

**BUREAU OF SUGAR EXPERIMENT STATIONS  
QUEENSLAND, AUSTRALIA**

**FINAL REPORT  
SRDC PROJECT BS6S**

**SELECTION OF SUPERIOR  
CROSSES OF SUGARCANE**

by

J K Bull and D M Hogarth

*This Project was funded by the Sugar Research Council/Sugar Research and Development Corporation during the 1988/89, 1989/90 and 1990/91 financial years.*

**October 1991**



## CONTENTS

	<b>Page No</b>
SUMMARY	1
INTRODUCTION	1
EXPERIMENTAL DETAILS	
Experiment 1	2
Experiment 2	3
Analytical methods	4
RESULTS AND DISCUSSION	
Nature and extent of interaction	4
Impact of interaction on gains from selection	8
CONCLUSIONS	13
RECOMMENDATIONS	14
ACKNOWLEDGEMENTS	14
LIST OF PUBLICATIONS	15
REFERENCES	16



## SUMMARY

The impact of GxE interaction on the response to three methods of selection was assessed over three locations and three crop-years. The three selection methods considered were two previously used procedures, mass (individual) selection using a visual appraisal of clonal performance and family selection using selection rate, and a new procedure, family selection using a grade based on weighed family plots. Within the two forms of family selection, light mass selection based on a visual appraisal of clonal performance was used to reject the poorest clones. The gains from selection, calculated as the deviation in performance of the select groups from the performance of a group of randomly chosen clones, were assessed for each of these three methods.

All three selection methods gave similar good gains over the random group when averaged over all locations and crop-years. Weighed family selection is recommended for routine use as it is the least labour intensive and most cost effective. Genotype x environment interaction, both on a family and clonal basis, was of sufficient magnitude to affect the gains made from selection. These effects were somewhat unpredictable but provided some support for location specific selection.

Further, selections based on the results from the Bundaberg Sugar Experiment Station produced relatively poor gains when assessed over all locations and crop-years. This indicates that the Station may be a poor location for central selection. The use of at least one other location, in addition to the Station, may provide a buffer against environmental factors rendering family or clonal discrimination worthless at any particular location.

## INTRODUCTION

Plant breeding trials are generally aimed at discriminating between a large number of genotypes over a range of representative environments. Commonly, the response of genotypes to the conditions encountered within the environments differs. This may result in a change in the relative performance of the genotypes and give rise to GxE interaction (Byth *et al*, 1976). When present this interaction complicates the selection of superior genotypes from a set of test genotypes. This interaction has been identified in sugarcane on both the clonal level (Arceneaux and Hebert, 1943; Pollock, 1978; Kang and Miller, 1984) and family level (Hogarth and Bull, 1990; Bull and Hogarth, 1990).

Historically it has been the practice to evaluate families (bi-parental crosses; Breaux, 1987) on a central experiment Station and then, when the number of clones has been substantially reduced (from approx 8500 to 150; Hogarth and Mullins, 1989), to evaluate this select group of clones over a range of environments. However the rationale behind this practice has been questioned (Hogarth and Bull, 1990) since clone by environment (CxE) and family x environment (FxE) interactions have been identified, and their effects found to be approximately as large as the main effect of clone or family, for the key evaluation characters.

The physical bulk of the sugarcane crop, coupled with the large number of families and clones within families, has precluded the efficient and rapid weighing of plots in the early

selection stages until recently (Hogarth and Bull, 1990). As a result, either mass (individual) selection or selection rate has been used to determine elite clones or families (Skinner *et al*, 1987). Both of these methods rely on a visual appraisal of clonal performance. The recent development of mobile weighing equipment (Hogarth and Mullins, 1989) has allowed the efficient and objective evaluation of families. Weighed clonal evaluation in the early selection stages is still impractical because of the large number of clones present. Also it may be somewhat undesirable, because the effects of competition will be exacerbated by the small plot sizes necessitated by the limited availability of planting material.

To examine the effectiveness of selection in such early selection stages, the actual gains were determined for three methods of selection over a random choice of clones. These three methods included the two previously used procedures (mass and selection rate) and one proposed procedure. The proposed method involved family selection using weighed family plots. The impact of CxE and FxE interactions on these selection methods and the suitability of the current centralised selection was investigated.

