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Studies on genetic variability parameters for yield and its component traits in advance hybrid clones of sugarcane

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Abstract

The present investigation was undertaken to estimate the genetic parameters on 14 quantitative traits of 35 clones selected from clonal-I population derived from a cross Co 7204 x Co Pant 97222 and 7 commercial sugarcane genotypes. Analysis of variance showed significant differences among the clones for all the characters studied, indicating the presence of a considerable amount of variability in the genetic material. The transgressive segregants *viz.*, SNK13101 and SNK13142 exhibited significantly superior cane and sugar yield over both the parents, with better potential compared to Co86032. These clones could be advanced for detailed yield trails for potential identification as parents and/or commercial clones in future. The estimates of GCV, PCV, heritability (broad sense) and genetic advance as percent of mean were recorded high for cane yield, commercial cane sugar yield, number of millable cane, brix yield and green top yield indicating that simple selection would be helpful for the improvement of these traits as these are governed by additive gene action whereas cane height recorded moderate heritability along with genetic advance suggesting that characters are governed by both additive and non-additive gene action.

Keywords: Genetic advance, heritability, variability, GCV, PCV, sugarcane

Introduction

Sugarcane is an economically important perennial, tall monocotyledon that belongs to the Andropogonae tribe of the grass family (Poaceae, subfamily Panicoide), class Monocotyledons and order Glumaceae. In general, the modern cultivated sugarcane varieties (*Saccharum* spp.) are derived from artificial interspecific hybridization between *S. officinarum* (2n = 80 chromosomes) and *S. spontaneum* (2n = 40–128) and also from back crosses involving the three major species namely *Saccharum officinarum* L., *Saccharum spontaneum* L. and *Saccharum sinensis* L. India is the original home of *Saccharum* species. New Guinea is the centre of origin of *S. officinarum*.

Globally sugarcane is cultivated in an area of 25.97 million hectares producing 1.84 billion tons with the productivity of 70.85 t ha⁻¹ (<http://www.fao.org/faostat>; 2017). India is next only to Brazil with respect to cane area and sugar production. In India, it is cultivated in an area of 4668.7 thousand hectares with the production of 337694.5 thousand tonnes with average productivity of 72.34 tonnes per hectare (<https://www.indiaagrstat.com>; 2017-18).

The major constraints in sugarcane production are low yield, lack of availability stable performing clones over different agro-ecological regions, abiotic stresses like drought, soil salinity and biotic stresses like diseases and pests. In this context, there is a huge demand for the development of sugarcane varieties with high tonnage and concentration of sucrose percent. Hence understanding the various genetic parameters is a basic step for improvement of any crop. Estimation of genetic variability in conjunction with heritability and genetic advance gives an idea of the possible improvement of the character through selection. Therefore, the present study was undertaken to assess genetic parameters for quantitative traits in sugarcane hybrid clones of a cross involving tropical Co7204 and subtropical Co Pant 97222

Materials and Methods

The trial was conducted at S. Nijalingappa Sugar Institute, Zadshapur farm during 2017-18. The experimental material for the present investigation consisted of 35 clones selected from clonal-I population derived from a cross Co 7204 x Co Pant 97222 and 7 commercial sugarcane genotypes. The experiment was laid out in RBD with two replications and all the recommended package of practices for cultivation of sugarcane crop was followed. Three sample canes were drawn at random from each replication and data were recorded for characters *viz.*, number of millable canes at 300 (DAP) days after planting (NMC), Single cane

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weight (SCW), Cane height (CH), Plant height (PH), Girth of cane (GTH), Number of Internodes (INT), Internodal length (INL), Green top yield (GTY), Brix percent (CB) at 10th month, Sucrose percent (%) at 10th month, Commercial cane sugar percent, Commercial cane sugar yield (CSSY), Brix yield (BY) and Cane yield (CY).

Statistical Analysis. The analysis of variance (ANOVA) was worked out according to the procedure of Randomized Block Design for each character as per methodology advocated by Panse and Sukhatme (1967) [10]. The analysis of variance was used to derive variance components (Cochran and Cox, 1957).

Estimation of the genotypic and phenotypic coefficient of variation: The formulae used to calculate PCV and GCV were given by Burton and De vane (1953) [4].

