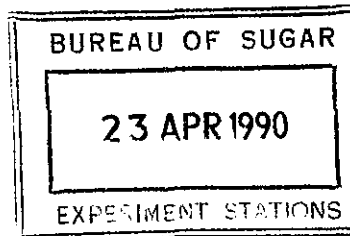


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PROJECT REPORT

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PROJECT 409

BUNCH FAMILY SELECTION

Efficiency of bunch-planted and single-planted seedlings for selecting superior crosses in sugar cane

by

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3.414 Effect of crop class on realized gains from selection.

Average gains in number of selections and NMGYOT, from selection of 20 characters in P or R crops of Bs and Ss seedlings do not differ significantly:

Ss crop selected	SEL8	NMGYOT
P	24.0	9.6
R	21.1	8.1

The above means are for the TePR trial (Table 95). They are based on a selection rate of 25 per cent. Because of differences between characters and class of seedling, the mean values have large standard errors. However, the result supports the use of only P crops of original seedlings. Additional land and resources are required for the R crop. R seedlings could only be recommended if selection was much more efficient in R than in P seedling crops.

There are significant interactions between the crop selected and the gain in each crop (P or R) of the Te trial (Table 95). The interactions are not marked for NMGYOT. The only significant difference (pr>rp) shows that selection in BsP seedlings gives a significantly larger gain in the TeR crop compared with selection in the BsR seedlings evaluated in the TeP crop. This effect also occurs for number of selections (SEL8) which shows several other highly significant differences.

If crop class (P, R) is important during selection of seedlings, selection in P seedlings should give higher gains in the TeP crop. Selection in R seedlings should give higher gains in the TeR crop. There is an indication of the latter effect (Table 95) but it is not statistically significant. For number of selections, selection in P seedlings gives much

higher gains in the R than in the P crop of the Te trial. This effect (pr>>pp) is highly significant in Bs and Ss seedlings. Furthermore, gains in the TeR trial are significantly higher for selection in P than in R seedlings (pr>rr for Ss and Bs+Ss). It shows that the class of crop is not very important for selection of seedlings.

The results indicate that genotype x years interactions are important in the project. When number of selections is used to evaluate the families, selection of P seedlings gives very poor gains in the TeP crop. It gives significantly higher gains in the TeR trial. This indicates there is a large genotype x years interaction between the year the P crop of the seedlings developed (year 1), and the following year (year 2) in which the TeP trial developed. The terms year 1 and year 2 are used, rather than calendar years. The year in which each crop developed occupied part of two calendar years. There are large ($P < 0.01$) interactions between year 2 and year 3 in which the TeR crop developed (#3.21, Table 29). The large interactions between family performance and years 1, 2, and 3 are probably due to atypical performance in year 2, in the Te trial.

NMGYOT for the commercial variety Q113 increased from 8.13 in year 2 to 12.26 in the TeR crop (#3.21). The grade of 8.13 for year 2 is exceptionally low for this variety, one of the main commercial varieties in the area. Three commercial varieties were used as an average standard for harvest characters. Visual net merit grade, which decided number of selections, was allotted only against Q113. Many other varieties, as well as Q113, would give atypical performance in year 2. Furthermore, the poor standard set by Q113 probably reduced the efficiency of visual selection that year.

For most characters selected, selection of P seedlings gives much lower gains in the TeP crop compared with the TeR crop, if evaluation is based on

number or selections (Table 92). For most characters, evaluation based on NMGYOT does not show this effect. The difference in evaluation based on selections compared with NMGYOT, may be due to the marked interaction shown by the standard variety Q113 in years 2 and 3.

The design of the project had a bias in favour of R original seedlings. They were grown in the same year as the TeP crop. Their performance was overestimated because of the absence of genotype x year interactions in year 2. They thus had an advantage compared with P seedlings which had no year in common with the Te trial.

This effect is illustrated by the following response when 25 per cent of families in Ss seedlings were selected using selection rate (SEL8, Table 92):-

Seedling crop selected	Gain in Te trial as % of mean			
	Number selected		NMGYOT	
	P	R	P	R
P	5.0	41.9	12.7	10.3
R	37.7	15.4	15.1	10.3

For evaluation based on number selected, selection in P seedlings gave a much higher realized gain in the R crop. This shows that the TeP crop (year 2) was atypical. Selection in the R crop gave a much higher realized gain in the P crop. This indicates bias due to the absence of families x years interaction, the TsR and the TeP crops being selected in the same year (year 2). Evaluation was based on NMGYOT also shows a higher gain in TeP than TeR, when selection was made in TsR.

The above evidence shows that year 2 was atypical for number of selections, and produced a large genotype x environment interaction. This large interaction is associated with unusually poor performance of the standard commercial variety (Q113) in the P crop of the Te trial. It would

not necessarily occur in the R crop of the Ts trial, which developed in the same year. A different standard variety (Q82) was used for selection in the Ts trial. However, the TsR crop would have an advantage because of the absence of a normal families x years interaction with the TeP crop. Without this advantage, it is likely that R seedlings would have been inferior, for family selection. Because of the land and time involved, R seedlings would only be efficient if they were found to be much superior to P seedlings. The results provide a clear conclusion that it would not be efficient to base family selection on R original seedlings.

3.415 Effect of selection rate on realized gains.

Realized gains were computed with selection rates of 50, 25 and 17 per cent (Table 92):-

% Selected	Gain in TePR trial, as % of mean	
	Number selected	NMGYOT
50	17.2	5.8
25	22.5	9.1
17	25.7	10.6
	17 > 50	25 >> 50
		17 >> 50

The results are for 46 observations on Bs and Ss seedlings. P and R selection for each character were treated as separate observations. Results for PR were excluded, except characters such as selection rate (e.g. SEL8plr) which applied to the mean result for each seedling.

Selection was effective, with improvements in realized gains with each increase in the severity of selection. More than half of the gains occur with very liberal selection (50 per cent). The incremental gain decreases with each increase in the severity of selection. The lowest selection rate

(17 per cent) does not give a significant gain over the 25 per cent rate. The lowest rate of 17 per cent does not represent severe selection by normal standards. However, the optimum selection rate is likely to be in the 25 to 50 per cent range. Severe selection gives the highest gains for one cycle of selection, but also causes the largest reduction in genetic variance. The risk of discarding superior families increases, especially if there are large families x years interactions.

The average gains include correlated responses for less important characters, including characters which gave negative gains in some cases. This gave large enough numbers for statistical analysis and significance tests, but the estimated gains are conservative.

Better estimates of gains from family selection are given by the main characters (Table 94). The values are for selection in the P crop, which the results show to be the appropriate crop for original seedlings. The gains are about 28 per cent for number of selections and 14 per cent for NMGYOT, with selection of 25 per cent of the families (Table 94, mean, Bs+Ss).

3.416 Comparison of realized gains from family vs modified mass selection.

Realized gains from modified mass selection are discussed above (#3.23). Results for the TePR crop (Table 36) can be compared with the above results for family selection (Table 92):-

Character (SsP crop)	Ts type	Gain as % of mean in TePR trial			
		Number of selections		NMGYOT	
		Selection method		Selection method	
		Mass	Family	Mass	Family
Visual plot grade	Bs	49.0		17.5	
Visual plot grade	Ss	27.3		14.5	
NMGYOT	Bs	25.7		14.1	
NMGYOT	Ss	33.5		12.4	
Selectable stalks	Bs	31.8	20.9	13.3	15.8
Selections (SEL8)	Ss	29.4	18.0	10.4	11.6

For family selection, a selection of rate of 17 per cent was used for Bs seedlings, and 25 per cent for Ss seedlings. The corresponding rates for modified mass selection were 17.25 per cent for Bs and 25 per cent for Ss seedlings. The selection rate for Bs seedlings is based on the number of surviving stalks, namely 52.18 per plot, 4.744 per bunch (BsSTp, Table 7). That is, about 47 per cent of the stalks planted in the bunch nursery survived for selection the following year. The visual plot grade includes brix information.

When selection is based on number of selections (or selectable stalks), family selection is inferior to modified mass selection, when evaluated by number of selections from the Te trial. It is superior to modified mass selection when evaluated by NMGYOT in the Te trial. Modified mass selection can only be based on number of selections (or selectable stalks). Family

selection can be based on other characters such as visual plot grade or NMGYOT. When allowance is made for this fact, the above results show family selection to be superior to modified mass selection. A later analysis (#3.6) shows that mean values seriously overestimate the value of modified mass selection. Thus family selection is clearly superior to modified mass selection. Normal mass selection, in which more selections are taken from better performing families, is expected to be superior to modified mass selection.

For family selection in seedlings, the above results clearly favour visual net merit grade of the whole plot, including brix, for both Bs and Ss seedlings. Selection rate would receive second preference, followed by NMGYOT, but neither of these characters is worthy of serious consideration. Selection rate is less effective and much more expensive than the visual plot grade. NMGYOT would only be efficient if it were far superior to the other characters, in realized gains from selection. Harvest characters such as NMGYOT involve destruction of the seedlings. If used in practical selection, it would be necessary to provide separate propagation material for the selected families. Additional seedlings would be required in the same crop, or the following year, for propagation. An alternative would be to ratoon the seedlings and propagate selected families from the ratoon crop. Original seedlings are expensive. For many families additional seedlings are not available when required. If the selection system already involved a delay of one year for autumn planting, ratoons could be used for planting material without loss of time or land. Except such special circumstances, all methods for using harvest characters involve considerable expense. They may also involve loss of time in the evaluation of families and their exploitation as proven crosses. Another alternative would be non-destructive green cane harvesting. Billets from selected

families could be used to provide propagation material. No such method has yet been developed. It might prove very difficult, and involve more research to estimate effects on germination, and other factors. However, the use of NMGYOT does not merit serious consideration in the present project. It did not show any superiority over other non-destructive selection methods. The present project clearly favours the use of experienced selectors, using visual net merit grade of the whole plot. A later analysis using cross ratios (#3.94) modified this conclusion.

3.417 Realized gains compared in old and current experiments.

Realized gains from selection in the present experiment differ considerably from those obtained in the old experiment conducted from 1976-79 (Table 96). For TCH and CCS the two experiments are fairly similar. The main difference is larger gains for CCS in the old experiment, from selection in both Bs and Ss seedlings.

Bs and Ss seedlings both performed poorly for selection of families for the important characters of TSH and NMGYOT, in the old experiment compared with the current one. Bs seedlings were especially poor. As a result, the relative gains in Bs and Ss seedlings differ considerably in the two experiments. In the present experiment, selection of families in Bs seedlings was much more efficient than expected, and about equal to selection in Ss seedlings. In the old experiment gains from selection were much lower in Bs than in Ss seedlings.

When drawing conclusions about realized gains from selection, results of both experiments must be considered. Although the old results appear to contradict the current results, there is no real contradiction. The current experiment was designed to give a better comparison of selection in Bs and Ss seedlings, and it achieved this. Part of this improvement is shown by

the F values in Table 96. The old and current experiments showed reasonable agreement for TCH and CCS. These were the only characters in the table with highly significant differences between families in the old experiment.

In the old experiment, there were no significant differences between families for TSH in Ss seedlings, or for NMGYOT in Bs or Ss seedlings. It is concluded that realized gains for TSH and NMGYOT were unreliable in the old experiment, because of lack of significant differences between families.

