

# HERITABILITY AND REPEATABILITY ESTIMATES OF A SUGARCANE POPULATION GROWN UNDER DRYLAND CONDITIONS

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## Abstract

Commercially important sugarcane traits were assessed in the early stages of the selection programme at the South African Sugar Association Experiment Station, Mount Edgecombe. The parents of a selected population were planted in the same field as their offspring to determine heritability values. The trial was planted in stage one of the plant breeding programme (single stools) and again in stage two (single lines) to calculate clonal repeatabilities and correlations between family means. Mid-parent-offspring regression was used to determine the narrow sense heritability of the traits investigated. Stalk population was the most heritable trait recorded at stage one, followed by stalk diameter, fibre % cane and brix % dry matter. Sucrose-related traits gave the highest estimates of heritability in stage two. Clonal repeatability and correlation between family means of traits were highest for stalk diameter, fibre % cane, and brix % dry matter.

## Introduction

The economic success of the South African sugarcane industry is dependent on the breeding, release and growth of, as well as the extraction of, sucrose from sugarcane varieties that are adapted to a number of different environmental conditions found throughout the industry.

For a sugarcane breeding programme to be successful it is important to know which traits give the highest estimates of heritability and which are the most repeatable over a number of seasons. Most sugarcane breeders select new clones from large seedling populations and usually discard a high proportion in the early stages of the selection programme. In the past this selection has been based mainly on traits which have since been found to have low heritability values, e.g. vigour, and are selected visually in the field. Although progress has been made in these early stages, it was very slow. It would be more beneficial to place stricter selection pressure at these early stages on traits of commercial importance with known higher heritability values, e.g. sucrose content and diameter (Stevenson, 1965).

Research indicates that heritability estimates are low for most characters affecting yield and fairly high for rust and smut resistance and brix % cane (Nageswara Rao *et al.*, 1983). However, when measuring heritabilities on a family basis, the heritabilities affecting yield have been found to be quite high (Skinner *et al.*, 1987).

The South African Sugar Association Experiment Station (SASEX) has carried out a number of inheritance trials, mainly under irrigation. Since the environmental variation under irrigation is less than that occurring in the non-irrigated areas (Blöse, 1992; Bond and van der Merwe, 1992), it was necessary to obtain heritability estimates under non-irrigated conditions. Hence a non-irrigated sugarcane popula-

tion was planted at SASEX, Mount Edgecombe, over two seasons, under dryland conditions, to determine heritability estimates.

## Methods and procedures

### Experimental procedures

A selection of 12 crosses was made from the terrace seedlings due to be planted into stage one of the routine selection programme at SASEX, Mount Edgecombe. The terrace seedlings, including the selections for the heritability trial, were planted into the same field in September 1992. The parental genotypes of these selections were also planted in the field as their offspring. The population was made up of single stools planted at 1 m intervals in rows 1,2 m apart. Each stool in the field represented a different genotype. 32 offspring were selected at random from each of the selected crosses. Two weeks before the harvest date (November 1993) the following traits were recorded: stool population (number of stalks in each stool), stalk diameter (mean of four stalks), stalk height (mean of 12 stalks), and two stalks from each stool were sampled to measure dry matter % cane, fibre % cane, brix % cane, brix % dry matter, pol % cane, ers % cane and purity.

The stool mass for this first stage was estimated using Bechet's method (Bond, 1979):

$$\frac{\text{No. of stalks/stool}}{4} \times \text{average stalk height (cm)} \times (\text{stalk diameter (cm)})^2 \times \frac{100}{30\,000} \text{ Kg}$$

In November 1993, these same crosses and parents were planted into a single line stage (stage two). Each genotype was planted into a 5 m line and the rows were 1,2 m apart. Both the parents and the crosses were replicated at this stage. The parents were replicated six times and each of the crosses was divided into four groups of eight offspring each. This indicates that, although the individuals themselves were not replicated, the crosses were replicated four times across the field. A control variety (NCo376) was planted at regular intervals in the trial to help measure field variation. The same traits as in stage one were studied, except that the stalk population was calculated by counting the number of stalks in four metres of each row and cane yield was the mass of each row expressed as tons per hectare. Data from the plots were used to calculate plot means, standard errors, heritabilities and repeatabilities of these traits over the two selection stages.