Heritability (Broad Sense): Heritability in broad sense was estimated by the formula given by Johnson *et al.* (1955) [7]. The heritability was categorized as low, moderate and high as given by Robinson *et al.* (1949) [13].

Genetic Advance: The estimates of genetic advance were obtained by the formula given by Lush (1949) [9], Johnson *et al.* (1955) [7] and Allard (1960) [3]. The range of genetic advance is classified as suggested by Johnson *et al.* (1955) [7].

Results and Discussion

Analysis of variance showed significant differences among the clones for all the characters studied, indicating the presence of a considerable amount of variability in the materials (Table 1 & 2). The transgressive segregants *viz.*, SNK13101 and SNK13142 exhibited significantly superior cane and sugar yield over both the parents and popular standard Co 86032. The clone, SNK 13096 also exhibited high mean performance for most of the traits studied *viz.*, brix yield, commercial cane sugar yield, commercial cane sugar percent, brix percent, Sucrose percent, green top weight, internodal length, number of millable canes and cane height.. Hence, these clones can be advanced for detailed yield trails for potential identification of parents and /or commercial clones in future.

In the present study, the estimates of the phenotypic coefficient of variation (PCV) for all the characters were higher than the estimates of the genotypic coefficient of variation (GCV), suggesting that the apparent variation is not only due to genetic but also due to environmental influences (Table 3). The highest estimates of phenotypic coefficients of variation and genotypic coefficient of variation were recorded for commercial cane sugar yield, green top yield, brix yield, cane yield, and number of millable canes respectively. All traits exhibited a relatively low magnitude of the difference between PCV and GCV indicating a less environmental influence on these traits (Patil *et al.*, 2014) [11]. These results are in accordance with the findings of Swamy Gowda *et al.* (2016) [15] for commercial cane sugar yield and cane yield, Guddadamath (2013) [6] for commercial cane sugar yield and cane yield and number of millable canes, Ahmed A.O. and Obeid A (2012) [1] for number of millable canes, cane yield, commercial cane and sugar yield.

Moderate estimates of the genotypic coefficient of variation and phenotypic coefficient of variation were recorded for single cane weight followed by cane height, the girth of cane and number of internodes. These results are in agreement with the findings of Guddadamath (2013) [6] for cane height and

number of internodes; Ahmed A.O. and Obeid A (2012) [1] cane height and the girth of cane; D.N. Kamat and J. R. P. Singh (2001) [8] single cane weight and cane height.

Heritability measures the relative amount of heritable portion of variability. It is a good index of the transmission of characters from parents to offspring. The perusal of Table 3 revealed the estimates of heritability in broad sense for fourteen characters studied, which ranged from 25.2 to 89 percent. High heritability was recorded for single cane weigh, cane yield, commercial cane sugar yield, number of internodes, number of millable canes, brix yield, the girth of cane, green top yield, and plant height respectively. This indicates that the least influence of environment on the expression of these characters. Therefore, for improving these traits through simple selection will be more effective on the basis of *per se* performance. These results are in correspondences with the findings of Swamy Gowda *et al.* (2016) [15] for single cane weigh, cane yield, brix yield, commercial cane sugar yield, girth of cane and number of millable canes; Relisha Ranjan *et al.* (2017) [12] for commercial cane sugar yield, cane yield, plant height, girth of cane and single cane weight; Guddadamath (2013) [6] for cane yield, commercial cane sugar yield, and number of millable canes.

Heritability estimates along with genetic advance are more useful than heritability alone in predicting the effectiveness of selection. Further, the heritability estimates coupled with expected genetic advance as percent of mean indicates the mode of gene action in choosing an appropriate breeding methodology. High heritability coupled with high genetic advance as percent of mean recorded for single cane weight, cane yield, commercial cane sugar yield, number of internodes, number of millable canes, brix yield, girth of cane and green top yield, indicate that additive gene action is involved in the genetic control of these traits. Hence, simple selection may help in improving these traits. These results are in correspondence with the findings of Swamy Gowda *et al.* (2016) [15] for commercial cane sugar yield, cane yield, single cane weight, number of internodes, girth of cane and number of millable canes, Relisha Ranjan *et al.* (2017) [12] for Cane yield, single cane weight and commercial cane sugar yield and Alam *et al.* (2017) [2] for single cane weight and number of millable canes Moderate heritability coupled with moderate genetic advance as percent of mean recorded for cane height Swamy Gowda *et al.* (2016) [15] and D.N. Kamat and J. R. P. Singh (2001) [8];