3.42 Realized gains from family selection in the evaluation trial.

In addition to normal realized gains from selection, realized gains from family selection in the Te trial were also computed. Results from the Ts trial were used to estimate these gains. In practice, this form of reverse selection is not possible because the Te trial was planted after the Ts trial. However, it provides additional information.

Comparison of normal and reverse selection for the random group is not likely to give much additional information. The two methods are not independent. In the extreme case of completely efficient selection in the seedlings, reverse selection would also be completely efficient. The same families would be selected by both methods. The main interest involves comparison of efficiency of reverse selection in the Re, Be and Se types in the Te trial (Tables 97, 98, 99, 100, 101, 102, 103).

Family selection is much more effective in Re than in the Se or Be types (Tables 102, 103). The superiority is highly significant in several comparisons. The Se and Be types were the result of modified mass selection in Ss or Bs seedlings. They had not been subjected to any previous family selection, the same number of selections (nine per plot) being taken from each family. The mass selection was effective, and significantly reduced

within-family variance (NMG_VAR, Table 35, #3.24). The present results would be explained if modified mass selection also reduced between family variances. However, variance ratios tend to be higher for Se and Be than for Re (variance ratios for RCB, Table 32).

The present results agree with those obtained from correlation analysis (Table 83, #3.3322) which showed Re>>Se>>Be.

Propagation material for the Re type was all obtained from one replicate (M) of Ss seedlings. That for the Be and Se types was obtained from plots in all three replicates. Thus, propagation material for the Re, Be and Se types was all obtained from the Ss seedlings. The type of bias discussed below (#3.7), is not expected to influence comparisons of reverse selection in the Re, Be and Se types. As a precaution, the three types were also evaluated, after omitting the replicate (M) which used to propagate the Re type (Table 103b). The Re type is still superior to the Se type, and much superior ($P<0.01$) to the Be type.

The Se type gives higher realized gains than the Be type. It is significantly superior in one case (NMGYOT, PR, 50 per cent selected, Table 101) when each selection rate is considered separately. It is not significant for the average gain over all selection rates within each crop (Table 102). However, it is highly significant for NMGYOT, 50 per cent selected, PR crop (Table 103). Other comparisons in Table 103 are not significant. However, Se has higher gains than Be at all three selection rates, for number selected, and for NMGYOT. When replicate M was removed from the analysis (Table 103b) Se > Be for number of selections at the 17 per cent rate, and Se>>Be for NMGYOT at the 50 per cent rate. Although much less marked than the superiority of Re over Be and Se, there is a real superiority of Se over Be.

3.421 Effect of crop class on realized gains from reverse selection.

With evaluation based on NMGYOT in the Ts trial, family selection in the Te trial is more effective ($P < 0.05$) in the TeR crop (Table 100). There is no such tendency with evaluation based on selection rate. This is an average result over all Te characters for the Re, Be and Se types, with a selection rate of 25 per cent.

When different selection rates are studied in each type, $R > P$ in several comparisons, for evaluation based on NMGYOT (Table 101). With 25 per cent selection, $R > P$ only for the Se type. With 17 per cent selection, $R > P$ in Be and Se types. With 50 per cent selection, $R > P$ in all three types, with $R \gg P$ for Re and Be.

When evaluation was based on number of selections, the only significant difference between crops is $R > P$ in the Be type, with 50 per cent selection. However, there is no general tendency for R selection to be superior to P.

For realized gains from normal selection, with evaluation based on number of selections, the TeP crop was atypical (#3.414, above). However, reverse selection is as effective in this "atypical" P crop, as in the R crop, when evaluation is based on number of selections. Evaluation of reverse selection is based on the average of both crops of Ss seedlings. The SsR crop developed in the same year as the TeP crop. Genotype x years interactions were important. There was no interaction between the TeP crop and one of the crops (TsR) on which evaluation was based. This would tend to counteract poor performance due to an atypical year.

3.422 Effect of selection rate on realized gains from reverse selection.

Selection in the Te trial was effective, with improvements in realized gains with each increase in the severity of selection (Table 101). For

selection based on both crops of the Re type, each improvement is highly significant for evaluation based on number of selections. It is highly significant or significant for evaluation based on NMGYOT. Significant differences are not so decisive for the Be and Se types. However, the data and the significant differences show the same general tendency for these types and the Re type.

Severe selection is more effective in the Te trial than in the Ts trial. The superiority of the 17 per cent over the 25 per cent rate is significant for selection in the Te trial (Table 101, Re). It is not significant in the Ts trial (#3.415, above).

3.52 Evaluation trial.

Error mean squares are fairly similar in the Ts and Te trials (mean values for Ss, Table 104, and Re, Table 105). F values, selection differential, genotypic coefficient of variation (GCV), heritability and theoretical gain are all lower in the Te trial than the Ts trial. Unlike the Ts trial, theoretical gains are not optimistic in the Te trial. Realized and theoretical gains are fairly similar. As a result, although theoretical gains are much lower in the Te trial, realized gains are slightly higher, for most characters (Ss, Table 104 vs Re, Table 105). However, the superiority of the Te trial, for realized gain, is not significant. Realized gains were higher in the Te trial in the old (1976) experiment. In the Te trial (Table 105) theoretical gains from selection, and the statistics used to compute it, show significant and highly significant differences between types. The Se type has the lowest error mean square and also the lowest selection differential. The Re type has the lowest F values and heritabilities. Be has the highest GCV and theoretical gain. The Se type is significantly higher than Re only for F and heritability.

Mean values for the five characters for which realized gains from selection are presented in Table 105 ($n = 15$) show fewer significant differences between the three types, compared with all characters ($n = 30$). However, the significant differences which do occur, are similar to those for $n = 30$. For GCV and theoretical gain, which are significant with $n = 30$ but not with $n = 15$, the order of means for the three types is similar.

Significant differences between types in the Te trial, for theoretical gains from selection, and the statistics used to compute it, involve selection effects. These effects on family means of the Be and Se types, were caused by modified mass selection within each family, in the Ts trial.

They differ from selection effects shown by realized gains from reverse selection (Tables 102 and 103, #3.42), and by correlations between the Ts and Te trials (Re >> Se >> Be, Table 83, #3.3322). Be is clearly superior to Re for F, GCV, heritability and theoretical gain from selection (Table 105, n = 30). Be is also significantly superior to Se for selection differential, GCV and theoretical gain from selection.

Modified mass selection within each family in Bs seedlings, resulted in inflated genotypic variances among families of the Be type in the Te trial (Table 105). Competition increases genotypic variances and it may be responsible in the present case. However, competition between families was not detected in the Te trial by normal competition analysis (#3.271). This type of analysis is not very sensitive when 3-row plots are used. Moderate amounts of competition may have occurred without being detected. However, it is not likely that competition too small to be detected, could have generated the large increase in genotypic variance which occurred in the Be type. Although selection normally reduces genotypic variance, it is likely that a selection effect, rather than competition, is responsible.

Selection in Bs seedlings is based mainly on a the single yield component, weight per stalk. It is concluded that some families respond much better than others to this selection. This could increase the genotypic variance among families for overall performance measured, for example, by NMGYOT. For example, families with good tillering ability would increase in weight of cane more than those with poor tillering ability. Thus genotypic variance for weight of cane, and overall performance, could be increased by selection. This could occur despite a reduction in the variance of the component (weight per stalk) selected.

The families which show the largest response to this type of selection may not be those which perform best in unselected (random) seedlings.

Selection based on weight per stalk may thus introduce families x types interactions. This would reduce the value of the Be type for predicting family performance, despite the increased genotypic variance among families. It may be argued that true family performance is predicted correctly, despite these differences from random seedlings. This argument is examined below (#3.635), and rejected.

The effect of selection for weight per stalk in Bs seedlings would depend on the size of the genotypic correlation between overall performance and weight per stalk. A high positive correlation would increase the range between the best and worst families without altering the ranking of families. This would increase correlations between the Ts vs Te trial, and make family selection in the Te trial more effective. A low correlation would increase the interaction between families in the Ts and Te trials. This would reduce correlations between the Ts and Te trials. It would make selection in the Be type in the Te trial less efficient.

The genotypic correlation between weight per stalk and NMGYOT in Bs seedlings is high in the P crop (0.93^{**} , Table 21) and moderate in the R crop (0.67^{**}). However, this genotypic correlation, when estimated as the phenotypic correlation between the TsPR and TePR trials is only 0.43^* for the Re type and 0.36 for the Be type (Table 74). These correlations are weak compared with 0.73^{**} for the Re type and 0.55^{**} for the Se type for visual NMG, which is used to select Ss seedlings. The lower correlations for the Be or Se type compared with the Re type indicate the effect of interactions due to modified mass selection of seedlings. The lower correlations for weight per stalk compared with visual NMG show there were additional large interactions when selection was made in Bs seedlings. This occurred because selection was necessarily based mainly on one component (weight per stalk) instead of overall performance (visual NMG) used for

selection of Ss seedlings.

The effect would not necessarily reduce gains from normal family selection in Bs seedlings compared with Ss seedlings. These gains were evaluated using the Re type. Lower gains would be expected from family selection in Bs seedlings, if the Be type were used for evaluation.

3.53 Correlations between gains from selection and other statistics.

Error mean squares had very little influence on gains from selection. None of the correlations with theoretical or realized gains from selection is significant, in the Ts or Te trials (Table 106). Heritability shows a highly significant correlation with theoretical gains from selection in Bs seedlings (0.673^{**} , $n = 19$). It shows no significant correlation with realized gains in Bs or Ss seedlings, or with theoretical gains in Ss seedlings. In the Te trial it shows no significant correlation with theoretical gains in any type, or with realized gains in the Re type. It shows significant negative correlations with realized gains in the Be and Se types, the latter correlation being highly significant. These negative correlations, compared with a low (not significant) correlation in the Re type, show a definite selection effect. The reason for it is not known.

The selection differential and genotypic coefficient of variation are closely correlated with theoretical and realized gains from selection. This occurs in both the Ts and Te trials (Table 106). Most of the correlations are highly significant, and some of them are close to 1.0. In one case (theoretical gain vs genotypic coefficient of variation, Ts trial, Ss seedlings) the correlation is 1.000.

The correlation between theoretical and realized gains is fairly high, 0.87^{**} in Bs seedlings and 0.79^* in Ss seedlings. In the Te trial this correlation is 0.93^{**} in the Re type and 0.90^{**} in Be, but only 0.51 (not

significant) in the Se type.

Correlations between types are also fairly high, 0.76* for theoretical and 0.89** for realized gains in the Ts trial. They range from 0.64* to 0.92** for the three types in the Te trial. The lowest correlation in the Te trial (0.64*) is for the Se type. This type also has the lowest correlation (0.51) between theoretical and realized gains. This is a selection effect. The Re type, which has relatively high correlations, corresponds to the Ss type in the Ts trial.

The fairly close correlations between theoretical and realized gains, and between types, in both the Ts and Te trials, presents a promising picture of effective selection. However, this picture is partly clouded by the probability that the correlations are partly spurious. They are probably inflated by competition in both trials, especially in the Be type.

3.6 A detailed analysis of NMGYOT.

Lower correlations between family means, and lower realized gains from family selection, in the Be and Se types compared with the Re type, are obviously due to modified mass selection. It is difficult to explain this effect because selection did not reduce the genotypic variance among families. The effect is largest in the Be type which also has the highest genetic variance among families (#3.52).

