Selection Criteria Used in Clonal Evaluation of Sugarcane (*Saccharum spp.*)

A. Wijesuriya, R.O. Thattil and A.L.T. Perera

Postgraduate Institute of Agriculture,
University of Peradeniya.
Peradeniya

ABSTRACT. *A knowledge of genetic architecture of the relationships between the components of yield are of great importance in deciding selection criteria for sugarcane. In early selection stages, the direct selection for yield has proved to be ineffective. This experiment was conducted using 9 biparental families, their parents and 2 standard varieties to estimate heritabilities, genetic and phenotypic correlations and expected direct and indirect responses to selection of yield components in sugarcane.*

High heritabilities were observed for brix (total soluble solids in juice), pol (sucrose % in juice), purity [(pol/brix) x 100], POCS (Pure Obtainable Cane Sugar), stalk diameter, fibre % and rind hardness. Tiller count, millable stalks/clump and clump weight had relatively low heritability values. In most cases, genetic and phenotypic correlations between the components of sugar and cane yields were found to be positive. Negative relationships were observed for brix verses purity and for millable stalks/clump verses cane diameter.

Indirect selection via selection of pol and purity proved to be effective in improving POCS. While selection on stalk length lead to selection of clones with high cane yield. Brix and stalk diameter were also positively correlated with sugar and cane yield. Rind hardness was positively correlated with fibre percent fresh weight and therefore can be used as proxy variable for fibre.

INTRODUCTION

The success of a sugarcane (*Saccharum spp.*) breeding programme depends on how effectively the test clones are selected for high yields of cane and sugar and moderate fibre content. Cane and sugar yields are complex characters determined by several components on which selections are made especially during initial selection stages (Gravois *et al.*, 1991).

Direct selection for sugar yield, cane yield and fibre content is practiced at the latter stages of selection where a lesser number of clones are involved.

Genetic and phenotypic correlations among characters and heritabilities provide expected response to selection and information in devising selection criteria for different stages of selection (Kang *et al.*, 1983, Punia *et al.*, 1983). Several sugarcane breeding institutes have conducted experiments to estimate these parameters in perfecting their breeding and selection programmes. This study was conducted to obtain such information under Sri Lankan conditions for further improvement of methodologies involved in present varietal development programmes.

The main objectives of this study were: (i) to estimate heritability values of important characters that determine cane, sugar yields and fibre content, (ii) to determine genetic and phenotypic correlations among these traits, (iii) to estimate direct and correlated response of characters and (iv) to suggest a suitable clonal selection system to be employed in the varietal development programme.

MATERIALS AND METHODS

Nine biparental families selected randomly from Stage 1 of the 1989 Series of sugarcane breeding programme were evaluated along with parents and 2 standard varieties. Fourteen parental clones were involved in deriving these biparental families. The 25 treatments were arranged in 5 complete blocks (Figure 1). The field design was obtained after randomization within each group of each block. This design was used to eliminate the two way variability observed in the experimental site.

Rep. Group 1	Rep. Group 2	Rep. Group 3	Rep. Group 4	Rep. Group 5
1 2 3 4 5	6 7 8 9 10	11 12 13 14 15	16 17 18 19 20	21 22 23 24 25
6 7 8 9 10	11 12 13 14 15	16 17 18 19 20	21 22 23 24 25	1 2 3 4 5
11 12 13 14 15	16 17 18 19 20	21 22 23 24 25	1 2 3 4 5	6 7 8 9 10
16 17 18 19 20	21 22 23 24 25	1 2 3 4 5	6 7 8 9 10	11 12 13 14 15
21 22 23 24 25	1 2 3 4 5	6 7 8 9 10	1 12 13 14 15	16 17 18 19 20

Figure 1. Randomized complete block arrangement with 5 replication groups across the blocks

A plot size of 34.25 m² was used to accommodate 50 individuals giving 0.5 m spacing between clumps within rows and 1.37 m between rows. The experiment was established in March 1991 at the Sugarcane Research Institute, Uda Walawe in the low country dry zone (DL₁) of Sri Lanka.

