RESEARCH ARTICLE

DIVERSITY ESTIMATES OF TEN CROSSES OF SUGARCANE (*SACCHARUM OFFICINARUM* L.) HYBRIDS FOLLOWING NORTH CAROLINA DESIGN-I

R. Alam[1], A. C. Deb[2]* and M. A. Khaleque[3]

Abstract

Nine characters of ten sugarcane hybrids were subjected to the estimation of diversity. The experiment was conducted in three different locations for two consecutive years viz. 2008-2009 and 2009-2010. Significant mean values and wide range of variation were found for all the characters. Variance based on genotype, location and year, and their interactions were found to be highly significant. The different components of variation and coefficient of variability were higher for the characters germination %, cane stalk girth (CSG), leaf length (LL), Brix % and cane yield / clump (CY/C). Broad sense heritability (h^2_b) was maximum (9.07) for germination %, followed by CYG, Brix % and cane stalk height (CSH) with a value of 3.23, 3.04 and 2.20 respectively. Genetic advance (GA) and genetic advance as percentage of mean (GA %) were low for all the characters in this study. The highest GA value of 1.50 was observed for CSH and the lowest 0.01 for NT/C, but in the case of GA%, the germination % and number of tillers/ clump (NT/C) showed the highest and the lowest values of 3.96 and 0.27 respectively. The results revealed the existence of high genetic variability in the sugarcane genotypes studied for achieving genetic progress through effective selection of the above characters.

Key words: Sugarcane hybrids, variance, coefficient of variability, heritability, genetic advance

R. Alam[1], A. C. Deb[2] and M. A. Khaleque[3]

[1]Bangladesh Sugarcane Research Institute, Ishurdi, Pabna.

[2]Department of Genetic Engineering and Biotechnology, University of Rajshahi, Bangladesh

[3]Department of Botany, University of Rajshahi, Bangladesh.
e-mail: anil_deb2001@yahoo.com

Introduction

Sugarcane cultivars are descendants of trispecific hybrids of *Saccharum officinarum*, *S. barberi* and *S. spontaneum*. The hybrid sugarcane cultivars are commercially cultivated all over the world for sugar production. However, genetic variability present in the sugarcane cultivars was a matter of concern as these are the products of six to ten generations of repeated backcrossing and intercrossing. For a successful sugarcane breeding programme it is important to identify the traits that give the highest estimates of heritability and repeatability over a number of seasons. In sugarcane breeding programme, breeders carry out experiments with promising clones from local and regional improvement programmes in the farms of various sugar mills and distilleries and compare the performance of the new clones with that of commercially grown cultivars. The yield and yield components in sugarcane are quantitative in nature and governed by polygenes, which are largely influenced by environmental factors. However, it is difficult to judge what proportion of observed variation of a particular character is heritable or due to environmental variation. In this situation, analysis of heritability is necessary (Lush, 1945). This study was carried out to estimate diversity and determine genetic variation in relation to the nature and magnitude of phenotypic and genotypic variability and to assess heritability, genetic advance and genetic advance as percentage of mean of nine agronomical and yield contributing characters in ten sugarcane genotypes.

Materials and methods

Fifteen sugarcane genotypes including five males, *viz*. I 149-00 (released as Isd 40), Isd 35, I 101-66, Co 642 and I 17-01, and 10 females, *viz*. Isd 31, Isd

29, Isd 25, I 4-71, I 157-94, I 216-92, I 34-95, I 324-86, Co 1148 and CPI 85-80 were mated as North Carolina Design I (NCD I) of Comstock and Robinson (1952) and 10 progeny families were produced. Each family consisted of five randomly selected F_1s. The field trials of these F_1's were conducted in three different locations, *viz*. BSRI-Ishurdi, Horian-Rajshahi and RSRS-Thakurgaon of Bangladesh for two consecutive years, i.e. 2008-2009 and 2009-2010. The F_1's were planted in RCB Design with three replications in plots of size 4m×4m with a row to row distance of 1 m. Fertilizers were applied according to the recommendation of BARC (2005). Data were collected for nine agronomical characters, namely germination percentage (Germi.%), number of tillers/clump (NT/C), number of millable canes/clump (NMC/C), cane stalk height (CSH), cane stalk girth (CSG), leaf length (LL), leaf breadth (LB), field brix percent (Brix%) and cane yield per clump (CY/C). Data of Germi.% and NT/C were collected after 45 and 150 days of planting, respectively and the rest at the time of harvesting of cane. The mean values of selected F_1 of a family were regarded as the hybrid's value and the data of 10 hybrids were analyzed following the biometrical techniques of analysis as developed by Mather (1949) based on the mathematical models of Fisher et al. (1932).