From the above discussion it can be concluded that, high estimates of GCV, PCV, heritability (broad sense) and genetic advance as percent of mean were recorded for cane yield, commercial cane sugar yield, number of millable cane, brix yield and green top yield indicating that simple selection would be helpful for the improvement of these traits as these are governed by additive gene action. The characters such as number of millable canes, girth of cane and number of internodes showed moderate estimates of GCV, PCV and high estimates of heritability (broad sense) and genetic advance as percent of mean indicating that there is high influence of environment on these characters, whereas cane height showed moderate heritability and genetic advance suggesting that character is governed by both additive and non additive gene action. Further, the transgressive segregants *viz.*, SNK 101 and SNK 142 can be advance for yield trial as it exhibited significantly high mean performance for cane yield and sugar yield compared to best standard Co 86032 and over both parents.

Table 1: Analysis of variance for fourteen characters in forty four sugarcane clones

Sl. No.	Characters (s)	Mean sum of squares		
		Replications (df: 1)	Genotypes (df:46)	Error (df:46)
1	Numer of Millable Canes (per plot)	127.68	238.80**	17.03
2	Single cane weight (kg)	0.01	0.09**	0.01
3	Cane height (m)	0.24	0.20**	0.07
4	Plant height (m)	0.01	0.11**	0.03
5	Girth of cane (cm)	0.00	0.29**	0.02
6	Number of Internode	0.22	9.48**	0.67
7	Internodal length (cm)	7.64	4.54*	2.71
8	Green top yield (t/ha)	30.10	58.06**	9.57
9	Brix percent (%)	0.00	3.41**	0.89
10	Sucrose percent (%)	1.74	2.88**	0.89
11	Purity percent (%)	1.85	1.62**	0.63
12	Commercial cane sugar percent (%)	10.59	25.96**	1.82
13	Commercial cane sugar yield (t/ha)	18.34	72.03**	5.42
14	Brix yield (t/ha)	352.64	1536.06**	95.79