Collection of data

Data collection was done on per clump basis. The number of tillers were recorded at 14 weeks after field establishment and data on other characters were recorded at harvest in March 1992. The average of 2 randomly selected stalks in a clump was taken for stalk height and diameter, hand refractometer brix (total soluble solids in juice measured by hand refractometer) and rind hardness. The weight of millable stalks in a clump was taken as clump weight. Cane juice analyses were made to determine laboratory brix and pol % (percentage sucrose in juice). A single stalk (randomly selected) per clump was fibrated to determine fibre percent fresh weight. Purity [(pol/brix)100] and POCS (Pure Obtainable Cane Sugar) were calculated accordingly (SRI laboratory procedures, 1987).

Statistical procedure

The parental population of sugarcane consist of commercial varieties which are complex inter-specific hybrids developed through 'nobilization' (Sreenivasan et al., 1987). Hence, the assumption of diploid inheritance is doubtful. Further, the random choice of parents from a population mating at random is unlikely to be met in experiments with sugarcane (Hogarth, 1987). Owing to cross fertilization, heterozygosity, incompatibility and male sterility of many varieties, most of the designs proposed for studying quantitative inheritance are not suitable for sugarcane (Hogarth, 1971). In such situations, planting a random set of biparental crosses in a replicated experiment is a useful design for showing the extent of genetic variation. The variance component due to differences between biparental crosses is a function of additive and non-additive genetic variance (Hogarth, 1987).

The following relationships established by Mather and Jinks (1982) for randomly mated biparental progenies were employed in this study to estimate the genetic parameters.

σ^2_b (variance of true biparental progeny means) $= 1/4\ D_r + 1/16 H_r$

σ^2_r (variance within families) $= 1/4\,D_r + 3/16H_r + E$

σ^2_w (variance of clonal replicates within individuals) $= E$

$D_r =$ Additive genetic variation

$H_r =$ Dominant genetic variation

$E =$ Environmental variation

Regression analysis of family means on mid parental values was carried out to estimate the narrow sense heritability (h^2_N). Variances and covariances for inter-families, intra-families and clonal (environmental) components were calculated from the mean squares and mean products presented in Table 1.

Heritability values and genetic correlations were calculated for the characters using the following equations.

Heritability (h^2) $\quad = 2$(Intra-class correlation)

$\quad\quad\quad\quad\quad\quad = 2[\sigma^2_b/(\sigma^2_r + \sigma^2_w)]$ _____(1)

Genetic correlation (r_A) for characters x and y

$\quad\quad\quad\quad\quad\quad = cov_b/(\sigma_{b_x}.\sigma_{b_y})$ _____(2)

Phenotypic correlations were also computed among characters studied. Expected direct and correlated responses to selection of characters were computed for 10% selection (90% discard) from the population as described by Falconer (1989).

RESULTS AND DISCUSSION

Heritability estimates

Analysis of variance indicated that there were significant differences among families and the rep individuals within families for all 12 characters studied. Heritability estimates derived from variance components and narrow sense heritability values computed through parent - off spring regression are listed against the characters in Table 2.

The highest narrow sense heritability (h^2_N) was observed for stalk diameter. Comparatively higher values were also observed for laboratory brix and hand refractometer brix. while the estimates of h^2_N for all other

Table 1   Expectations of mean squares and cross products of analysis of variance and covariance for characters X and Y

