

REFEREED PAPER

FAMILY EVALUATION FOR QUALITY TRAITS IN SOUTH AFRICAN SUGARCANE BREEDING PROGRAMMES

ZHOU M, LICHAKANE M AND JOSHI SV

South African Sugarcane Research Institute, P/Bag X02, Mount Edgecombe, 4300, South Africa
Marvellous.Zhou@sugar.org.za

Abstract

Family evaluation involves the selection or rejection of entire families of seedlings based on information derived from replicated family plots, and is widely practised in sugarcane breeding programmes. After family evaluation, individual seedling selection is restricted to the selected elite families. Family evaluation data is also used to determine breeding values of parent populations. The objectives of this study were to determine the effectiveness of family evaluation and determine potential selection gains over time for quality traits across South African Sugarcane Research Institute regional breeding and selection programmes. Data for various quality traits were collected from Stage I (Single Stools) of all the regional breeding programmes and analysed using the Mixed Procedure of the Statistical Analysis System. There were highly significant ($P < 0.001$) differences between families for the effectiveness of family selection. There were increasing family effects differences with advancing series, indicating the cumulative benefits of family selection. Estimated recoverable crystal (ERC) % cane, Pol % cane and Brix % cane produced the largest gains from family selection, indicating that the current approach is effective. Brix % cane, a trait that can be easily measured with a hand held refractometer, could be used to evaluate within-family variability, an important parameter for family evaluation. The 12-month programmes produced larger gains from family selection than the longer cycle programmes. Future studies should determine the breeding values of parent populations.

Keywords: sugarcane, plant breeding, covariance parameters, broad sense heritability, selection gains

Introduction

Selection is the cornerstone of plant breeding and is practised across all stages of a sugarcane breeding programme (Skinner *et al.*, 1987). Although sugarcane is clonally propagated, the first stage of selection involves evaluating segregating seedlings planted from true seed obtained after crossing. Referred to as the Seedling Stage or Stage I, this is the only stage established from true seed. The seedlings are appraised either as individual seedlings or in family plots.

Family selection involves the selection or rejection of whole families of seedlings based on information derived from family plots (Falconer and Mackay, 1996). Family selection is now widely practiced in Stage I among sugarcane breeding programmes including Australia (Hogarth *et al.*, 1990; Cox and Stringer, 1998; Kimbeng *et al.*, 2000, 2001; Jackson *et al.*, 1995a,b; Stringer *et al.*, 2011), USA (Milligan and Legendre, 1990; Chang and Milligan, 1992a,b), India (Shanthi *et al.*, 2008; Babu *et al.*, 2009); Brazil (Pedrozo *et al.*, 2011; de Resende and Barbosa, 2006) and South Africa (Bond, 1977, 1989). After family selection, individual seedling selection is restricted to the elite families. The advantage is that families

can be planted in replicated plots across locations and the plots can be harvested mechanically and weighed (Hogarth and Mullins, 1989). This cannot be achieved with individual seedlings not only because of the lack of planting material but, more importantly, because of the large number of seedlings involved. The ability to replicate families across time and space would allow for the evaluation of genotype by environment interaction effects and estimation of gains to selection. This analysis is particularly important for traits controlled by several genes with additive effects such as cane yield.

Prior to family selection, sugarcane breeders relied on the proven cross system to assess the potential of a family or cross to produce elite progeny (Heinz and Tew, 1987). The proven cross system defined elite families using the proportion of seedlings advanced to later stages of the programme, and was widely used in Australia and South Africa (Heinz and Tew, 1987; Skinner *et al.*, 1987) and other countries. Its value was questioned by Walker (1963) because larger numbers of seedlings were planted from elite families at the expense of new crosses, creating a bias against new families. Another disadvantage of the proven cross system was the lack of statistical tests to compare the families. Proven cross took several years to evaluate family potential because of the need to wait for advancement numbers (Milligan and Legendre, 1990).

The availability of objectively measured data from family plots, such as cane yield and sucrose content, prompted sugarcane breeders to rely increasingly on information obtained from family appraisals to make selection decisions that impact several other important aspects of the breeding programme. Decisions relating to the breeding value of parents (Balzarini, 2000; Cox and Stringer, 1998; Stringer *et al.*, 1996; Chang and Milligan, 1992a,b) retained for future crossing, cross combinations, and the number of crosses and seedlings per cross to plant and selection intensity per cross, are guided by family appraisal.

The objectives of this study were to determine the effects of family selection over time for quality traits across South African Sugarcane Research Institute (SASRI) regional breeding and selection programmes and identify the quality traits that produced larger gains during family selection. The trends in broad sense heritability and family selection gains were evaluated and compared across series and among selection programmes.

Materials and Methods

Trial sites

The data were collected from single stool trials established from seedlings planted in the field in 2006 to 2010 (Table 1) across the regional breeding programmes. The Midlands programmes represent a climate with long cold winters and shorter summers (Nuss, 1998). The coastal long cycle represents the ideal harvest age for growing areas along the Indian Ocean coast line of KwaZulu-Natal in South Africa. The coastal short cycle average potential represents a shorter growing cycle that provides for harvest before borer damage causes significant yield losses. The coastal short cycle high potential represents the areas with good soils, and high and well distributed rainfall conducive to high yields. The irrigated programme represents low rainfall areas with irrigation cropping systems.

Experiment design and data collection

The number of families planted in each series ranged from 100 to 400. Each family was planted to three replicates. A randomised complete block design was used. Sampling was done at harvest age. In each family plot, one stalk was taken randomly from each of the first

20 seedlings. The stalks were bundled together and sent for analysis at the sucrose laboratory using the standard method (Shoonees-Muir *et al.*, 2009).