## **EXPERIMENTAL DETAILS**

### **Experiment 1**

This experiment was described by Hogarth and Bull (1990), and was planned to simulate the initial family selection stage in a sugarcane breeding program. It consisted of 35 families and five standard cultivars (CP44-101, H56-752, Q110, Q125, Q137) each grown on three locations in south east Queensland, Australia. The standard cultivars were included to provide an agronomic bench mark (Basford *et al*, 1990). The three locations were Bingera Plantation, a substation near Nambour and the Bundaberg Sugar Experiment Station, to be referred to as Bingera, Nambour and Station, respectively. This experiment was harvested as plant and first ratoon crops, and therefore could be considered as six environments.

At each location, 42 clones were planted from each of the 35 families giving 1470 clones. Similarly, 42 repeats were planted from each of the five standard cultivars, giving an additional 210 clones. Three blocks were used at each location and 14 clones from each family or standard were planted as 'family' plots in each block. There were three rows each with five 2 m plots per 'family plot'. To facilitate visual appraisal of clones, the first position in the central row of each of these 'family' plots was occupied by standard cultivar CP44-101.

Visual net merit grades (VNMG) were given to each clone in the plant crop of this experiment prior to harvest. These were based on a visual appraisal of the cane yield and on a hand refractometer brix value of each clone relative to the nearest CP44-101 standard cultivar (Skinner, 1965).

The characters which were assessed on a family basis at each location in both plant and first ratoon crops included tonnes of cane per hectare (TCH), commercial cane sugar (CCS), tonnes of sugar per hectare (TSH) and net merit grade (NMG) (Skinner, 1965). CCS for each family was determined by taking stalk samples from five random clones and sampling the mixed juice.

## Experiment 2

This was designed to assess the gains from three selection strategies when applied to Experiment 1. The selection strategies chosen were practical and directly applicable to the core breeding program and included:

- (i) Mass selection based on clonal VNMG (Skinner *et al.*, 1987). A total of 126 clones was selected from the 1470 clones present in the plant crop at each location.
- (ii) Modified family selection based on selection rate (referred to as 'family SR') determined by the number of clones superior for VNMG within each family (Skinner *et al.*, 1987). Seven families were selected from the 35 present at each location based on plant crop results. The selection of clones superior for VNMG from within elite families was conducted in the first ratoon crop at each location. This would be the practice if this method was adopted as, by limiting clonal selection to those families already chosen, labour requirements would be minimised. So, within each of the selected families, 18 clones were chosen from the 42 clonal members based on their VNMG, at each location.
- (iii) Modified family selection based on NMG (to be referred to as 'family NMG') derived from weighing family plots and determining CCS. Seven families were selected from the 35 families present at each location based on their plant crop results. As for method (ii), clonal evaluations were based on first ratoon crop results. Within each of the selected families, 18 clones were chosen from the 42 clonal family members based on their VNMG, at each location.

To facilitate the measurement of the gains made from each of these three selection methods, 126 clones were chosen randomly from the 1 470 clones present. However, only 103 clones were common to all locations over the three crop-years due to germination failures, establishment failures and limited planting material precluding the re-planting of failed clones. The failed clones were replaced at each location by other randomly chosen clones giving 126 in total at each location. To provide an agronomic bench mark, five standard cultivars (CP44-101, H56-752, Q110, Q137, Q141) were included. Each of these five standards was planted 18 times at each location.

Of all the clones chosen by mass selection at each of the three locations, 288 were different, and of all the families chosen by either method at the three locations 17 were different. Thus 810 clones were planted at each location - this was comprised of 288 clones from mass selections, 306 clones from family selections (17 families each of 18

clones), 126 clones from the random group, and 90 clones from the standard cultivars (five standard cultivars each repeated 18 times).

All clones were planted in single row 10 m plots. In an effort to decrease competition effects, clones from the same selection origin were planted into 'family' plots, each with three rows and two contiguous plots per row. These 'family' plots were randomly positioned in each block at each location in the plant crop. Each clone was harvested and weighed individually while CCS was determined from a two stalk sample. The characters TCH, TSH and NMG were derived from this information.

The same three locations were used for this experiment as for Experiment 1, ie, Bingera, Nambour and Station. Plant, first, and second ratoon crops were harvested enabling nine environments to be considered. Selections from each location using each method in Experiment 1 were planted on every location in Experiment 2.

### **Analytical methods**

To analyse the data, a completely random model was assumed as inference was to be drawn from these analyses to wider applications. Negative variance component estimates were reported as calculated but are assumed to be due to sampling errors. Other reasons are discussed by Thompson and Moore (1963).

