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OPTIMUM SELECTION STRATEGIES

IN ORIGINAL SEEDLINGS PARTICULARLY

FOR HEAVILY LODGED CROPS

by

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SUMMARY

In the Burdekin region, sugarcane is grown under irrigation, which results in large and frequently lodged crops. Mass (individual clone) selection is impractical under such conditions, and selection under conditions that minimise lodging has proved to be ineffective. The introduction of mobile weighing machines in Australia has made it possible to implement family selection using weighed whole family plot data. This study investigated the effectiveness of family selection on original seedlings grown to full crop potential followed by visual selection on the ratoon crop in the Burdekin region.

The results demonstrated that family selection based on the selection index, net merit grade (NMG), was effective in identifying families with a high frequency of elite clones (clones that combine good cane yield and sugar content). However, the results also suggested that any form of family selection would have to be liberal as a few elite clones could be found in relatively poor families. Combined family and visual selection was even more effective than family selection alone, and visual selection was effective in identifying elite clones in both the good and relatively poor families.

Gain from family selection was consistent up till about 30% of selection. It is proposed that the top 30% of families be chosen for routine visual selection. Thereafter, progressively fewer clones should be selected from the intermediate 40 to 50% of families. Families with moderate to low NMG, that have extremely high sugar content but otherwise low cane yield and vice versa, should also be targeted for any outstanding clones. The time required to select from these relatively poor families would not be a limiting factor in the field as such plots can be predetermined using family data.

An added advantage of family selection is the use of family data to select parents, since the breeding value of parents can be determined from progeny performance. Overall, this can only mean a more effective and efficient breeding program for the Burdekin region.

1.0   INTRODUCTION

Sugarcane is grown commercially as a clonally propagated crop. Identification of the most appropriate clones is critical in any sugarcane selection program. Many sugarcane selection programs commence with a large population of seedlings and employ mass selection, based on visual assessment of individual seedlings, to select the best clones. Because it is impractical to replicate such trials, the genetic expression of individual seedlings (clones) is confounded by uncontrollable environmental error. Realised heritability or response to selection is, therefore, low. To guard against discarding superior individuals at this stage of selection, such programs relax the selection intensity (selecting more individuals than necessary) putting a strain on available resources.

Research by BSES has shown family selection to be more efficient than mass selection at this early stage of selection (Cox, 1996). Family selection is particularly useful for traits with low heritability because families could be replicated across years and sites, thereby improving estimates of family mean as well as aiding in the identification of stable families (Falconer, 1989; Jackson and McRae, 1998). With family selection, entire families are selected on the basis of the mean phenotypic value (Falconer, 1989). However, in sugarcane, the rationale for family selection is not to produce superior families with commercial value, but rather to identify families with a higher frequency of superior clones. Family selection makes it possible to focus the selection for superior clones on the best families, as the probability of finding superior clones at later stages of selection is greatest within these families. This makes for more efficient use of available resources, as the need for relaxed selection intensity is reduced. An added advantage of family selection is that family data can be used to select parents, based on progeny performance.

In the Burdekin region of Australia, sugarcane is grown under irrigation, which results in large and frequently lodged crops. Since visual selection is impractical under such conditions, the practice was to restrict crop growth, by minimising irrigation and fertilisers, in order to prevent lodging and enable visual selection to be conducted (Hogarth *et al.,* 1990). However, because the crop's growth potential was not realised under such conditions, this probably had a negative impact on selection response, as visual estimation of cane yield was poorly correlated with actual cane yield in heavily lodged crops (Pollock, 1982). Indeed, neither family nor mass selection was effective under these conditions (Hogarth *et al.,* 1990), since the selection conditions (environments) were atypical of the target environment. The development of mobile weighing machines in Australia (Hogarth and Mullins, 1989) has made it feasible to harvest and weigh whole family plots. Using mobile weighing machines, it is now possible to objectively measure the full potential of original seedlings in family plots in the Burdekin region without having to restrict crop growth. Visual (mass) selection of superior clones within the promising families can then be carried out on the first ratoon crop using family data from the plant crop.

2.0   PROJECT OBJECTIVES

a) To evaluate the effectiveness of family selection in the plant crop of original seedlings of sugarcane grown to full crop potential in the Burdekin region. The crop will probably be heavily lodged.
b) To evaluate the effectiveness of visual (mass) selection in the young first ratoon crop.
c) To determine the level of family performance in seedling populations required for a family to be selected.

Information derived from this study would enable the breeder to design the most cost effective and efficient selection scheme for this stage of the breeding program for the Burdekin region.

3.0   METHODOLOGY

3.1   Stage 1 trial

Original seedlings from 100 full-sib families were planted to the field at the Burdekin station (147° 19' 50" E; 19° 33' 50" S) in May 1990. These seedlings represented a sample of seedlings in the BSES Burdekin's core breeding program. Seedlings were planted into single-row plots at the rate of 15 seedlings per row, with intra- and inter-row spacings of 0.6m and 1.5m, respectively. The experimental layout was a randomised complete block design with four replicates. Ten control plots, five each of the cultivars Q96 and Q117, were planted in each replicate.

The plant crop of this seedling trial was harvested in September 1991. The crop was lodged at time of harvest, but the extent of lodging was not as severe as anticipated. Whole family plots were mechanically harvested and weighed to obtain cane yield (tonnes of cane per hectare, TCH). Eight stalks, one from each of eight randomly chosen clones (stools) in a plot, were crushed and the extracted juice used to estimate sugar content (commercial cane sugar, CCS) using standard procedures (BSES, 1984). The above data (TCH and CCS) were used to calculate sugar yield (tonnes of sugar per hectare, TSH) and selection index (net merit grade, NMG) for each family. NMG is a selection index incorporating TCH and CCS with other agronomic characteristics of economic importance. It is calculated relative to standard cultivars (controls), which are adjusted to a mean of 10 (Skinner, 1965).