Table 1. Regional programmes, age at harvest and trials.

Programme	Harvest age (months)	Trials
Midlands humic soils	20-24	BSS06, BSS07, BSS08, BSS09
Midlands sandy soils	20-24	SSS06, SSS07, SSS08, SSS09
Coastal long cycle	18	GSS07, GSS08, GSS09
Coastal hinterland	15-18	KSS07, KSS08, KSS09
Coastal short cycle average potential	12-15	USS07, USS08, USS09, USS10
Coastal short cycle high potential	12	TSS07, TSS08, TSS09, TSS10
Irrigated	12	FSS07, FSS08, FSS09, FSS10

Data analysis

Data were subjected to analysis of variance using the following linear mixed model:

$$Y_{ij} = \mu + R_i + F_j + RF_{ij} \quad \text{Equation 1}$$

where Y_{ij} = observation for family j ($j = 1, 2, \dots, f$), and replication i ($i = 1, 2, 3$); μ = overall mean; R_i = the random effect of the i th replication; F_j = the fixed effect of the j th family and RF_{ij} = the random interaction effect of the i th replication by the j th family, and was also the residual error and was used to test the family effects. The same model was used to estimate variance components where the family effects were treated as random. The data were analysed using the mixed procedure of the Statistical Analysis System (SAS) (SAS Version 9.2, 2009). The estimates of variance components, their standard errors and probability tests were calculated using the COVTEST option in the model statement (Littell *et al.*, 2008). The standard error was multiplied by the t-statistic of 2 (derived from the statistical tables of Freund and Wilson, 2003). The product of the standard error was added and subtracted from the heritability (H) value to estimate the confidence limits. If the confidence limits included zero in their interval, then the H was not significantly ($P < 0.05$) greater than zero. When the confidence limits excluded zero, then the H was significantly ($P < 0.05$) larger than zero.

The estimates of H or genetic repeatability on a plot mean basis were calculated as:

$$H = \sigma_F^2 / (\sigma_F^2 + \sigma_{FR}^2 / r), \quad \text{Equation 2}$$

where σ_F^2 was the variance component of family effects; σ_{FR}^2 was the residual variance component and r the number of replications. The estimates of the standard errors (SEs) for H were estimated using (Becker, 1992):

$$SE = \sqrt{\frac{2(1-H)^2[1+H(k-1)]^2}{k(k-1)(n-1)}} \quad \text{Equation 3}$$

where k is the number of observations per family and n is the number of families in the trials. Selection gains (Gs) were estimated using the formula described by Allard (1960):

$$G_s = k\sigma_F H \quad \text{Equation 4}$$

where k is selection intensity and σ_F is the phenotypic standard deviation. The G_s was estimated in units of quality and expressed as a percentage of the overall family means to allow easy comparisons across traits and series of trials.

Results and Discussion

Statistical parameters

The F-values for dry matter (DM) % cane and Fibre % cane in the Midlands increased from the BSS07 series to the BSS09 series while the opposite trend was evident from SSS07 to SSS09 (Table 2). This result indicated the greater potential of selecting elite families in BSS than in SSS. The F-values for Brix % cane, Purity %, Pol % cane and estimated recoverable crystal (ERC) % cane consistently increased from the BSS06 to BSS09 series, indicating that these traits could be significantly improved using family selection. The increasing F-values were also associated with increasing r^2 and decreasing CV% indicating the improved quality of the data, particularly for BSS. An opposite trend was apparent from the SSS06 to SSS09 series. All traits (except DM % cane) for SSS06 to SSS09 showed decreasing F-values. The SSS programme is relatively young compared to BSS. The SSS programme was established after the 1997 relocations, and the BSS was relocated to Bruyns Hill from the adjacent Windy Hill research station (Nuss, 1998). Windy Hill research station had been running for several years before relocation. There were highly significant differences ($P < 0.0001$) among families for all traits except for the SSS09 series. The crop cycle for the SSS09 series included a drought year (2010) and, coupled with the poor sandy soils, could have been negatively affected by the drought resulting in more variable data. The SSS09 series was associated with lower r^2 and larger CV%, an indication of the larger variability in the data leading to poorer detection of differences among families. The SSS09 series produced non-significant ($P > 0.05$) F-values across all traits. There were larger CV% for ERC % cane, Fibre % cane and Pol % cane, while Purity % had the smallest. The F-values for Purity % were generally the smallest among the traits. Therefore, there was likely to be small variability among the values for Purity %. There were generally low r^2 values with all traits across all series, producing less than 0.80 and nearly half below 0.60, indicating that most variability in the data remained unexplained. There may be a need to determine the optimum number of replications for family evaluation, as well as to investigate whether ratooning the families would improve the precision. Generally, ratooning ability is considered important in South Africa. Purity % produced the smallest F-values, indicating the small family differences for this trait.