An attempt was made to clarify the situation. A detailed analysis was made of the important character NMGYOT. This involved linear regression, and realized gains from selection of the best six and the worst six families. Second order (quadratic) regressions gave no improvement over linear regressions, and are not reported.

3.61 Evaluation (Y) vs single seedling (X) trial.

3.611 Regression of random type on seedling trial.

The regression line gave an unbiased fit for good and poor families (Figure 2). However, the regression equation ($Re = 4.06 + 0.47 \times Ss$ seedling value) shows that the best six families increase less than the mean (-0.94). The worst six families increase more than the mean ($+1.01$).

3.612 Fitted values.

For the best families in the Ss seedlings, fitted values for the Re, Be and Se types in the Te trial are fairly similar (Figure 5a). That is, the fitted values show that modified mass selection had very little effect on good families.

For the worst families there are marked differences between the three types, with $Be \geq Se \geq Re$. That is, modified mass selection had much more effect on poor than on good families. It is more effective in the Be than

in the Se type for poor families. However, the Se type is slightly superior to Be for good families.

3.613 Residuals vs fitted values.

Plots of residuals vs fitted values show that the best families in the Ss seedlings are estimated less accurately than the poor families. This occurs in all types (Re, Be, and Se).

The range of the residuals is Be (4.4) > Se (3.2) > Re (2.8). This is inversely related to the correlation coefficients which were in the order Re (0.70) > Se (0.49) > Be (0.14).

3.614 Realized gains (best six - worst six families).

The realized gains from modified mass selection are:-

Type	Be or Se minus Re type		
	Worst 6	Best 6	Worst - Best
Bs	1.75	0.32	1.43
Ss	1.12	0.47	0.65

The realized gain from modified mass selection is slightly higher for selection in Ss than in Bs seedlings for the best families. It is higher in Bs than Ss for the worst families. Bs and Ss both gave much higher gains in the *worst* families. Realized gains were small in the best families, being less than the gains in the means. Gains in the best families are only 18 per cent of that in the worst families for the Be type, and 42 per cent for the Se type.

These results are illustrated in Figure 3. The Re type is significantly worse than the Be and Se types for the worst and second-worst groups. There are no significant differences between any types in the best or second best groups.

3.6141 Realized gains from family selection.

Realized gains in NMGYOT in the TePR trial, from family selection based on NMGYOT in BsP or SsP seedlings, are:-

Group of 6 crosses	Selection in Bs seedlings			Selection in Ss seedlings		
	Evaluation in Te Type			Evaluation in Te type		
	Re	Be	100 x Re/Be	Re	Se	100 x Re/Se
Best	15	10	150	12	8	150
Worst	-12	- 3	400	-12	- 6	200
Best - Worst	26	13	200	25	14	179

The above values are expressed as per cent of the mean for each Te type.

Genotypic correlations for NMGYOT, as measured by the phenotypic correlation between TsP and TePr, are:-

For BsP, 0.68** vs RePR and 0.34 vs BePR (Table 75)

For SsP, 0.70** vs RePr and 0.49* vs SePR (Table 74)

For SsP, 0.14 vs BePR (Table 74).

3.615 Families included in the best or worst group in both trials.

The number of families in the best six or worst six in the Ts trial, which were also in the same group in the Te trial, are as follows:-

Type	Best	Worst	Best + Worst
Re	5	4	9
Be	3	2	5
Se	4	4	8
By chance	1.5	1.5	3

These results give a similar ranking to those given by regression and realized gains, for effectiveness of family selection, with $Re \geq Se \geq Be \geq$ Chance.

3.62 Single seedling (Y) vs Evaluation (X) trial.

3.621 Regression of single seedling value on random type.

The regression line gave an unbiased fit for good and poor families (Figure 4). The regression equation (S_s seedling value = $-1.13 + 1.02 \times Re$ value) has a constant about equal to the difference in the general means (-0.97). The slope shows a 1 : 1 correspondence between performance in the two trials. Thus there is no tendency for the best families to increase less than the mean, or for the worst families to increase more than the mean.

3.622 Fitted values.

The efficiency of prediction of family means is in the same order ($Re > Se > Be$) when based on trials T_e and T_s (Figure 5). Trial T_s gives much larger differences in prediction for poor than good families. For poor families, predicted values for the Be and Se types are much higher than Re (Figure 5a). By contrast, trial T_e gives larger differences in prediction of good than poor families (Figure 5b). For poor families, there is very little difference between the three types. Better prediction with Re means that predicted values for good families are much higher for Re than for Be , with Se intermediate.

3.623 Residuals vs fitted values.

Plots of residuals versus fitted values were produced, but are not presented. They showed that, for the Re and Be types, the best and worst

families were estimated in Ss seedlings with about the same accuracy. There was a tendency for the best families in the Se type to be estimated more accurately than the worst families.

The range of residuals was Be (5.5) \geq Se (4.4) \geq Re (3.8). These residuals are larger than the corresponding residuals for Te trial vs Ss seedlings (#3.613), but the order of types is the same.

3.624 Realized gains (best six - worst six families).

Realized gains are in the order Re \geq Se \geq Be, as shown by the following values in Ss seedlings:-

Group	Be - Re	Se - Re
Best 6	-1.47	-0.67
Worst 6	+1.05	+0.59
Best - Worst	-2.52	-1.26

The differences (Best six - Worst six) are:-

Evaluation (Y)	Selection (X)	Re	Be	Se
Ts	Te	2.99 (100%)	0.47 (16%)	1.73 (58%)
Te	Ts	1.69 (100%)	0.26 (15%)	1.04 (62%)

Realized gains are much higher for selection in trial Te than for normal selection in Ts. This is probably due to the larger genotypic variance among families in Ss seedlings. Relative gains are very similar, for selection in trials Ts and Te. Realized gains are about 60 per cent as high for Se, and only 15 or 16 per cent as high for Be, compared with Re.

These results are illustrated in Figure 6. The only significant difference in the figure is the superiority of Re over Be for the best families. The error bars for Re indicate some other significant differences. However, these differences are not significant because errors are

higher for Be and Se than Re.

Although reverse selection in the Te trial provided some new information, its value is limited. It was evaluated by the Ss seedlings which provided the Re, Be and Se types. The above per cent gains for the Be and Se types are similar for normal and reverse selection. They both estimate the difference in response of the best and worst family groups, to modified mass selection in Bs and Ss seedlings.

3.63 Discussion of detailed analysis.

3.631 Environmental selection effects.

Although the Re type has no selection effects, discussion of best and worst groups within it automatically involves selection effects. The best families are above average genetically. However, they also have positive environmental deviations. The worst families are genetically inferior but they also have negative environmental deviations.

When selections are planted in another trial, the genetical effects are kept, but the environmental deviations are lost. This produces an environmental selection effect. The best families increase less than average families. The worst families increase more than average families.

The expected size of this selection effect depends on the size of the interactions between the two trials. It also depends on the ratio of environmental to genotypic variance. If there are large interactions, a large environmental selection effect is expected. If there is little or no interaction, little or no environmental selection effect is expected. With no interaction, the same families would make up the best group in both trials, and same families would be in the worst group. These families are not likely to have the same positive (best) or negative (worst group) environmental deviations in both trials. Absence of interactions between

the two trials indicates that environmental variance is small relative to genotypic variance. The best (or worst) families may be so good (or poor) that they occupy the best (or worst) group regardless of the environmental deviations. Such families do not require positive or negative environmental deviations to occupy these groups. Thus the best and worst groups may have environmental deviations which sum to zero. That is, there is no selection effect.

Interactions are smallest between the Ss seedlings and the Re type. Large interactions occur between the Ss seedlings and the Be type. The Se type is intermediate. This is shown by the size of the correlations between the two trials (0.70 for Re, 0.49 for Se and 0.14 for the Be type). It is also shown by the number of families common to the best and worst groups (9 for Re, 8 for Se, and only 5 for Be). Thus the largest environmental selection effect is expected with the Be type. The smallest effect is expected with the Re type, the Se type being intermediate.

The effect would occur in the Be and Se types, but it is difficult to measure. It is confounded with effects due to modified mass selection. In the Re type, selection in the Ts trial appears to produce a large environmental selection effect (#3.611). However, only a small effect is expected. No effect is observed from selection in the Te trial (#3.621). The environmental effect is confounded with another factor. This factor is a change in scale, due to a difference in variances among families in Ss seedlings compared with Re clones in the Te trial.

3.632 Variance among families in the two trials.

The range between the best six and the worst six families is 3.51 in Ss seedlings. This is much higher than the range of 2.47 in the Re type. This indicates that the genotypic as well as the phenotypic variance among

families was larger in Ss seedlings. This is also shown by analysis of variance, the genotypic variances being 1.86 (Table 107) for Ss seedlings and 0.67 for the Re type in the Te trial. These differences are accompanied by a change of scale in the two trials.

This change of scale adds to the normal environmental selection effect for selection in Ss seedlings (#3.611). It also subtracts from this effect for reverse selection in the Re type (#3.621). The difference between the best and worst families in the Re type was larger in Ss seedlings than in the Re type itself. This occurred despite the selection effect which would tend to make this range smaller in Ss seedlings.

Thus two factors are operating, an environmental selection effect, and a change of scale. For the Re type the selection effect is expected to be fairly small. It is less important than the change of scale. The selection effect would be largest in the Be type which has the largest interactions (#3.633), and intermediate in the Se type. The results fit this expectation but, because of confounding with other factors, the size of the selection effect was not estimated separately.

3.633 Interactions between families in seedlings and in evaluation trial types.

Interactions between families in the Ts and Te trials are smallest in the Re type and largest in the Be type. This is shown by the correlations (Re 0.70 > Se 0.49 > Be 0.14). It is confirmed by the number of families in the best (or worst) group in both Ts and Te trials. For the total of 12 families in both groups, the numbers in common are 9 for the Re type, 8 for Se and only 5 for Be. By chance, three families are expected to be in common.

Interactions are smallest in the Re type. This indicates that it is the

appropriate type for evaluating families in the project.

3.634 Interactions between types in the evaluation trial.

There are marked interactions between families in Ss seedlings and in the three Te trial types (#3.633). This means that families x types interactions also occur within the Te trial.

The presence of these interactions is confirmed by correlations between the three types. The correlations for Re vs Be (0.66) and Be vs Se type (0.61) are less than Re vs Ss seedlings (0.70). Only Re vs Se type (0.79) is higher, but the four correlations do not differ significantly.

Correlations between the seedling and Te trial were reduced by families x years and families x locations interactions. These interactions did not influence correlations within the Te trial. If there were no families x types interactions within the Te trial, correlations within the Te trial would be much higher than those between the Ts and Te trials. Correlations between types within the Te trial are about equal to the correlation between the Ts and Te trials, for the Re type. This shows there are important families x types interactions within the Te trial. These interactions are roughly equal to the families x environment interactions between the two trials.

Analysis of variance (#3.22) did not detect the families x types interaction in the Te trial.

3.635 Genotypic variance among families in the three types in the evaluation trial.

A distinction is made between effective and actual genotypic variance among families. The effective genotypic variance among families is in the order $Re \geq Se \geq Be$. The actual genotypic variance is in the order $Be \geq Re \geq$

Se. The effective genotypic variance is estimated by the range in each Te type, for the best six - worst six families in Ss seedlings. The actual genotypic variance is estimated by the range, best six - worst six families within each type. It is also estimated, more accurately, by normal analysis of variance for each type (Table 107).