Results and discussion

In this study the mean values of different characters were significant against their respective standard errors. Remarkable range of variation for the characters indicated that these were quantitative in nature and under polygenic control. The highest range of variation was observed for CSH (240.40 - 285.14) followed by Germi.% (24.87 - 38.62), LL (117.92 - 130.92) and Brix % (17.07 - 19.66), while the lowest was for CSG (2.41 - 2.85) (Table 1). Similar results were observed in sugarcane by Nahar and Khaleque (1996), Kadian et al. (1997) and Tyagi and Singh (2000). The highly significant genotypic (G) item indicated that genotypes (hybrids) were significantly and genetically different from each other and justified their inclusion in the present investigation as materials (Table 2). Nahar (1997) observed highly significant difference among genotypes in sugarcane and Dutonde et al. (2006) in chilli. Other factors such as location (L), year (Y) and their different interactions (G × L, G × Y, L × Y and G × L × Y)

were highly significant for all the characters when tested against within error, which indicated that the genotype significantly interacted with the locations and years, and they differently interacted with themselves. Similar results were obtained by Nahar (1997) in sugarcane and Bicer and Sakar (2004) in lentil.

Phenotypic component of variation (s^2p) was higher than genotypic component (s^2_G), year (s^2_Y), location (s^2_L), their interaction (s^2_{GL}, s^2_{GY}, s^2_{LY} and s^2_{GLY}) and error (s^2_E) component of variation for all the characters except LL where year ($s^2 Y$) and location × year ($s^2 LY$) interaction components of variation were higher than $s^2 P$ (Table 3). These results are similar with the findings of Nahar (1997), Devagiri *et al.* (1997) and Goni et al. (2000). The difference between phenotypic and genotypic variations was greater in magnitude for all the characters studied, indicating that the location (environment) had considerable effect on these characters. The greater magnitude of phenotypic variation was also found in sugarcane by Podder (1993) and Devagiri et al. (1997).

Coefficients of variability based on phenotypic (PCV), genotypic (GCV), location (LCV) and year (YCV), their interactions (G ×Y CV, G ×L CV, L ×Y CV and G×L×Y CV) and within error (ECV) coefficient of variability of nine quantitative characters are provided in Table 4. The highest phenotypic (1096.51) and genotypic (24.11) variations were observed for CSH, followed by Germi.%, Brix % and NT/C with values of 49.83, 4.52 and 0.64 for phenotypic and 0.01, 1.78 and 0.01 for genotypic variation respectively. These results were in conformity with Mian and Awal (1979) in sugarcane and Khan et al. (2006) in Brassica. High genotypic value resulted in high phenotypic value and larger genotypic value for any character would always be helpful for effective selection. Cane height (CSH) also exhibited greater value of 10.72, 178 and 910.67, respectively for the component of variation of s^2GL, s^2GLY and s^2E and indicated better scope for improvement of this character through selection.