To simplify interpretation, the gains were calculated as deviations from the mean of the random group, and were assessed for each selection method. To determine whether gains were significantly different, least significant difference (LSD) tests were used (Steel and Torrie, 1980). For all the analyses of the gains from selection, the error mean square values used to calculate the LSD value were obtained from the selection method x environment interaction mean square in an appropriate analysis of variance (ANOVA).

## **RESULTS AND DISCUSSION**

### **Nature and extent of interaction**

#### Clones

The pooled ANOVA over all environments and the ANOVA over all locations and crop-years were constructed for clones. The variance components for the effects of interest were estimated from this analysis for the characters TCH, CCS, TSH and NMG, and were based on the individual performance of clones from the random group in Experiment 2 (Table 1). Since each clone was unreplicated within a location, the trial was considered to be completely random in design and the sampling variability from the repeated standards was used to calculate the variance components for the CxE and clone x location x crop-year (CxLxY) interactions. Clonal measurements for TCH, CCS TSH and NMG were not obtained in Experiment 1, due to time and labour constraints.

Table 1

The estimated variance component and associated standard error for clone (C), clone x environment (CxE), clone x location (CxL), clone x crop-year (CxY) and clone x location x crop-year (CxLxY) effects for the 103<sup>1</sup> random clones for each character over plant, first and second ratoon crops in Experiment 2

Source	df	TCH	CCS	TSH	NMG
C	102	286.9 ± 49.9	0.91 ± 0.15	4.51 ± 0.79	3.02 ± 0.54
CxE	816	218.1 ± 39.5	0.87 ± 0.08	1.61 ± 0.69	1.89 ± 0.48
C	102	186.7 ± 52.5	0.82 ± 0.15	2.97 ± 0.83	1.98 ± 0.57
CxL	204	374.9 ± 48.9	0.37 ± 0.08	5.79 ± 0.77	3.90 ± 0.54
CxY	204	26.1 ± 16.1	-0.01 ± 0.05	0.35 ± 0.26	0.30 ± 0.20
CxLxY	408	-82.6 ± 33.5	0.61 ± 0.09	-2.99 ± 0.62	-1.26 ± 0.43

<sup>1</sup> Only 103 out of 126 random clones grown at each location in each year were common across all locations and crop-years.

These analyses demonstrated that:

- CxE interaction effects existed and were almost as large as the main effect of clone.
- Clone x location (CxL) interaction effects existed for TCH, TSH and NMG and were of similar magnitude to the main effect of clone.
- Clone x crop-year interaction effects were small relative to the main effect of clone.
- CxYxL interaction effects were non-significant (except for CCS).

On a clonal basis, therefore, the performance of clones differed mostly between locations and not between crop-years or due to location x crop-year interaction. Hence, there may be little need to use multi-year evaluation when selecting on a clonal basis.

### Families

Similarly for families, the pooled ANOVA over environments and the ANOVA over locations and crop-years were constructed. From these analyses the variance components for the effects of interest were estimated for TCH, CCS, TSH and NMG (Tables 2a to 2c). This was done using Experiment 1 results (all 35 families), Experiment 1 results for the 17 families selected from Experiment 1, and Experiment 2 results (all 17 families).

These analyses demonstrated that:

- The selection of families decreased the estimated family variance component for CCS, TSH and NMG.
- FxE interaction effects existed and were as large as the main effect of family for all characters in at least one analysis.
- Family x location (FxD) interaction effects existed and were as large or larger than the main effect of family for all characters in at least one analysis.
- Family x crop-year (FxD) interaction effects were mostly non-significant.
- Family x location x crop-year (FxDxY) interaction effects were mostly significant, but generally not as large as the main effect of family.