The actual genotypic variance in all types, especially the Be type, is increased by interactions between families in the Ts and Te trials (#3.633). These interactions were increased most in the Be type because selection of Bs seedlings was necessarily based mainly on a single yield component (weight per stalk, #3.52). Some families responded much more than others to this type of selection. The increase due to interactions may consist of two portions, only one of which is effective in predicting true family performance. The effective portion would exist if original seedling families showed seedling effects not shown by commercial crops. The limit of this effective portion would be the interaction shown by the Re type. Additional interaction shown by the Be and Se types would be ineffective, for prediction of true family value.

The Be type has very little effective genotypic variance among families. Its large actual genotypic variance is due to a large portion which is not effective for predicting family value.

This conclusion is based on the assumption that random seedlings estimate the true value of families. This assumption may not be correct, and it is desirable to examine it in more detail.

Random seedlings certainly provide the best estimate of the relative value of unselected seedling families. However, the true value of a family is the proportion of commercial varieties it contains. With each stage of effective selection the true value of a family will improve. Some families respond more than others to selection. This produces interactions so the

relative true values of the families will change at each stage of selection. The relative true values may also differ for different selection systems such as modified mass selection in Bs compared with Ss seedlings. Thus it is possible to have different relative true values for different selection systems at each stage of selection. This provides a complicated picture which could be exploited in practice by the proven cross system better than any other known system.

However, in this form the picture does not provide a method for comparing different selection systems. Evaluation of families by the Be and Se types appears to be appropriate for those types. It could lead to a conclusion that true evaluation is equal in those types, and superior to the Re type which only applies to unselected seedlings. It could even lead to a conclusion that the Be type gives true evaluation superior to any other type, because it has a higher genotypic variance.

The complicated picture is only partly true. Some of the conclusions drawn from it are false. The idea that true family evaluation is different but equally valid in the Be and Se types compared with the Re type, is refuted by realized gains from family selection (#3.6141).

There are real gains from family selection in the Ts seedlings. The estimate of these gains in the Te trial would be zero, if estimation of true family value in the Te trial were completely inefficient. It would increase as the efficiency of estimation of family value increased. It would reach a maximum with completely efficient estimation of true family value. The Te type giving the best estimate of true family value is the one giving the highest estimate of realized gains from selection. This is the Re type which was much more efficient than the Be and Se types. Estimated gains using the Re type were twice those with the Be type following selection in Bs seedlings. This occurred despite the higher genotypic

variance in the Be type. Gains using the Re type were 80 per cent higher than the those with the Se type following selection in Ss seedlings.

Random seedlings (Re) provide by far the best estimate of true value of families, available in the project. The Re type provides the best estimate, not only at the seedling stage, but also at stage 2. Correlations (#3.6141) and realized gains from selection in the Te trial (#3.624) show the Be type inferior to the Re and Se types. The Be type is so poor that it seems to have very little value for family evaluation. Estimates of realized gains from family selection in the Ts trial (#3.6141) confirm that the Re type is best at stage 2. However, this analysis also shows that the Be type is better than indicated by the other analyses. Estimated gains, as per cent of the Re type, are 50 per cent for Be and 56 per cent for Se. That is, this analysis shows Be and Se to be about equal. Although inferior to Re, the Be and Se types both estimate true family value well enough to give gains from selection. Selection based on weight per stalk in Bs seedlings is expected to distort estimates of true family value. However, this seems to reduce correlations more than estimates of the value of the best and worst six families. Correlations are based on all 24 families.

Stage 2 evaluation of families would be different after normal mass selection. However, the same problem is expected with selected groups as with the Be and Se groups provided by modified mass selection. This will make family selection less efficient after stage 1, although progress can still be made.

3.636 Effects of modified mass selection.

The large gains from modified mass selection of poor families shows that they can be improved a lot by selection. The high positive genotypic correlation between mean and variance in Ss seedlings (#3.115) means that

the poor families have below average genotypic variances. Despite this, there is a large amount of genetic variance in poor families. It can be exploited by modified mass selection. However, gains in poor families may not be large enough to give much chance of selecting commercial varieties. Thus gains are much less important in poor than in good families.

The small gains from modified mass selection of good families, shows that good families cannot be exploited effectively by modified mass selection. The best 17 per cent of the Ss or Bs seedlings in a poor family are well above the mean of that family. However, the best 17 per cent of the Ss or Bs seedlings in a good family are only slightly above the mean of that family. This indicates that much of the high phenotypic performance of the best clones in the best families is due to high positive environmental deviations. Because of this, large genetic gains in mean values are not likely to be achieved in the best families by any form of mass selection. Higher selection rates than those used by modified mass selection are necessary to exploit them. This increases the chance that superior clones with high genotypic values will be included in the selected group.

The results indicate that normal mass selection, which gives very high selection rates in good families and very low or zero selection rates in poor families, is much superior to modified mass selection. This superiority is not due to a large increase in the mean value of good families, but to the selection of more clones from them. Its main superiority is due to unconscious family selection. The poorest families are eliminated, or make a very small contribution to the selected group. The best families make a large contribution to the selected group.

Plant breeders often regard mass and family selection as separate systems. However, in a crop such as sugarcane, mass selection automatically involves family selection. The breeder using mass selection may not realize

that he is using any family selection at all. However, most of the gains he achieves in the population mean are probably due to indirect family selection.

Without its capacity to improve families, mass selection would always be inferior to family selection. A gain of ten per cent from mass selection would be much less valuable than a gain of ten per cent from family selection. These gains are equal, for selection of superior varieties from one series of seedlings. However, the proven cross system uses gains from family selection to improve the general mean in later seedling populations. This is an important source of long-term progress from breeding, more important than the gain in any particular season.

Mean values overestimate the value of modified mass selection. The means show modified mass selection to be very effective but it has very little value in good families. The mean values also overestimate the value of modified mass selection in Bs compared with Ss seedlings. The mean values indicate Bs superior to Ss but this occurs because Bs gives a much higher improvement in the poorest families. For the best families, modified mass selection was slightly more effective in Ss than in Bs seedlings. Commercial varieties are most likely to be produced by gains in the best families. The value of a selection system in sugarcane depends on production of commercial varieties. Improvement of means has no value, unless it corresponds to an increase in proportion of commercial varieties. This occurs for most comparisons, but not for modified mass selection. There is a substantial increase in means with little or no increase in the expected proportion of commercial varieties. Thus it has very little value.

The regression analysis indicates that modified mass selection was slightly more effective in Ss than in Bs seedlings, because of the improvement in the best families. However, modified mass selection had little

benefit in the best families. Very little importance can be attached to results for modified mass selection.

Realized gains and regressions (fitted values for Re, Be and Se types vs Ss seedlings) give similar conclusions concerning the three types. By both methods, gains from modified mass selection are much smaller in the best families, with Se better than Be. In the worst families, gains are much larger, with Be much better than Se.

Poor families are improved much more than good ones by modified mass selection. It therefore reduces the effective genotypic variance among families. This range, for realized gains (six best - six worst), was 1.69, 0.26, and 1.04 for Re, Be and Se respectively. This reduction in effective genotypic variance among families is fairly big for Se and very serious for Be. This is also shown by fitted regression values for Re, Be and Se types vs Ss seedlings. The reduction explains why correlations between the Ts and Te trial are in the order Re >> Se >> Be. It also explains why realized gains from reverse family selection in the Te trial are also in the order Re > Se > Be. Despite this, the results indicate that the Be and Se types do have some value for family selection.

3.64 Other characters.

The detailed analysis was confined to NMGYOT. However, partial analyses of TCH and TSH gave conclusions similar to those for NMGYOT.

The main characters in the project are NMGYOT and number of selections (SEL8). TSH is the most important completely objective character. SEL8 was not subjected to a detailed analysis. However, the detailed analysis of NMGYOT, and the partial analysis of TCH and TSH, are sufficient to explain average selection effects shown by important characters. These analyses are sufficient for general conclusions to be drawn about selection effects due

to modified mass selection.

3.65 Conclusions from detailed analysis of NMGYOT.

- Modified mass selection gives very little improvement in the best families, but a large improvement in the worst families. Improvements in the best families are much more likely to produce commercial varieties.
- The value of modified mass selection, as shown by mean values, is seriously overestimated. The mean gains are mainly due to the improvement of poor families.
- For the best families, modified mass selection was slightly better in Ss than in Bs seedlings. For the worst families, selection in Bs was much superior to Ss. Thus the mean values seriously over-estimate the efficiency of Bs seedlings, as well as the efficiency of modified mass selection.
- Since poor families are improved much more than good ones, the range of true genetic differences between families is reduced by modified mass selection. This reduction in effective genotypic variance among families was fairly big for the Se type and very serious for the Be type.
- This reduction in effective genetic variance explains why correlations between the seedling and Te trial were in the order $Re \gg Se \gg Be$. It also explains why realized gains from reverse family selection in the Te trial are also in the order $Re > Se > Be$.
- The Be type had the highest actual genetic variance but the lowest effective genetic variance. The actual genetic variance was inflated by interactions which are of no value for estimating true family performance.
- Random seedlings (Re) provide the best available estimate of true family performance, at stage 2 as well as the seedling stage. The Be type is

about equal to the Se type for family evaluation at stage 2. Although inferior to Re, Be and Se do have some value. The value of the Be type for family evaluation is higher than it appears from correlation analysis.

- Important families x types interactions were present in the Te trial, but were not detected by analysis of variance (#3.22). Analysis of variance does not provide a sensitive method for detecting interactions.
- The detailed analysis for NMGYOT explained why correlations between family means, and realized gains, were much poorer in the Be than the Re type. It also showed that the value of modified mass selection, and its high effectiveness in the Be type, as shown by mean values, were an illusion. For the more important good families, Ss seedlings gave slightly better results than Bs, and modified mass selection had very little value.

3.7 Possible bias due to genetic sampling and rust disease.

Propagation material to plant the Re type in the Te trial was taken from only one replicate (M) of Ss seedlings. This introduced the possibility of bias due to genetic sampling.

If there had been sufficient seedlings, a separate propagation area would have been planted. However, it was later realized that this would involve the possibility of bias due to genetic sampling, in other comparisons. The Be and Se types were planted in the Te trial using selections from the Bs and Ss seedlings. If propagation material for the Re type had not been taken from these seedlings, correlations involving Bs and Ss seedlings and the three types in the Te trial would have been subject to this bias. Realized gains from reverse selection in the Re, Be and Se types in the Te trial, with evaluation using Ss seedlings (#3.42), would also have been subject to it. No such bias is expected with the design adopted. Planting material for the Be and Se types was obtained from all three replications of the seedlings. That for the Re type was all obtained from one replicate. However, this difference is expected to have a negligible effect on the comparisons.

If the number of seedlings was sufficient to give an accurate genetic sample of each family mean, bias would not be important. The smallest sample (27 clones per family) occurred in the Te trial. Bias would not affect comparisons made within the Ts trial or within the Te trial. If present, it would inflate realized gains from selection of Ss seedlings compared with Bs seedlings. Most of the clones in Ss seedlings in replicate M (27/36) were the same as those in the three replicates of the Re type. None of the clones in Bs seedlings were in the Re type, because they did not provide any propagation material for it. Realized gains were evaluated using the Re type in the Te trial. If present, bias would also inflate

correlations between Ss seedlings and the Re type, compared with similar correlations involving Bs seedlings.