Source of Variance	df	Expectations		
		$MS_{(xx)}$	$MS_{(xy)}$	$MS_{(yy)}$
Blocks (p)	4	$\sigma^2_{wx}+ c\sigma^2_{rx}+ cr\sigma^2_{bx}+ crbq\sigma^2_{px}$	$cov_w+ ccov_r+ crcov_b+ crbqcov_p$	$\sigma^2_{wy}+ c\sigma^2_{ry}+ cr\sigma^2_{by}+ crbq\sigma^2_{py}$
Replication groups (q)	4	$\sigma^2_{wx}+ c\sigma^2_{rx}+ cr\sigma^2_{bx}+ crbp\sigma^2_{qx}$	$cov_w+ ccov_r+ crcov_b+ crbpcov_q$	$\sigma^2_{wy}+ c\sigma^2_{ry}+ cr\sigma^2_{by}+ crbp\sigma^2_{qy}$
Between families (b)	8	$\sigma^2_{wx}+ c\sigma^2_{rx}+ cr\sigma^2_{bx}$	$cov_w+ ccov_r+ crcov_b$	$\sigma^2_{wy}+ c\sigma^2_{ry}+ cr\sigma^2_{by}$
Between rep individuals within families (r)	441	$\sigma^2_{wx}+ c\sigma^2_{rx}$	$cov_w+ ccov_r$	$\sigma^2_{wy}+ c\sigma^2_{ry}$
Between clonal reps within individuals within families (c)	1792	σ^2_{wx}	cov_w	σ^2_{wy}

characters were not significant. Yet, a relatively higher value was observed for stalk length.

Table 2. Heritability estimates through parent-offspring regression and variance components

Character	Narrow sense heritability (h^2_N)	Heritability calculated through intra-class correlation
1. Stalk length	0.36	0.66**
2. Stalk diameter	0.82**	0.68**
3. Clump weight	0.02	0.42**
4. Tiller count/clump	0.06	0.41**
5. Millable stalks/clump	0.03	0.42**
6. Hand refractometer brix	0.42**	0.36**
7. Laboratory brix	0.46**	0.70**
8. Pol (%)	0.06	0.89**
9. Purity (%)	0.01	0.84**
10. POCS	0.04	0.71**
11. Fibre % fresh weight	0.20	0.70**
12. Rind hardness	0.02	0.74**

** - Significantly greater than zero in absolute value at 1% probability level.

Mather and Jinks (1981) reported that the heritability estimates through intra-class correlation fall in between narrow sense and broad sense heritabilities and are usually larger than h^2_N, as observed for all the characters. Similar results were reported by Tai et al., (1991) for sugarcane indicating differences in magnitude of estimates from these two methods. This may be due to the presence of non additive genetic variation that can be exploited in breeding clonally propagated crops such as sugarcane.

In this study, tiller count, clump weight and millable stalks per clump had comparatively low heritability values. Relatively higher heritablity values were observed for pol %, purity. POCS, fibre % fresh weight and rind hardness while a moderate estimate was noted for stalk length. These results are in reasonable agreement with Kang et al., (1983) for sugarcane.

Correlations

The matrix of phenotypic and genetic correlation coefficients among the characters are presented in Table 3. The magnitude of phenotypic and genetic correlations are important in deciding selection criteria for cane and sugar yield.

Pure Obtainable Cane Sugar (POCS) determines sugar yield. The biochemical characters; brix (hand refractometer and laboratory), pol and purity had significant positive phenotypic correlations with POCS. The signs of the phenotypic correlations matched with genetic correlations except for the weak negative relationship observed with laboratory brix.

Hand refractometer brix had a strong positive relationship with laboratory brix. Hence, it can be used effectively in selecting clones for brix during the early stages of selection where thousands of genotypes are involved.

Phenotypic and genetic correlations observed between POCS and fibre percent fresh weight were smaller in magnitude and dissimilar in direction. Moreover, no significant relationships were found between fibre percent fresh weight and other bio-chemical characters. These results confirm that the sugar content in cane can be improved by breeding while keeping the optimum fibre content (13%) needed for sugar factories. A conventional factory requires fibre within 11-15% range. In the early stages of selection, these extremes are approximated by testing rind hardness. The accuracy of this test has been subjected to much criticism. Significant phenotypic and genetic correlations between fibre % and rind hardness in this experiment would suggest that the rind hardness test is reasonably accurate as a measure of fibre % in cane.