* Significant at 5% level; ** Significant at 1% level

Table 2: Mean performance of forty four sugarcane clones for fourteen characters

SL. NO	NAME	NMC	SCW	CH	PH	GTH	INT	INL	GTY	CB	CP	CCS%	CCSY	BY	CY
1	Co 94012	52.50	1.02	1.92	3.40	2.59	18.67	10.28	28.59	23.45	19.92	13.88	13.73	23.20	98.94
2	Co 92005	41.50	1.33	1.92	3.38	2.83	20.00	9.62	14.20	19.95	17.17	12.04	12.20	20.26	101.67
3	SNK 044	33.00	1.14	2.36	3.68	2.50	18.17	12.98	10.92	22.20	19.17	13.47	9.35	15.39	69.37
4	Co 86032	50.00	1.19	1.74	3.47	2.39	16.67	10.44	19.49	20.45	17.09	11.81	15.53	26.90	110.13
5	SNK 632	35.50	1.43	1.80	3.69	3.25	18.34	9.91	16.06	22.45	18.49	12.68	11.86	21.15	94.19
6	CoM 0265	37.00	1.33	2.33	3.53	2.74	20.00	11.61	11.91	21.45	17.48	11.92	10.72	19.32	89.97
7	Co 2001-15	42.50	1.10	2.35	3.75	2.35	21.34	11.03	13.20	19.70	16.40	11.31	9.77	16.94	86.12
8	Co 7204	28.00	0.84	2.30	3.45	2.14	15.17	15.24	9.84	21.70	18.90	13.34	5.78	9.36	43.08
9	Co Pant 97222	29.50	0.79	1.68	3.38	2.56	13.00	12.89	9.37	22.70	18.69	12.82	5.46	9.69	42.69
10	SNK-13012	43.00	0.87	2.11	3.69	2.23	16.17	13.07	12.15	19.70	16.10	10.99	7.62	13.66	69.26
11	SNK-13013	39.00	0.86	2.02	3.60	2.15	15.50	13.03	13.58	21.45	18.03	12.49	7.76	13.33	62.12
12	SNK- 13033	42.00	0.99	2.24	3.63	2.26	16.00	13.98	14.13	21.45	17.92	12.38	9.64	16.62	77.20
13	SNK-13035	34.50	1.04	2.13	3.58	2.61	14.17	15.06	13.14	21.95	18.15	12.47	8.22	14.50	66.05
14	SNK-13044	33.00	1.62	2.34	3.47	2.73	22.34	10.47	14.04	19.20	16.10	11.14	11.07	19.10	99.24
15	SNK-13148	27.50	1.15	1.78	3.02	1.98	12.33	14.72	6.19	21.70	16.98	11.31	6.67	12.69	58.73
16	SNK-13049	26.50	1.23	2.29	3.65	2.55	18.50	12.35	8.48	20.95	17.85	12.46	7.62	12.77	60.44
17	SNK-1350	15.50	1.00	2.28	3.39	2.64	17.17	13.26	5.48	20.20	16.27	11.02	3.17	5.80	28.72
18	SNK-13053	36.50	1.20	2.39	3.92	2.29	17.17	13.91	15.76	19.95	16.65	11.49	9.27	16.10	80.71
19	SNK-13054	30.50	1.14	2.40	3.90	2.23	18.84	12.72	10.26	21.45	17.58	12.03	7.73	13.82	64.46
20	SNK-13067	38.00	1.69	2.63	3.93	3.34	20.50	12.82	15.71	22.45	17.98	12.14	14.37	26.74	118.70
21	SNK-13071	51.50	1.01	2.44	3.91	2.61	20.33	12.01	14.50	23.20	19.76	13.79	13.28	22.30	95.90
22	SNK-1376	56.50	0.96	2.24	3.75	2.40	16.67	13.43	20.97	22.70	18.93	13.07	13.11	22.76	100.22
23	SNK-13095	53.50	1.01	1.99	3.40	2.42	18.83	10.53	23.97	18.45	15.55	10.79	10.93	18.67	100.39
24	SNK-13096	51.50	1.26	2.67	3.71	2.35	18.00	14.83	23.75	23.45	20.69	14.69	17.59	28.11	119.86
25	SNK-13101	50.00	1.47	2.73	3.95	2.56	18.34	14.94	24.96	20.70	17.66	12.33	16.74	28.06	135.42
26	SNK-13109	26.50	1.12	2.50	3.48	2.59	17.34	14.43	14.81	18.95	15.71	10.81	5.91	10.35	54.55
27	SNK-13120	26.00	1.26	2.28	3.63	2.85	18.17	12.52	10.57	21.45	18.29	12.77	7.72	12.98	60.63
28	SNK-13123	37.00	0.94	2.18	3.17	2.49	19.17	11.36	16.31	19.70	16.26	11.16	7.17	12.68	64.38
29	SNK-13125	31.50	1.14	2.38	3.33	2.60	17.67	13.44	12.82	21.20	17.39	11.90	7.84	14.04	66.25
30	SNK-13134	36.50	1.10	2.40	3.87	2.65	16.84	14.30	15.10	19.95	16.81	11.66	8.72	14.91	74.71
31	SNK-13135	51.50	1.01	2.44	3.53	2.27	18.34	13.32	21.14	20.70	16.99	11.63	11.13	19.86	96.00
32	SNK-13142	49.00	1.46	3.10	3.96	2.51	22.34	13.84	21.88	20.70	17.72	12.40	16.47	27.44	132.41
33	SNK-13144	32.00	1.00	2.60	3.70	4.29	19.17	13.55	13.39	21.70	17.97	12.36	7.26	12.75	58.98
34	SNK-13145	39.00	1.09	2.75	3.77	2.24	20.84	13.17	18.15	20.70	17.72	12.40	9.75	16.30	78.52
35	SNK-13153	46.00	1.17	2.16	3.59	2.37	17.33	12.48	19.95	20.45	17.21	11.94	11.95	20.44	99.69
36	SNK-13158	28.00	1.13	2.48	3.98	2.35	17.84	13.91	13.99	20.45	17.24	11.96	6.97	11.89	58.23
37	SNK-13178	24.00	0.95	2.17	3.90	2.34	19.34	11.20	11.12	19.70	16.55	11.47	4.60	7.92	40.36
38	SNK-13187	25.50	1.04	2.13	3.39	2.24	17.50	12.16	7.67	21.95	18.07	12.39	6.05	10.72	48.84
39	SNK-13188	16.00	1.41	2.59	3.56	2.47	18.34	14.10	6.39	20.95	17.23	11.80	4.93	8.75	41.79
40	SNK-13196	26.50	0.73	1.49	3.13	2.10	13.67	10.87	10.07	19.70	16.54	11.46	4.13	7.07	35.93
41	SNK-13201	38.00	0.99	1.91	3.48	2.43	17.50	10.88	14.42	19.45	16.36	11.34	7.89	13.52	69.70
42	SNK-13205	30.50	1.18	2.24	3.77	2.42	17.17	13.05	16.02	18.95	15.58	10.67	7.06	12.55	66.28
43	SNK-13207	34.50	0.78	2.12	3.52	2.64	18.00	11.74	16.97	19.20	15.70	10.73	5.25	9.45	49.27
44	SNK-13209	57.50	1.14	2.05	3.69	2.41	17.50	11.73	24.53	18.95	16.22	11.35	13.72	22.92	120.96
	Mean	37.36	1.12	2.25	3.60	2.52	17.87	12.66	14.91	20.86	17.43	12.04	9.40	16.22	77.55
	C.V.	11.05	6.48	11.99	4.48	6.10	4.58	13.01	20.75	4.51	5.40	6.61	14.35	14.35	12.62
	F ratio	14.02	17.20	2.70	4.10	12.17	14.17	1.67	6.07	3.85	3.24	2.56	14.26	13.30	16.04
	F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	S.E.	2.92	0.05	0.19	0.11	0.11	0.58	1.16	2.19	0.67	0.67	0.56	0.95	1.65	6.92
	C.D. 5%	8.32	0.15	0.54	0.33	0.31	1.65	3.32	6.24	1.90	1.90	1.61	2.72	4.69	19.74

