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VARIABILITY PATTERN IN CULTIVAR x SPECIES PROGENIES IN SUGARCANE

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ABSTRACT

Variability pattern of the progenies (25 per mating group) of the Indian commercial hybrids crossed with *S. officinarum* (HO), *S. spontaneum* (HS) and *S. barberi/sinense* (HB) were studied. The HB mating group had clear advantage over HO and HS groups for quality characters, whereas HO genotypes were superior for cane yield and its contributing characters, except NMC. The maximum genetic variability was observed among HS progenies for all the characters except cane yield. The HB mating group was found advantageous for obtaining promising clones as compared to other groups. It is suggested that a more extensive use of advanced breeding material could be made in a deliberate programme of bridging crosses amongst the progenies of three mating groups for the genetic base broadening of the Indian sugarcane cultivars.

Key words: Variability, mating groups, genetic base broadening, *Saccharum* species.

Crossing of clones of *Saccharum* species to a commercial hybrid forms a dependable and quick method of incorporation of new and varied germplasm into a genotype selected for adaptation to a particular environment. Moreover, this practice hastens the gains in performance and steps up the variance among commercial hybrids which, at present, is diminishing to that of experimental error level in the commonly adopted intervarietal crossing programmes. The need for a new cycle of nobilization using diverse clones of *S. officinarum, S. spontaneum, S. sinense/barberi* and *S. robustum* has been suggested by many workers [1–5]. But little published information exists on the effect of nobilization on quantitative characters. The present study aims to understand the variability pattern in the progenies of *S. officinarum, S. spontaneum* and *S. barberi/sinense* crosses with the Indian commercial varieties.

MATERIALS AND METHODS

The experimental material comprised F_1 progenies from crosses involving Indian commercial hybrids and *S. officinarum* (HO), *S. spontaneum* (HS) and *S. barberi/sinense* (HB). Eight clones each of *S. officinarum, S. spontaneum* and *S. barberi/sinense* were used in hybridization. The progenies at seedling stage were subjected to selection pressure so as to surpass the threshold limits set up for each group for H.R. brix 18% in all groups, NMC (number of millable canes) in HO, and cane diameter and single cane weight in HS and HB groups to bring down the number to a manageable level. Hybridity of the progenies was ensured by the distinct economic characteristic of each species. Twenty five progenies in each mating group were taken at random. The progenies along with three checks, viz. Co 62175, Co 6304 and CoC 671, were evaluated in randomized block design with three replications. Each F_1 clone was grown in a single-row plot, 6 m long, spaced at 90 cm. Twenty three-budded setts were planted in a plot at equal distance. The trial was harvested after 360 days and the data on nine quantitative characters recorded following the standard procedures. The genotypic and phenotypic coefficients of variation (GCV and PCV) [6], broad sense heritability [7], and genetic advance [8] were computed.

RESULTS AND DISCUSSION

The analysis of F_1 genotypes showed significant differences between genotypes for all the traits (Table 1). Significant differences were also observed between mating groups for all the characters except CCS per plot, indicating the potential of certain parents involved in the crosses to produce better genotypes. A comparison was made between mating groups. The genotypes derived from the HO mating group significantly differed from the HB genotypes for all the characters except CCS per plot, whereas differences were significant only for contributing characters of cane yield between HO and HS mating groups. Significant differences were also observed between the genotypes of the HS and HB mating groups for all the characters except cane yield and CCS per plot.

Differences were also significant between genotypes within each mating group. While comparing the magnitude of mean squares among genotypes within the mating groups, it was evident that the variation among the genotypes of HS group was more than that of HO and HB groups for all the characters except single cane weight, cane yield, and CCS per plot. Such high variability in the genotypes of HS mating group could be due to high frequency of unfavourable alleles. The variability among HB genotypes was minimum for the characters except NMC. This provides sufficient evidence to conclude that *S. sinense/barberi* is the closest relative of the Indian commercial hybrids. Parthasarathy [9] reported the resemblance of some early Indian commercial hybrids, such as, Co 205 and Co 285 and the seedlings of Co 421 with *S. barberi* in respect of chromosome number, taxonomic characters and juice quality.

Coefficient of variation gives an idea of relative variability in a population. The genotypic coefficient of variation in HS genotypes was higher than that of HO and HB groups for all the characters except cane yield (Table 2). The high variability among progenies of HS mating group revealed that the HS genotypes were not able to utilise effectively the existing environment. The relative genetic variability appeared to be the same in the HO and HS mating groups for cane yield and quality characters and was the minimum in the HB genotypes. Comparison between genotypic and phenotypic coefficients of variation revealed that cane diameter and cane length in the HO and HB mating groups are largely influenced by environment.