Detection of bias depended on statistical analyses of realized gains and correlations. All three replicates (KLM) in the Ts trial were compared with the two (KL) which did not provide any propagation material for the Re group.

3.71 Reverse selection in the random type.

Gains from reverse selection in the Re type were evaluated using two (KL, Table 108) or three (KLM, Table 97) replicates in Ss seedlings.

Three replicates are significantly superior to two replicates at all selection rates for evaluation based on NMGYOT. Three replicates are also superior at the 17 per cent rate, for evaluation using number of selections (Table 109). The use of two or three replicates had no influence on the selection of families. The same families were evaluated in two or three replicates at each selection rate. Significant superiority of KLM over KL could be due to increased precision, or to bias.

If there had been no significant differences between KLM and KL, it would have shown that there was no important bias during selection. The results show there is a possibility of significant bias when replicate M is included in the evaluation. The results do not show that bias occurred. Other tests are necessary to determine whether the significant results are due to bias, or to an increase in precision with an additional replicate.

3.711 Reverse selection in the Re, Be and Se types.

Gains from reverse selection in the Re, Be and Se types were computed with evaluation in Ss seedlings based on two replicates (KL, Tables 108, 110, 111 respectively). They were compared with gains evaluated using all

three replicates (KLM, Tables 97, 98, 99). Selection effects made it difficult to draw conclusions from comparisons involving the Be and Se types, so conclusions were based on the Re type (#3.71).

3.72 Bias in gains from selection in the seedling trial.

There is an indication of bias in gains from normal family selection. Gains were higher in Bs than in Ss seedlings with selection in two replicates (KL, Tables 112, 113). They were higher in Ss than in Bs seedlings with selection in all three replicates (KLM, Table 113a). However, the effect is not significant at any selection rate. It is not significant when tested on means over all selection rates, based on 72 observations (Table 113a, footnote). None of the comparisons between Bs and Ss approach significance. For Ss, three replicates (KLM) gave significantly higher gains than two replicates (KL) but this could be a result of more reliable estimates with three replications, without bias.

No definite conclusions can be drawn because there is no significant interaction between gains in Bs and Ss seedlings. If bias is present, it is very small compared with other factors such as different selection rates. Selection rates show highly significant differences in several comparisons (Table 113a).

Realized gains from selection provide a useful practical estimate. However, they have large standard errors, especially with only two replications in the Ss seedlings. The large standard errors are indicated by the lack of significant differences between the Bs and Ss classes (Table 113a) and confirmed by examination of the main characters (Table 113b). For TSH, $Ss \geq Bs$ with two and three replications. For NMGYOT, $Ss = Bs$ for three replicates, but $Bs \geq Ss$ for two replicates. For visual plot grade including brix, $Bs \geq Ss$ with two and three replicates, but its superiority is more with

two replicates. However, the poor performance of Ss seedlings for this character in two replicates seems to be due to a chance fluctuation rather than genetic bias. Ss seedlings performed very well for this character in the ratoon crop (Table 113b), being superior to Bs seedlings in two as well as three replications.

Omission of replicate M tends to strengthen the conclusion, that family selection in Bs seedlings was surprisingly effective. There is an indication of genetic sampling error. However, omission of the replicated (M) which supplied the propagation material does not alter the main conclusion. Gains from family selection were about equal in Bs and Ss seedlings, with no significant differences between the them.

3.73 Bias in correlations between the seedling and evaluation trials.

Some bias was detected when correlations between the Ts and Te trials were computed using three (KLM) or two (KL) replications in the Ts trial (Tables 114, 115, 116, 117, and 118). Replicates K and L contained no clones present in Re type in the Te trial, all planting material for it coming from replicate M.

Correlations are higher for replicates KLM than for KL. This occurs in seven of the eight cases in which they differed significantly (Tables 117, 118). In six cases the superiority of KLM is highly significant. Two of these cases involve Bs seedlings. Such superiority does not necessarily involve bias. Better estimates of means provided by three replications would give higher correlations.

For the important character NMGYOT, correlations are significantly higher in replicates KL for Bs. However, KLM >> KL for Ss seedlings (Table 117). In replicates KLM, Ss >> Bs, but there is no significant difference between Bs and Ss in replicates KL. This indicates that bias is present for

NMGYOT. Ss>>Bs in replicates KLM because the correlations for Ss are inflated by genetic sampling. Of the 14 characters analyzed, only NMGYOT shows evidence of bias.

Considering both gains from selection and correlations, bias due to replicate M was absent or negligible for most characters. It assumes importance because it occurred for correlations involving the important character NMGYOT. However, the analysis makes it possible to allow for this when drawing conclusions. It does not provide any reason for excluding replicate M from the project, and basing conclusions only on replicates KL in the Ts trial. That would introduce bias for other comparisons such as correlations and gains from selection involving the Ts trial and the Re, Be and Se types. It would also involve a serious loss of precision, as shown for realized gains from selection in Table 109 and for correlations in tables 117 and 118.

3.74 Bias due to rust disease.

Common rust (*Puccinia melanocephala* H. & P. Syd.) was first recorded in Australia, near Cairns, in October, 1978 (Egan and Ryan, 1979). It caused serious damage to susceptible varieties. It had a major impact on the breeding program. Most of the major commercial varieties in North Queensland were susceptible, as were most proven crosses, and most seedlings in the selection program.

Rust would have had an important influence on the experiment, which started with the 1980 seedlings. However, the effect could not be measured in the experiment, and only general comments can be made. Selection for rust resistance was very effective in small plots (Berding, Skinner and Ledger, 1984). Rust probably made all forms of selection (family, modified mass and normal mass selection) more effective than usual. Selection for

resistance to rust disease is still very important. However, it has less effect now than in the experiment. Most families and seedlings are now resistant to rust disease whereas many in the experiment were susceptible.

Progress from selection was probably over-estimated more in bunch than in single seedlings. Bunch seedlings tend to develop more rust on the seedling benches compared with single seedlings. In 1980 this would have been an advantage because rust epidemics on the seedling benches were light. This would have become a liability in later years when rust epidemics became more severe. Seedlings which would be resistant in the field give a susceptible reaction on the seedling benches, if the epidemic is too severe. This indicates that the value of Bs seedlings for family and modified mass selection may be over-estimated relative to Ss seedlings, because of rust disease. However, there was no direct evidence in the experiment to prove this. Early growth observations on the Bs and Ss seedlings may have given such evidence. Rust research, including rating of the parent collection, required all available staff at that time of the year. Early growth notes were not taken on the experiment.

3.8 Mass selection.

3.81 Mass selection trial.

Normal mass selection is slightly less effective in the R than the P single seedlings. However, the difference is not significant (Tables 119, 120, Visual NMG and SEL8, TmP, class B vs class C). Mean values for visual NMG and number of selections are higher in class B than in class C. Class B consists of clones selected in SsP seedlings but rejected in SsR. Class C consists of clones selected in SsR but rejected in SsP. Normal selection in the SsP crop would provide classes A+B (or A+B+D), selection in SsR providing classes A+C. Although classes B and C are artificial, they provide the most sensitive measure of the effect of selection in the two crops.

Class A (seedlings selected in both crops) is superior to classes B and C for visual NMG and number of selections. This shows that selection in both crops was effective. Only 45 per cent (176/392) of the seedlings were selected in both crops. This shows there is a fairly marked interaction between the two crops for selection rate. Analysis of variance shows a highly significant interaction for number of selections (SEL8, $(R - P)/2$, Table 15, Cross x Year, Table 18).

The main selection results, for visual NMG, are shown in Table 121. The above classes have been combined to show results for selection in SsP (classes A+B), SsR (classes A+C), and SsPR seedling crops. The selection rate is 15.1 per cent ($100 \times 392/2592$). Numbers for selected and random groups are each two less than the number selected because of missing plots in trial Tm. Selection was effective in SsP and SsR seedlings. Mean net merit grade increased by about 28 per cent. Number of selections from 4-sett more than doubled. Selection was slightly more effective in SsP than in SsR seedlings. Selection based on SsPR was no better than the P crop

only. The results do not support ratooning of original seedlings.

Selection prospects seemed better in the R than the P crop of the Ts trial. The R crop appeared very even. There were very attractive seedlings with many stalks. However, in the random group, seedlings graded highest (11 to 14 visual NMG) in SsR performed no better in trial Tm than those graded about 8.0 (Table 127). This suggests that outstanding performance in ratoon seedlings was mainly determined by environmental effects or competitive ability rather than true yielding ability or ratoon performance.

For ratooning of original seedlings to be efficient, it would be necessary for selection in SsR to produce a substantial increase in selections from stage 2. More time, and 50 per cent more land, would be required for SsR seedlings. Since the ratoon seedlings produced 11 per cent less selections in trial Tm (85 from SsR and 95 from SsP, Table 121) ratooning of Ss seedlings for mass selection would be very inefficient.

The correlation between the value for each Ss seedling in the Ts and Tm trials (Table 122, 123) estimates the broad sense heritability (or degree of genetic determination). For visual NMG, these estimates are:-

	Correlation
	Ts vs Tm
Selections from SsP seedlings	-0.017
Selections from SsR seedlings	0.111
Random seedlings, grade in SsP	0.307
Random seedlings, grade in SsR	0.344
Random seedlings, grade in SsPR	0.361

These estimates are for (true yield + competition). Lower estimates would be expected if true yield could be measured. For true yield + competition, random seedlings give unbiased estimates. In practice,

estimates based on selections are often used. The results show that estimates from selections are strongly biased (reduced). Furthermore, they are not valid statistically, because the distribution of values is abnormal for selections from Ss seedlings in the Ts trial. In this case, the distribution consists of only the extreme upper portion truncated from the whole normal distribution. Selection in Ss seedlings (for true yield + competition) is much more efficient than we have assumed, from correlations based on selected groups. Hogarth (1973, page 177) obtained an even higher correlation of 0.56 between random SsP seedlings and 4-sett plots.

Competition may be the main factor in both original seedlings and 4-sett plots. Without large plots, it is very difficult to estimate the true efficiency of mass compared with family selection. For example, Hogarth (1973, page 170) obtained the following estimates of per cent gain, for selection based on net merit grade:

	Mass selection	Family selection
Predicted	9.2	10.3
Actual, 4-sett P	31.1	15.4
Actual, 4-sett R	31.0	13.6

The actual gains from mass selection are over twice as high as those from family selection. This is one of the reasons we use mass rather than family selection. Hogarth used 3-row plots, so competition may have inflated the estimated gains for families. However, estimated gains for mass selection would be much more inflated. The actual gains for true yield may be less for mass than for family selection, despite the estimates which show mass selection far superior to family selection.

In the present project, the selected and random seedlings were planted at random in 4-sett plots in the Tm trial. Usually random allocation is an efficient procedure, but competition may make it very inefficient. The gain

from selection for true yield is likely to be much less than the results indicate.

Possible bias caused by competition could be reduced in future experiments by grouping selections with similar grades into larger plots (e.g. 4-row plots). Gains from selection in original seedlings may be mainly due to selection for competitive ability. The selected clones are also likely to gain from competition in 4-sett plots allotted at random, as in the present experiment. However, the selections graded 10 (for example) could be planted in 4-sett sub-plots grouped into 4-row main plots. Competition effects would sum to zero inside the 4-row plots. Average gains in competitive ability would disappear in the inner portion. Gains over the whole 4-row plot would be similar to those for selected families planted in 4-row plots.

