

CROSSING POTENTIAL ON SEVEN QUANTITATIVE CHARACTERS IN SUGARCANE

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ABSTRACT

Seven quantitative characters viz. germination percentage, number of tillers/clump, number of millable canes/clump, cane stalk height (cm), cane stalk girth (cm), field brix and cane yield/clump were considered for inheritance study. In this study, ten crosses were carried out. Among the ten crosses the highest 7.2 g and the lowest 2.5 g fuzz were produced by the cross I 34-95 × Co 642 and cross Isd 25 × I 101-66, respectively. Seedling production and its survivability was higher from the fuzz developed from the cross I 157-94 × I 101-66 and the cross, the highest 65 number of seedlings were produced by 4.4 g fuzz and among them finally 49 were survived. The varieties were different regarding the selected characters. The maximum range of variation was observed for germination % followed by field brix, number of tillers/clump and number of millable canes/clump. In general, the magnitude of dominance component (H) was higher than that of additive component (D). Both broad and narrow sense heritability were found to be low. Comparatively high genetic advance (GA) in narrow and broad senses were shown by number of tillers/clump and germination %, respectively. The highest genetic advance expressed as percentage of mean (GA%) was recorded for number of tillers/clump in case of narrow sense heritability and for cane stalk height in case of broad sense heritability.

Key words: Sugarcane, heritability, additive and dominance components.

INTRODUCTION

Sugarcane is a major sugar yielding crop and is cultivated in more than 69 tropical and sub tropical countries throughout the world (Humbert, 1968). The major sugar producing countries of the world are Brazil, India, Cuba, China, Australia, Philippines and Thailand (Bartens, 1985). All varieties of sugarcane are either species or hybrids under the genus *Saccharum* of the family Gramineae. The genus has three cultivated species, viz., *S. officinarum*, *S. sinensis* and *S. barberi* and two wild species *S. spontanium* and *S. rubastum*. The tropical noble cane *S. officinarum* is indigenous to the New Guinea and thought to have been originated from wild species, *S. rubastum* of medium thickness and low sucrose content with chromosome number, $2n = 60$. *Saccharum officinarum* ($2n = 80$) is characterized by thick stem, soft rind, high cane and sugar yield and low fibre. *Saccharum sinensis* and *Saccharum barberi* are indigenous to north India, Bangladesh, Burma and China (Podder, 1983). These two species are characterized by thin stalk, large vigor, wide adaptability but poor cane yield and intermediate to low sucrose content. *Saccharum sinensis* having chromosome number, $2n = 116$ and *S. barberi* the $2n$ varies from 82. *S. spontanium* the wild species is perennial, having slender stalks, high tillering capacity, high fiber and low sucrose content but resistant to major diseases. The $2n$ chromosome of this species varies from 40.

The aim of any plant breeding programme is to develop commercial varieties having high production

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potential and this potential may be due to inherent genetic superiority of yield/quality and resistant to pest and diseases. But the success of breeding programme depends on the knowledge of genetic variability and the nature of gene actions governing the various qualitative traits. The model of genetic analysis of heterogeneous F₂ generation maintained by random mating was developed by Comstock and Robison's (1952) North Carolina Designs (NCDs). Since the role of heterozygosity is predominant in cross pollinated crops, a model that can measure most precisely the average degree of dominance would be the most desirable. North Carolina Designs (NCDs) are capable to estimating the two most crucial components, additive and dominance genetic variances which tend to define the breeding strategy for crop improvement.

Genetical work of sugarcane is a great problem due to the high polyploid number and the difficulties involved in selfing and crossing (Bhat *et al.*, 1962). Although several information on genetical work of different crops are available in the world but it is scanty in Bangladesh. Study of "North Carolina Design I" (NCD I) in sugarcane is not also available in the world. Keeping this view in mind, present investigation was under taken to study the nature of variability and to estimate the magnitude the gene actions following NCD I.

MATERIALS AND METHODS

Seedlings developed from 10 crosses using 15 sugarcane clones/varieties that have been maintaining in the germplasm bank of Bangladesh Sugarcane Research Institute (BSRI), Ishurdi, Pabna in the cropping year 2005-2006 were considered as the experimental materials in this investigation. The list of the clones/varieties is as follows:

Table 1. List of the clones/varieties of sugarcane.

Sl. No.	Clone/Variety	Sl. No.	Clone/Variety	Sl. No.	Clone/Variety	Sl. No.	Clone/Variety	Sl. No.	Clone/Variety
1.	Isd 35	4.	I 101-66	7.	CPI 85-80	10.	I 205-94	13.	Isd 29
2.	I 149-00	5.	I 17-01	8.	I 34-95	11.	I 4-71	14.	Isd 25
3.	Co 642	6.	Co 1148	9.	I 157-94	12.	I 216-92	15.	I 324-86

Pollen viability of the selected clones/varieties was done before set crossing. Due to higher viability of pollen Isd 35, I 101-66, I 149-00, Co 642 and I 17-01 were considered as male parents and remaining 10 clones/varieties viz. Isd 25, Isd 29, Co 1148, CPI 85-80, I 4-71, I 34-95, I 157-94, I 216-92, I 205-94 and I 324-86 were considered as female parents. Each of the males mated with two females. All the crosses were done in crossing shed at BSRI and were shown in Table 2.