3.2   Stage 3 trial

Each stage 1 seedling family plot was sampled in April, 1992 (first ratoon crop), by randomly taking three clones and by selecting the best three clones based on visual appraisal for yield and agronomic characteristics of economic importance. Clones taken at random could also have been selected. The two border clones in a plot were not sampled, thus, limiting sampling to 13 clones per plot. These clones were planted into a stage 3 trial to assess the effectiveness of family selection in the plant crop of original seedlings grown to full crop potential, followed by visual selection in the young first ratoon crop in the Burdekin region. Each clone was planted to a single row (20-sett

plot, 10 m long). The experimental layout was a split-plot arrangement replicated into four randomised complete blocks, with whole plots assigned to families and sub-plots to sampling methods (random vs. selected). Each whole (family) plot comprised six rows, including three rows of random and three rows of selected clones. Thus, families but not clones were replicated. The control plots were planted to six rows of the cultivars Q96 and Q117 in each replicate.

The plant crop of this stage 3 trial was harvested in September 1993 and the first ratoon crop in July 1994. Each row/clone was mechanically harvested and weighed to estimate TCH. A two-stalk sample was taken from each row and used to estimate CCS using standard procedures (BSES, 1984). The above data, TCH and CCS, were used to calculate TSH and NMG.

3.3   Statistical analyses

Data from the stage 1 trial were subjected to analyses of variance (ANOVA) for a randomised complete block design using the generalised linear model (GLM) procedure in SAS (SAS Institute, 1990). Variance components were estimated, assuming all effects as random, by equating the means squares to their respective expected mean squares in the ANOVA (Table 1).

Table 1.   Expected mean squares for analysis of variance in the plant crop of 100 full-sib families (stage 1) of sugarcane.

Source of variation	d.f	Expected mean squares
Blocks, B	3	$\sigma_e^2 + 100\sigma_r^2$
Families, F	99	$\sigma_e^2 + 4\sigma_f^2$
Error, (B x F)	297	σ_e^2

** $P< 0.01$.

Broad sense heritability, on an entry mean basis, with appropriate confidence intervals (Knapp *et al*., 1985), was estimated for each trait as the ratio of the genotypic to the phenotypic variance component. The genotypic coefficient of variation, which measures the magnitude of genotypic variability among full-sib families and allows for comparison among traits with different measurement units, was estimated for each trait as follows:

$$CV_g = \frac{\sqrt{2\sigma_f^2}}{\bar{x}} \text{ x } 100$$

where, σ_f^2 is the family variance component, and $\bar{x}$ is the mean of the trait.

Genotypic, phenotypic and environmental correlation coefficients were estimated between each pair of traits among the full-sib families. Predicted response to direct full-sib family selection for a trait was estimated using the following formula (Falconer, 1989):

$$R = k. h^2. \sigma_p$$

where, R is predicted gain from selection; k is the standardised selection differential; h^2 is the broad sense heritability of the trait; and σ_p is the phenotypic standard deviation of the trait. Correlated responses to indirect selection were estimated using the following formula:

$$CR_Y = k. \sqrt{h^2}_X. \sqrt{h^2}_Y. \sigma p_Y. r_{XY}$$

where CR_Y is the predicted gain for trait Y by indirect selection for trait X; k is the standardised selection differential; h^2_X and h^2_Y are broad sense heritabilities for traits X and Y; σp_Y is the phenotypic standard deviation for trait Y; and r_{XY} is the genetic correlation between traits X and Y. For the above calculations (predicted direct and correlated responses), k was assumed at 20% selection intensity.

Data from the stage 3 trial were subjected to analyses of variance (ANOVA) using the generalised linear model (GLM) procedure in SAS (SAS Institute, 1990). The GLM procedure estimated type III sums of squares, which corrected for a few missing values in the stage 3 trial. The analysis followed a randomised complete block design with a split-plot treatment arrangement, with family treated as whole plot and sampling method within family (random vs. selected) as subplot. Differences between families were tested using the family by replication interaction. Differences between sampling methods (random vs. selected) and between family by sampling methods were tested using the family by sampling method interaction and the replication within family by sampling method interaction, respectively, as the appropriate error terms.

The effectiveness of family selection was assessed as the gain (%) in performance in stage 3 of randomly selected clones (23% random selection) from selected (family selection) stage 1 families, over the overall performance of random clones in stage 3. Similarly, the effectiveness of combined family and visual selection was assessed as the gain (%) in performance in stage 3 of visually selected clones (23% visual selection) from selected (family selection) stage 1 families, over the overall performance of random clones in stage 3.

The magnitude of the selection response, R, measured in stage 3 using random clones, relative to that of the selection differential, S, measured in stage 1, was determined as a measure of relative response. Selection differential, S, was calculated as the difference between the mean of selected stage 1 families and the overall stage 1 mean. Similarly, selection response, R, was calculated as the difference between the overall mean of the random stage 3 clones, and the mean of random stage 3 clones of selected stage 1 families. This formula is analogous to that used in estimating realised heritability (Fehr, 1987), except that the selected families were evaluated as clones rather than their derived progeny.

4.0   RESULTS AND DISCUSSION

Table 2.   Analysis of variance for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in the plant crop of 100 full-sib families (stage 1) of sugarcane.