For brix, hardness and visual NMG, standard deviations in the random type are fairly similar in the TsP, TsR and TmP trials (Table 124). For number of stalks the standard deviation is higher in the TsR than the TsP crop, the variance ratio being highly significant ($F = 2.7^{**}$). This indicates that number of stalks was strongly influenced by competition in the ratoon crop. The CV for number of stalks is similar in the TsP and TmP trials (39, 37, Table 124). The Tm trial had larger plots (4-sett vs single plant for the Ts trial), so the planting method for Ss (potted seedlings) probably reduces variation.

Effective selection is expected to reduce the genetic variance. The CVs in Table 124 tend to support this theory. In trial Tm, they are lower in the selected classes (A+B, A+C) than in the random class, for brix, number of stalks, and NMG.

Data in Tables 122 and 124 were used to compute gains from selection and realized heritabilities (Table 123). The table also includes

correlation coefficients which estimate broad sense heritability. The correlations for visual NMG in classes A+B and A+C in the Ts trial are invalid. There is also some doubt about correlations for other characters in the Ts trial (for the same reason, namely distortion of normal distributions by selection). Despite this, the results show that heritabilities estimated from correlations are much more reliable than realized heritabilities.

The realized heritabilities are so erratic that little or no notice can be taken of them. Those for brix (0.8, 0.9, Table 123) and hardness (1.8, 0.65) are too high. Those for number of stalks were too low, especially in the TsR crop. The variance for stalks was probably inflated in the Ts trial by competition between seedlings, especially in the TsR crop. The realized heritability for visual NMG in the TsR crop (0.38) is reasonable. That for the TsP crop (0.56) is rather high. The most reliable estimates of broad sense heritability are given by correlations for the random class (E). However, these are also expected to be inflated for number of stalks and visual NMG, because of competition effects in both the Ts and Tm trials.

Because small plots were used in the Tm trial, the project has not given any reliable estimate of broad sense heritabilities, or realized gains from mass selection. This fault is present in previous research to estimate these values, both by BSES and by research workers in other countries. The problem was defined at Meringa during the present project.

When visual NMG in the Ts trial is evaluated by number of selections produced from the Tm trial (Table 125), the results favour liberal selection. Peak production is given by seedlings graded 10, production falling for seedlings graded higher than 10. The optimum truncation point will be well below 10, because many good clones are discarded at that level. However, the random class (SsP, SsR, and SsPR, Table 125) indicates

that the optimum truncation point is about 7.0. Productivity is very poor from grades much below 7. This shows that mass selection is effective. The results show that selection is more effective in eliminating very poor clones than in selecting very good ones. Ss seedlings graded 1 or 2 in the Ts trial produced no selections from the Tm trial. Ss seedlings graded 11 or higher were less productive than those graded 10.

Performance of the random class is examined in more detail in Tables 126 (TsP crop), 127 (TsR) and 128 (TsPR). The tables show the number of clones receiving each grade in the Tm trial, for each grade in the Ts trial. The results show successful mass selection and confirm the importance of liberal selection. Productivity increases occur up to about 9 grade in the Ts trial. Grades above 10 are inferior to 10, and grade 10 appears to achieve its high per cent productivity because of a chance non-normal distribution.

As the proportion of the population discarded is increased by raising the truncation point, the proportion of Tm selections which are lost also increases (Table 129). However, this increase is not linear, the curve becoming steeper as selection becomes more severe (P crop, Figure 7, R crop, Figure 8). A change in the slope of the curve occurs with about 60 per cent discarded in the TsP crop and 70 per cent discarded in TsR. These values both correspond to a Ts grade of 6, that is, a truncation point of 7.0. This shows that a truncation point of 7.0 approximates the optimum selection rate. When cost of seedlings is considered, the optimum truncation point would tend to be below 7.0 rather than above it. This would reduce the relative size of the seedling stage, the most expensive stage in the program. However, a truncation point of 7.0 is satisfactory. Figures 7 and 8 show that a truncation point of 8.0 (76 per cent discard in the TsP crop, 84 per cent in TsR) is too severe. It is on the steep part of

the curve.

In the TsP crop, increasing the truncation point from 7.0 to 8.0 (that is, moving from 6 to 7 NMG, Table 129) discards 17 per cent more Ss seedlings. However, it gives a larger loss (19 per cent) of Tm selections. Thus it is less efficient to use a truncation point of 8.0 than 7.0. Efficiency declines further if selection is made more severe. Increasing the truncation point from 8.0 to 10.0 discards 18 per cent more Ss seedlings. However, 29 per cent of the selections from the Tm trial are lost. In ratoon seedlings, severe selection is even more harmful. An increase of the truncation point from 7.0 to 8.0 discards 17 per cent more SsR seedlings, but loses 22 per cent of the Tm selections. An increase in the truncation point from 8.0 to 10.0 discards only 11 per cent more SsR seedlings, but 22 per cent of the Tm selections are lost.

Effective selection at low truncation points automatically results in excessive losses of superior varieties, if selection becomes too severe. For example, if 50 per cent of the SsP seedlings are selected, 71 per cent of the Tm selections are selected. This corresponds to a truncation point of about 6.0, and is a satisfactory result from mass selection. The selected group contains an above-average proportion of the Tm selections. It is inevitable that, as the truncation point is raised further, a level will be reached at which more severe selection becomes inefficient. The proportion of Tm selections lost becomes higher than the proportion of the TsP population discarded.

This method, using increments of the Ss population and Tm selections discarded, provides the best method available for deciding optimum selection rates. The optimum truncation point in the Ts trial is the one just below that at which per cent Tm selections lost \geq per cent Ss population discarded. This optimum truncation point is 6.0 in SsP, SsR and

SsPR (Table 129). This method gives a more definite estimate of the optimum truncation point compared with other methods. It gives a lower estimate (6.0 compared with 7.0).

This method is based on the assumption that the genetic value of clones receiving the same visual NMG in the T_m trial, is independent of their visual NMG in the T_s trial. For example, T_m selections graded 9.0 are assumed to be equal in genetic value, even if they differed in grade in Ss seedlings. This is a reasonable assumption. There were large environmental and competition effects in the Ss seedlings. Seedlings graded above 10.0 were slightly less productive than those graded 9 or 10 (Tables 126, 127, 128).

3.82 Random type in the evaluation trial.

In addition to the T_m trial, information on normal mass selection can be obtained from the T_e trial. Performance of individual clones of the Re type in the T_e trial can be compared with the same clones in the Ss seedlings. The P crop of these seedlings provided the planting material for the Re type. For mean, standard deviation and CV (Table 130) these seedlings are similar to those which provided the random class (E) for the T_m trial (Table 124). In 4-sett plots the Re type has higher brix and NMG. Mean number of stalks and all CVs, are fairly similar in the T_eP and T_mP trials. The T_m trial was not ratooned, the T_e trial having lower brix but more stalks in the R compared with the P crop. The Re type can provide information on possible effects of mass selection on ratoon performance, not available from the T_m trial.

Correlations between Ss seedlings and 4-sett plots are higher for brix in the T_m trial, but slightly higher for visual NMG in the T_e trial (Tables 131 and 122):

Character	SsP vs 4-settP		SsR vs 4-settP	
	Te	Tm	Te	Tm
Brix	0.314	0.533	0.326	0.505
Stalks	0.419	0.470	0.498	0.451
Visual NMG	0.357	0.307	0.386	0.344

The correlations for visual NMG show little or no crop effect:

	Te trial	
	ReP	ReR
SsP	0.357	0.379
SsR	0.386	0.427

The four correlations do not differ much, but there is a tendency for $R \geq P$ in both the Ts and Te trials. Thus, although the highest correlation is SsR vs ReR, the lowest is SsP vs ReP. If there were a strong crop effect, SsP vs ReP would be higher than SsP vs ReR. The correlations also fail to show any dominant genotype x year effect. SsR vs ReP is lower than SsR vs ReR, although SsR and ReP developed in the same year.

As occurred for class E in the Tm trial, results for the Re type show that selection in original seedlings should be very liberal, with a truncation point of 6.0. The last two columns in Table 132 (a-g) show that per cent loss of selections from 4-sett plots exceeds the per cent of the Ss seedlings discarded, if the truncation point in the Ss seedlings is raised above 6.0. This corresponds to the grade class of 5 in the tables. This occurs in Tables a, b, c and e. The optimum truncation point is higher (7.0) only in Table 132f, but lower (5.0) in d and g. The results show the standard truncation point of 8.0 results in an inefficient discard of about one-third of the seedling population.

More liberal selection would increase efficiency if land could be made available for the additional selections. There would be an increase of more

than 100 per cent in the number of selections. The estimated increase is 160 per cent (Table 132a) or 119 per cent (Table 126a). A reduction in the seedling population, in order to select more liberally, may not be efficient. Efficiency of family selection and the proven cross system is promoted by the use of large seedling populations. Too big a reduction in these seedling populations, although desirable for mass selection, would reduce progress through the proven cross system. It would be especially important not to reduce seedling populations until liberal selection had been used for several years. This is essential to test the assumption that the genetic value of clones receiving the same grade in 4-sett plots, is independent of their visual NMG as original seedlings. This assumption would be tested by the number of advanced selections from seedlings graded 6 or 7 compared with advanced selections produced by seedlings graded 8 or higher. It is reasonable to make the assumption when deciding optimum selection rates. It is not reasonable to decide that the assumption is infallible, if more liberal selection is introduced.

A possible method for liberal selection at the seedling stage would involve no selection for brix of individual seedlings. This would reduce the cost of seedling selection. Brix sampling for numerous seedlings requires a considerable amount of time and resources. It is not desirable to eliminate brix measurements completely during seedling selection. Before 1970, problems occurred from families with high vigour and low sugar content, even with selection for brix. Such families produced selections from Ss seedlings, but had low selection rates at later stages of selection.

If individual seedling brix were not measured, it would be desirable to measure brix on a plot basis, as was done for family selection in the present project. Selection rates could then be increased in high brix plots

and reduced in low brix plots. Measurement of plot brix is much less expensive than measurement of seedling brix.

The results do not prove that it would be efficient to stop measuring individual seedling brixes. However, modified mass selection was much less efficient in Ss than Bs seedlings, for improvement of weight of cane. This indicates that brix measurements of each seedling were of little or no value for mass selection. Although sugar content was improved, the selection differential for weight of cane was reduced.

3.83 Mass selection in 4-sett plots.

There were 68 clones of the Re type which were planted in the Tm trial as well as the Te trial. They supply some information about mass selection in 4-sett plots. Their value is limited because of the small number, and they were not deliberately allotted at random to the Te and Tm trials. This carries the risk that they are not a completely random sample of the Ss seedlings.

Correlations between 4-sett plots (Re vs Tm) are higher than those between Ss seedlings and Tm (Table 133), although they are not very high.

Correlation	NMG	Brix	Stalks
SsP vs Tm	0.189	0.322	0.496
SsR vs Tm	0.392	0.404	0.477
ReP vs Tm	0.378	0.423	0.577
ReR vs Tm	0.523	0.500	0.522

In both Ss and Re, $R \geq P$ for NMG and Brix, but not for number of stalks.