**Table 2**

**The estimated variance component and associated standard error for family (F), family x environment (FxE), family x location (FxD), family x crop-year (FxD) and family x location x crop-year (FxDxY) effects for each character.**

**2a All 35 families in Experiment 1 evaluated over plant and first ratoon crops in Experiment 1 (from Hogarth and Bull, 1990)**

Source	df	TCH	CCS	TSH	NMG
F	34	56.0 ± 16.9	0.44 ± 0.11	1.25 ± 0.37	0.79 ± 0.22
FxE	170	39.3 ± 10.6	-0.01 ± 0.02	0.77 ± 0.19	0.42 ± 0.10
F	34	42.9 ± 17.7	0.43 ± 0.11	1.01 ± 0.33	0.68 ± 0.23
FxD	68	19.8 ± 12.5	-0.02 ± 0.02	0.51 ± 0.23	0.29 ± 0.12
FxD	34	13.6 ± 8.0	0.02 ± 0.01	0.21 ± 0.13	0.07 ± 0.06
FxDxY	68	18.7 ± 9.6	0.00 ± 0.02	0.29 ± 0.16	0.17 ± 0.09

**2b The 17 families selected from Experiment 1 evaluated over plant and first ratoon crops in Experiment 1**

Source	df	TCH	CCS	TSH	NMG
F	16	56.6 ± 24.7	0.19 ± 0.07	0.80 ± 0.38	0.43 ± 0.20
FxE	80	53.0 ± 16.6	0.01 ± 0.02	1.16 ± 0.33	0.60 ± 0.17
F	16	42.9 ± 25.8	0.18 ± 0.07	0.48 ± 0.41	0.27 ± 0.22
FxD	32	45.2 ± 22.9	-0.02 ± 0.02	0.99 ± 0.45	0.56 ± 0.24
FxD	16	2.4 ± 7.4	0.02 ± 0.02	0.15 ± 0.17	0.03 ± 0.07
FxDxY	32	19.1 ± 12.7	0.02 ± 0.04	0.34 ± 0.23	0.16 ± 0.11

2c The 17 families selected in Experiment 1 evaluated over plant, first, and second ratoon crops in Experiment 2

Source	df	TCH	CCS	TSH	NMG
F	16	57.9 ± 21.6	0.08 ± 0.03	0.78 ± 0.30	0.51 ± 0.20
FxE	128	13.5 ± 8.8	0.09 ± 0.03	0.35 ± 0.16	0.22 ± 0.12
F	16	51.4 ± 21.9	0.05 ± 0.04	0.64 ± 0.31	0.40 ± 0.21
FxL	32	3.5 ± 11.1	0.04 ± 0.03	0.07 ± 0.18	0.06 ± 0.13
FxY	32	-0.1 ± 4.3	0.03 ± 0.02	0.15 ± 0.11	0.13 ± 0.08
FxLxY	64	16.5 ± 8.0	0.04 ± 0.03	0.26 ± 0.14	0.14 ± 0.10

Thus the performance of families for all characters differed mostly between locations and to a lesser extent due to location x crop-year interaction.

Impact of CxE interaction on selection

The clones selected at each location in the plant crop of Experiment 1 were compared to assess the effect of CxL interaction on selection. This was not possible for the first ratoon crop because planting material was removed and would have unduly biased the results on a clonal basis.

Relatively few selected clones were common between all locations (15 out of the 126). Hence, only about 12% of clonal selection was independent of location. The Station and Bingera and the Station and Nambour had 38 and 35 clones in common, respectively, whilst Bingera and Nambour only had 28 clones in common.

Impact of FxE interaction on selection

The families selected using either family NMG or family SR at each location in the plant crop of Experiment 1 were compared to assess the effect of FxL interaction on selection (Table 3). Using family NMG, three families out of seven were selected at all three locations and therefore were considered to be somewhat broadly adapted. Hence about 40% of family selection was independent of location. The location specific family selections, however, would only have been identified under the set of environmental conditions operating at each location in the plant crop. Using family SR, two families were common to the select groups from each location, and thus about 30% of family selection was independent of location for this method.

Table 3

The number of families selected in common (out of seven) between locations in experiment 1 for family SR and family NMG in the plant crops and also for family NMG in the ratoon crops

Selection method	Crop class	Location combination			
		Station and Bingera	Station and Nambour	Bingera and Nambour	All three locations
Family SR	Plant	3	3	4	2
Family NMG	Plant	4	4	4	3
Family NMG	Ratoon 1	3	3	4	3

Considering the family NMG performance in the first ratoon crop, similar conclusions may be drawn. However, the first ratoon family SR performance will not be considered as it may have been unduly affected by the removal of planting material.

Considering family NMG performance in both crop-years, only one family would have been selected from all locations, highlighting the effect of FxE interaction. However, all except two of the 17 families selected from the plant crop would have been selected from the first ratoon crop, highlighting the small effect of the FxY interaction. This may indicate that similar environmental challenges were occurring in the two crop-years but were occurring at different locations, thus giving rise to FxLxY interaction. From these data, the use of ratoon crops at the expense of sampling additional locations is difficult to justify in the core plant breeding program.

