (cm)	1.000							
Stalk weight (kg)	0.730**	1.000						
Number of stalks/fed	0.278**	-0.366	1.000					
Cane yield (ton/fed)	0.969**	0.610**	0.496**	1.000				
Brix(%)	0.230**	-0.331	0.587**	0.189**	1.000			
Sucrose (%)	0.360**	-0.023	0.278**	0.223**	0.748**	1.000		
Purity (%)	0.149**	0.424**	-0.430	0.026*	-0.366	0.343**	1.000	
Sugar yield (ton/fed)	0.895**	0.493**	0.463**	0.864**	0.448**	0.663**	0.277**	0.660**

* and ** denote significance at 0.05 and 0.01 levels of probability, respectively

(6.03%); indicating the possibility of selecting clones with high number of stalks for further improvement. These results are in line with those reported by El-Hinnawy and Masri (2009) and Jamoza et al. (2014), whereas high heritability for stalk weight, stalk diameter and moderate heritability for stalk height was observed. The heritability and the expected genetic advance obtained by stalk weight, followed by stalk diameter indicate the importance of these traits for sugarcane selection and breeding strategy. The study also identified potential crosses for different traits and clones for further evaluation.

Sugar yield and juice quality traits

The study (Table 4) revealed that phenotypic variance (σ^2_p) and genotypic variance (σ^2_g) increased from plant cane to first ratoon for quality traits viz., sucrose%, purity% and sugar yield, but they decreased for Brix%. Similar trend was observed for the trait Brix % for PCV%GCV%, but with an increase in others traits. A range of

estimates of GCV% were obtained (%28.18 and 8.99%) for sugar yield and purity%, respectively. As in plant crop the small differences between GCV% and PCV% indicated the possibility of genetic improvement in these traits.

Broad-sense heritability estimates were high for Brix% (98.63%) and low for purity% (74.38%). Broad - sense heritability (H%) decreased for Brix, sucrose% and sugar yield , while it increased for purity%. The highest expected genetic gain was recorded in sugar yield (43.81%), while, sucrose% (20.51%) and purity% (13.65%) had low genetic gain. Similar results were reported by Mohamed and El-Taib (2007) and Mali et al. (2009), who observed that the heritability and the expected genetic advance obtained by sugar yield followed by cane yield indicate the importance of these traits for sugarcane selection in both crops.

Genotypic correlation across crops

The genotypic (r_g) correlation coefficients between all pairs of the studied characters across

crops are presented in Table 5. Cane yield showed positive and highly significant correlations with each of stalk diameter, stalk weight and number of millable canes. Our results are in agreement with Masri et al. (2015) and Kumar and Kumar (2014), who reported that the cane yield is considered as the most important character of sugarcane, was positively and significantly correlated with number of millable canes, stalk diameter and stalk weight. A strong positive correlation was recorded between sugar yield and Brix %, sucrose % and cane yield. These results are in agreement with those found by Singh et al. (2013), who showed significant positive genotypic correlations between sugar yield and each of cane weight, cane yield, Brix% and sucrose.

Conclusion

The results suggest that 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. 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. High heritability was observed for Brix%, sucrose% and number of stalks/ha, indicating direct selection of these traits will help in improvement of cane and sugar yield and identification of potential crosses and superior clones for future improvement.

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