Table 2. Pattern of crosses following NCD I.

Sl. No.	Female	Male	Sl. No.	Female	Male
1	Co 1148	× Isd 35	7	Isd 25	× I 101-66
2	I 4-71	×	8	I 157-94	×
3	I 34-95	× Co 642	9	I 324-86	× I 17-01
4	Isd 29	×	10	I 205-94	×
5	CPI 85-80	× I 149-00			
6	I 216-92	×			

Marcot Techniques in Sugarcane:

The selected parents, when initiate its last leaf in the field, then 2 or 3 portion of internodes were marcotted using wet sawdust and wrapping paper at the 1.5- 2 feet higher from the base of cane stalk to develop root at marcotting portion. After development of flower, selected parents were cut under the

marcotted area and were taken to the crossing shed for crossing with desired plants. Flower of male was shaken over the females for pollination up to one week.

Techniques of Analysis of Data:

The collected data were analyzed following Singh and Chaudhary, (1985) and North Carolina Design I of Comstock and Robinson, (1952).

For the present investigation, analysis of variance was done and the expectations of mean squares are as follows:

Item	df	Mean square (MS)	Expected mean square (EMS)
Blocks	b-1		
Crosses	c-1= mf-1	MS _c	$\sigma_w^2 + \sigma_{bc}^2 + b\sigma_c^2$
Males	m-1	MS _m	$\sigma_w^2 + \sigma_{bf}^2 + b\sigma_f^2 + bf\sigma_m^2$
Females males (sets)	m(f-1)	MS _f	$\sigma_w^2 + \sigma_{bf}^2 + b\sigma_f^2$
Blocks × crosses	(b-1)(mf-1)	MS _{bc}	$\sigma_w^2 + \sigma_{bc}^2$
Blocks × males	(b-1)(m-1)	MS _{bm}	$\sigma_w^2 + \sigma_{bm}^2$
Blocks × females in males	(b-1)[m(f-1)]	MS _{bf}	$\sigma_w^2 + \sigma_{bf}^2$
Within crosses	bmf(k-1)	MS _w	σ_w^2
Total	bmfk-1		

Where,

b= number of blocks (replications)

m= number of males

f= number of females crossed to each male

k= constant number of individuals scored in each of the mf progeny families

From EMS of sums due to additive variance and EMS of differences due to dominance variance, additive component (D) and dominance component (H) were measured separately as follows:

(i) Additive component D:

$$1/8 D = MS_m - MS_f/bf$$

(ii) Dominance component H:

$$1/8 D + 1/16 H = MS_f - MS_{bf}/b$$

(iii) The degree of dominance was calculated as follows: $(H/D)^{1/2}$

(iv) Heritability in narrow sense (h_n^2) and broad sense (h_b^2) was computed as follows:

$$h_n^2 = 1/2D / (1/2 D + 1/4 H + E)$$

$$h_b^2 = 1/2 D + 1/4 H / (1/2 D + 1/4 H + E)$$

Where, $E = \sigma_w^2 - 1/4 D - 3/16H$

(v) Genetic Advance: Genetic advance was calculated as per formula of Lush (1949).

$$GA = K (\sigma_p) \times \sigma_g / \sigma_p$$

Where,

GA = genetic advance

K = the selection differential in standard units, for the present study it was 2.06 at 5% level of selection intensity.

(σ_p) = square root of the phenotypic variance

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

(vi) Genetic advance as % of Mean: It was measured by the following formula:

$$GA \% \text{ of mean} = (GA / \bar{x}) \times 100$$

Where,

GA% = genetic advance as % of mean

\bar{x} = grand mean for a particular character.

RESULTS AND DISCUSSION

Among the ten crosses, I 43-95 × Co 642 produced the highest 7.2 gm fuzz followed by the cross Isd 29 × Co 642, I 4-71 × Isd 35 and Co 1148 × Isd 35, and the lowest 2.5 gm fuzz from the cross Isd 25 × I 101-66 (Table 3).

Table 3. Performance of crosses to produce seeds (fuzz).