#### Impact of interaction on gains from selection

The gains were determined for each of the three methods of selection, using the deviations in performance of the select groups from the performance of the random group at each location in each crop-year. The gains from each method were averaged over the three locations and three crop-years in Table 4. All three selection methods gave significantly better performance for each character than did the random group, indicating that each method of selection was effective.

Table 4

Gains from each of the three methods of selection for each character, expressed as deviations from the performance of the random group, averaged over all locations and crop-years

Method	TCH	CCS	TSH	NMG
Mass	10.04 <sup>a</sup>	0.56 <sup>a</sup>	1.67 <sup>a</sup>	1.50 <sup>a</sup>
Family SR	9.86 <sup>a</sup>	0.40	1.52 <sup>a</sup>	1.33 <sup>a</sup>
Family NMG	9.80 <sup>a</sup>	0.51 <sup>a</sup>	1.60 <sup>a</sup>	1.44 <sup>a</sup>
LSD 5%	2.35	0.08	0.31	0.23
Percentage gain <sup>1</sup>	12.6	4.4	17.0	19.4

<sup>a</sup> Indicates for each character, those methods whose gains are not significantly different from the method with the highest gain.

<sup>1</sup> (Mean of superior methods/mean of the random group)\*100

Mass and family NMG selection methods were found to be more effective for CCS than was family SR. However, there was no significant difference between selection methods for the other characters.

The percentage gain over the mean of the random group was high for all characters except CCS, where genetic variation may have been somewhat limiting (Roach, 1980; Hogarth *et al.*, 1981). Thus, all three methods were essentially equally effective, and the decision as to which to adopt in the core breeding program depends upon the relative efficiency, cost effectiveness and practicality of each method. Currently these factors favour family NMG which is rapid and requires less labour to assess.

#### Centralised selection

To assess the utility of basing selection solely on Station results, the gains for the select groups from each of the three locations using each of the three methods were averaged over all locations and crop-years (Table 5). The select groups from each of these locations and methods gave significantly better performance for each character than did the random group. This indicates that each method of selection was effective and that CxE and FxE interactions were not of sufficient magnitude to completely frustrate advance from selection.

However, irrespective of method, the select groups from the Station gave significantly poorer gains than the highest performing select groups did, for the characters TCH, TSH, and NMG (Table 5).

Table 5

**Gains for each character averaged over the three locations  
and three crop-years for each of the three selection methods  
applied at each of the three locations**

Method	TCH	CCS	TSH	NMG
<b>Mass</b>				
Bingera	11.14 <sup>a</sup>	0.53 <sup>a</sup>	1.76 <sup>a</sup>	1.58 <sup>a</sup>
Nambour	10.07	0.55 <sup>a</sup>	1.68 <sup>a</sup>	1.51 <sup>a</sup>
Station	8.91	0.59 <sup>a</sup>	1.57	1.41
<b>Family SR</b>				
Bingera	11.08 <sup>a</sup>	0.35	1.65 <sup>a</sup>	1.42
Nambour	9.25	0.45	1.46	1.30
Station	9.25	0.42	1.45	1.27
<b>Family NMG</b>				
Bingera	13.50 <sup>a</sup>	0.43	1.99 <sup>a</sup>	1.74 <sup>a</sup>
Nambour	9.32	0.58 <sup>a</sup>	1.62	1.47 <sup>a</sup>
Station	6.57	0.52 <sup>a</sup>	1.19	1.11
LSD 5%	2.72	0.13	0.36	0.30

<sup>a</sup> Indicates for each character, those methods whose gains are not significantly different from the method with the highest gain.

To further assess the performance of selections based on the Station, the gains for the select groups based on each of the three locations using each of the three methods were averaged over crop-years for each location (Tables 6a to 6c). These select groups gave significantly better performance than the random groups for all characters, with only one exception. This indicates that selection based on each location using each method of selection was effective. This also demonstrated that the magnitude of CxE and FxE interactions was not sufficient to completely frustrate the advances from selections based at any location.