Source of variation	d.f.	Mean squares			
		TCH	CCS	TSH	NMG
Blocks, B	3	1402.82*	14.58**	5.01	15.72**
Families, F	99	1103.80**	1.68**	27.03**	4.49**
Error, (B x F)	297	396.66	0.87	10.58	1.85
C.V. (%)		17	6	19	23

There were significant differences ($P < 0.01$) among families for TCH, CCS, TSH, and NMG in the plant crop of the stage 1 trial (Table 2). These results suggest that there is sufficient variability for these traits among the families tested for family selection to be effective. Estimates of coefficient of variation in this study are comparable to those reported in other trials in the Burdekin region (McRae *et al*., 1993).

Heritability estimates on an entry mean basis for TCH, CCS, TSH and NMG are reported in Table 3. Similar estimates of heritability on a plot mean basis for TCH, CCS, TSH and NMG are 31, 19, 28 and 26, respectively. The results reveal that TCH is the most heritable of the traits measured, and was estimated with the most precision as demonstrated by the relatively narrow width of the confidence limits. Heritability estimates for the derived traits, TSH and NMG were moderate, and one can assume that TCH was a more important determinant of these traits than CCS. The relatively low heritability estimate for CCS in this study contradicts a previous report of a similar study (McRae *et al*., 1993). Also surprising is the fact that heritability for CCS was estimated with low precision, especially since the CV, which measures the precision with which a trait is measured, portrayed that CCS was measured with high precision relative to the other traits (Table 2). The narrow genotypic variability for CCS (Table 3) within the studied population may be responsible for its low heritability value.

Table 3.   Coefficient of genotypic variability and heritability on an entry mean basis, with 90% confidence limits, for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in the plant crop of 100 full-sib families of sugarcane.

Trait	Coefficient of Genotypic variability (%)	Heritability (%)	Lower limit	Upper limit	Width[A]
TCH	16.8	64	49	75	41
CCS	4.3	48	26	64	79
TSH	19.1	60	44	72	47
NMG	19.9	59	42	71	49

[A] Expressed as the ratio (%) of the confidence interval width relative to the heritability point estimate.

Differences ($P < 0.01$) among families for TCH, CCS, TSH, and NMG in both the plant and ratoon crops of the stage 3 trial (Table 4) corroborate the conclusion drawn from the stage 1 analysis, that family selection would be effective for the traits measured. The effect of sampling method (random vs. selected) was significant ($P < 0.01$) for all traits in both the plant and ratoon crops, with the exception of CCS in the ratoon crop. Where sampling method was significant, the selected mean was greater than the random mean, indicating that selection based on visual appraisal of yield in the ratoon crop of original seedlings was effective for these traits. Also, the effectiveness of visual selection was consistent across families for these traits as indicated by the lack of significance of the family by sampling method interaction effect.

Table 4. **Analysis of variance for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in the plant and first ratoon crops of a stage 3 trial in sugarcane.**

Source of variation	d.f.	Mean squares							
		Plant crop				Ratoon crop			
		TCH	CCS	TSH	NMG	TCH	CCS	TSH	NMG
Blocks, B	3	7604.15**	52.52**	148.94*	56.14**	29004.21**	101.08**	359.66**	78.35**
Family, F	99	5211.66**	9.91**	123.78**	14.14**	2421.78**	9.02**	52.57**	11.25**
Error a	297	1935.05	6.82	53.72	6.74	941.73	2.77	22.66	4.70
Selection Method, M	1	98352.58**	33.01**	2714.37**	294.56**	67531.49**	0.10	1378.85**	236.09**
F x M	99	1459.15	3.89	43.56	5.42	631.54	1.71	17.37	3.80
Error b	300	1325.91	3.56	41.18	5.08	584.26	1.83	14.85	3.21
Sampling error	1598	3181.03	3.82	85.76	9.58	1622.01	1.90	42.44	8.54
CV (a), %		15	11	17	23	15	6	16	18
CV (b), %		12	8	15	20	12	5	13	15
Grand mean		172.40	13.92	24.32	6.62	118.24	14.94	17.73	6.97
Visual mean (V)		178.78	14.04	25.38	6.97	123.54	14.93	18.49	7.29
Random mean (R)		165.97	13.80	23.24	6.26	112.94	14.94	16.97	6.66
% Difference of V over R		7.7	1.7	9.2	11.3	9.4	-0.1	9.0	9.5

$P < 0.05$, ** $P < 0.01$.

Compared to the other traits, the improvement in CCS resulting from visual selection was minimal. Indeed, the response was slightly negative in the ratoon crop (Table 4). This can be attributed partly to the low, negative correlation between TCH and CCS in the population studied (Table 5), which effected a negative albeit low correlated response in CCS (Table 6). The normal breeding practice is to select the best families based on the selection index, NMG, before applying visual selection on the selected families. Furthermore, during visual selection, the brix of putative clones is taken to give an estimate of CCS, and clones with low brix (low CCS) are discarded. Therefore, a greater improvement in CCS than was observed in this study would be expected under normal circumstances. However, judging from the low heritability for CCS in this population (Table 3) and the low predicted response in CCS from selecting directly for CCS and indirectly for NMG (Table 6), the improvement would probably not have been very significant.