Response to selection

As suggested by Falconer (1989), the correlated response may be used to progress rapidly when compared to that from selection for the desired character itself. Accordingly, the ratio of correlated response to direct response was proposed as an index to assess the merit of indirect selection.

Table 3 The Coefficients of Phenotypic and Genetic Correlations among some Important Characters of Sugarcane

	ER.Brix	Pol %	Purity %	POCS	Stalk length	Stalk diameter	Clump weight	Fibre %	Tiller/clump	Millable stalks/clump	Rind hardness
L.Brix[1]	0.6373*** 0.8869	0.7161*** 0.6676	0.0599 -0.4040	0.4899*** -0.1442	0.0940 -0.2121	-0.0430* -0.1136	0.0346 0.5493	-0.0279 0.1788	-0.0577** -0.2245	0.0056 -0.3936	-0.0719** 0.0307
ER.Brix[2]		0.4982*** 0.4072	0.0767** -0.3600	0.3631*** 0.2392	0.1328** -0.3988	-0.1286** -0.3672	0.0885** -0.6639	-0.0105 -0.3512	0.0077 -0.1044	0.0354 -0.1381	-0.0091 -0.2326
Pol %			0.7125*** 0.8847	0.4540*** 0.9746	0.0217 -0.2708	-0.0096 0.2316	0.0799** 0.1023	-0.0212 0.3568	-0.0703** -0.6010	0.0319 -0.4615	0.0213 0.1614
Purity %				0.8703*** 0.9615	-0.0129 -0.1716	0.0295 0.2545	0.0729** -0.2141	-0.0028 0.3698	-0.0438** -0.4442	0.0364 -0.2462	0.0949** 0.1368
POCS					0.0114 -0.2390	0.0094 0.2028	0.0736** -0.3977	-0.1259** 0.2911	0.0729** -0.5287	0.0215 -0.3792	0.0194 0.1287
Stalk length						0.0423** 0.5726	0.4687*** 0.8368	0.0210 0.1716	-0.0256 -0.0505	0.1957** -0.0066	0.2496*** 0.6124
Stalk diameter							0.2206*** 0.3451	-0.0425** 0.8118	-0.0935*** 0.8172	-0.0215 -0.5282	0.1450** 0.0474
Clump weight								0.0855*** 0.1376	0.2028*** 0.1386	0.7735*** 0.4690	0.2599*** 0.3960
Fibre %									0.0733** -0.5056	0.1416** -0.0632	0.3591*** 0.6577
Tiller/clump										0.3203*** 0.8693	0.0056 -0.5990
Millable stalks/clump											0.1865** -0.3171

(N = 2250)

*,*** Significant at the 0.01 and 0.001 levels respectively

1/ L.Brix   - Laboratory brix
2/ ER.Brix - Hand refractometer brix

Note : Upper and lower values represent phenotypic and genetic correlation coefficients, respectively.

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The estimates of response to selection for characters determining sugar and cane yields are given in Tables 4a and 4b. As illustrated in Table 4a, POCS had the advantage of being selected through pol and purity, which suggests that selection for pol and purity would be beneficial over direct selection for POCS in sugarcane. Similarly, indirect selection via stalk length was substantially better than direct selection for improving cane weight (Table 4b).