However, when assessed over the three crop-years at Bingera, the Station select groups gave significantly poorer gains than the highest performing groups, for all characters except CCS using the family NMG selection method (Table 6a). When assessed over the three crop-years at Nambour, the Station mass selections performed well for all characters except for TCH, but both methods of family selection gave significantly poorer gains for all characters than did those from the highest groups (Table 6b). In addition and irrespective of method, the Station selections assessed at the Station generally gave significantly poorer gains for each character than the best gains obtained (Table 6c).

These poor responses for selections from the Station, when evaluated at either Bingera or Nambour, indicate that the Station may not be a suitable location for central selection. However, the reason for the lack of performance of selections from the Station when evaluated at the Station is unknown. It may be related to the incidence of low frequency environmental challenges in the crop-years of Experiment 1 relative to the evaluation crop-years of Experiment 2. Research expressly designed to characterise the impact of environmental challenges on family and clonal discrimination is therefore required.

Considering the gains from the three selection methods from the other two locations, Bingera was found to give the greatest gains for each character (except for CCS) when averaged over all locations and crop-years. However, these gains were non-significantly different for CCS, TSH and NMG from those from the highest performing selection methods from Nambour. The greatest gains from selection when averaged over crop-years for Bingera or Nambour came from location specific selections. However, these gains for most characters were non-significantly different from some of the gains obtained from select groups from the other locations. However, if CxE and FxE interactions were not important, the gains from selection at any location using any particular method should be non-significantly different. Thus, there was some indication that location specific selection may be warranted.

**Table 6**

**Gains, for each character, from the three methods of selection from each of the three locations, expressed as deviations from the mean of the random group, when averaged over all crop-years in turn for each location**

**6a Assessed at Bingera**

<b>Method</b>	<b>TCH</b>	<b>CCS</b>	<b>TSH</b>	<b>NMG</b>
<b>Mass</b>				
Bingera	14.65 <sup>a</sup>	0.50	1.99 <sup>a</sup>	1.92 <sup>a</sup>
Nambour	10.49	0.66 <sup>a</sup>	1.66 <sup>a</sup>	1.68 <sup>a</sup>
Station	7.63	0.50	1.16	1.18
<b>Family SR</b>				
Bingera	9.79	0.43	1.40	1.40
Nambour	5.53	0.56 <sup>a</sup>	1.02	1.07
Station	7.08	0.47	1.09	1.20
<b>Family NMG</b>				
Bingera	11.39 <sup>a</sup>	0.43	1.60	1.56
Nambour	10.22	0.69 <sup>a</sup>	1.67 <sup>a</sup>	1.70 <sup>a</sup>
Station	5.86	0.57 <sup>a</sup>	1.07	1.11
LSD 5%	3.76	0.16	0.37	0.33

<sup>a</sup> Indicates for each character, those methods whose gains are not significantly different from the method with the highest gain.

**6b Assessed at Nambour**

Method	TCH	CCS	TSH	NMG
<b>Mass</b>				
Bingera	11.91	0.59 <sup>a</sup>	2.05 <sup>a</sup>	1.75 <sup>a</sup>
Nambour	15.08 <sup>a</sup>	0.54 <sup>a</sup>	2.41 <sup>a</sup>	2.00 <sup>a</sup>
Station	10.43	0.73 <sup>a</sup>	1.97 <sup>a</sup>	1.71 <sup>a</sup>
<b>Family SR</b>				
Bingera	11.54	0.15	1.58	1.27
Nambour	10.02	0.34	1.46	1.33
Station	8.77	0.50	1.50	1.25
<b>Family NMG</b>				
Bingera	16.21 <sup>a</sup>	0.25	2.20 <sup>a</sup>	1.82 <sup>a</sup>
Nambour	9.08	0.47	1.60	1.40
Station	7.87	0.45	1.35	1.26
LSD 5%	3.23	0.21	0.48	0.42

<sup>a</sup> Indicates for each character, those methods whose gains are not significantly different from the method with the highest gain.