The GSS trials had greater variability in the data with larger CV% than KSS (Table 3), indicating the large inherent variability that exist at Gingindlovu research station. The r^2 values were low with only a third of the series by trait combination showing values larger than 0.60, and indicating that large variability in the data remained unexplained. All the series by trait combination had less than 0.80 r^2 values. There were smaller CV% and larger r^2 values in KSS than GSS, indicating the greater uniformity in data for KSS. The F-values increased from GSS07 to GSS08 and decreased to GSS09. This trend was consistent across traits. The GSS08 series had the largest F-values that were generally highly significant ($P < 0.0001$) followed by GSS07, while GSS09 had the smallest F-values that were largely non-significant ($P > 0.05$) except for Fibre % cane. The GSS09 trial was severely affected by termite damage, which reduced the populations by more than 80%. The damage was patchy and largely concentrated around termite mounds scattered in the field. This trend in termite damage led to larger unexplained variability in the data and non-significant family differences. Series KSS07 had the smallest F-values, KSS09 the largest, and KSS08 was intermediate. The trend in F-values increased consistently from KSS07 to KSS09 and was

evident across all the traits. All traits for all series except Purity % in KSS07 had highly significant ($P < 0.0001$) F-values. These trends indicated the high and increasing efficiency of family selection for quality traits in KSS. There was a general increase in r^2 values from KSS07 to KSS09. KSS07 had the largest CV% while KSS08 and KSS09 had lower CV%. For both GSS and KSS series, DM% cane, Brix % cane and Purity % had lower CV% than Fibre % cane, Pol % cane and ERC % cane, indicating the variability in data from the different traits. Purity % produced the smallest F-values, indicating the smaller family differences compared to other traits. Brix % cane, Pol % cane and ERC % cane had the largest F-values, indicating larger family differences.

The F-values for all traits were highly significant ($P < 0.0001$) (Table 4), indicating the efficiency of family evaluation in the short cycle programmes. The order of magnitude of F-values for the TSS programme was TSS07 < TSS08 > TSS09 > TSS10. This trend was apparent across all traits except for Fibre % cane that peaked in TSS09. The r^2 and CV% had similar trend to F-values. The r^2 values were smaller for smaller F-values and vice versa. Larger CVs were associated with smaller F-values and vice versa. The order of magnitudes for the F-values for the USS programme was USS07 < USS08 < USS09 > USS10 except for Purity % which decreased from USS07 to USS08. The trends in r^2 and CV% followed that of F-values. As expected, the r^2 values were smaller for smaller F-values and larger for larger F-values. The CV% values were larger for smaller F-values and smaller for larger F-values. Generally, DM% cane, Brix % cane and Purity % showed lower CV% than Fibre % cane, Pol % cane and ERC % cane. The decreasing F-values in older series indicate the smaller family differences that exist in these populations. The small F-values for Purity % indicated narrow family differences.

The order of magnitude of F-values across series for the irrigated programme was FSS07 < FSS08 < FSS09 > FSS10 for DM % cane and Fibre % cane, while that of Brix % cane, Purity %, Pol % cane and ERC % cane was FSS07 < FSS08 < FSS09 < FSS10 (Table 5), indicating a consistent increase across stages. The consistent increase highlights the increased value of family selection with advancing series. Of great interest is that the lower F-values for DM % cane and Fibre % cane coincide with large increases in F-values for Brix % cane, Purity %, Pol % cane and ERC % cane. This trend could be indicating the presence in these later series of high sucrose populations that naturally possess low fibre and thus lower dry matter. The F-values for FSS08, FSS09 and FSS10 were all highly significant ($P < 0.0001$) for all traits while the F-values for DM% cane and Fibre % cane were not significant ($P > 0.05$) in FSS07. As expected, the r^2 values followed the trends of F-values and increased from FSS07 to FSS10. Large CV% values were recorded for Fibre % cane, Pol % cane and ERC % cane. ERC % cane produced the largest CV% values. Generally, Purity % had the smallest CV% values, indicating probably greater precision of measurement.

Table 2. F-value, P-value, r² and CV% of the quality traits for the Midlands breeding programmes.

Trait	Statistic	BSS06	BSS07	BSS08	BSS09	SSS06	SSS07	SSS08	SSS09
DM	F value	2.40	1.17	1.70	3.69	3.25	2.50	3.11	1.01
	P value	<0.0001	0.1952	0.0038	<0.0001	<0.0001	<0.0001	<0.0001	0.4717
	r ²	0.57	0.45	0.51	0.55	0.67	0.61	0.67	0.46
	CV%	4.02	3.74	2.98	3.65	2.52	2.97	2.52	4.32
Fibre	F value	1.97	1.47	1.84	2.76	2.82	3.66	2.72	1.05
	P value	0.0007	0.0189	0.0011	<0.0001	<0.0001	<0.0001	<0.0001	0.3954
	r ²	0.53	0.49	0.52	0.48	0.64	0.72	0.65	0.47
	CV%	7.92	8.96	7.83	7.55	5.22	6.09	5.23	8.77
Brix	F value	1.99	2.64	4.32	4.68	3.35	4.30	3.28	0.84
	P value	0.0006	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.8022
	r ²	0.53	0.68	0.72	0.60	0.68	0.78	0.69	0.34
	CV%	3.84	4.49	3.30	3.91	2.84	3.85	2.84	4.87
Purity	F value	1.39	1.93	2.61	2.10	1.78	1.76	1.74	0.69
	P value	0.0621	0.0002	<0.0001	<0.0001	0.001	0.0013	0.0012	0.9651
	r ²	0.43	0.63	0.64	0.40	0.52	0.79	0.54	0.34
	CV%	4.19	2.07	1.58	2.45	1.41	1.94	1.41	2.80
Pol	F value	1.80	2.84	4.20	4.45	3.48	5.01	3.38	0.83
	P value	0.0028	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.8157
	r ²	0.50	0.65	0.72	0.59	0.69	0.76	0.70	0.35
	CV%	6.95	5.50	4.39	5.30	3.60	4.23	3.60	6.68
ERC	F value	1.68	2.28	4.00	4.03	3.34	4.66	3.25	0.82
	P value	0.0072	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.832
	r ²	0.48	0.64	0.71	0.57	0.68	0.76	0.69	0.35
	CV%	9.84	6.68	5.43	6.71	4.32	5.11	4.32	8.42

Table 3. F-value, P-value, r^2 and CV% of the quality traits for the coastal long cycle and coastal hinterland breeding programmes.

