

Variability Trends for Brix Content in General Cross Combinations of Sugarcane (*Saccharum* spp.)

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ABSTRACT

The study was undertaken to determine the potential of general cross combinations in sugarcane, obtained by open pollinating the female parents CoSnk 05103, Co8313, Co 1148, CP 44-101 and CoSnk 03632, to generate variants for Brix content and frequency distribution pattern of variants. Using Brix as selection criterion, 1638 seedlings raised from five general cross combinations, comprising high sugared commercial varieties were investigated. The Brix values of test genotypes evaluated in augmented design, inferred the generation of highly variable population with significant differences. Highly significant negatively skewed leptokurtic distribution of the progeny for Brix content in GCs obtained from Co 8313, CoSnk 05103 and CoSnk 03632 female parents indicated that the tail on the left side of probability density function was longer than the right side and the bulk of the values (including the median) lie to the right of the mean. This indicated that Co 8313, CoSnk 05103, and CoSnk03632 are potential female parents to generate high frequency of elite seedlings for Brix. The evaluation of elite clones from each GC in the next clonal stage led to a higher selection rate in progenies of Co 8313, CoSnk 05103, and CoSnk 03632 as compared to other GCs. The study suggested the scope of general cross combinations, which are less laborious, cost effective and generally yield more fuzz, to generate elite segregants for quantitative traits like sucrose content in sugarcane.

MODERN sugarcane (*Saccharum* spp.) is an important grass that contributes 60 per cent of the raw sugar produced worldwide and has a high biofuel production potential. It was created about a century ago from the combination of the polyploid species *S. officinarum* and *S. spontaneum* (D' hont *et al.*, 1995). Proper exploitation of variability in a crop like sugarcane with a complex ploidy and a high level of heterozygosity is a complicated process (Babu *et al.*, 2009). The main difficulty in improvement of sugarcane is selection at seedling stage. Further, it is a vital stage of selection because it provides the base population for remaining and more effective stages of selection (Ram Bakshi *et al.*, 2009). New sugarcane cultivars are developed through the selection of vegetatively propagated genotypes, obtained from true seed after hybridization of superior parents. Selection at early stages in sugarcane breeding programmes is generally based on refractometer Brix as the only juice quality characteristic. Many breeders indicated that heritability of juice quality in sugarcane, including Brix (Shanthi *et al.*, 2005) is moderate to high and therefore, can be improved with the correct selection pressure. Brix was highly correlated with sucrose and selection for high sucrose could begin as early stage and most of the

genetic variation for Brix could be attributed to additive effects (Ram Bakshi *et al.*, 1997).

The main objective of the experiment was to investigate the potential of general cross combinations which are not laborious to execute like biparental crosses in sugarcane and to estimate the influence of maternal parent on frequency of elite segregants in the population for Brix value, a trait of high heritability and an indicator of sugarcane quality. Five general cross combinations were effected from five open pollinated female parents sown in same block at National Hybridization Garden, SBI, Coimbatore, India in 2013. In GCs female parents were allowed to open pollinate and fuzz was hence, collected from female arrows. The seedling stage refers to a selection stage where clones are grown from true seed (fuzz) after hybridization and the subsequent stage that develops from regeneration of the seedling clumps after harvest, is referred to as ratooned seedling stage. After germination tests, the fuzz was sown in the ground nursery, three-month-old seedlings were transplanted to main field and all seedlings of crosses were evaluated as per the specifications of AICRP(sugarcane) at ZARS, V.C. Farm, Mandya.

The experiment was established as an augmented design along with three checks *viz.*, Co 99463, Co 86032 and Co 62175. Six meters of row length with four feet of row to row spacing were maintained. Seedling to seedling spacing was one ft. 1638 seedlings derived from different crosses were evaluated for Brix using a hand refractometer after 270 days of transplanting. The Brix was recorded from seedling and the average Brix was used for all statistical analysis. The individual seedlings were evaluated on

unreplicated plots in an augmented design. Descriptive statistics were worked out for each cross, the class intervals were constituted for Brix. The frequency distribution of progeny for Brix content for each general cross combination was determined and represented graphically. The seedlings were evaluated in an augmented design using Brix as the selection criterion. The critical differences and standard error of deviation for a total of 1638 test genotypes and test treatment are presented in Table Ia, b and c.

TABLE Ia
Analysis of variance for Brix value of the progenies from CoSnk 03632 cross based on augmented design.