Table 4a   Expected Direct and Correlated Response of Characters which Determine Sugar Yield

Y X	L Brix	HR Brix	Pol % .	Purity	POCS
L Brix	2.950[1] (1)	2.582[2] (1.173)[3]	0.239 (0.060)	−4.820 (−0.360)	−0.438 (−0.142)
HR Brix	1.880 (0.637)	2.201 (1)	1.036 (0.259)	−3.097 (−0.235)	0.521 (0.169)
Pol %	0.225 (0.015)	1.337 (0.607)	3.994 (1)	11.900 (0.909)	3.338 (1.085)
Purity	−1.309 (−0.444)	−1.148 (−0.483)	3.421 (0.857)	13.097 (1)	3.199 (1.040)
POCS	−0.429 (−0.145)	0.701 (0.319)	3.466 (0.868)	11.542 (0.881)	3.077 (1)

Table 4b   Expected Direct and Correlated Response of Characters which Determine Cane Yield

Y X	Tillers/ Clump	Millable Stalks/ Clump	Stalk Length	Stalk Diameter	Clump Weight
Tillers/ Clump	1.723 (1)	1.522 (0.888)	−2.236 (−0.040)	.−2.430 (−0.637)	523.052 (0.332)
Millable Stalks/ Clump	1.568 (0.910)	1.713 (1)	−0.296 (−0.005)	−1.584 (−0.416)	764.46 (0.485)
Stalk Length	−0.110 (−0.064)	−0.014 (−0.008)	56.085 (1) .	2.160 (0.567)	1643.533 (1.044)
Stalk Diameter	−1.813 (−1.053)	−1.147 (−0.660)	32.659 (0.582)	3.812 (1)	686.439 (0.436)
Clump Weight	0.590 (0.342)	0.838 (0.489)	37.587 (0.670)	1.039 (0.273)	1574.62 (1)

Note: 1/ All diagonal values (R_x) − Direct response to selection
 2/ CR_y − Correlated response of character Y when selection is done on character x
 3/ The ratio of correlated response to direct response

CONCLUSION

During the early selection stages, more weight should be given to heritable and easily measurable characters such as stalk length and stalk diameter in selecting clones for cane yield. Hand refractometer brix can be used effectively in determining sugar yield during these stages. The rind hardness test provides a sufficient accurate measure of fibre percent fresh weight and can be used for determination of fibre during the initial stages of selection.

Selection for pol and purity was found to be beneficial for selection of sugar yield during the latter stages of selection. A considerable response for cane yield can be attained through the selection of stalk length. Moreover, cane and sugar yield can be improved without affecting the optimum fibre content required for the factories.

REFERENCES

Falconer, D.S. (1989). Introduction to quantitative genetics, Longman Group UK Ltd., UK.

Gravois, K.A., Milligan, S.B. and Martin, F.A. (1991). Indirect selection for increased sucrose yield in early sugarcane testing stages. Field Crops Res. 26: 67-73.

Hogarth, D.M. (1971). Quantitative inheritance studies in sugarcane I. Estimation of variance components. Aust. J. Agric. Res. 22: 93-102.

Hogarth, D.M. (1987). Genetics of sugarcane. pp. 255-271. In: Heinz, D.J. (Ed). Sugarcane Improvement through Breeding, Developments in Crop Science II, Elsevier, USA.

Kang, M.S., Miller, J.D. and Tai, T.Y.P. (1983). Genetic and phenotypic path analyses and heritability in sugarcane. Crop Sci., 23: 643-647.

Mather, K. and Jinks, J.L. (1982). Biometrical genetics, University press, Cambridge.

Punia, M.S., Paroda, R.S. and Hooda, R.S. (1983). Correlation and path analysis of cane yield in sugarcane. ..dian J. of Genet. 43: 109-112.

Sreenivasan, T.V., Ahloowalia, B.S. and Heinz, D.J. (1987). Cytogenetics. pp. 211-253. *In*: Heinz, D.J. (Ed). Sugarcane Improvement through Breeding, Developments in Crop Science II, Elsevier, USA.

SRI Laboratory Procedures (1987). Sugarcane Res. Inst., Uda Walawe, Sri Lanka.

Tai, P.Y,P., Hong He, Haipeng Gan and Miller, J.D. (1991). Flowering of hybrids from commercial sugarcane x *Saccharum spontaneum* crosses. J. ASSCT 11: 69-74.