Majority of the characters, except LL, showed higher values for phenotypic coefficient of variability (PCV). In case of LL, year (Y) and year × location (YL)

coefficient of variation were higher than PCV. These are in agreement with the findings of Samad (1991), Hossain et al. (2000) and Khan (2009). The difference between PCV and GCV was greater in magnitude for Germi. % followed by NT/C, CY/C and Brix % (149.35 and 13.55, 33.12 and 0.17, 23.72 and 0.46, and 12.06 and 0.37, respectively) indicating that environment had considerable effect on these characters. Similar findings was reported by Podder (1993), Chubbey and Richharia (1993), Nahar (1997) and Khan (2009). The existence of higher PCV and GCV for NT/C, Brix % and CY/C showed wide scope of selection for these characters. In general coefficient of variability was low and hence difficulties to improve through selection. The low variability in cane length, cane thickness, Brix% and sucrose % in sugarcane was reported by Singh *et al*. (2002), Venkatachalam et al. (2002), Lourdusamy and Selvan (2009) and Anbanandan and Saravanan (2010). The low GCV and broad sense heritability coupled with low genetic gain were observed for all the characters under study, indicating predominance of non- additive gene action under polygenic control that makes selection difficult. These results were in conformity with Mukopadhya et al. (1986) and Geeta and Prabhakaran (1987).

In this investigation, comparatively higher broad sense heritability (h^2_b) was estimated for Germi. % (9.0746) followed by CSG, Brix % and CSH (3.2336,

3.0419 and 2.1984 respectively). This result differed with the findings of Bakshi Ram (1994), Singh et al. (1996) and Hapase and Repale (1999) who reported high heritability coupled with high genetic advance for some traits in the crop. The low values of heritability for different characters indicated that the environment constituted a major portion of total phenotypic variation for these characters. Earlier, low heritability in some traits of sugarcane was supported by Podder (1993) and Anbanandan and Saravanan (2010). Nageswara Rao et al. (1983) reported that heritability estimates were low for the characters affecting yield and Brix% and was fairly high for rust and smut resistance. Maximum genetic advance (1.4996) was observed for CSH, followed by Germi.% (1.3195), Brix % (0.0936) and CY/C (0.0317) (Table 5).

The results of this investigation showed that Germi.% had the highest value for PCV, GCV, h^2_b GA and GA%, and second and third highest value for $\sigma^2 L$ and $\sigma^2 GLY$. The characters that followed were CSH, CSG, NT/C, Brix % and CY/C. As higher magnitude of PCV was observed for all characters, it was evident that the characters included were quantitative in nature and large amount of genetic variability existed in the genotypes studied. Therefore, genetic improvement of sugarcane could be achieved through practicing effective selection of these characters.

Table 1. Ranges and means with standard errors of different characters for overall genotypes in sugarcane

Character	Range	Mean ± SE
Germination (%)	24.8683 - 38.6162	33.363 ± 0.4156
NT/C	4.5889 - 6.5839	5.3649 ± 0.0698
NMC/C	3.1500 - 4.4219	3.6172 ± 0.0424
CSH (cm)	240.4000-285.1389	262.2796 ± 1.6449
CSG (cm)	2.4056 - 2.8533	2.6139 ± 0.0163
LL (cm)	117.9156-130.9203	124.2991± 0.4626
LB (cm)	2.9656 - 3.5836	3.3433 ± 0.018
Brix	17.0706 - 19.66	18.4959 ± 0.0775
CY/C (kg)	2.0214 - 3.5194	2.7092 ± 0.0473

Table 2. Analysis of variance of genotype and its interaction with location and year
for different characters in sugarcane

			Germination (%)		
Source	df	SS	MS	VR1	VR2
Genotype(G)	9	5344.8987	593.8776	16.95**	7.59**
Location (L)	2	3994.7070	1997.3535	57.00**	25.53**
Year (Y)	1	1271.0929	1271.0929	36.27**	6.8*
G × Y	9	1682.4839	186.9427	5.33**	
G × L	18	1407.9669	78.2204	2.23**	
L × Y	2	2418.2953	1209.1476	34.51**	6.36**
G × L × Y	18	3420.1139	190.0063	5.42**	
Within error	840	29434.7749	35.0414		

			NT/C		
Source	df	SS	MS	VR1	VR2
Genotype(G)	9	122.5428	13.6159	9.97**	3.54*
Location (L)	2	78.2671	39.1336	28.64**	10.17**
Year (Y)	1	5.7217	5.7217	4.19**	
G × Y	9	114.9663	12.7740	9.35**	2.72*
G × L	18	69.2823	3.8490	2.82**	
L × Y	2	189.7521	94.8761	69.44**	20.21**
G × L × Y	18	84.5077	4.6949	3.44**	
Within error	840	1147.7088	1.3663		