Trait	Statistic	GSS07	GSS08	GSS09	KSS07	KSS08	KSS09
DM	F value	1.49	2.34	1.37	2.54	2.56	4.29
	P value	0.0259	<0.0001	0.052	<0.0001	<0.0001	<0.0001
	r^2	0.46	0.62	0.48	0.59	0.58	0.71
	CV%	6.36	4.01	4.86	4.58	3.55	3.78
Fibre	F value	1.27	1.95	1.74	1.96	2.25	6.63
	P value	0.1222	0.0005	0.0021	<0.0001	<0.0001	<0.0001
	r^2	0.41	0.56	0.55	0.56	0.56	0.79
	CV%	10.11	5.63	7.24	8.46	5.96	6.09
Brix	F value	1.64	4.09	0.96	2.12	4.68	6.43
	P value	0.0082	<0.0001	0.5781	<0.0001	<0.0001	<0.0001
	r^2	0.48	0.73	0.35	0.62	0.72	0.78
	CV%	7.03	4.20	6.26	5.12	3.63	4.10
Purity	F value	1.17	1.56	0.88	1.28	2.70	4.45
	P value	0.2183	0.0147	0.7257	0.0526	<0.0001	<0.0001
	r^2	0.42	0.51	0.35	0.43	0.59	0.71
	CV%	5.95	3.37	4.11	4.32	2.10	2.70
Pol	F value	1.51	2.98	0.94	2.12	4.30	6.52
	P value	0.0227	<0.0001	0.6096	<0.0001	<0.0001	<0.0001
	r^2	0.47	0.67	0.36	0.57	0.70	0.78
	CV%	11.67	6.57	9.57	7.42	5.09	5.90
ERC	F value	1.44	2.48	0.92	1.91	4.00	6.30
	P value	0.0391	<0.0001	0.6473	<0.0001	<0.0001	<0.0001
	r^2	0.46	0.63	0.35	0.53	0.69	0.77
	CV%	16.86	9.04	13.12	10.09	6.45	7.89

Table 4. F-value, P-value, r^2 and CV% of the quality traits for the coastal short cycle breeding programmes.

Trait	Statistic	TSS07	TSS08	TSS09	TSS10	USS07	USS08	USS09	USS10
DM	F value	2.41	5.82	4.40	3.13	1.65	1.96	2.98	2.28
	P value	<0.0001	<0.0001	<0.0001	<0.0001	0.0092	0.0004	<0.0001	<0.0001
	r^2	0.60	0.78	0.73	0.62	0.51	0.55	0.65	0.57
	CV%	4.02	2.45	2.65	3.05	3.62	2.74	2.83	3.79
Fibre	F value	2.30	5.09	5.14	2.37	1.18	2.49	5.11	2.83
	P value	<0.0001	<0.0001	<0.0001	<0.0001	0.2125	<0.0001	<0.0001	<0.0001
	r^2	0.59	0.75	0.77	0.56	0.45	0.61	0.74	0.62
	CV%	4.77	5.37	5.99	6.48	8.44	6.08	5.69	8.23
Brix	F value	2.30	4.95	4.90	3.41	1.71	3.16	6.89	3.52
	P value	<0.0001	<0.0001	<0.0001	<0.0001	0.0055	<0.0001	<0.0001	<0.0001
	r^2	0.59	0.76	0.79	0.65	0.51	0.67	0.80	0.67
	CV%	4.77	4.03	3.33	3.99	4.60	3.98	3.92	6.81
Purity	F value	1.49	3.14	2.32	2.02	1.74	1.68	6.09	2.11
	P value	0.0031	<0.0001	<0.0001	<0.0001	0.0043	0.0052	<0.0001	<0.0001
	r^2	0.49	0.66	0.65	0.52	0.56	0.53	0.79	0.54
	CV%	4.36	1.86	1.86	2.22	3.71	1.94	2.27	3.41
Pol	F value	2.22	5.37	4.83	3.35	1.94	3.00	7.68	3.23
	P value	<0.0001	<0.0001	<0.0001	<0.0001	0.0008	<0.0001	<0.0001	<0.0001
	r^2	0.57	0.78	0.76	0.64	0.55	0.66	0.83	0.65
	CV%	7.46	5.04	4.37	5.35	7.01	5.04	5.53	8.83
ERC	F value	2.04	5.24	4.56	3.16	1.92	2.74	7.73	3.00
	P value	<0.0001	<0.0001	<0.0001	<0.0001	0.001	<0.0001	<0.0001	<0.0001
	r^2	0.55	0.77	0.74	0.63	0.56	0.65	0.83	0.63
	CV%	10.24	6.23	5.51	6.70	9.53	6.34	7.07	11.15

Table 5. F-value, P-value, r^2 and CV% of the quality traits for the irrigated breeding programme.