### Statistical procedures

The degree of resemblance between relatives for the traits was determined from the ratio of additive to phenotypic variance (narrow sense heritability). Mid-parent-offspring

regression was used to determine these estimations. Mid-parent-offspring regression was calculated as follows:

$$b_{OM} = \frac{COV_{OM}}{\sigma_p^2}$$

where  $COV_{OM}$  is the covariance of offspring on mid-parent value and  $\sigma_p^2$  is the variance of the parents, which is the phenotypic variance of the population. The covariance between the offspring and mid-parent value is equal to the additive genetic variance, therefore this  $b_{OM}$  is equal to the heritability in the narrow sense (Falconer, 1989).

The degree of genetic determination (DGD), which is the ratio of genotypic to phenotypic variance (broad sense heritability), was also calculated for this population. The following formula was used to determine repeatability:

$$V_{P(n)} = V_G + V_{Eg} + V_{Es} / n \text{ (Falconer, 1989)}$$

where  $V_{P(n)}$  is the total phenotypic variance for n measurements of the trait,  $V_G$  is the genetic variance,  $V_{Eg}$  is the general environmental variance, which is the environmental variance contributing to the between-individual component arising from permanent or non-localised circumstances, and  $V_{Es}$  is the special environmental variance, which is the within-individual variance arising from temporary or localised circumstances. Repeatability is the ratio of ( $V_G + V_{Eg}$ ) to  $V_P$ . The term 'clonal repeatability' is used when the correlation refers to different plants of the same sugarcane genotype, usually planted at two different locations. Clonal repeatability can provide an estimate for DGD when  $V_{Eg}$  is non-existent or very small.

Table 1

Family means and mid-parent values for stage one – single stools

Cross no.	Diameter (cm <sup>2</sup> )		Stool Population		Height (cm)		Stool mass (kg)	
	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent
	1	5,3	6,5	25,1	19,3	85,0	80,0	9,3
2	6,2	7,7	19,2	19,8	91,6	108,3	9,0	13,6
3	5,9	6,5	22,6	18,3	102,2	106,7	11,2	10,7
4	7,9	8,7	14,3	12,8	76,6	100,0	7,2	9,2
5	5,8	7,4	18,0	16,2	88,1	82,5	7,8	8,1
6	5,2	6,5	23,0	20,1	99,4	99,2	9,7	10,8
7	6,8	6,6	17,2	17,8	81,6	84,2	7,9	7,9
8	6,8	8,1	15,6	12,1	85,6	99,2	7,5	7,9
9	6,6	8,0	24,2	16,5	85,0	105,0	11,1	10,9
10	8,0	6,7	17,0	18,5	79,7	73,3	8,8	7,4
11	5,3	5,8	22,4	29,2	96,9	89,2	9,6	8,2
12	6,3	7,2	18,0	12,9	93,1	98,3	8,7	7,5
mean	6,4	7,1	19,9	16,9	88,7	93,8	9,0	9,2
SD % mean	14,2	11,3	17,4	16,4	8,7	11,8	13,8	19,7