			NMC/C		
Source	df	SS	MS	VR1	VR2
Genotype (G)	9	43.8021	4.8669	6.94**	3.46**
Location (L)	2	83.7945	41.8973	59.74**	29.78**
Year (Y)	1	27.6466	27.6466	39.42**	
G × Y	9	53.8623	5.9847	8.53**	
G × L	18	25.3221	1.4068	2.01**	
L × Y	2	31.7736	15.8868	22.65**	4.17*
G × L × Y	18	68.5894	3.8105	5.43**	
Within error	840	589.1242	0.7013		

			CSH (cm)		
Source	df	SS	MS	VR1	VR2
Genotype (G)	9	45002.2816	5000.2535	5.49**	
Location (L)	2	44420.2417	22210.1208	24.39**	5.68*
Year (Y)	1	19372.9282	19372.9282	21.27**	6.84*
G × Y	9	25477.0318	2830.7813	3.11**	
G × L	18	70405.6472	3911.4248	4.30**	
L × Y	2	47815.5110	23907.7555	26.25**	6.66**
G × L × Y	18	64614.8223	3589.7124	3.94**	
Within error	840	764960.0200	910.6667		

			CSG (cm)		
Source	df	SS	MS	VR1	VR2
Genotype (G)	9	5.0625	0.5625	6.41**	
Location (L)	2	5.9472	2.9736	33.88**	6.48**
Year (Y)	1	2.0881	2.0881	23.79**	8.61*
G × Y	9	2.1823	0.2425	2.76**	
G × L	18	8.2541	0.4586	5.22**	
L × Y	2	5.2990	2.6495	30.19**	6.16**
G × L × Y	18	7.7372	0.4298	4.90**	
Within error	840	73.7227	0.0878		

LL (cm)

Source	Df	SS	MS	VR$_1$	VR$_2$
Genotype(G)	9	3666.5165	407.3907	4.05**	
Location (L)	2	161408.6545	80704.3272	802.01**	135.77**
Year (Y)	1	96539.7720	96539.7720	959.37**	81.93**
G × Y	9	10605.3179	1178.3687	11.71**	2.98*
G × L	18	10699.8634	594.4369	5.91**	
L × Y	2	137563.5691	68781.7846	683.52**	174.00**
G × L × Y	18	7115.2884	395.2938	3.93**	
Within error	840	84527.6011	100.6281		

LB (cm)

Source	df	SS	MS	VR$_1$	VR$_2$
Genotype(G)	9	5.1826	0.5758	3.96**	
Location (L)	2	52.6335	26.3168	180.88**	28.56**
Year (Y)	1	2.9685	2.9685	20.40**	
G × Y	9	5.5767	0.6196	4.26**	
G × L	18	16.5881	0.9216	6.33**	
L × Y	2	108.5328	54.2664	372.99**	66.20**
G × L × Y	18	14.7545	0.81969	5.63**	
Within error	840	122.2111	0.145		

Brix%

Source	df	SS	MS	VR$_1$	VR$_2$
Genotype (G)	9	159.7280	17.7476	11.27**	3.28*
Location (L)	2	11.8710	5.9355	3.77**	
Year (Y)	1	151.5525	151.5525	96.25**	13.02**
G × Y	9	104.7749	11.6417	7.39**	
G × L	18	97.2676	5.4038	3.43**	
L × Y	2	129.7631	64.8816	41.21**	6.64**
G × L × Y	18	175.8287	9.7683	6.20**	
Within error	840	1322.6561	1.5746		

CY/C (kg)