**6c Assessed at Station**

Method	TCH	CCS	TSH	NMG
<b>Mass</b>				
Bingera	6.86	0.51 <sup>a</sup>	1.25	1.07
Nambour	4.65	0.46	0.99	0.84
Station	8.66	0.54 <sup>a</sup>	1.59	1.34
<b>Family SR</b>				
Bingera	11.89 <sup>a</sup>	0.46	1.95 <sup>a</sup>	1.60 <sup>a</sup>
Nambour	12.19 <sup>a</sup>	0.44	1.91 <sup>a</sup>	1.51 <sup>a</sup>
Station	11.89 <sup>a</sup>	0.28	1.77	1.34
<b>Family NMG</b>				
Bingera	12.91 <sup>a</sup>	0.61 <sup>a</sup>	2.19 <sup>a</sup>	1.83 <sup>a</sup>
Nambour	8.66	0.58 <sup>a</sup>	1.60	1.32
Station	5.97	0.54 <sup>a</sup>	1.17	0.97
LSD 5%	2.75	0.12	0.41	0.38

<sup>a</sup> Indicates for each character, those methods whose gains are not significantly different from the method with the highest gain.

### Implications for selection

The three methods of selection evaluated over all locations and crop-years performed similarly for the two key evaluation characters, TSH and NMG. The decision as to which selection method to adopt must therefore rest with its practicality and efficiency. These considerations presently favour weighed family selection. However, if the mass selection method and mass selection within families for either of the family selection methods were based on weighed clonal plots rather than on the VNMG system, a greater response to selection may be anticipated when evaluated by NMG. At present this is impractical due to the large number of clones in the initial plant breeding trials. The use of weighed plots to evaluate response to selection is desirable however, because it is more objective and is relevant to commercial harvesting.

One must be careful not to infer too much from these two experiments. However, if similar poor results from selection at the Station are recorded over a number of crop-years, then its utility as a selection location must be severely questioned. In the short term, it seems prudent to consider at least two locations at this stage of selection in case any particular location is subjected to infrequently occurring environmental challenges. Such challenges may render family or clonal discrimination worthless, as may have occurred to some extent in these experiments at the Station.

Further research is needed to determine the environmental factors responsible for family and clonal adaptation. An understanding of such adaptation may permit a managed environment approach to selection. In the long term the use of such an approach would be anticipated to enhance the repeatability of family and clonal discrimination and therefore increase gains from selection.

Further research is also required to determine the worth of a system of differential clonal selection intensities within selected families. Under such a system more clones would be selected from the higher ranked families (low intensity) than from lower ranked families (high intensity). This may also be anticipated to increase gains from selection.

### **CONCLUSIONS**

The following conclusions may be drawn from these experiments:

- Both CxE and FxE interactions were of sufficient magnitude to affect gains from selection.
- Substantial advances were made using each of three methods of selection considered.

- Of the methods considered family NMG selection is the preferred method for routine use as it is presently the most efficient and cost effective.
- The use of a single selection location to determine the elite clones or families may limit the gains from selection when these clones or families are evaluated over multiple-locations or crop-years.
- Selection at more than one location may be warranted to guard against infrequent environmental factors rendering selection at any one location worthless.
- Further rationalisation of the core plant breeding program is restricted by the current limited understanding of the specific environmental challenges causing differential clonal and/or family adaptation.

### **RECOMMENDATIONS**

- Undertake research to identify specific environmental challenges which lead to differential clonal and/or family adaptation. A project with this express focus has been submitted to SRDC for funding.
- Adopt the family NMG selection method for routine evaluation of families in the core breeding program. (Based on preliminary results from these experiments, BSES began to use family NMG selection in 1990 for the routine evaluation of families.)
- Evaluate clones and families on at least one location in addition to the central Experiment Station. (From 1991, BSES will use two contrasting environments for early clonal and family evaluation in the core breeding program.)
- Determine the utility of imposing different clonal selection intensities within selected families. (The design of a project to study this will be agreed upon at the 1992 BSES plant breeding conference.)

### **ACKNOWLEDGMENTS**

The conduct and analysis of this project was funded by the Sugar Research and Development Corporation. We are thankful for the technical assistance of Messrs J Panitz, J Reimers and P Hansen throughout this project. Grateful acknowledgment is also made to Dr Kaye Basford, University of Queensland, who assisted with supervision of the project.

**LIST OF PUBLICATIONS****Accepted or published**

Bull, J K, Basford, K E, DeLacy, I H and Cooper, M (1991). Determining appropriate group number and composition for data sets containing repeated check cultivars. *Field Crops Res.*, (In press).

Bull, J K, Basford, K E, DeLacy, I H and Cooper, M (1992). Determining group number following clustering data from trials containing repeated checks. In: *Proceedings of the Statistical Society of Australia Incorporated, STATCOMP/BIOSTATS 91, Coolangatta, 1991.* Abstract to appear.