Cross no.	DM % cane		Fibre % cane		Brix % cane		Brix % DM	
	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent
1	29,1	27,9	15,7	13,0	13,3	14,9	46,1	53,6
2	28,0	27,8	13,4	12,6	14,6	15,2	52,3	55,0
3	30,5	29,3	16,3	14,7	14,2	14,6	46,7	50,0
4	29,8	*	16,0	*	13,8	*	46,2	*
5	30,3	28,4	16,8	14,5	13,5	13,9	44,7	49,1
6	30,4	29,0	15,8	14,1	14,6	15,0	48,3	51,6
7	29,2	29,4	15,8	15,3	13,4	14,0	46,1	47,9
8	29,1	28,7	15,8	15,2	13,3	13,5	46,0	47,6
9	29,8	28,9	16,3	15,3	13,5	13,5	45,4	47,4
10	29,0	28,3	15,3	13,7	13,7	14,7	47,5	52,1
11	29,5	26,3	15,8	13,3	13,8	13,0	46,8	49,2
12	30,7	30,2	16,9	15,5	13,8	14,8	45,1	48,9
mean	29,6	28,6	15,8	14,3	13,8	14,3	46,8	50,2
SD % mean	2,5	3,4	5,4	6,9	3,2	4,8	4,1	4,8

Cross no.	Pol % cane		Ers % cane		Purity	
	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent
1	11,2	11,5	9,3	9,0	83,8	76,7
2	12,4	12,9	10,5	11,1	84,0	84,6
3	12,3	12,3	10,4	10,4	86,1	84,0
4	11,6	*	9,7	*	84,3	*
5	11,4	10,6	9,4	8,2	84,3	76,2
6	12,5	12,2	10,6	10,0	85,3	81,0
7	11,0	10,7	9,0	8,2	82,0	76,1
8	10,7	11,0	8,5	9,0	79,7	81,2
9	11,1	11,6	8,9	9,8	81,6	85,9
10	11,3	12,0	9,2	9,9	81,8	81,3
11	11,6	10,5	9,6	8,5	84,0	80,4
12	11,6	12,0	9,6	9,7	83,8	80,6
mean	11,6	11,6	9,6	9,4	83,4	80,7
SD % mean	4,7	6,5	6,6	9,4	2,0	3,9

\* the male parent variety of cross 4 did not perform well in stage one but was included in the analyses as a missing plot.

The family means of stage two were estimated using the residual maximum likelihood (REML) method (Robinson, 1987). REML is used to analyse unbalanced data (Genstat 5 Release 3 Reference Manual, 1993).

**Results and discussion**

The mid-parent values and family means of both stages were calculated and used to determine narrow sense heritabilities. Family means for diameter, population, and stool mass varied for the different crosses (Tables 1 and 2) whereas the family means for the other traits varied only slightly. The difference between the family means for stalk population were fairly high in stage one but were less in stage two.

High narrow sense heritabilities were observed for stalk population, diameter, fibre % cane, brix % dry matter and pol % cane for stage one (Table 3). The narrow sense heritability was very high for stalk population at stage one because there were fairly large differences in stalk numbers within and between crosses (between 14 and 25 stalks per stool). The difference between the cross means became much smaller at stage two (between 13 and 19 stalks per stool) when (Table 2). With the low variance between crosses, only a small gain would be made when selecting for this trait. The standard errors for population and diameter were also quite high. The lower standard error in stage two was possibly due to better planting conditions, trial layout and field adjustments.

Stalk diameter, population, fibre % cane/and brix % dry matter had high heritability estimates, whereas stalk height, stool mass, dry matter % cane/and purity were found to have very low heritability estimates at stage one. The estimate

Cross no.	DM % cane		Fibre % cane		Brix % cane		Brix % DM	
	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent
1	28,9	29,7	14,9	14,7	14,0	14,9	48,7	50,3
2	28,0	28,5	12,2	12,5	15,9	16,0	56,6	56,3
3	30,2	29,4	14,8	14,6	15,5	14,8	51,3	50,3
4	30,9	29,7	15,4	14,3	15,5	15,5	50,6	52,2
5	30,4	30,5	16,3	16,0	14,0	14,6	46,4	47,7
6	30,1	29,6	14,8	14,2	15,4	15,4	51,0	51,9
7	28,8	31,1	15,2	15,9	13,5	15,2	46,8	49,1
8	27,9	28,8	14,8	15,7	13,0	13,2	46,8	46,3
9	28,6	30,1	14,4	15,6	14,2	14,5	49,7	48,4
10	29,2	29,6	14,0	13,6	15,2	16,0	52,0	54,2
11	30,1	29,7	17,0	15,8	13,2	13,9	44,1	46,9
12	30,4	31,8	15,4	16,1	15,0	15,6	49,6	49,1
mean	29,5	29,9	14,9	14,9	14,5	15,0	49,5	50,2
SD % mean	3,3	2,9	7,6	7,2	6,6	5,4	6,3	5,7