Trait	Statistic	FSS07	FSS08	FSS09	FSS10
DM	F value	1.28	1.92	2.81	1.02
	P value	0.0521	<0.0001	<0.0001	0.4273
	r^2	0.50	0.53	0.65	0.38
	CV%	8.83	5.11	5.52	8.38
Fibre	F value	1.26	2.84	3.98	1.94
	P value	0.064	<0.0001	<0.0001	<0.0001
	r^2	0.50	0.60	0.72	0.53
	CV%	16.24	8.93	11.84	17.63
Brix	F value	1.48	4.09	5.37	7.16
	P value	0.005	<0.0001	<0.0001	<0.0001
	r^2	0.50	0.64	0.79	0.80
	CV%	10.21	4.34	8.56	6.34
Purity	F value	1.40	2.73	4.19	10.09
	P value	0.0128	<0.0001	<0.0001	<0.0001
	r^2	0.50	0.57	0.74	0.84
	CV%	6.36	3.04	8.78	6.44
Pol	F value	1.51	3.73	4.44	8.24
	P value	0.0035	<0.0001	<0.0001	<0.0001
	r^2	0.51	0.63	0.75	0.82
	CV%	13.54	6.62	15.22	11.58
ERC	F value	1.45	3.60	3.84	8.30
	P value	0.0077	<0.0001	<0.0001	<0.0001
	r^2	0.50	0.62	0.72	0.82
	CV%	19.20	8.67	24.24	17.70

Covariance parameters

In the Midlands, the variance component for family effects was highly significant ($P < 0.0001$) for all traits across series except for SSS09, BSS07 (DM % cane and Fibre % cane) and BSS06 (Purity %) that were non-significant ($P > 0.05$) (Table 6). The highly significant variance components indicated the large variability for family effects. The variance component for Brix % cane, Purity %, Pol % cane and ERC % cane in the SSS09 series were zero due probably to the drought associated moisture stress in sandy soils. Broad sense heritability (H) for families was tested for significance using standard errors. All traits had significantly ($P < 0.05$) larger H than zero, except for DM % cane in the BSS07 series. This significant H indicated that potential gains would be made using family selection. There was no trend in H for DM % cane and Fibre % cane across series. Brix % cane, Pol % cane, Purity % and ERC % cane showed a consistent increase in H from BSS06 to BSS08, with a marginal decrease from BSS08 to BSS09. These traits showed an increase in H from SSS06 to SSS07 and a decrease from SSS07 to SSS08. These increases in H were also associated with increases in family selection gains. ERC % cane followed by Pol % cane and Brix % cane had high selection gains while Purity % had low gains. Therefore family selection for ERC % cane as currently practised was effective. Purity % had the smallest H and gains compared to other traits.

From the coastal long cycle, Purity % was non-significant ($P < 0.05$) in GSS07, GSS09 and KSS07, while ERC % cane was non-significant in GSS07 and GSS09 (Table 7). DM % cane, Brix % cane and Pol % cane were non-significant ($P < 0.05$) in GSS09, while Fibre % cane

was non-significant ($P < 0.05$) in GSS07. All traits except Fibre % cane were non-significant ($P > 0.05$) in GSS09. Brix % cane, Purity %, Pol % cane and ERC % cane were non-significant ($P < 0.05$) H in GSS09, while Purity % was non-significant ($P < 0.05$) in GSS07. For the GSS series, H increased from GSS07 to GSS08 and decreased in GSS09. The GSS09 series was severely damaged by termites which reduced the populations to less than 20%. The inherent variability in the trial due to termite damage could have caused the larger variability in the trials and low H. Gains to family selection followed similar trends to H. The KSS series produced a consistent increase in H and family selection gains from KSS07 to KSS09. ERC % cane, Pol % cane and Brix % cane had the largest gains, while Purity % had the least. Therefore family selection using ERC % cane as currently practised is efficient. ERC % cane, Pol % cane or Brix % cane could be a candidate trait for future family selection, depending on which will be the easiest to measure. In other sugar industries, such as in Louisiana in the USA, selection for quality is done using the hand held refractometer for Brix (personal communication¹). South African results suggest a potential benefit from adopting such a system. Measurements can be done on individual clones, the method is non-destructive and could provide data to determine distribution among populations, thus providing feed-back for parent evaluation.

All variables across all series except for Fibre % cane in USS07 were significant ($P < 0.05$) (Table 8), indicating large population variability. The H increased from TSS07 to TSS09 for all traits, and the family selection gains followed the same trend. For USS, H increased from USS07 to USS08 for all traits. The gains from family selection increased consistently from USS07 to USS10. Generally, ERC % cane followed by Pol % cane, Brix % cane and Fibre % cane showed large selection gains indicating that the current selection method of using ERC % cane was effective. There is also potential to use the hand held refractometer that measures brix. Purity % produced the lowest selection gains. The H for Purity % was also consistently the lowest for all traits, indicating that it was unsuitable for family evaluation.

In the irrigated programme, the family variance components were highly significant ($P < 0.0001$) except for DM % cane in FSS07 and FSS10, and Fibre % cane in FSS07 (Table 9), indicating large population variability for the quality traits. The H values for all traits increased from FSS07 to FSS09 but decreased in FSS10. Gains to family selection produced a similar trend to H. ERC % cane produced the largest gains followed by Pol % cane, while Brix % cane and Fibre % cane were similar in third place. The current approach of using sucrose content in family selection is efficient. The smallest gains were produced by DM % cane and Purity %. The low family selection gains for Purity % and DM % cane were evident despite fairly high H values and significant family variance component, indicating that these traits were not suitable for family evaluation.

The irrigated and 12-month cycle programmes showed potential for large family selection gains compared to the long cycle and Midlands programmes. This trend could be caused by the larger variability in growing conditions that the longer cycles get exposed compared to the short cycles. Generally, the short cycles, particularly the irrigated areas, produced the largest selection gains that were consistent across series. The irrigated programme has the most uniform soils and growing conditions, where moisture stress via mid-season drought is limited. The weakest programme was the Midlands sandy soils, where the 24-month cycle exposes the crop to greater variability in growing conditions associated with moisture stress during mid-season or seasonal droughts.