Table 1. Analysis of variance of genotypes derived from three mating groups in sugarcane

Sources	d.f.	N.M.C.	Cane diameter	Cane length	Single cane weight	Cane yield	Sucrose %	Purity %	CCS %	CCS per plot
Genotypes	74	5610.9**	0.48**	2098.8**	0.45**	1070.9**	18.2**	78.9**	11.1**	13.6**
Genotypes/HO	24	374.3**	0.21**	1618.0**	0.41**	1275.7**	17.5**	80.9**	11.0**	14.3**
Genotypes/HS	24	9688.5**	0.56**	2754.7**	0.28**	1143.5**	19.7**	89.4**	12.3**	13.6**
Genotypes/HB	24	1439.9**	0.20**	1274.9**	0.19**	853.7**	13.5**	45.7**	8.3**	13.6**
Mating groups	2	69569.1**	6.20**	9883.3**	6.19**	346.2*	65.2**	326.7**	32.3**	4.7
HO vs. HS	1	129477.7**	11.87**	19494.0**	12.33**	11.9	0.0	10.8	0.0	0.0
HO vs. HB	1	8986.1**	1.21**	3082.7**	3.84**	591.2**	97.4**	412.5**	48.2**	7.1
HS vs. HB	1	70243.4**	5.51**	7072.7**	2.41**	435.5	98.1**	556.8**	47.6**	6.8
Checks vs. genotypes	1	11011.1**	1.09**	869.0	0.77**	1143.1**	98.0**	378.1**	65.1**	1.7
Error	154	24.09	0.05	583.9	0.03	129.4	3.3	16.44	2.0	3.3
CD (for group mean)		1.57	0.07	7.73	0.06	3.64	0.58	1.30	0.45	0.58

*,**Significant at $P = 0.05$ and $P = 0.001$, respectively.

The differences were evident among three mating groups for contributing attributes of cane yield (Table 2). The mean of HO genotypes exceeded the means of HS and HB genotypes for cane yield and its traits, except NMC. For quality characters, the mean of HB genotypes was significantly higher than the means of other two groups. No differences were noted for the means of cane yield and quality characters of the genotypes from HO and HS mating groups. It is quite clear that the absence of genetic variation in CCS per plot between the HO and HS mating groups was mainly due to cane yield. The negative effect of NMC in the HO group in comparison with HS group was compensated by the positive effect of other component traits of cane yield, resulting in similar cane yields in the two mating groups. The performance of HB genotypes was intermediate for yield contributing characters but significantly superior for quality characters than the other groups.

The heritability (broad sense) estimates provide a measure of the potential effectiveness of selection amongst parents prior to hybridization. The heritability estimates for all the characters were higher in the HS mating group than the other groups (Table 2). Heritability values were quite high for NMC, single cane weight, and cane yield in comparison with quality characters. It seems that environment played a major role in sugar accumulation in these early generation (F_1) genotypes. In other words, selection for component characters of cane yield will be more reliable than the quality characters while selecting the parents for further hybridization keeping sucrose content at the economic threshold level. Variation in heritability values is expected due to differing degrees of genetic variability in the parents

Table 2. Mean range, CV, PCV, heritability (broad sense) and expected genetic advance (GA) in F_1 progenies of three mating groups of sugarcane