Table 5. **Genotypic (top value), phenotypic (middle value) and environmental (bottom value) correlation coefficient (± SE) between cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in the plant crop of 100 full-sib families (stage 1) of sugarcane.**

	CCS	TSH	NMG
TCH	-0.07 ± 0.19	0.97 ± 0.01	0.91 ± 0.03
	0.00 ± 0.03	0.96 ± 0.00	0.90 ± 0.00
	0.10 ± 0.06	0.95 ± 0.00	0.88 ± 0.01
CCS	-	0.17 ± 0.18	0.35 ± 0.17
	-	0.27 ± 0.02	0.44 ± 0.02
	-	0.40 ± 0.05	0.55 ± 0.04
TSH	-	-	0.98 ± 0.01
	-	-	0.98 ± 0.00
	-	-	0.98 ± 0.00

Table 6. **Predicted response from direct and indirect selection for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in the plant crop of 100 full-sib families (stage 1) of sugarcane.** *A 20% selection intensity was assumed.*

Direct response		Indirect response	
Trait	Value	Trait	Value
TCH	21.45	CCS	-0.06
		TSH	3.20
		NMG	1.25
CCS	0.69	TCH	-1.30
		TSH	0.50
		NMG	0.41
TSH	3.22	TCH	20.03
		CCS	0.48
		NMG	1.29
NMG	1.31	TCH	18.79
		CCS	0.27
		TSH	3.12

4.1 Simulated selection and selection efficiency

The effectiveness of family selection in stage 1 was assessed by comparing the mean in stage 3, of random clones from selected stage 1 families, with the overall mean of random clones (Tables 7 to 10). Different scenarios where family selection was imposed for TCH, CCS, TSH and NMG were simulated, although normally family selection is based on NMG. Generally, the results show that family selection was

effective in predicting families with a high frequency of superior clones. For example, in Tables 7 to 10, the percent gain from family selection (Random) was generally greater at higher selection intensities and decreased as selection intensity approached 100%. This was especially true when selection was imposed directly for the trait. Exceptions were recorded for TCH (Table 7), where percent gain at 70% selection intensity was slightly greater than expected and for CCS (Table 8), where percent gain was slightly greater than expected at 30 and 70% selection intensities. The response in CCS when selection was based on TCH (Table 7) and vice versa (Table 8) was not too encouraging, and probably reflects the unfavourable association between CCS and TCH in this population (see Tables 5 and 6). This underpins the importance of basing selection on the selection index, NMG (Skinner, 1965), which takes into account both TCH and CCS as well as other agronomic characteristics of economic importance.

When family selection was based on NMG, the response in TCH and TSH decreased progressively as the selection intensity was relaxed from 10 to 100% (Table 11). The response for NMG also followed a similar pattern. These results indicate that family selection based on NMG was effective in identifying families with a high proportion of clones that are superior in TCH, TSH and NMG. The response in CCS was not consistent, and was negative at 10% of selection and peaked at 30% and again at 70% of selection. The ultimate goal of a family selection program is to select families with a high proportion of clones that are superior in both TCH and CCS and that have commercial value (superior in NMG). Judging from the response in NMG, it can be concluded that family selection based on NMG was effective in identifying families with a high proportion of elite clones. Additional evidence to this point can be visualised in Appendix A.16 and B.16, which shows the ranked performance for NMG in stage 3 of random families (Appendix A.16) or individual clones (Appendix B.16) at different rates of family selection for NMG in stage 1. As family selection was relaxed from 10 to 100%, the number of families or individual clones occurring in the top 50% of stage 3 tended to decrease.

However, some families performed better in stage 3 whereas others performed worse than would be expected on the basis of their family performance in stage 1. This is indicated by the lack of a uniform value for the estimates of relative response (Table 11) and from the performance (frequency distribution) in stage 3 of randomly derived families and individual clones at different rates of family selection in stage 1 (Appendix A and B). The above observation was also supported by the fact that correlation coefficients between stage 1 (family means) and stage 3 (family mean of random clone) were moderate [TCH, r = 0.53; CCS, r = 0.49; TSH, r = 0.50; NMG, r = 0.48], and explained less than 50% of the variation. Thus, although family selection was important for predicting families with a high frequency of superior clones, some form of liberal selection needs to be practised, as superior clones can be found in relatively poor families.

The effectiveness of combined family and visual (mass) selection in stage 1 was assessed by comparing the mean, in stage 3, of visually selected clones from selected stage 1 families, with the overall mean of random clones (Tables 7 to 10). In the model, visual or random selection of individual clones within families was fixed at 23%, whereas family selection was simulated from 10 to 100%. As was the case with family selection, the response to combined family and visual selection (Selected) generally was greater at

higher selection intensities and decreased as selection intensity approached 100%. However, as expected from the lack of association between TCH and CCS (Table 5), the response in CCS, and other traits when family selection was based on CCS, did not follow this trend. But importantly, when visual selection was preceded by family selection for NMG, the response in TCH and TSH decreased as the selection intensity was relaxed from 10 to 100% (Tables 7 and 9). A similar trend was recorded for NMG except that at 20% of family selection the response was slightly lower than expected (Table 10). This slight discrepancy is to be expected since the computation of NMG takes into account both TCH and CCS. In spite of the discrepancy, the overall results confirmed that family selection was effective, and also demonstrated the importance of visual selection in identifying elite clones within families.

In fact, the results showed that combined family and visual selection was more effective than family selection alone. At every rate of family selection, percent gain was always greater when family selection was accompanied by visual (Selected) rather than random (Random) selection (Tables 7 to 10). It is interesting to note that this occurred for all the traits, even when initially, family selection was not imposed for that trait. Furthermore, when the performance in stage 3 was ranked from 10 to 100%, a greater proportion of families (Table 12) or individual clones (Table 13) from the selected group occurred in the top 0 – 40% rank compared to the random group. The reverse was true at the lower ranks (> 40%). Additional evidence can be visualised in Appendix A.16 and B.16 which shows the ranked performance for NMG in stage 3 of random versus selected families (Appendix A.16) or individual clones (Appendix B.16) at different rates of family selection for NMG in stage 1. It is clear from the frequency distribution that combined family and visual selection was more effective than family selection alone in identifying elite families or individual clones from the top as well as relatively poor families. BSES breeders often are only interested in clones with mean NMG $\geq$ 9.0. Were it not for visual selection, only 197 clones with NMG $\geq$ 9.0 would have progressed to the next stage of the breeding program (Table 12, Appendix B.16). With visual selection, the number of clones was increased to 283.