Two-way frequency tables (Table 134, a-c) are variable, because of the small numbers. However, they confirm that liberal selection is desirable in 4-sett plots as well as in original seedlings. The optimum truncation

points, estimated from the last two columns of each table, are 7.0 in ReP, 6.0 in ReR and 7.0 in RePR. Overall, the truncation point for 4-sett plots is about 7.0, slightly higher than that of 6.0 for Ss seedlings. This is reasonable, considering the larger plot size. However, liberal selection is necessary, confirming that the 4-sett plot is not very reliable for selection.

3.84 Value of normal mass selection.

If family selection were used, about 20 per cent of the Ss seedlings (seedlings graded 3 or less) could be discarded efficiently using mass selection (Tables 126, 127, 132). Very poor seedlings could be discarded rapidly without considering brix of individual seedlings, when using the plots to propagate the selected families. With this method, the value of the selected families could be increased, with minimum risk of losing good clones. This very liberal selection is not likely to reduce the value of the selections for estimating family value at the next stage. This shows that mass selection could be used to supplement family selection. However, it does not answer the question: should the main selection system be based on family or mass selection?

The mass selection trial was mainly designed to answer the question: should ratoon original seedlings be used in the selection system? It gives a clear answer. Ratoon seedlings would be inefficient and should not be used. The experiment was not designed to estimate the efficiency of normal mass selection compared with family selection. Because of this, it does not tell whether mass or family selection should be used. It does show that modified mass selection is less efficient than family selection. It provides some information about the value of mass selection, without providing any definite conclusion.

When used to evaluate mass selection in Ss seedlings, results for the Re type (#3.82) are fairly similar to those for the Tm trial (#3.81). However, these results also cast doubt on the value of the estimates provided by 4-sett plots in both the Re type and the Tm trial. They also raise some doubts about the value of normal mass selection.

For selection in SsP and SsR seedlings, the Tm trial estimated large gains from mass selection. Mean visual net merit grade was increased by about 28 per cent. Number of selections from the Tm trial was more than doubled (#3.81). Random Ss seedlings graded 8.0 or higher (SEL8) gave improved selection rates at the next (4-sett) stage. Two random groups are involved, namely that used for the Re type, and class E in the Tm trial. The improvements, expressed as per cent of all random seedlings in the group, are as follows:

	ReP trial	TmP trial
Number in group	646	237
SsP vs 4-sett P	51**	85*
SsR vs 4-sett P	75**	131**

These gains were calculated from tables 132a, 132d, 126 and 127. Significance was tested using chi-square tests on 2x2 contingency tables for numbers graded 8 or higher. A continuity correction of 0.25 was used.

Selection in SsR is indicated to be superior to SsP. However, this is not a real difference. The whole population, from which the random groups were sampled, showed SsR slightly inferior to SsP. There is a stronger indication that the improvement was higher in the Tm than the Te trial. This is likely to be a real effect. Different fields and different years were involved. Another difference was that, in the Te trial, clones from the same family were planted in the same 3-row plot.

In the Te trial, gains from normal mass selection in the SsP crop were

estimated in 4-sett plots of the Re type. These gains were much higher than gains from modified mass selection estimated in three-row plots of the Re, Be and Se types in the same trial (SEL8, Tables 34, 35 and 36 compared with 132a, 132b and 132c):

Evaluation crop	3-row	Re 4-sett
TeP	25.6*	51**
TeR	22.9*	76**
TePR	29.4*	78**

Furthermore, there was a big reduction when the gains from modified mass selection, estimated in 3-row plots, were estimated using the middle row. The middle row is protected from lateral competition. Gains for TCH fell from 5.5** per cent estimated in 3-row plots to 1.4 per cent (not significant) in the middle row (#3.231, Table 39).

Normal mass selection, as tested by clones in the Re type, would have given higher real gains than modified mass selection estimated by the 3-row plots. However, it is not likely that this could explain all the large difference in the above estimates. It is likely that some of the difference is due to inflation of the estimates for 4-sett plots, due to competition between clones.

This would apply to the Tm trial as well as the Te trial. Overall, the results leave some doubts about the value of normal mass selection in Ss seedlings. These doubts arise because estimates of the value of mass selection are inflated by competition at the evaluation (4-sett) stage. Family selection is attractive because the estimates of its value, although lower, are more reliable. They are less affected by competition. However, this is not sufficient reason to conclude that family selection should replace mass selection.

Family and normal mass selection were evaluated using different trials

planted in different years, so no accurate comparison can be made between the two trials. However, such a comparison does show mass selection to be far superior to family selection. The following comparison shows the effect of family and mass selection in SsP seedlings:

Character	Family	Mass	100 x Mass/Family
evaluated	TeP trial	TmP trial	
SEL8	28.0	114.0**	407

The selection rates are 16.7 per cent for family selection (4/24 selected, S3SEL8p, Table 92), and 15.1 per cent for mass selection (Table 121).

The results show that the estimated gains from mass selection are inflated by competition in the 4-sett plots used for evaluation. However, it remains possible that, if competition effects were removed, normal mass selection may still be much superior to family selection.

The proven cross system combines mass and family selection, and it may be superior to family selection alone. Its only disadvantage is that the family selection it performs is necessarily based on selection rate. Pure family selection could use the less expensive character, visual net merit grade of the whole plot. However, this may be more than balanced by advantages of the proven cross system. It uses additional gains from mass selection, as well as those from family selection based on selection rate.

This project does not attempt to answer the question: should mass or family selection be used as the main system? However, it draws attention to this question, and shows that BSES must conduct further research to answer it. Inflation of estimated gains from mass selection, due to competition, will continue to be a problem. However, now that this problem has been defined, experiments can be designed to reduce its effect.

The results show that, except for a possible improvement using pure

family selection, the most efficient selection system is the proven cross system based on normal mass selection of Ss seedlings. This is the current selection system at Meringa.

3.9 Advanced selections.

Selections produced by 4-sett plots in the Te and Tm trials entered the normal selection program. Their performance in later stages of selection can be used to estimate the value of different treatments in the experiment.

3.91 Normal mass selection in plant and ratoon crops of single seedlings.

Normal mass selection in SsP or SsR seedlings was effective, producing a much higher proportion of selections compared with random seedlings (Table 135a). The effect is highly significant at the 30-sett stage (P, R >> Random). The numbers surviving after the 30-sett stage are too small to give significant differences. Mass selection was slightly more effective in SsP than in SsR seedlings. However, the difference is well below the level required for statistical significance.

Clones selected in both SsP and SsR crops are superior to those selected only in one crop (A > B, A >> C, Table 135b). This is considered to be a year effect rather than a crop effect. The SsP and SsR seedling crops sample two different years as well as two crops. Clones which perform well in both years are likely to be genetically superior in future years, compared with those which perform well in one year and not in the other, at the seedling stage. This does not mean that ratoon seedlings should be grown. Class A involves more severe selection than classes B and C. Classes B and C do not occur in practice as separate selection classes.

The results for advanced selections confirm conclusions drawn in the experiment. Unfortunately, the numbers reaching the YOT and SYT stages are too small to give statistically significant differences. Thus the advanced selections do not add much to the main experimental results. Mass selection was effective, giving a large increase in numbers reaching the 30-sett

stage. However, this could be due to selection for competitive ability rather than true yielding ability. In order to exclude this possibility, it would be necessary to have large enough numbers to produce significant differences at the YOT stage.

3.92 Modified mass selection.

There are no significant differences between numbers of advanced selections produced by the Re, Be and Se types (Table 136). Numbers reaching the 30-sett stage were large enough to produce significant differences, if effects were important. The Be and Se types were produced by modified mass selection in Bs and Ss seedlings respectively. Thus the results show that modified mass selection was ineffective. There are no significant differences between numbers of advanced selections produced by the three selection levels within the Be and Se types. This shows that more severe modified mass selection (e.g. use of level L1 instead of L1+L2+L3) would be ineffective.

The lack of significant differences between types seems to conflict with the mean values which show Be,Se >> Re for the important characters (#3.23, Table 36). However, a detailed analysis of NMGYOT (#3.6) showed that the mean values overestimate the value of modified mass selection. The main gains in the means were due to improvement of the poor families which were not likely to produce advanced selections. Results for advanced selections support the final conclusion drawn from the detailed analysis of NMGYOT, namely that modified mass selection has very little value (#3.65).

3.93 Comparison of normal and modified mass selection.

Normal mass selection gave a large improvement in production of advanced selections, with a highly significant improvement at the 30-sett

stage. Modified mass selection gave no improvement in advanced selections, with no significant difference at the 30-sett stage. Thus normal mass selection is clearly superior to modified mass selection. However, this superiority may be due to selection for competitive ability rather than true yielding ability. Severe competition would occur in 4-sett plots in the T_m trial. If clones selected in S_s seedlings were superior in competitive ability, this would give them an advantage in the T_m trial. It would increase their chance of selection for 30-sett plots. Random clones would have a reduced chance of selection. Competition between 4-sett plots would be reduced in the T_e trial. Selections were planted together in 3-row plots where competition effects produced by selection in the T_s trial would tend to be lost. Thus gains from selection for competitive ability in the T_s trial would increase selections more in the T_m trial than the T_e trial.

A reasonable conclusion, considering all results, is as follows. Estimated gains from modified mass selection and from normal mass selection are both inflated because of competition between clones. The inflation is larger for normal mass selection. Despite this, normal mass selection is much superior to modified mass selection, for selection based on true yielding ability without competition. Most of the real gains from normal mass selection are not due directly to mass selection. They are due to indirect selection of superior families. Many more selections are obtained from the better families, whereas the poor families produce few or no selections.

3.94 Cross ratios.

Advanced selections from the experiment resulted in changes to proven crosses and cross ratios (Table 1, cross ratios 1989 vs 1980). For the 80N series, the 1989 cross ratios were decided by selections produced by

modified mass, mass and family selection from Ss seedlings, and modified mass selection in Bs seedlings. Because of the unequal contribution from Bs and Ss seedlings, and from P and R crops, these cross ratios were not suitable for evaluation of treatments in the experiment.

The cross ratios omitting the 80N series provide estimates of family value which are completely independent of the experiment. They are suitable for testing the value of treatments in the experiment. These cross ratios could not be computed for some families. Some were planted only in the experiment, gave poor results, and were not replanted. Cross ratios were computed for all families with 80N cross ratios above 1.0, except one (number 16).

Only five crosses had 1989 cross ratios above 1.0. Only three (numbers 8, 18 and 22) can be regarded as superior crosses. One of them (18. NCo310 x 54N7096, ranked third) has produced several commercial varieties in different parts of Queensland. The crosses ranked fourth and fifth had cross ratios of 1.2 and 1.3, not much above average performance for the whole population. They had been replanted more than once. Such declining proven crosses are of doubtful value. One of them (number 20) had a cross ratio of 2.8 for the 80N series, so it may have some value. However, it is necessary to ignore this, if bias is to be avoided. It is only one of several marked discrepancies between the 1989 cross ratios for 80N and 80N omitted. An extreme case is number 15 with 9.0 for 80N and 0.8 for 80N omitted. In the following discussion, the term 1989 cross ratio refers to those with 80N series omitted.

The top three crosses were compared with the worst four crosses (cross ratio 0.0), and with the general mean, in the Ts trial (Table 137, Bs and Ss seedlings) and in the Te trial for the Re (Table 138), Be (Table 139) and Se (Table 140) types. In addition to average performance, the number of

crosses which must be selected in order to include the top three (or top five) crosses was computed. Results for the main characters are summarized in Table 141.