Sl. No.	Parentage		Fuzz collected (g)
	Female	Male	
1.	Co 1148	Isd 35	5.0
2.	I 4-71		6.0
1.	I 34-95	Co 642	7.2
2.	Isd 29		7.0
1.	Isd 25	I 101-66	2.5
2.	I 157-94		4.4
1.	CPI 85-80	I 149-00	3.3
2.	I 216-92		4.4
1.	I 324-86	I 17-01	4.2
2.	Isd 31		4.0

After preservation in deep freeze to control the viability, the fuzz was shown in the month of July 2006 to raise seedlings. Data on seedling germination and its survivability is presented in Table 4. It was observed from the table that seedling production and its survivability was higher from the fuzz developed from the cross I 157-94 × I 101-66, (4.4 g fuzz) and this cross produced maximum 65 number of seedlings, among these finally 49 were survived in the field.

Table 4. Development of seedling from sugarcane fuzz and its survivability.

Crosses		Quantity of fuzz sowing (gm)	No. of seedling germinated	No. of seedling survived in nursery	No. of seedling transplanted in field	No. of seedling survived in field
Female	Male					
Co 1148	Isd 35	5.0	57	40	40	35
I 4-71		6.0	15	14	14	11
I 34-95	Co 642	7.2	33	27	27	25
Isd 29		7.0	21	17	17	14
CPI 85-80	I 149-00	3.3	23	21	21	18
I 216-92		4.1	41	33	33	32
I 157-94	I 101-66	4.4	65	52	52	49
Isd 25		2.5	28	20	20	17
I 324-86	I 17-01	4.2	19	16	16	14
Isd 31		4.0	23	20	20	18

Table 5. Ranges and means with standard errors of seven agronomical characters in sugarcane.

Characters	Range	Mean with standard error
Germination %	30.38 – 59.17	40.7499 ± 1.6239
Number of tiller/clump	2.70 – 5.93	4.446 ± 0.1657
Number of millable cane/clump	2.14 – 5.35	3.5535 ± 0.1146
Cane stalk height	2.05 – 2.99	2.4914 ± 0.0564
Cane stalk girth	1.74 – 2.22	2.0236 ± 0.0101
Field brix	11.05 – 18.62	15.3526 ± 0.1510
Cane yield/clump	1.55 – 3.78	2.8479 ± 0.0882

The estimates of range and mean with standard error of seven characters are shown in Table 5. Mean values were highly significant for all the characters when tested with their respective standard error and indicated that the varieties were different regarding these characters. Considerable range of variation was observed for all the characters, the maximum range of variation was observed for germination % followed by field brix, number of tillers/clump and number of millable canes/clump. The lowest range of variation was exhibited by cane stalk girth.

Analysis of variance was done following NCD I for seven agronomical characters are shown in Table 6. It is evident from the table that replications × crosses, replications × males and replications × females interaction were non significant against all the characters. But female sets in males interaction are found to be significant in germination %, number of tillers/clump, cane stalk girth and field brix, and rest of characters viz. number of millable canes/clump, cane stalk height and cane yield/clump showed non significant when tested against within crosses. Again, males showed significant results for all the characters except cane yield/clump. Significance of males and females in different set indicated substantial contribution of males and females, to the variation among biparental crosses.

In the present study, additive (D) and dominance (H) components were estimated and the estimated values of additive (D) and dominance (H) components, degree of dominance, narrow and broad sense heritability, genetic advances and genetic advance percentage of mean for seven agronomic characters are presented in Table 7. The table showed that the magnitude of additive component (D) was higher than that of dominance component (H) for number of tillers/clump and field brix but the latter was higher for germination %, number of millable canes/clump, cane stalk height, cane stalk girth and cane yield/clump. The dominance was negative in direction for number of millable canes/clump, cane stalk girth and cane yield/clump. These results indicated that additive component of variation was more important than the dominance component for the expression of these characters. These findings corroborated with the findings of Hogarth (1977 and 1980), Wu *et al.*, (1980 & 1988), Skinner (1981) and Hogarth and Kingston (1984) in sugarcane. Nahar and Khaleque (2000) also obtained similar results in their materials following Bip's. In the present investigation, negative additive component was estimated in germination % and cane stalk height. The negative dominance component in maximum cases is also supported by Moll *et al.*, (1960), Lindsey *et al.*, (1962) and Willium *et al.*, (1965) in maize and Nahar and Khaleque (2000) in sugarcane. Probably negative estimation of dominance component might be the genotype × environmental interaction (Hill, 1966).

The degree of dominance was measured following the ratio $(H/D)^{1/2}$ for the characters separately and the results are put in Table 7. It was observed from Table 7 that about 71% cases showed over dominance and rest of the cases showed partial dominance and both were in negative direction. Over dominance were found in germination %, number of millable canes/clump, cane stalk height, cane stalk girth and cane yield/clump and field brix and number of tillers/clump showed partial dominance. Nahar and Khaleque (2000) noticed over dominance in negative direction in sugarcane.

Table 6. Analysis of variance for seven agronomical characters in sugarcane following NCD I.