¹CA Kimbeng, Sugarcane Breeder, LSU AgCenter, Sugar Research Station, Baton Rouge, Louisiana, USA

Table 6. Variance components for family, residual and the estimated broad sense heritability (H), selection gains (Gs) and % gains to selections (%Gs) for the Midlands breeding programmes.

Trait	Statistic	BSS06	BSS07	BSS08	BSS09	SSS06	SSS07	SSS08	SSS09
DM	Family	0.67±0.21**	0.04±0.09ns	0.18±0.08**	0.57±0.14**	0.51±0.11**	0.42±0.11**	0.50±0.11**	0.02±0.11ns
	Residual	1.37±0.18**	1.17±0.14**	0.74±0.09**	0.84±0.08**	0.60±0.07**	0.72±0.09**	0.60±0.07**	1.42±0.17**
	H	0.59±0.06	0.10±0.07	0.43±0.07	0.67±0.06	0.72±0.04	0.64±0.05	0.71±0.04	0.04±0.06
	G _s	1.13	0.18	0.70	1.13	1.11	1.03	1.10	0.08
	%G _s	3.89	0.65	2.43	4.49	3.60	3.60	0.34	0.28
Fibre	Family	0.42±0.17**	0.17±0.11ns	0.29±0.10**	0.31±0.09**	0.32±0.08**	0.65±0.14**	0.31±0.07**	0.03±0.11ns
	Residual	1.26±0.16**	1.16±0.14**	0.88±0.10**	0.72±0.07**	0.47±0.05**	0.63±0.08**	0.47±0.05**	1.37±0.17**
	H	0.50±0.07	0.31±0.07	0.49±0.07	0.57±0.07	0.67±0.05	0.76±0.04	0.69±0.06	0.06±0.06
	G _s	0.93	0.56	0.85	0.91	0.97	1.19	0.97	0.12
	%G _s	6.60	4.70	6.95	8.23	7.45	9.14	7.43	0.89
Brix	Family	0.12±0.04**	0.30±0.07**	0.35±0.07**	0.24±0.06**	0.22±0.05**	0.46±0.09**	0.22±0.05**	0±0ns
	Residual	0.33±0.04**	0.49±0.06**	0.30±0.04**	0.30±0.03**	0.25±0.03**	0.36±0.04**	0.26±0.03**	0.45±0.04**
	H	0.51±0.07	0.64±0.05	0.78±0.04	0.71±0.05	0.72±0.04	0.79±0.03	0.73±0.04	0±0
	G _s	0.68	0.95	1.01	0.93	0.90	1.08	0.91	0
	%G _s	4.57	6.06	6.11	6.65	5.09	6.93	5.11	0
Purity	Family	1.75±1.24ns	1.06±0.36**	1.04±0.28**	1.18±0.41**	0.45±0.17**	0.82±0.32**	0.45±0.17**	0±0ns
	Residual	12.87±1.64**	3.17±0.37**	1.82±0.22**	4.49±0.44**	1.57±0.18**	2.82±0.34**	1.57±0.18**	5.23±0.52**
	H	0.29±0.08	0.50±0.06	0.63±0.06	0.44±0.07	0.46±0.06	0.47±0.06	0.46±0.06	0±0
	G _s	0.97	1.17	1.29	1.13	0.91	1.06	0.92	0
	%G _s	1.12	1.37	1.50	1.30	1.03	1.23	1.03	0
Pol	Family	0.23±0.10**	0.36±0.09**	0.44±0.09**	0.32±0.07**	0.29±0.06**	0.50±0.09**	0.30±0.06**	0±0ns
	Residual	0.81±0.10**	0.54±0.06**	0.39±0.05**	0.42±0.04**	0.32±0.04**	0.32±0.04**	0.32±0.04**	0.65±0.06**
	H	0.46±0.07	0.67±0.05	0.77±0.04	0.70±0.05	0.73±0.04	0.82±0.03	0.73±0.04	0±0
	G _s	0.76	1.01	1.08	0.99	0.97	1.09	0.97	0
	%G _s	5.90	7.54	7.52	8.15	6.17	8.13	6.18	0
ERC	Family	0.30±0.14*	0.34±0.09**	0.48±0.11**	0.36±0.09**	0.32±0.07**	0.52±0.10**	0.33±0.07**	0±0ns
	Residual	1.23±0.16**	0.71±0.08**	0.46±0.05**	0.52±0.05**	0.37±0.04**	0.36±0.04**	0.37±0.04**	0.79±0.08**
	H	0.42±0.08	0.59±0.06	0.76±0.04	0.68±0.05	0.72±0.04	0.81±0.03	0.72±0.04	0±0
	G _s	0.78	0.91	1.10	1.01	0.99	1.11	0.99	0
	%G _s	6.87	7.81	8.80	9.39	7.07	9.38	7.04	0

Table 7. Variance components for family, residual and the estimated broad sense heritability (H), selection gains (Gs) and % gains to selections (%Gs) for the coastal long cycle and coastal hinterland breeding programmes.