One objective of this study was to determine the level of family performance in seedling populations required for a family to be selected. From a breeding standpoint, only clones with mean NMG $\geq$ 9.0 are worthy of consideration, which in this study corresponds to the top 20% performance in stage 3 (Table 13). Assuming the same 20% performance for the families, Appendix A.16 and B.16 show that gain from family selection in stage 1 was consistent up till about 30% of selection. For example, 6 of the 8 random families and 20 of the 32 selected families that performed in the top 20% in stage 3, occurred within the 10 to 30% range of family selection in stage 1 (Appendix A.16). Similarly, a relatively greater number of individual clones from the random and selected groups that performed in the top 20% in stage 3 occurred within the 10 to 30% range of family selection in stage 1 (Appendix B.16). Therefore, the top 30% of families should be chosen for routine visual selection in the breeding program.

Table 7. **Response of cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in stage 3, from family selection for TCH in stage 1 followed by either random (random) or visual (selected) selection of individual clones within family.** *Random and Selected are taken to represent the effects of family and combined family plus visual selection, respectively.*

Rate of family selection	Selection method for individual clones within family [A]	Gain (%) over population mean of random clones in stage 3			
		TCH	CCS	TSH	NMG
10	Random	12.24	-0.43	11.03	11.04
	Selected	18.99	0.26	19.19	20.36
20	Random	6.85	-0.37	6.14	5.92
	Selected	14.56	0.61	15.07	16.51
30	Random	4.37	0.04	4.14	4.08
	Selected	13.43	1.06	14.46	15.95
40	Random	4.21	0.02	3.95	4.00
	Selected	12.74	0.70	13.38	14.62
50	Random	3.21	-0.17	2.89	2.75
	Selected	12.05	0.47	12.38	13.45
60	Random	2.41	-0.07	2.22	2.15
	Selected	10.99	0.30	11.24	12.11
70	Random	2.73	-0.16	2.51	2.49
	Selected	10.77	0.23	10.89	11.70
80	Random	1.70	-0.08	1.57	1.57
	Selected	10.14	0.46	10.52	11.46
90	Random	0.98	-0.18	0.81	0.73
	Selected	9.68	0.57	10.13	11.18
100	Random	0.00	0.00	0.00	0.00
	Selected	8.40	0.77	9.10	10.29
Population mean of random clones in stage 3		139.45	14.38	20.10	6.46

[A] 23% of individual clones were selected from each family.

Table 8. **Response of cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in stage 3, from family selection for CCS in stage 1 followed by either random (random) or visual (selected) selection of individual clones within family.** *Random and Selected are taken to represent the effects of family and combined family plus visual selection, respectively.*

Rate of family selection	Selection method for individual clones within family [A]	Gain (%) over population mean of random clones in stage 3			
		TCH	CCS	TSH	NMG
10	Random	-2.68	2.89	0.14	2.10
	Selected	3.49	4.04	7.52	10.77
20	Random	0.01	2.32	2.22	4.01
	Selected	7.25	3.22	10.69	13.92
30	Random	-1.15	2.34	1.04	2.76
	Selected	6.26	2.60	8.96	11.66
40	Random	-0.61	1.84	1.27	2.64
	Selected	7.62	2.57	10.22	12.86
50	Random	0.27	1.16	1.47	2.38
	Selected	8.27	2.02	10.28	12.55
60	Random	0.16	1.09	1.16	1.91
	Selected	8.44	1.88	10.29	12.44
70	Random	-0.13	1.16	0.96	1.75
	Selected	8.63	1.73	10.30	12.29
80	Random	-0.10	0.78	0.59	1.07
	Selected	8.36	1.32	9.60	11.25
90	Random	-0.02	0.57	0.49	0.86
	Selected	8.76	1.14	9.82	11.33
100	Random	0.00	0.00	0.00	0.00
	Selected	8.40	0.77	9.10	10.29
Population mean of random clones in stage 3		139.45	14.38	20.10	6.46

[A] 23% of individual clones were selected from each family.

Table 9. **Response of cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in stage 3, from family selection for TSH in stage 1 followed by either random (random) or visual (selected) selection of individual clones within family.** *Random and Selected are taken to represent the effects of family and combined family plus visual selection, respectively.*

Rate of family selection	Selection method for individual clones within family [A]	Gain (%) over population mean of random clones in stage 3			
		TCH	CCS	TSH	NMG
10	Random	9.82	-0.17	9.28	9.40
	Selected	17.50	1.41	18.89	20.65
20	Random	7.29	0.26	7.41	7.63
	Selected	14.99	0.38	15.35	16.65
30	Random	5.77	0.37	5.91	6.26
	Selected	13.86	0.99	14.84	16.42
40	Random	3.52	0.57	3.85	4.28
	Selected	13.17	1.17	14.33	16.03
50	Random	2.72	0.53	3.16	3.63
	Selected	11.81	1.11	12.86	14.47
60	Random	2.75	0.15	2.97	3.21
	Selected	11.57	0.49	11.93	12.98
70	Random	2.60	0.19	2.68	2.92
	Selected	10.69	0.41	10.96	11.87
80	Random	2.15	0.07	2.11	2.22
	Selected	10.32	0.36	10.60	11.54
90	Random	1.05	-0.10	0.95	0.92
	Selected	9.60	0.64	10.13	11.19
100	Random	0.00	0.00	0.00	0.00
	Selected	8.40	0.77	9.10	10.29
Population mean of random clones in stage 3		139.45	14.38	20.10	6.46

[A] 23% of individual clones were selected from each family.