Character	Mating group	Mean	Range	G.C.V.	P.C.V.	Heri tabi- lity	GA % of mean
N.M.C.	HO	54.81a*	33–71	19.9	21.3	0.87	20.9
	HS	113.60b	43–231	49.9	50.2	0.99	116.4
	HB	70.29c	49–136	30.9	31.7	0.95	43.7
Cane diameter	HO	2.66a	2.23–3.53	7.8	13.2	0.35	0.3
	HS	2.10b	1.32–2.70	19.9	21.9	0.83	0.8
	HB	2.48c	1.90–2.93	9.3	12.3	0.57	0.4
Cane length	HO	247.27a	195–283	7.0	13.0	0.29	19.0
	HS	224.47b	153–282	12.3	15.7	0.61	44.3
	HB	238.20c	193–273	6.9	11.4	0.37	20.6
Single cane weight	HO	1.31a	0.83–2.57	26.4	31.5	0.71	0.6
	HS	0.74b	0.27–1.25	40.5	42.7	0.90	0.6
	HB	0.99c	0.55–1.39	23.3	29.2	0.64	0.4
Cane yield	HO	70.64a	45.8–114.6	27.6	32.1	0.74	34.7
	HS	70.27ab	36.7–117.5	26.8	29.7	0.81	34.9
	HB	66.87b	43.6–108.2	23.3	28.7	0.66	26.1
Sucrose %	HO	14.71a	11.14–18.85	14.7	19.4	0.57	3.4
	HS	14.70a	11.08–19.58	16.2	19.8	0.67	4.0
	HB	16.32b	11.83–20.36	11.1	16.1	0.48	2.6
Purity %	HO	81.90a	73.42–90.53	5.6	7.6	0.54	6.9
	HS	81.36a	67.11–89.65	6.0	7.9	0.57	7.6
	HB	84.37b	75.37–89.94	3.8	5.8	0.42	4.3
CCS %	HO	9.83a	7.04–12.98	17.5	23.0	0.58	2.7
	HS	9.82a	6.73–13.63	18.9	23.0	0.67	3.1
	HB	10.96b	7.50–14.16	12.9	19.0	0.46	2.0
CCS/plot	HO	6.90a	4.26–11.94	27.7	38.3	0.52	2.8
	HS	6.91a	3.92–11.55	28.2	35.4	0.64	3.2
	HB	7.33a	4.02–11.52	24.6	36.4	0.46	2.5

*Different letters indicate significant differences at $P = 0.05$.

and the environmental and competitional variance in small plots which had to be used in these experiments [10]. The heritability estimates and genetic variability have similar and supplementary effect on the expected genetic advance. As the genetic coefficient of variation for HS group was generally high for the majority of characters, the expected genetic advance was also higher.

In the sugarcane breeding programme at Sugarcane Breeding Institute, Coimbatore, the genotypes at par or significantly superior to the best local check for CCS per unit area are selected and promoted to multilocation testing. For this reason, the number of genotypes at par and significantly outyielding the midlate check, Co 6304, was used as a measure for comparing the efficiency of the three mating groups. On this basis, the HB mating group showed clear advantage over the other groups for number of promising genotypes (Table 3). There was no difference between HO and HS mating groups. The mean CCS per plot of the promising genotypes was also the highest in the HB group, reflecting its superiority over other groups.

The occurrence of promising genotypes among the progenies of all the three mating groups is remarkable. It may be mainly due to the use of the commercial hybrids, resulting into better progenies [2, 10, 11]. According to Roach [12], this may be due to the superiority of the gametes contributed by the commercial hybrids, better balance of noble and wild chromosomes and n + n chromosome transmission, which resulted in total diploid chromosome number within the range 100–125, as in the commercial varieties. Kandasami [13] also reported n + n chromosome transmissiom from hybrid x *S. spontaneum* and *S. spontaneum* x hybrid crosses with one exception. It is evident that not only the chromosome constitution but also the genetic constitution of the individual is important.

The interspecific hybrids currently under cultivation were derived from hybridization of *S. officinarum* with *S. spontaneum* and *S. sinense/barberi*. Utilization of a commercial clone may not reduce fibre content and increase sugar content as rapidly as the noble clone, but may have other desirable effects. Roach [14] has shown that a commercial clone would generally increase the vigour of its offspring when compared to noble canes, and in Barbados it has been observed that offsprings of commercial clones were generally more tolerant to stress conditions [15].

Thus, the present study indicates that HB mating group had clear advantage over HO and HS groups for quality characters, whereas HO genotypes were superior for cane yield and its component traits except NMC. The maximum genetic variability was observed among HS

Table 3. Number of genotypes at par and significantly superior to the midlate standard cv. Co 6304 for CCS/plot in three mating groups of sugarcane

Mating group	No. of genotypes in comparison to Co 6304			Mean CCS/ plot
	superior	at par	total	
HO	0	4	4	8.29
HS	1	3	4	8.92
HB	2	5	7	9.30

genotypes. The improvement in CCS per plot was mainly due to increase in cane yield through increase in NMC in comparison to the standards. Therefore, for improvement in sugar yield, it is suggested that the average cane yield should be increased, however, maintaining the threshold economic level of sucrose content of the genotypes. To make effective use of selected germplasm, a deliberate programme for bridging crosses among the three groups seems desirable. It is suggested that a more extensive use of advanced breeding material could profitably be made in the interest of a broader genetic base and to exploit the accumulated effects of specific selection pressure.

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