Trait	Statistic	GSS07	GSS08	GSS09	KSS07	KSS08	KSS09
DM	Family	0.37±0.21*	0.65±0.19**	0.21±0.13ns	0.85±0.18**	0.57±0.13**	1.24±0.20**
	Residual	2.13±.26**	1.38±0.17**	1.52±0.18**	1.53±0.14**	1.04±0.10**	1.08±0.09**
	H	0.34±0.08	0.59±0.06	0.29±0.07	0.62±0.04	0.62±0.05	0.77±0.03
	G _s	0.73	1.12	0.56	1.22	1.10	1.39
	%G _s	3.16	3.83	2.21	4.52	3.85	5.08
Fibre	Family	0.11±0.11ns	0.27±0.10**	0.21±0.09**	0.47±0.13**	0.36±0.09**	1.25±0.17**
	Residual	1.28±0.16**	0.80±0.10**	0.85±0.10**	1.39±0.13**	0.82±0.08**	0.67±0.06**
	H	0.20±0.08	0.49±0.07	0.43±0.07	0.50±0.05	0.57±0.05	0.85±0.02
	G _s	0.37	0.81	0.72	0.96	0.95	1.35
	%G _s	3.35	5.18	5.71	6.91	6.23	10.06
Brix	Family	0.15±0.07*	0.33±0.07**	0.00±0.04ns	0.18±0.05**	0.30±0.05**	0.57±0.08**
	Residual	0.69±0.09**	0.32±0.04**	0.63±0.07**	0.45±0.04**	0.24±0.02**	0.32±0.03**
	H	0.40±0.08	0.76±0.04	0.02±0.07	0.55±0.05	0.79±0.03	0.84±.02
	G _s	0.64	1.01	0.03	0.79	0.98	1.12
	%G _s	5.39	7.42	0.27	6.02	7.22	8.05
Purity	Family	1.25±1.57ns	1.62±0.69**	0±0ns	1.43±0.91ns	1.93±0.41**	5.07±0.78**
	Residual	19.32±2.39**	7.14±0.85**	9.48±0.90**	13.88±1.28**	3.24±0.31**	4.46±0.37**
	H	0.16±0.08	0.41±0.07	0±0	0.24±0.06	0.64±0.04	0.77±0.03
	G _s	0.60	1.17	0	0.80	1.52	1.98
	%G _s	0.81	1.46	0	0.93	1.76	2.52
Pol	Family	0.19±0.10*	0.34±0.09**	0.01±0.05ns	0.29±0.07**	0.40±0.07**	0.74±0.10**
	Residual	1.05±0.13**	0.50±0.06**	0.85±0.10**	0.71±0.07**	0.35±0.03**	0.41±0.03**
	H	0.35±0.08	0.67±0.05	0.04±0.07	0.55±0.05	0.77±0.03	0.84±0.02
	G _s	0.62	1.00	0.06	0.88	1.05	1.19
	%G _s	7.10	9.15	0.64	7.80	8.99	10.89
ERC	Family	0.20±0.12ns	0.33±0.09**	0.01±0.06ns	0.33±0.09**	0.44±0.08**	0.83±0.12**
	Residual	1.30±0.16**	0.65±0.08**	0.99±0.11**	0.99±0.09**	0.43±0.04**	0.49±0.04**
	H	0.32±0.08	0.50±0.07	0.03±0.07	0.50±0.05	0.76±0.03	0.84±0.02
	G _s	0.60	0.79	0.05	0.87	1.08	1.23
	%G _s	8.80	8.88	0.64	8.83	10.62	13.87

Table 8. Variance components for family, residual and the estimated broad sense heritability (H), selection gains (Gs) and % gains to selections (%Gs) for the coastal short cycle breeding programmes.