Table 3: Mean, the coefficient of variability, heritability (broad sense) and genetic advance as percent of the mean for fourteen characters in sugarcane.

Sl. No.	Character (s)	Mean	Range		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of the mean (%)
			Min.	Max.	Genotypic	Phenotypic			
1	Numer of Millable Canes (per plot)	37.36	15.50	60.00	28.18	30.27	86.70	20.20	54.05
2	Single cane weight (kg)	1.12	0.73	1.69	18.45	19.56	89.00	0.40	35.87
3	Cane height (m)	2.25	1.49	3.10	11.06	16.31	46.00	0.35	15.45
4	Plant height (m)	3.61	3.02	3.98	5.58	7.16	60.80	0.32	8.97
5	Girth of cane (cm)	2.52	1.98	4.29	14.41	15.65	84.80	0.69	27.35
6	Number of Internode	17.87	12.33	22.3	11.75	12.61	86.80	4.03	22.54
7	Internodal length (cm)	12.66	9.62	15.24	7.55	15.04	25.20	0.99	7.81
8	Green top yield (t/ha)	14.91	5.48	28.59	33.06	39.01	71.70	8.59	57.62
9	Brix percent (%)	20.86	18.45	23.45	5.39	7.03	58.80	1.76	8.51
10	Sucrose percent (%)	17.43	15.55	20.69	5.72	7.87	52.90	1.49	8.57
11	Purity percent (%)	12.04	10.67	14.69	5.84	8.82	43.80	0.96	7.95
12	Commercial cane sugar percent (%)	9.40	3.17	17.59	36.96	39.65	86.90	6.67	70.98
13	Commercial cane sugar yield (t/ha)	16.22	5.80	28.11	35.58	38.37	86.00	11.03	67.99
14	Brix yield (t/ha)	77.55	28.72	135.42	34.60	36.83	88.30	51.94	66.97

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