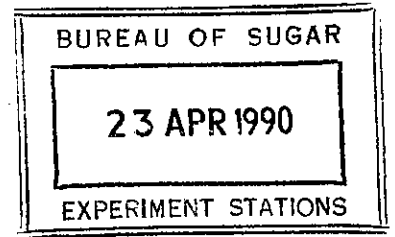


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PROJECT REPORT

Volume 1 of 7

PROJECT 409

BUNCH FAMILY SELECTION

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

by

J.C. Skinner, N. Berding and D.M. Hogarth

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SUMMARY.

Mass and family selection were studied in bunch and single seedlings from 24 families (12 proven and 12 experimental) planted at Meringa in 1980. The families were planted in an evaluation trial in 1981, using selections from bunch and single seedlings, as well as random seedlings. The selections were obtained by modified mass selection, nine selections being taken from each plot. A third (mass selection) trial planted in 1982 compared equal numbers of selections from the plant and ratoon crops of single seedlings. Random seedlings were included as a control.

In 1990, cross ratios were computed using all series available since 1979, except the 80N series used in the experiment. This estimate of family value was completely independent of the experiment. It was used to estimate the value of treatments in the experiment. This cross ratio analysis altered some of the conclusions from the main experiment.

The mass selection trial showed that it is not efficient to ratoon original seedlings. They do not give better results than plant cane, and use additional time and land. The main experiment gave a similar result for family selection. There was no indication that the ratoon seedlings provided special information about ratoon performance of families.

Ratoon seedlings gave better evaluation of families in the evaluation trial, giving higher correlations with values in the seedling trial. The old (1976) experiment on this subject also showed better evaluation in ratoons in sett-planted material.

Some superficial differences between the present and the old experiment were traced to a lack of significant differences between seedling families in the old experiment. The seedling trial in the present project used more replications and was much more precise. It had much higher F values, not

only compared with the old experiment, but also compared with the evaluation trial. Family selection was more effective in the sett-planted evaluation trial than in the seedling trial, in the previous experiment. The evaluation trial was slightly better in the present experiment. However, cross ratio analysis showed family selection to be better in single seedlings than in the evaluation trial.

There is no real difference in weight of cane produced by bunch and single seedlings, despite intense natural selection in bunch seedlings. Single seedlings were slightly (not significantly) higher in this project. Bunch seedlings were higher in the old experiment.

Gains were much higher than expected from modified mass selection, and from family selection, in bunch seedlings. Modified mass selection gave significantly higher gains, for weight of cane, in bunch than in single seedlings.

No competition between families was detected. Number of stalks per row was analyzed in the seedling and evaluation trials. Weight per stalk and weight of cane were also analyzed in the evaluation trial.

Competition between types occurred for weight of cane and weight per stalk in the evaluation trial. The bunch and single types gained at the expense of the random type. However, the bunch type retained its highly significant superiority when lateral competition was avoided by using only the middle row of each 3-row plot. Without competition, gains for weight of cane in the single type became very small (about 1.5 per cent) and not significant.

A detailed analysis for NMGYOT showed that the highly significant gains from modified mass selection in bunch seedlings were an illusion. The means were improved mainly by improving poor families which are less likely to produce commercial varieties. For the more important good families, there

was very little improvement from modified mass selection, and the single type was slightly superior to the bunch type.

Three selection levels (8 to 25 per cent for single seedlings) showed that more severe selection gives little or no improvement with modified mass selection. Modified mass selection is of no practical value. It is inferior to family selection and to normal mass selection.

Although modified mass selection gave no practical improvement, marked selection effects were shown by the bunch and single types. The size of correlations between the seedling trial and the evaluation trial types were in the order random >> single >> bunch. Realized gains from selection in the evaluation trial, measured by performance of seedling families, showed a similar order. Realized gains from family selection in bunch seedlings were estimated to be much lower by the bunch type than the random type. This occurred although the bunch type had a higher genotypic variance than the random type. Realized gains from selection in single seedlings were also estimated to be lower by the single type than the random type. The random type gives the best estimates of true family performance. It is superior to the bunch and single types at stage 2, as well as the seedling stage.

Cross ratio analysis also showed the random type superior to the bunch and single types, for family evaluation. However, it showed that the bunch type is better than the estimate given by correlation analysis in the main experiment. It showed that the bunch and single types are about equal in value, and both give highly significant gains from family selection.

Visual net merit grade of the whole plot gave good results for family selection in original seedlings. In the main experiment, it was the most successful character. This was shown for both bunch and single seedlings, by realized gains from selection, by correlations between the seedling and

evaluation trials, and by multiple regression analysis. However, cross ratio analysis showed family selection most effective using selection rate in single seedlings. It showed NMGYOT the most successful character in bunch seedlings, and in the evaluation trial.

Harvest characters such as NMGYOT involve destruction of the seedlings. This is a serious disadvantage if selections are to be replanted the same year. Family selection using NMGYOT in bunch seedlings, is probably only worth consideration if autumn planting is used. For autumn planting, selections can be cut from the young ratoon crop. In single seedlings, selection rate is efficient for the proven cross system, but is probably too expensive for pure family selection. Visual net merit grade of the whole plot is the preferred character for pure family selection in single seedlings. It is the most successful character in the main experiment, and second only to selection rate for the cross ratio analysis. It is a very economical character. However, it can only be used if experienced selectors are available.

Family selection is effective in bunch seedlings. This answers one of the main questions studied in the project. It reverses a previous opinion that family selection was not effective.