Trait	Statistic	TSS07	TSS08	TSS09	TSS10	USS07	USS08	USS09	USS10
DM	Family	0.66±0.14**	0.83±0.12**	0.73±0.11**	0.49±0.09**	0.28±0.14*	0.23±0.09**	0.58±0.14**	0.53±0.14**
	Residual	1.28±0.12**	0.48±0.04**	0.58±0.05**	0.68±0.06**	1.24±0.16**	0.71±0.09**	0.81±0.09**	1.13±0.12**
	H	0.61±0.04	0.84±0.02	0.79±0.03	0.68±0.04	0.49±0.07	0.49±0.07	0.68±0.05	0.58±0.05
	G _s	1.13	1.23	1.21	1.10	0.91	0.79	1.14	1.06
	%G _s	4.04	4.34	4.25	4.02	2.97	2.60	3.57	3.76
Fibre	Family	0.56±0.13**	0.64±0.098**	0.76±0.11**	0.33±0.07**	0.11±0.15ns	0.44±0.14**	1.30±0.25**	1.10±0.24**
	Residual	1.28±0.12**	0.46±0.04**	0.51±0.05**	0.70±0.06**	1.79±0.23**	0.85±0.11**	0.86±0.10**	1.66±0.17**
	H	0.57±0.04	0.81±0.02	0.82±0.02	0.58±0.04	0.16±0.08	0.61±0.06	0.82±0.03	0.66±0.04
	G _s	1.06	1.17	1.22	0.94	0.32	1.03	1.39	1.33
	%G _s	8.08	9.27	10.19	7.25	2.02	6.85	8.47	8.48
Brix	Family	0.24±0.05**	0.54±0.08**	0.42±0.06**	0.26±0.04**	0.12±0.06*	0.28±0.07**	0.81±0.15**	0.66±0.13**
	Residual	0.51±0.05**	0.39±0.03**	0.30±0.03**	0.32±0.03**	0.47±0.06±**	0.37±0.05**	0.37±0.04**	0.72±0.08**
	H	0.59±0.04	0.80±0.02	0.81±0.02	0.71±0.03	0.42±0.08	0.69±0.05	0.87±0.02	0.73±0.04
	G _s	0.88	1.12	1.06	0.94	0.62	0.96	1.19	1.19
	%G _s	5.84	7.17	6.37	6.57	4.14	6.21	7.69	9.52
Purity	Family	2.60±1.01**	1.79±0.31**	1.15±0.26**	1.29±0.31**	2.71±1.19*	0.69±0.27**	6.85±1.27**	3.24±0.94**
	Residual	13.93±1.25**	2.34±0.20**	2.39±0.22**	3.67±0.30**	10.08±1.30**	2.61±0.31**	3.62±0.42**	8.24±0.87**
	H	0.63±0.04	0.70±0.03	0.59±0.04	0.51±0.05	0.45±0.07	0.44±0.07	0.85±0.03	0.54±0.05
	G _s	2.17	1.52	1.29	1.25	1.40	1.00	2.07	1.61
	%G _s	2.52	1.84	1.56	1.45	1.42	1.18	2.46	1.92
Pol	Family	0.42±0.09**	0.64±0.09**	0.48±0.07**	0.34±0.06**	0.27±0.10**	0.30±0.08**	1.29±0.23**	0.70±0.15**
	Residual	0.92±0.08**	0.42±0.04**	0.36±0.03**	0.43±0.04**	0.80±0.10**	0.43±0.05**	0.52±0.06**	0.87±0.09**
	H	0.58±0.04	0.82±0.02	0.80±0.02	0.70±0.03	0.50±0.07	0.68±0.05	0.88±0.02	0.71±0.04
	G _s	0.99	1.16	1.09	1.00	0.83	0.97	1.32	1.20
	%G _s	7.69	9.01	7.98	8.13	6.52	7.69	10.12	11.42
ERC	Family	0.51±0.12**	0.68±0.10**	0.51±0.08**	0.38±0.07**	0.37±0.14**	0.31±0.09**	1.55±0.28**	0.73±0.16**
	Residual	1.32±0.12**	0.46±0.04**	0.41±0.04**	0.52±0.04**	1.12±0.14**	0.52±0.06**	0.62±0.07**	1.00±0.11**
	H	0.54±0.05	0.82±0.02	0.79±0.03	0.68±0.04	0.50±0.07	0.65±0.06	0.88±0.02	0.68±0.04
	G _s	1.02	1.19	1.11	1.03	0.90	0.97	1.38	1.20
	%G _s	8.98	10.82	9.53	9.47	8.08	8.46	12.39	13.44

Table 9. Variance components for family, residual and the estimated broad sense heritability (H), selection gains (Gs) and % gains to selections (%Gs) for the irrigated breeding programme.

Trait	Statistic	FSS07	FSS08	FSS09	FSS10
DM	Family	0.40±0.44ns	0.51±0.16**	1.20±0.32**	0.20±0.17ns
	Residual	6.82±0.63**	2.06±0.16**	1.69±0.22**	3.75±0.30**
	H	0.15±0.05	0.43±0.05	0.68±0.05	0.14±0.05
	G _s	0.42	0.90	1.37	0.34
	%G _s	1.49	3.23	5.78	1.42
Fibre	Family	0.10±0.56ns	0.79±0.16**	2.27±0.52**	1.31±0.29**
	Residual	7.81±0.78**	1.49±0.12**	1.97±0.26**	3.73±0.30**
	H	0.04±0.05	0.61±0.04	0.78±0.04	0.51±0.05
	G _s	0.11	1.19	1.62	1.27
	%G _s	0.06	8.77	13.61	11.37
Brix	Family	0.27±0.12**	0.34±0.06**	1.70±0.36**	1.25±0.17**
	Residual	1.58±0.14**	0.38±0.03**	0.99±0.13**	0.62±0.05**
	H	0.34±0.05	0.73±0.03	0.84±0.03	0.86±0.02
	G _s	0.67	1.01	1.48	1.34
	%G _s	5.52	7.11	12.61	10.78
Purity	Family	3.23±1.51*	3.19±0.63**	47.18±10.62**	60.67±7.84**
	Residual	22.88±2.04**	6.36±0.49**	37.59±4.95**	20.88±1.75**
	H	0.30±0.05	0.60±0.04	0.79±0.04	0.90±0.01
	G _s	1.13	1.68	3.44	3.38
	%G _s	1.55	2.02	4.93	4.75
Pol	Family	0.28±0.11**	0.48±0.08**	2.15±0.47**	2.51±0.33**
	Residual	1.48±0.13**	0.61±0.05**	1.58±0.21**	1.07±0.09**
	H	0.35±0.05	0.70±0.04	0.80±0.03	0.88±0.02
	G _s	0.69	1.10	1.59	1.57
	%G _s	7.84	9.27	19.17	17.5
ERC	Family	0.28±0.12**	0.57±0.10**	2.42±0.56**	3.32±0.44**
	Residual	1.66±0.15**	0.76±0.06**	2.16±0.28**	1.41±0.12**
	H	0.33±0.05	0.69±0.04	0.77±0.04	0.88±0.02
	G _s	0.66	1.14	1.64	1.68
	%G _s	10.03	11.31	27.12	25.03

Conclusion

There were highly significant family effects indicating the existence of differences that can be utilised during selection. Populations in the programmes possessed large variability as well as potentially large selection gains, making them suitable for progress using family selection. ERC % cane and Brix % cane were the major traits that emerged most suitable for the application of family selection, while Purity % was unsuitable. The short crop cycle programmes produced the largest potential gains compared to the longer cycle programmes. Programmes with inherently large variability such as the coastal long cycle and the Midlands sandy soils produced the least gains.

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