3.941 Ss vs Bs seedlings.

Number of selections in Ss seedlings is the most successful character and method for family evaluation. Family evaluation is thus better in Ss than Bs seedlings. It is better in Ss seedlings than in the evaluation trial.

In Ss seedlings, net merit grade of the whole plot was second in value to selection rate. Omission of brix from this grade made it less successful.

In Bs seedlings, NMGYOT is the most successful character, although TSH and TCH are almost equal to it. These harvest characters are all more successful in Bs than Ss seedlings. TCH is poor in Ss seedlings, especially for number of families including the top three. In Bs seedlings, selectable stalks gives average gains equal to NMGYOT. However, it is not acceptable because the family ranked third in cross ratio was ranked 19th for this character (BsSELST in Tables 8, 137, SEL8 Table 141). Weight per stalk was much more successful in Bs than Ss seedlings. For number of families selected, Bs was significantly superior to Ss ($P < 0.01$) in the P, R and PR crops.

3.942 P vs R seedling crops.

For Bs seedlings, P is superior to R. For the most successful character in Ss seedlings, selection rate, P and R crops are equal for mean gain, but P is slightly superior to R for families selected. For the other successful characters, $P > R$ for mean gain and $R > P$ for families selected. However, the

difference between P and R is more marked for families selected than for means, the superiority of R over P being significant for TSH.

More land and time are required for ratoon seedlings. When this is considered, these results support the conclusion from the experiment, that ratoon seedlings are not efficient for family selection. However, if visual plot grade were used in single seedlings, instead of the most successful character (SEL8), the cross ratio results would tend to favour ratoon seedlings for family selection in single seedlings. Overall, the results indicate that only plant crops of seedlings should be grown.

3.943 Ss seedlings vs Re type.

For selection rate Ss seedlings are much superior to the Re type. This occurs for both mean and number of selected families. For selected families, Ss is significantly superior to Re in P, R and PR crops. For selected crosses, selection rate is unacceptable in the Re type, because only nine families give poorer performance than cross 22 (Tables 10, 141). Selection rate for a family is determined by the within-family variance as well as the mean. Unpublished research has shown that more clones are required to estimate variances than means. The poor results for selection rate in the Re type indicate that the 27 clones planted for each family, are not enough for reliable estimation of variances, or family value using selection rate. For mean gains, Ss and Re are about equal for NMGYOT and TSH. However, for both these characters, ReP is significantly superior to SsP for families selected. Thus, for NMGYOT, family evaluation is more successful in Re than Ss. However, the best result is provided by selection rate in Ss seedlings. This does not agree with results from the main experiment, or the earlier experiment, which showed the sett-planted evaluation trial to be superior to original seedlings for family selection.

It would agree, if NMGYOT were used for selection.

The ReP and ReR crops were about equally effective for family selection. This differs from the main experiment, and the earlier experiment, which show family selection to be more efficient in the ratoon crop of the sett-planted evaluation trial. Overall, it is concluded that selection is more efficient in the ratoon evaluation trial. Lack of a clear difference in the present analysis is not sufficient reason to change the earlier conclusion.

3.944 Re, Be and Se types.

Selection rate gives the highest mean gains in the Te trial but it is poor for crosses selected. The latter is especially poor in the Re type, but it is unacceptable in the BeR, SeR and SePR crops. Overall, NMGYOT is the most successful character. In the Re type, CCS is surprisingly successful for crosses selected, being significantly superior to TCH in the P, R and PR crops, and almost equal to NMGYOT. Mean gains are low, but this is expected because of the low genotypic variance for CCS. CCS is not successful in the BeR or in the Se type.

For the most successful character, NMGYOT, the Re type is superior to the Be and Se types for family selection. This occurs for mean gains and families selected, although differences are fairly small for mean gains. For families selected, the three types are fairly similar in the TeR trial. However, the superiority of Re over both Be and Se is highly significant in the TeP crop. The superiority of Re over Be and Se, for families selected, is also significant for TSH.

Overall, the results show the Re type to be superior to the Be and Se types for family evaluation. This confirms the conclusion reached in the main experiment. Although inferior to the Re type, the Be type shows

substantial and highly significant mean gains. For families selected it is significantly inferior to Re for NMGYOT and TSH in the P crop, but is significantly superior to Re for SEL8 in the P and PR crops. For correlations, Se was intermediate between Re and Be. It was thought that Be was especially poor because selection was based on a single yield component, weight per stalk. The cross ratio results indicate that Be is about equal to Se. A similar conclusion was drawn from estimated gains from selection (#3.635).

It is concluded that populations produced by modified mass selection are inferior to random seedlings for evaluation of families. This probably also occurs with family selection. However, the effect occurs with single as well as bunch seedlings. Both types remain useful for further family selection.

3.945 Support for proven cross system.

The cross ratio analysis gives strong support for the proven cross system, based on normal mass selection of single seedlings. Selection rate in single seedlings was the most successful character. It gave better family evaluation than any character in Bs seedlings, or in the sett-planted evaluation trial. Selection rate would be expensive for pure family selection, but it is efficient for the proven cross system.

3.95 Conclusion from advanced selection results.

Except for cross ratios, results for advanced selections do not add much to results from the main experiment. Numbers reaching the YOT and SYT stages were too small to give reliable statistical comparisons. Despite this, the advanced selections support conclusions from the main experiment.

The present project, like most other research on selection and breeding

methods for clonal crops, uses early stages of selection. There are enough individuals to give reliable statistical comparisons. This research is based on the hypothesis that statistical results obtained from such populations apply to commercial varieties. Commercial varieties are rare superior clones. Statistical methods have never been developed for them. Reliable statistical tests of different treatments can be made in advanced stages, if numerous clones reach these stages. This occurs in the main selection program. For example, advanced stages are proposed (#3.82) to determine whether the genetic value of clones receiving the same grade at stage 2, is independent of their grade as seedlings. If liberal selection is introduced, enough selections will reach advanced stages for valid statistical tests. Most selection experiments are too small to produce enough clones in advanced stages for reliable statistical tests. Even if resources were provided, some experiments mainly based on advanced selections would not be efficient, because of the many years required to reach conclusions.

A new method may produce a significant improvement when applied at an early selection stage (e.g. 4-sett or 30-sett). If the design avoids factors such as competition which may bias the results, it is assumed that the method will produce an improvement in production of rare commercial varieties. Experience in the past, when improved selection methods developed by research have produced more commercial varieties, supports this assumption. Advanced selections from the present project do not provide critical evidence. Conclusions concerning family selection are more likely to be valid than those concerning mass selection. Conclusions concerning family selection are much less likely to be subject to bias caused by competition.

Cross ratio analysis made a valuable contribution to the project. Cross

ratios omitting the 80N series gave estimates of family value which were completely independent of the experiment. These cross ratios were used to define superior families. Their performance, in the experiment, was used to evaluate treatments in the experiment. In this way, the precision provided by replicated plots in the Ts and Te trials could be used. This method avoids the problem of lack of significant differences, which occurs when small numbers of advanced selections are used directly in statistical tests. As might be expected from an independent method, the cross ratio analysis upset some conclusions drawn in the main experiment. However, the modified conclusions are expected to provide a more reliable picture of mass and family selection.

3.10 Practical applications.

The project was successful, answering the main questions it was designed to answer. It showed that BSES must conduct more research to answer some other questions, especially the question of whether pure family selection is more efficient than mass selection using the proven cross system. The project was designed to answer general questions about family selection in bunch and single seedlings, rather than assess particular systems for direct application in the practical program. However, it provided enough information for the following proposed applications.

Meringa experiment station.

Single planting should continue. Half of the seedling area should be used for pure family selection, selection of families being made using visual plot grade, including plot brix. The other half would use normal mass selection. An effort should be made to avoid bias when allotting families to the family and mass areas. Experimental crosses of equal expected value should be allotted to each area. The same proven cross should be allotted to both areas. In the family area the seedlings from a proven cross should be subdivided into separate treatments. Each treatment should be equal to the number of seedlings planted from an experimental cross (e.g. 36 x 2 replicates = 72 seedlings). Each treatment from the same proven cross should be graded and selected independently. A better method may be devised for proven crosses. Unless a method such as that proposed is used, a proven cross planted on a large area would have no selections for stage 2, if its mean grade was just below the truncation point. Equal allocation of genetic material to the mass and family area is very important. It is the most difficult part of the proposal.

Selections from the seedlings should be planted in 20-sett plots, as at present. An equal number of selections should be taken from the mass and

family areas. Selections from the family area should be given a distinctive set of selection numbers (e.g. starting at 6001). No change would be made to the proven cross or other record systems. The proven cross system should be based on both systems. The pseudo treatments in a proven cross should be combined with one another, and with selections from the mass area, before entering data. Standard procedures should be followed in stage 2 and later stages.

If improvements are found to the mass or family selection systems, they can be introduced at any time during the course of the project. This may include more liberal mass selection (#3.82), if land is available. The object is to compare the best available mass and family systems, not necessarily the initial systems adopted. Records should be kept to provide an objective comparison of resources used by the two systems.

After several years, the value of the two systems should be assessed by chi-square and possibly other statistical tests on numbers of selections reaching YOT and SYT. The better system would be adopted, based on this evaluation. Information may also be available on success in prediction of proven crosses.

The present results indicate that pure family selection is promising enough for a field trial such as that proposed. They do not show whether or not it is superior to mass selection, so there is no basis for recommending a complete change to family selection. The proposal is preferred to the alternative of using a small plot replicated experiment to provide similar information. Estimates of the value of mass selection are inflated by competition in small plots. In the proposed system, selections reaching SYT should provide a unbiased comparison of the two systems.

The proposal turns the whole selection program into a large experiment, as was done at Ayr. An important difference is that mass selection already

provides an effective selection system at Meringa. In testing possible improvements, it is important to avoid the risk of introducing a less efficient system. The proposal involves minimum risk, while taking advantage of the economies of family selection for half of the seedling area. The proposed pure family selection does not eliminate mass selection. It transfers mass selection from stage 1 to stage 2. Poor families are eliminated but large numbers still reach stage 2. Mass selection per clone is expected to be much more effective in 20-sett plots compared with single seedlings. Mass selection within good families may be effective in 20-sett plots. It has very little effect in seedlings.

Ayr experiment station.

No change is proposed at Ayr. The large experiment in progress has been delayed by cyclones and atypical seasons. The present project may provide some useful information, but it is not desirable to complicate the designed experiments.

Mackay and Bundaberg.

No detailed practical proposal is made for Mackay and Bundaberg. If the present bunch planting system is continued, an experiment comparing it with pure family selection would be likely to provide an improved system. If planting material is taken in autumn, selection would be based on NMGYOT of the plant crop. However, if about ten seedlings per bunch are planted, as in the present project, it does not provide a good basis for mass or family selection. It wastes too many seedlings, for Queensland conditions. A small number of seedlings per bunch, or close spaced single seedlings, are likely to provide a more efficient basis for family and mass selection. Research could be carried out to determine the optimum planting system for family selection, before conducting a large field comparison. An alternative would be to include two or three planting systems in a comparison with the proven

cross system. The type of design proposed for Meringa, could be used.

4. ACKNOWLEDGEMENTS

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