Table 10. **Response of cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in stage 3, from family selection for NMG in stage 1 followed by either random (random) or visual (selected) selection of individual clones within family.** *Random and Selected are taken to represent the effects of family and combined family plus visual selection, respectively.*

Rate of family selection	Selection method for individual clones within family [A]	Gain (%) over population mean of random clones in stage 3			
		TCH	CCS	TSH	NMG
10	Random	9.82	-0.17	9.28	9.40
	Selected	17.50	1.41	18.89	20.65
20	Random	7.48	0.36	7.63	7.96
	Selected	15.25	0.70	16.03	17.45
30	Random	5.24	0.81	5.84	6.59
	Selected	14.51	1.42	15.96	17.95
40	Random	3.15	0.70	3.62	4.19
	Selected	12.67	1.10	13.74	15.37
50	Random	3.08	0.56	3.61	4.15
	Selected	12.13	1.03	13.09	14.64
60	Random	2.64	0.42	3.14	3.59
	Selected	11.31	0.74	11.93	13.22
70	Random	2.46	0.52	2.99	3.50
	Selected	11.05	0.72	11.72	13.03
80	Random	1.95	0.30	2.17	2.43
	Selected	10.21	0.60	10.71	11.83
90	Random	0.66	0.14	0.77	0.91
	Selected	9.27	0.82	9.96	11.15
100	Random	0.00	0.00	0.00	0.00
	Selected	8.40	0.77	9.10	10.29
Population mean of random clones in stage 3		139.45	14.38	20.10	6.46

[A] 23% of individual clones were selected from each family.

Table 11.   **Relative response for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG) in stage 3, from different rates of family selection for these traits in stage 1.**

Rate of family Selection in stage 1	Relative response from family selection in stage 1[A]			
	TCH	CCS	TSH	NMG
10	0.58	0.41	0.40	0.32
20	0.42	0.42	0.41	0.35
30	0.33	0.52	0.40	0.35
40	0.38	0.48	0.31	0.26
50	0.35	0.35	0.31	0.31
60	0.32	0.40	0.37	0.35
70	0.46	0.53	0.44	0.45
80	0.40	0.47	0.49	0.45
90	0.41	0.55	0.39	0.30
100	0.00	0.00	0.00	0.00

[A] Relative response estimated as the ratio of the selection response, R, measured in stage 3 using random clones, and the selection differential, S, measured in stage 1.   See Materials and Methods for details.

As previously mentioned, the current practice at BSES is to select the best families in stage 1 based on the selection index, NMG, before applying visual selection on the selected families. Taking the brix of putative clones during visual selection should guard against selecting clones with extremely low CCS. This should at least off set the adverse correlation between TCH and CCS such that eventually, only clones with moderate to high NMG are selected. We currently select more clones from the top families (which according to this study should comprise the top 30% of families) and progressively fewer clones from the intermediate families. A few families with moderate to low NMG, that have extremely high CCS but otherwise low TCH and vice versa, are also targeted during visual selection in the hope of identifying any exceptional clones. Fortunately, the time required to select from these relatively poor families in the field is not a limiting factor as such plots are predetermined based on family data.

5.0   DIFFICULTIES

Original seedlings were first planted in 1989 but were destroyed by greyback grubs. This was the first report of such an attack in this region. The experiment was replanted in 1990, delaying the project by one year. Dr McRae, the principal investigator, resigned from the BSES before a final report could be written; he has been replaced by Dr Collins A. Kimbeng. Despite these problems, it should be noted that the results from this project have had a positive impact on the selection program in the Burdekin and have led to the release of some promising new cultivars.

6.0 CONCLUSION

Selection based on family data in the plant crop of original seedlings was effective in identifying families with a high proportion of superior clones. However, family selection would have to be liberal as superior clones could be found in relatively poor families. Visual selection practised on the young first ratoon crop of original seedlings was also effective in selecting superior genotypes within families and would be particularly useful in selecting such genotypes in relatively poor families. Gain from selection was much greater with combined family and visual selection than with family selection alone. An appreciable number of elite clones were found in the top 30% of families. Therefore, the top 30% of families should be chosen for routine visual selection in the breeding program.

Table 12. Ranked performance in stage 3, for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection Index (NMG), of families derived from either random (Random) or visual (Selected) selection in stage 1. *Random and Selected are taken to represent the effects of family and combined family plus visual selection, respectively.*