Bull, J K, Cooper, M, DeLacy, I H, Basford, K E and Woodruff, D R (1991). Utility of repeated checks for hierarchical classification of data from plant breeding trials. *Field Crops Res.*, (In press).

Bull, J K, Hogarth, D M (1990). The implications of genotype x environment interactions for evaluation of sugarcane families. II. Alternative methods of analysis. In: Kang, M S, (Ed) *Symposium on genotype-by-environment interaction and plant breeding.* Louisiana State University, Baton Rouge, Louisiana, pp 347-363

Hogarth, D M, Bull, J K (1990). The implications of genotype x environment interactions for evaluation of sugarcane families. I. Effect on selection. In: Kang, M S, (Ed) *Symposium on genotype-by-environment interaction and plant breeding.* Louisiana State University, Baton Rouge, Louisiana, pp 335-344.

**In preparation**

Bull, J K (1992). Utility of classificatory techniques in assisting in the analysis and interpretation of plant breeding trials. PhD Thesis, Univ. of Qld. Australia.

Bull, J K, Basford K E, DeLacy, I H and Cooper, M (1992). Weighting environments when classifying genotypic data from plant breeding trials containing repeated checks.

Bull, J K, Basford K E, DeLacy, I H and Cooper, M (1992). Classifying environments using genotypic data from plant breeding trials that contain repeated check cultivars.

Bull, J K, Hogarth, D M and Basford, K E (1992). Impact of genotype x environment interaction on response to selection.

## REFERENCES

- Arceneaux, G and Hebert, L P (1943). A statistical analysis of varietal yields of sugarcane obtained over a period of years. *J. Amer. Soc. Agron.* 35:148-160.
- Basford, K E, Kroonenberg, P M and DeLacy, I H (1990). Three-way methods for multiattribute genotype by environment data: An illustrated partial survey. *Field Crops Res.* (in press).
- Breaux, R D (1987). Some breeding strategies with bi-parental and polycrosses. In: *Copersucar international sugarcane breeding workshop*. Copersucar Technology Centre, Piracicaba-SP, Brasil. pp 71-86.
- Bull, J K and Hogarth, D M (1990). The implications of genotype x environment interactions for evaluation of sugarcane families. II. Alternative methods of analysis. In: M S Kang (Editor), *Genotype-by-environment interaction and plant breeding*. Louisiana State University, Baton Rouge, Louisiana, pp 347-363.
- Byth, D E, Eisemann, R L and DeLacy, I H (1976). Two-way pattern analysis of a large data set to evaluate genotypic adaptation. *Heredity*, 37:215-230.
- Hogarth, D M and Bull, J K (1990). The implications of genotype x environment interactions for evaluation of sugarcane families. I. Effect on selection. In: M.S. Kang (Editor), *Genotype-by-environment interaction and plant breeding*. Louisiana State University, Baton Rouge, Louisiana, pp 335-344.
- Hogarth, D M and Mullins, R T (1989). Changes in the BSES plant improvement program. *Proc. Int. Soc. Sugar Cane Technol.*, 20:956-961.
- Hogarth, D M, Wu, K K and Heinz, D J (1981). Estimating genetic variance in sugarcane using a factorial cross design. *Crop Sci.* 21:21-25.
- Kang, M S and Miller, J D (1984). Genotype x environment interactions for cane and sugar yield and their implications in sugarcane breeding. *Crop Sci.* 24:432-440.
- Pollock, J S (1979). Variety-environment interaction and selection of sugar cane. M.Agr.Sc. Thesis, Univ. of Qld. Australia.
- Roach, B T (1980). Selection trial data as a basis for breeding and selection strategies. *Proc. Int. Soc. Sugar Cane Technol.*, 17:1090-1102.
- Skinner, J C (1965). Grading varieties for selection. *Proc. Int. Soc. Sugar Cane Technol.*, 12:938-949.
- Skinner, J C, Hogarth, D M and Wu, K K (1987). Selection methods, criteria, and indices. In: D.J. Heinz (Editor) *Sugarcane improvement through breeding*. Elsevier Science Publishers B.V., Amsterdam. pp 409-453.
- Steel, G D and Torrie, J H (1980). Principles and procedures of statistics. McGraw-Hill, Kogakusha Ltd, Tokyo. pp 173-194.
- Thompson, W A and Moore, J R (1963). Non-negative estimates of variance components. *Technometrics* 5:441-449.