Source	df	SS	MS	VR$_1$	VR$_2$
Genotype (G)	9	42.8734	4.7637	8.89**	3.48*
Location (L)	2	58.8761	29.4381	54.93**	21.48**
Year (Y)	1	4.4005	4.4005	8.21**	
G × Y	9	32.8691	3.6521	6.81**	3.32*
G × L	18	24.6645	1.3702	2.56**	
L × Y	2	44.0298	22.0149	41.08**	20.04**
G × L × Y	18	19.7773	1.0987	2.05**	
Within error	840	450.1993	0.5360		

* and ** indicate significance at 5% and 1% level, respectively

VR$_1$ denominator is within error and VR$_2$ denominator is respective interaction

Table 3. Phenotypic ($\sigma^2 P$), genotypic($\sigma^2 G$), location ($\sigma^2 L$), year ($\sigma^2 Y$), interaction ($\sigma^2 G \times Y$, $\sigma^2 G \times L$, $\sigma^2 L \times Y$ and $\sigma^2 G \times L \times Y$) and within error ($\sigma^2 E$) component of variation of selected sugarcane genotypes

Component	Germination (%)	NT/C	NMC/C	CSH	CSG	LL	LB	Brix	CY/C
$\sigma^2 P$	49.83	1.78	0.94	1096.51	0.11	129.11	0.19	2.23	0.64
$\sigma^2 G$	4.52	0.01	-0.01	24.11	0.00	-8.57	0.00	0.07	0.01
$\sigma^2 L$	2.63	-0.19	0.09	-5.66	0.00	39.74	-0.09	-0.20	0.02
$\sigma^2 Y$	2.75	0.01	0.06	41.03	0.00	214.31	0.01	0.33	0.01
$\sigma^2 GY$	-0.07	0.18	0.05	-16.87	0.00	17.40	0.00	0.04	0.06
$\sigma^2 GL$	-3.73	-0.03	-0.08	10.72	0.00	6.64	0.00	-0.15	0.01
$\sigma^2 LY$	6.79	0.60	0.08	135.45	0.01	455.91	0.36	0.37	0.14
$\sigma^2 GLY$	10.33	0.22	0.21	178.60	0.02	19.64	0.04	0.55	0.04
$\sigma^2 E$	35.04	1.37	0.70	910.67	0.09	100.63	0.15	1.57	0.54

Table 4. Phenotypic (PCV), genotypic (GCV), location (LCV), year (YCV), interaction (G ×Y CV, G ×L CV, L ×Y CV and G×L×Y CV) and within error (ECV) coefficient of variability of nine quantitative characters in sugarcane genotypes

Coefficient of variability	Germination (%)	NT/C	NMC/C	CSH	CSG	LL	LB	Brix	CY/C
PCV	149.35	33.12	26.11	4.21	4.21	103.87	5.55	12.06	23.72
GCV	13.55	0.17	-0.34	0.17	0.14	-6.89	-0.01	0.37	0.46
LCV	7.88	-3.46	2.40	-0.02	0.04	31.97	-2.79	-1.06	0.91
YCV	8.23	0.18	1.66	0.21	0.17	172.41	0.19	1.80	0.32
G×YCV	-0.20	3.35	1.34	-0.15	-0.16	14.00	-0.13	0.23	2.09
G×LCV	-11.17	-0.53	-2.22	0.06	0.04	5.34	0.10	-0.79	0.33
L×YCV	20.37	11.21	2.23	0.66	0.57	366.78	10.66	1.99	5.15
G×L×YCV	30.97	4.14	5.73	0.80	0.87	15.80	1.34	2.95	1.38
ECV	105.03	25.47	19.39	3.39	3.36	80.96	4.35	8.51	19.78

Table 5. Heritability (h^2_b), genetic advance (GA) and genetic advance expressed as percentage of mean (GA %) of different characters in sugarcane genotypes

Component	Germination (%)	NT/ C	NMC/C	CSH	CSG	LL	LB	Brix	CY/C
h^2_b	9.07	0.53	-1.32	2.20	3.23	-6.64	-0.26	3.04	1.92
GA	1.32	0.01	-0.03	1.50	0.02	-1.55	0.00	0.09	0.03
GA%	3.96	0.27	-0.73	0.57	0.85	-1.25	-0.07	0.51	1.17

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