Ranked performance in stage 3		Selection strategy in stage 1[A]	Number (proportion) of families in the random and selected group within each rank[B]			
Percent	NMG Range		TCH	CCS	TSH	NMG
10	≥ 7.9	Random	3 (15)	7 (35)	2 (10)	3 (15)
		Selected	17 (85)	13 (65)	18 (90)	17 (85)
20	≥ 7.4	Random	4 (20)	12 (60)	6 (30)	5 (25)
		Selected	16 (80)	8 (40)	14 (70)	15 (75)
30	≥ 7.2	Random	7 (35)	8 (40)	6 (30)	7 (35)
		Selected	13 (65)	12 (60)	14 (70)	13 (65)
40	≥ 7.0	Random	9 (45)	8 (40)	10 (50)	10 (50)
		Selected	11 (55)	12 (60)	10 (50)	10 (50)
50	≥ 6.7	Random	11 (55)	10 (50)	7 (35)	11 (55)
		Selected	9 (45)	10 (50)	13 (65)	9 (45)
60	≥ 6.5	Random	10 (50)	10 (50)	11 (55)	9 (45)
		Selected	10 (50)	10 (50)	9 (45)	11 (55)
70	≥ 6.3	Random	9 (45)	13 (65)	14 (70)	11 (55)
		Selected	11 (55)	7 (35)	6 (30)	9 (45)
80	≥ 6.1	Random	13 (65)	12 (60)	14 (70)	16 (80)
		Selected	7 (35)	8 (40)	6 (30)	4 (20)
90	≥ 5.6	Random	17 (85)	9 (45)	13 (65)	12 (60)
		Selected	3 (15)	11 (55)	7 (35)	8 (40)
100	≤ 5.6	Random	17 (85)	11 (55)	17 (85)	16 (80)
		Selected	3 (15)	9 (45)	3 (15)	4 (20)

[A] 23% of individual clones were selected from each family in stage 1.
[B] Data based on family mean. There were 100 families each of random and selected clones for a total of 200 families.

Table 13. **Ranked performance in stage 3, for cane yield (TCH), sugar content (CCS), sugar yield (TSH) and selection index (NMG), of individual clones derived from either random or visual (selected) selection in stage 1**. *Random and Selected are taken to represent the effects of family and combined family plus visual selection, respectively.*

Ranked performance in stage 3		Selection strategy in stage 1[A]	Number (proportion) of clones in the random and selected group within each rank[B]			
Percent	NMG Range		TCH	CCS	TSH	NMG
10	≥ 10	Random	96 (40)	111 (46)	94 (39)	97 (40)
		Selected	144 (60)	129 (54)	146 (61)	143 (60)
20	≥ 9.0	Random	100 (42)	120 (50)	100 (42)	100 (42)
		Selected	140 (58)	120 (50)	140 (58)	140 (58)
30	≥ 8.2	Random	111 (46)	116 (48)	108 (45)	108 (45)
		Selected	129 (54)	124 (52)	132 (55)	132 (55)
40	≥ 7.6	Random	123 (51)	122 (51)	120 (50)	120 (50)
		Selected	117 (49)	118 (49)	120 (50)	120 (50)
50	≥ 6.9	Random	125 (52)	115 (48)	130 (54)	131 (55)
		Selected	115 (48)	125 (52)	110 (46)	109 (45)
60	≥ 6.3	Random	106 (44)	112 (47)	116 (48)	114 (47)
		Selected	134 (56)	128 (53)	124 (52)	126 (53)
70	≥ 5.5	Random	116 (48)	121 (50)	118 (49)	112 (47)
		Selected	124 (52)	119 (50)	122 (51)	128 (53)
80	≥ 4.5	Random	134 (56)	132 (55)	115 (48)	125 (52)
		Selected	106 (44)	108 (45)	125 (52)	115 (48)
90	≥ 3.2	Random	127 (53)	122 (51)	144 (60)	144 (60)
		Selected	113 (47)	118 (49)	96 (40)	96 (40)
100	≤ 3.2	Random	162 (67)	129 (54)	115 (65)	149 (62)
		Selected	78 (33)	111 (46)	85 (35)	91 (38)

[A] 23% of individual clones were selected from each family in stage 1.
[B] Data based on mean of individual clones. There were 1200 each of random and selected clones for a total of 2400 clones.

In the Burdekin region where crop lodging is regular, visual selection is impractical and restricting crop growth to facilitate selection has been shown to impede selection progress. This study has shown that, for this region, family selection on the plant crop of original seedlings followed by visual selection within selected families in the ratoon crop is a practical and efficient method of selecting sugarcane. In this study, visual selection was fixed at 23%. Future studies should look at differential rates of family and visual selection to optimise the advantages of visual selection.

7.0   PUBLICATIONS

This report will be edited for format and content and submitted for publication at a later date. The target journals are the Australian Journal of Experimental Agriculture and the Australian Society of Sugarcane Technologists.

8.0   REFERENCES

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9.0   ACKNOWLEDGMENTS

Appendix A. Continued

9 Rate of family selection for TSH in stage 1

Rate of family selection for TSH in stage 1	Ranked performance for TCH in stage 3										Total stage 1
	10	20	30	40	50	60	70	80	90	100	
Selected (S)											
10	6	1	1	1	1	0	0	0	0	0	10
20	3	1	2	2	1	1	0	0	0	0	10
30	1	3	3	1	1	0	0	1	0	0	10
40	2	3	1	1	0	1	2	0	0	0	10
50	0	2	2	0	2	1	2	1	0	0	10
60	2	1	2	2	0	2	1	0	0	0	10
70	0	1	0	4	1	1	1	2	0	0	10
80	2	2	0	0	2	1	1	2	0	0	10
90	1	1	2	0	0	2	0	1	3	0	10
100	0	1	0	0	1	1	4	0	0	3	10
Total stage 3 (S)	17	16	13	11	9	10	11	7	3	3	100
Random (R)											
10	2	1	2	1	1	1	1	0	1	0	10
20	1	0	1	0	3	1	2	2	0	0	10
30	0	1	1	1	2	0	1	1	3	0	10
40	0	0	1	0	0	3	1	0	2	3	10
50	0	0	1	1	1	1	0	2	3	1	10
60	0	0	0	3	2	1	1	2	1	0	10
70	0	1	1	0	1	1	1	2	3	0	10
80	0	1	0	1	1	1	1	2	0	3	10
90	0	0	0	1	0	1	1	0	2	5	10
100	0	0	0	1	0	0	0	2	2	5	10
Total stage 3 (R)	3	4	7	9	11	10	9	13	17	17	100
Total S + R	20	20	20	20	20	20	20	20	20	20	200