SOV	DF	SS	MS	F	5%	1%
Treatments	293	1702.141	5.8094	35.7866	2.315*	3.397**
Checks	2	13.7013	6.8507	42.2012	3.885*	6.927**
Test entries	290	1556.193	5.3662	33.0566	2.315*	3.398**
Check v test entries	1	132.2463	132.2463	814.659	4.747*	9.330**
Error	12	1.948	0.1623			
Total	305	1704.089				

Parameters	SE	SED	CD(P=05)	CD(P=01)
Test Entries	0.4029	0.5698	1.2422	1.7436
Checks	0.1802	0.2548	0.5555	0.7797
Test V Check		0.4414	0.9622	1.3506

TABLE Ib
Analysis of variance for brix value of the progenies from Co 8313 cross based on augmented design

SOV	DF	SS	MS	F	5%	1%
Treatments	933	4373.991	4.6881	28.8794	2.302*	3.372**
Checks	2	13.7013	6.8507	42.2012	3.885*	6.927**
Test entries	930	4168.541	4.4823	27.6117	2.302*	3.372**
Check v test entries	1	191.7486	191.7486	1181.203	4.747*	9.330**
Error	12	1.948	0.1623			
Total	945	4375.939				

Parameters	SE	SED	CD(P=05)	CD(P=01)
Test Entries	0.4029	0.5698	1.2422	1.7436
Checks	0.1802	0.2548	0.5555	0.7797
Test V Check		0.4414	0.9622	1.3506

TABLE IC
Analysis of variance for brix value of the progenies from CoSnk 05103 cross based on augmented design

SOV	DF	SS	MS	F	5%	1%
Treatments	412	2128.304	5.1658	31.8221	2.309*	3.387**
Checks	2	13.7013	6.8507	42.2012	3.885*	6.927**
Test entries	409	1976.749	4.8331	29.7729	2.310*	3.387**
Check v test entries	1	137.8542	137.8542	849.2044	4.747*	9.330**
Error	12	1.948	0.1623			
Total	424	2130.252				

Parameters	SE	SED	CD(P=05)	CD(P=01)
Test Entries	0.4029	0.5698	1.2422	1.7436
Checks	0.1802	0.2548	0.5555	0.7797
Test V Check		0.4414	0.9622	1.3506

The heterogeneity was observed within a given cross. The treatments were, therefore adjusted and compared using respective critical differences. Highly significant differences in the test genotypes for Brix content indicated the generation of highly variable population from general cross combinations in sugarcane. The augmented design, though not equal to lattice design in statistical efficiency, is quite useful to sugarcane breeders who have to evaluate a large number of clones as precisely as possible, no possibility of further reduction of error variance as in lattice design. The highest values of L.S.D. and C.V. are usually recorded in case of augmented design (Bhagyalakshmi *et al.*, 1999).

The general statistics for each type of general cross combination *viz.*, CoSnk 05103 (GC I), Co8313 (GC II), CoSnk 03632 (GC III), Co 1148 (GC IV) and CP 44-101 (GC V) were described in Table II. The mean Brix was 19.09 in the progeny of GC IV followed closely by GC III, GC I, GC II and GC V.

None of the seedlings had mean Brix value lower than 10.0, whereas, in GC I the lowest limits of the variants was 9.50. Difference were observed in coefficient of variance in all general cross combinations (19.57 in GC IV to 13.67 in GC II). To assess the distribution of progeny and its deviation from a normal distribution, skewness and kurtosis in progeny of each GC was worked out.

Left skewed distribution (Skewness<0) was observed in all GCs though the value was statistically significant in GC I, II, III and V. thereby indicating that most values are concentrated on the right of the mean (Table II). Graphically, the frequency distribution in the progeny of each GC is presented in Fig. 1, 2 and 3. Significant leptokurtic distributions in progeny of GCI, GCII and GC III derived from Cosnk 05103 and Co 8313, inferred that distribution of progeny presented higher peaks around the mean compared to normal distributions, which leads to thick tails on both sides. This signified that the most of the seedlings from CoSnk 05103 and CoSnk 03632 performed superior to the population mean and in the direction of higher scale and hence, surfaced as potential female parents to generate high frequency of elite seedlings for Brix content. The non- significant skewness was observed in the progeny of Co 1148 with the low percentage of extreme segregants.

Based on Brix value, the categorization of seedlings in three classes *viz.*, poor (<16.0 Brix content), average (16.1-20.0 Brix content) and elite (> 20.1.0 Brix content), was done (Table III). Cp-44-101 generated the highest per cent of elite (33.0) seedlings followed by GC III (29.60) ,GCIV (27.30) and GCI (26.80) and GCII Co8313 (14.70) having Brix content >20 per cent.