Item	df	Germination %		Number of tillers/clump		Number of millable canes/clump		Cane stalk height		Cane stalk girth		Field brix		Cane yield/clump	
		SS	MS	SS	MS	SS	MS	SS	MS	SS	MS	SS	MS	SS	MS
Replications	2	244.2876		1.0912		1.1817		0.2865		0.015		2.0542		0.701	
Crosses	9	780.576	86.7296	17.245	1.9161	12.033	1.337	2.4443	0.2715	0.216	0.0240	39.135	4.3483	9.0312	1.0034
Males	4	339.476	84.8697*	12.554	3.1386**	6	10.5031	2.6257**	1.0067	0.176	0.0441**	25.7296	6.4324**	7.5600	1.8900 ^{NS}
Females	5	441.1037	88.2207**	4.6909	0.9381**	1.5298	0.3059 ^{NS}	1.5610	0.3122*	0.039	0.0079 ^{NS}	13.4059	2.6812*	1.4711	0.2942 ^{NS}
Replications × crosses	18	396.377	22.0209 ^{NS}	3.6678	0.2037 ^{NS}	3.8175	0.21208 ^{NS}	0.2064	0.0114 ^{NS}	0.060	0.0033 ^{NS}	27.6578	1.5365 ^{NS}	2.0101	0.1116 ^{NS}
Replications × males	8	223.9394	27.9924 ^{NS}	2.1345	0.2668 ^{NS}	2.4159	0.3019 ^{NS}	0.0476	0.0059 ^{NS}	0.035	0.0044 ^{NS}	9.4665	1.1833 ^{NS}	1.2892	0.1611 ^{NS}
Replications × females in males	10	172.4376	17.2437 ^{NS}	1.5333	0.1533 ^{NS}	1.4016	0.14016 ^{NS}	0.1588	0.0158 ^{NS}	0.024	0.0024 ^{NS}	15.4109	1.5411 ^{NS}	0.7209	0.0720 ^{NS}
Within crosses	270	7157.456		105.48		106.1792	0.3932	6.1434	0.0227	2.441	0.0090	334.4388	1.2387	330.9675	1.2258
Total	299														

*, ** and NS indicates significant at 5% and 1% level and non significant, respectively.

Table 7. Estimates of different genetic components for seven agronomical characters in sugarcane.

Components	Germination %	Number of tillers/clump	Number of millable canes/clump	Cane stalk height	Cane stalk girth	Field brix	Cane yield/clump
Additive (D)	-4.4680	2.9336	3.0928	-0.0808	0.0480	5.0016	2.1272
Dominance (H)	387.4800	-1.6816	-5.3024	1.7424	-0.0672	-3.9227	-3.0704
Degree of dominance (H/D ^{1/2})	-9.3125	-0.7571	-1.3093	-4.6437	-1.1832	-0.8856	-1.2014
Narrow sense heritability (h ² _n)	-0.0077	0.3235	0.3234	-0.1279	0.2443	0.1867	0.0844
Broad sense heritability (h ² _b)	0.3283	0.2307	0.0504	1.2581	0.0733	0.1135	0.0234
Genetic advance in narrow sense (GA _n)	-0.3808	1.4508	0.9286	-0.3419	0.1348	1.3840	0.5831
Genetic advance in broad sense (GA _b)	16.2391	1.0346	0.1447	3.3469	1.9975	0.8414	0.1624
Genetic advance expressed as % of mean in narrow sense (GA% _n)	-0.9344	31.6837	26.1319	-	6.6650	9.0151	2.8479
Genetic advance expressed as % of mean in broad sense (GA% _b)	39.8506	22.5944	4.0720	13.7232	134.338	1.9975	5.4805
				1			5.7024

Heritability estimated was computed separately both in narrow sense (h^2_n) and broad sense (h^2_b) based on components of variation of all the characters are given in Table 7. Both narrow and broad sense heritability values were low for the characters indicating that environmental effect upon the expression of the characters. In this investigation, heritability in narrow sense was lower than broad sense in germination % and cane stalk height but in the rest of the characters it is higher than broad sense due to dominance in negative direction.

Genetic advance (GA) and genetic advance expressed as percentage of mean (GA%) were estimated as low both in narrow sense (h^2_n) and broad sense (h^2_b) and are shown in Table 7. In case of number of tillers/clump, number of millable canes/clump, field brix and cane yield/clump genetic advance in narrow sense was higher than broad sense. The highest GA% in narrow sense was recorded for number of tillers/clump followed by number of millable canes/clump and in broad sense noted for cane stalk height followed by germination %.

Thus, the present investigation revealed that additive gene action was important in the expression of most of the characters under studied. Moreover, for five characters namely number of tillers/clump, number of millable canes/clump, cane stalk girth, field brix and cane yield/clump showed comparatively high above of narrow sense heritability than broad sense heritability might be best to improve through selection for higher yield.

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