10 Rate of family selection for TSH in stage 1

Rate of family selection for TSH in stage 1	Ranked performance for CCS in stage 3										Total stage 1
	10	20	30	40	50	60	70	80	90	100	
Selected (S)											
10	2	0	2	2	0	1	1	0	2	0	10
20	2	1	1	0	0	0	0	1	3	2	10
30	3	1	1	2	0	1	0	0	1	1	10
40	1	0	1	2	3	1	0	2	0	0	10
50	1	1	2	0	1	3	0	0	1	1	10
60	0	0	0	2	1	0	1	1	2	3	10
70	1	0	0	1	2	2	1	1	2	0	10
80	0	0	3	1	1	0	3	1	0	1	10
90	1	3	1	1	2	0	0	2	0	0	10
100	2	2	1	1	0	2	1	0	0	1	10
Total stage 3 (S)	13	8	12	12	10	10	7	8	11	9	100
Random (R)											
10	0	2	2	0	0	1	2	1	0	2	10
20	1	2	1	0	1	1	1	1	1	1	10
30	1	1	1	1	2	0	0	3	1	0	10
40	1	1	0	2	2	0	3	0	1	0	10
50	1	2	1	0	0	1	2	2	0	1	10
60	0	0	0	3	0	1	2	1	1	2	10
70	1	1	1	1	1	2	0	0	3	0	10
80	0	0	0	1	2	2	1	3	1	0	10
90	0	2	0	0	1	2	1	0	1	3	10
100	2	1	2	0	1	0	1	1	0	2	10
Total stage 3 (R)	7	12	8	8	10	10	13	12	9	11	100
Total S + R	20	20	20	20	20	20	20	20	20	20	200

Appendix B. Frequency distribution in stage 3, of individual clones derived from family selection in stage 1 followed by either visual (selected) or random (random) selection of individual clones within family. *23% of individual clones were selected from each family.*

1 Rate of family selection for TCH in stage 1

Rate of family selection for TCH in stage 1	Ranked performance for TCH in stage 3										Total stage 1
	10	20	30	40	50	60	70	80	90	100	
					Selected (S)						
10	18	19	17	19	13	13	6	11	3	1	120
20	16	11	13	18	13	7	13	13	14	2	120
30	15	13	20	14	8	13	13	6	13	5	120
40	14	21	11	8	14	14	11	10	11	6	120
50	16	16	10	5	13	12	20	9	12	7	120
60	16	10	14	10	10	10	15	9	16	10	120
70	14	13	13	14	10	14	16	9	10	7	120
80	13	13	13	9	11	12	17	12	9	11	120
90	13	18	6	10	11	22	5	13	12	10	120
100	9	6	12	10	12	17	8	14	13	19	120
Total stage 3 (S)	144	140	129	117	115	134	124	106	113	78	1200
					Random (R)						
10	14	16	7	19	23	13	8	8	7	5	120
20	9	10	12	12	19	5	10	19	12	12	120
30	9	11	12	10	13	6	19	10	11	19	120
40	13	8	13	16	7	13	11	18	12	9	120
50	10	8	7	16	17	8	14	11	14	15	120
60	8	10	12	8	10	11	13	18	14	16	120
70	8	12	19	14	10	15	9	12	8	13	120
80	6	5	13	10	6	14	13	15	18	20	120
90	7	15	8	9	9	14	8	11	15	24	120
100	12	5	8	9	11	7	11	12	16	29	120
Total stage 3 (R)	96	100	111	123	125	106	116	134	127	162	1200
Total S + R	240	240	240	240	240	240	240	240	240	240	2400

2 Rate of family selection for TCH in stage 1

Rate of family selection for TCH in stage 1	Ranked performance for CCS in stage 3										Total stage 1
	10	20	30	40	50	60	70	80	90	100	
					Selected (S)						
10	9	12	11	9	17	17	11	12	12	10	120
20	12	12	14	14	16	8	9	13	12	10	120
30	15	10	14	10	15	11	13	15	8	9	120
40	13	12	10	14	10	14	12	11	8	16	120
50	11	8	11	17	7	14	17	14	8	13	120
60	12	8	9	14	12	17	8	10	14	16	120
70	11	10	13	3	14	14	15	9	20	11	120
80	15	16	12	13	10	13	14	7	12	8	120
90	12	14	17	10	13	12	11	8	13	10	120
100	19	18	13	14	11	8	9	9	11	8	120
Total stage 3 (S)	129	120	124	118	125	128	119	108	118	111	1200
					Random (R)						
10	9	13	10	14	10	15	12	14	10	13	120
20	11	13	5	14	11	13	14	12	15	12	120
30	10	11	10	11	16	12	16	13	16	5	120
40	11	7	12	13	12	12	16	14	12	11	120
50	8	9	11	14	12	15	10	10	16	15	120
60	14	13	9	11	13	9	13	17	6	15	120
70	9	11	16	9	13	11	8	14	12	17	120
80	9	17	13	17	8	9	10	11	13	13	120
90	9	9	12	12	10	8	15	19	17	9	120
100	21	17	18	7	10	8	7	8	5	19	120
Total stage 3 (R)	111	120	116	122	115	112	121	132	122	129	1200
Total S + R	240	240	240	240	240	240	240	240	240	240	2400