Table 2

Family means and mid-parent values for stage two – single lines

Cross no.	Diameter (cm <sup>2</sup> )		Population (per metre)		Height (cm)		Cane yield (t/ha)	
	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent
1	4,8	5,3	18,9	15,7	102,1	119,4	50,4	49,4
2	6,2	7,1	17,7	16,5	136,4	133,0	79,3	76,3
3	5,2	5,7	16,3	15,2	117,0	116,9	54,9	55,8
4	6,7	8,1	13,1	10,7	132,5	123,2	63,4	47,2
5	5,0	5,8	16,4	13,2	118,5	115,9	53,5	45,2
6	4,8	5,4	17,7	17,1	114,0	125,9	54,3	62,4
7	5,9	6,1	15,6	13,8	115,3	127,3	68,3	53,5
8	6,1	7,0	14,8	13,9	128,6	141,1	56,6	72,1
9	6,0	7,0	15,6	15,7	129,7	138,8	65,8	72,8
10	7,4	6,1	13,9	12,0	116,6	121,1	56,9	42,7
11	4,6	4,9	16,5	18,3	117,1	136,9	47,1	70,3
12	5,6	6,4	15,8	11,8	124,2	131,5	62,2	56,0
mean	5,7	6,2	16,0	14,5	121,0	127,6	59,4	58,6
SD % mean	14,6	14,1	9,7	15,3	7,6	6,5	14,3	19,3

Cross no.	Pol % cane		Ers % cane		Purity	
	Family mean	Mid-parent	Family mean	Mid-parent	Family mean	Mid-parent
1	12,0	13,3	10,3	11,7	85,8	88,9
2	14,1	14,4	12,5	13,0	88,3	90,0
3	13,8	13,1	12,1	11,4	88,7	87,7
4	13,9	13,9	12,2	12,3	89,2	89,6
5	12,1	13,0	10,3	11,3	86,2	88,8
6	13,5	13,9	11,7	12,3	87,7	89,6
7	11,5	13,5	9,6	11,7	84,4	88,2
8	10,4	10,8	8,3	8,8	79,5	81,3
9	12,3	12,8	10,5	11,0	86,2	87,7
10	13,3	14,4	11,7	12,8	87,8	89,3
11	11,2	12,3	9,3	10,6	84,4	87,9
12	13,3	14,2	11,5	12,6	88,0	90,6
mean	12,6	13,3	10,8	11,6	86,4	88,3
CV %	9,2	7,4	11,9	9,5	3,0	2,6

Table 3

Family heritability in the narrow sense calculated from the data recorded in the field

Sugarcane traits	Heritabilities in the narrow sense and their standard errors	
	Stage one — Single stools	Stage two — Single lines
Stalk diameter	0,618 ± 0,294	0,687 ± 0,208
Stalk population	0,802 ± 0,298	0,508 ± 0,153
Stalk height	0,294 ± 0,199	0,580 ± 0,299
Cane yield	0,311 ± 0,192	0,234 ± 0,226
Dry matter % cane	0,410 ± 0,229	0,492 ± 0,324
Fibre % cane	0,629 ± 0,218	0,813 ± 0,211
Brix % cane	0,389 ± 0,180	0,950 ± 0,223
Brix % dry matter	0,618 ± 0,182	0,992 ± 0,150
Pol % cane	0,518 ± 0,188	0,976 ± 0,211
Ers % cane	0,465 ± 0,192	0,989 ± 0,201
Purity	0,008 ± 0,186	0,978 ± 0,176