TABLE II

Descriptive statistics for HR brix in progeny of different general cross combinations

General cross combination	Total no. of seedlings	Mean	Min	Max	Median	Variance	Skewness	Kurtosis	CV
CoSnk 03632 (GC III)	291	18.93	10.50	22.70	17.00	5.366	-1.134*	1.285	15.29
Co 1148 (GC IV)	11	19.09	17.00	21.50	19.00	1.741	-0.320	-0.556	19.57
CP 44-101 (GC V)	23	17.08	12.00	20.50	18.00	5.864	-0.837*	-0.74	18.96
Co 8313 (GC II)	931	18.37	10.00	23.00	19.00	4.482	-0.893*	0.913	13.67
CoSnk 05103 (GC I)	410	18.89	9.50	22.50	19.00	4.833	-1.164*	2.329	14.15

TABLE III

Performance of progeny in different general cross combinations

General cross combination	% Poor seedlings/ population (<16.0 HR Brix)	% Average seedlings/ Population (16.1 - 20.0 HR Brix)	% Elite seedlings/ Population (>20.1 HR Brix)
CoSnk 03632 (GC III)	13.7	56.7	29.6
Co 1148 (GC IV)	-	72.7	27.3
CP 44-101 (GC V)	26.1	40.9	33
Co8313 (GC II)	15.4	69.9	14.7
CoSnk 05103 (GC I)	9.00	64.2	26.8

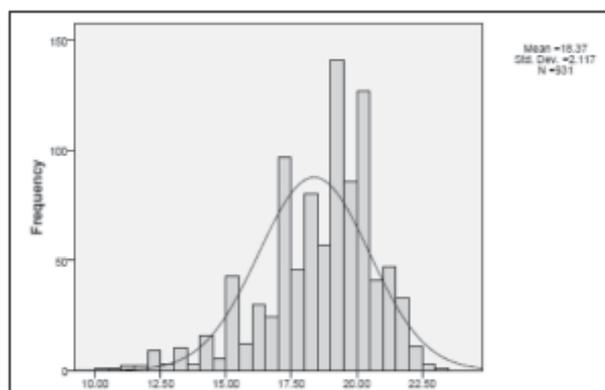


Fig. 2: Frequency distribution of progeny of general cross combination of Co8313 (GC II), for Brix content.

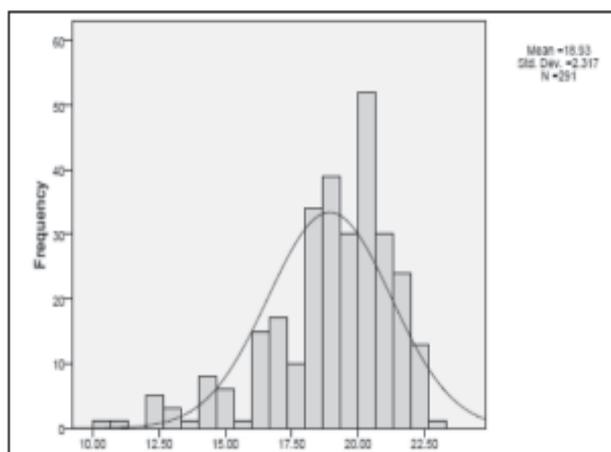


Fig. 1: Frequency distribution of progeny of general cross combination of CoSnk 03632 (GC III) for brix content.

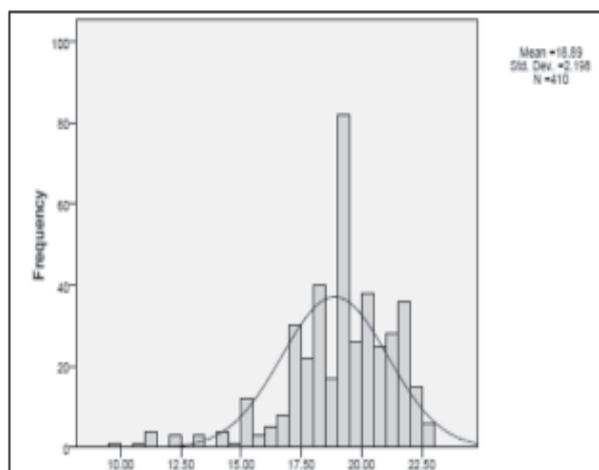


Fig. 3: Frequency distribution of progeny of general cross combination of CoSnk 05103 (GC I), for brix content.

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(Received : May, 2016 Accepted : June, 2016)