for purity was very low when compared with the other sucrose-related traits. The cane was mature when it was sampled, resulting in there being very little difference between varieties. Stalk diameter, fibre % cane and brix % dry matter were consistently high over the two stages, which indicated the stability of these characters under the dryland conditions that existed for the duration of these trials. The heritability estimate of cane yield was very low in both stages, which suggests that less attention should be given to this trait when choosing parents. When considering the sucrose-related traits, the heritabilities were found to be consistently high in stage two. This may be due to the larger stalk sample being taken from a longer row at stage two and less competition between neighbouring rows giving a more accurate estimate of each of the clones. This indicates that the use of results obtained from stage two would be more reliable when selecting parents for crossing. Apart from heritabilities being low, the standard errors obtained for stalk height, cane yield and dry matter % cane were very high at both stages, which suggests that the breeder should be cautious when selecting parents for these traits.

The clonal repeatabilities (correlation coefficients for all individuals) within crosses over the two seasons were calculated and found to be highest for stalk diameter, fibre % cane and brix % dry matter (Table 4). On an individual basis, cane yield, brix % cane, pol % cane and purity were not very repeatable over the two years. The correlations between family means over the two seasons were high for most traits, with stalk diameter, fibre % cane, brix % dry matter, dry matter % cane and cane yield giving the highest estimates (Table 4).

The lowest correlation between family means at single line stage was measured for stalk height. From these results the breeder should be able to predict the expression of most traits in the offspring over a few seasons, but should be careful when looking at stalk height.

Table 4

Repeatability estimates over two seasons at the Mount Edgecombe Experiment Station

Sugarcane traits	Phenotypic correlations between seasons (stages one and two)	
	Clonal repeatabilities — on an individual basis — (DGD)	Correlations between family means (r)
Stalk diameter	0,554	0,953
Stalk population	0,395	0,738
Stalk height	0,416	0,173
Cane yield	0,247	0,591
Dry matter % cane	0,468	0,779
Fibre % cane	0,610	0,758
Brix % cane	0,248	0,763
Brix % dry matter	0,510	0,742
Pol % cane	0,264	0,757
Ers % cane	0,338	0,746
Purity	0,216	0,718

These results show that clonal repeatabilities are greater than narrow sense heritability values. Brown *et al.* (1968) and Kang *et al.*, (1984) also observed this in their research. This is to be expected since clonal repeatability approximates broad sense heritability and the latter is never smaller than narrow sense heritability (Kang *et al.*, 1984).

These estimates were calculated for this particular sugarcane population. The actual values themselves are not critically important here, but rather those traits that are the most or least heritable. A population of different sugarcane crosses and parents is likely to give different estimates of heritability, as the heritabilities are dependent on the population being studied at the time. These findings are similar to other studies although, in some cases, slightly lower heritability estimates were obtained (Nageswara Rao *et al.*, 1983; Skinner *et al.*, 1987; Bloose, 1992).

### Conclusions

Useful information was obtained from these studies. Stage one could be used to determine heritability values, although stage two would give more realistic and reliable estimates of narrow sense heritability. This is due to the larger plot sizes and the ability to adjust the data for field variability more efficiently.

The use of mid-parent-offspring regression to estimate heritability is effective, although it does not account for the variation within the crosses. A high heritability estimate by itself does not necessarily mean that a trait will be useful for selection, because the response to selection is dependent on the amount of variation present. A trait with a low heritability value and wide genetic variation will result in a better gain than a trait which has a high heritability estimate and narrow genetic variation.

Some traits are more heritable than others and the breeder can make progress with these more heritable traits. Some traits are also more repeatable than others and this is important to know for selection purposes.

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