In the main experiment, gains from family selection are about equal in bunch and single seedlings. There is no significant difference between them. However, cross ratio analysis showed single seedlings (using selection rate) superior to bunch seedlings using the most successful character (NMGYOT). Although they require about six times the seedling area, single seedlings have the more important advantage of requiring only about one-third the number of seedlings. BSES may not have the resources to maintain efficient family selection with bunch planting on all experiment stations. If supply of seedlings from good families is a limiting factor,

inclusion of poorer families in bunch nurseries would reduce the efficiency of family selection.

Random single seedlings in one replicate provided the propagation material for all replicates of the random type in the evaluation trial. The random type was used to evaluate family selection. There was an indication that this caused some bias in gains from family selection. Single seedlings had an advantage over bunch seedlings which did not provide any propagation material. Gains from selection were also computed without the replicate which was used for propagation. Family selection improved in bunch compared with single seedlings. However, the change was not statistically significant.

Correlations between the seedling and evaluation trials were also computed with and without the replicate used for propagation in the seedling trial. The important character, NMGYOT, showed significant bias due to genetic sampling. Bias was negligible for all other characters. Bias, as shown by correlations and gains from selection, was fairly small. It did not have much effect on the main conclusions.

Rust disease, which entered Queensland in 1978, probably increased gains from selection in the experiment. The experiment contained more susceptible clones and families, compared with modern populations.

The project was successful, answering the main questions it was designed to answer. It was not designed to give an accurate comparison of family selection with normal mass selection. It showed that more research is important for a decision between mass and family selection. This research should include a range of planting systems for family selection. It is not likely that the two standard planting systems used in the present project are best for family selection. Possible improvements include bunch planting with a small number of seedlings per bunch, and closer single

planting.

Estimated gains from normal mass selection were inflated by competition between clones in original seedlings and in 4-sett plots in the mass selection trial. However, the estimated gains for number of selections, using normal mass selection, were very high. They were about 300 per cent higher than those from family selection when different trials were compared, and 78 per cent higher in the same trial. Even allowing for serious inflation of these estimates by competition, and other errors, mass selection may be much more effective than family selection.

Modified mass selection is pure mass selection free from family selection. The same number of selections is taken from each family. Normal mass selection is often regarded as completely different from family selection, the family being ignored when selecting individual clones. However, normal mass selection includes family selection, some families producing numerous selections, and others producing none. The failure of modified mass selection indicates that most of the gains from normal mass selection are due to unconscious family selection, not to mass selection within families. Normal mass selection, combined with the proven cross system, may be the most efficient system of family selection available.

Results from the main experiment indicate that the most efficient system is normal mass selection of single seedlings, using the proven cross system. This is the standard system at Meringa. The cross ratio analysis gives strong support to this system. It showed that family selection was most successful using selection rate in single seedlings. Selection rate is too expensive for pure family selection, but it is efficient for the proven cross system.

The optimum selection rate for family selection is estimated to be between 25 and 50 per cent. Liberal selection should also be used for mass

selection. The optimum truncation point for mass selection of single seedlings is about 6.0. This was estimated from two-way frequency tables showing the number of clones receiving each visual NMG at two stages of selection. It would involve an increase of over 100 per cent in seedlings selected, compared with the standard truncation point of 8.0.

More liberal mass selection would increase efficiency, provided land is available for the increased selections. More liberal selection with a reduction in seedling numbers may not work. The proven cross system may become less efficient if seedling numbers are too small. The results indicate that it may be efficient to select more liberally by not measuring brix of each seedling. Plot brix could be measured and less selections taken from low brix families. This method would be less expensive than measurement of seedling brix, especially with more liberal selection. Poor response to modified mass selection in single seedlings indicates that selection using brix of each seedling is of little value, and may be harmful. More research is necessary to decide this.

Results for advanced selections from the experiment confirm conclusions drawn in the experiment. However, they do not add much information because the numbers reaching YOT and SYT were too small to give significant differences. Cross ratios based on advanced selections were effective. The method took advantage of the precision provided by the main replicated experiments, giving numerous significant differences. This analysis made it necessary to modify some conclusions from the main experiment. However, cross ratio analysis and the main experiment both support the proven cross system based on normal mass selection of single seedlings. They indicate that this is the best available selection system. They also indicate that pure family selection is promising and worth large-scale trial.

Successful selection is accompanied by a reduction in genetic variance.

Within family variance for brix was significantly reduced by modified mass selection in single seedlings. Within family variance for visual NMG was significantly reduced by selection in bunch and single seedlings. It is desirable for BSES to increase genetic variance within and among families deliberately, probably by increased wild cane breeding.

There were highly significant genotypic, phenotypic and environmental correlations between family mean and variance in the seedling and in the evaluation trial. The correlations were positive for number of stalks and visual NMG, and negative for brix. The negative brix correlations fit the hypothesis that brix is approaching a physiological limit, high sugar families having lower within-family variances. The positive correlations for visual NMG make it easier to use means for family selection, ignoring variances. They may also explain why selection rate, and the proven cross system based on it, have been so successful. However, these correlations may be produced by competition between clones in small plots. If so, they would not help selection for true yield.

Families x years interactions were not significant for NMGYOT in the evaluation trial, but were highly significant for visual NMG. The mean of three varieties (Q82, Q90 and Q113) was used as standard for NMGYOT whereas only one standard (Q113) was used for visual NMG. Q113 showed a large interaction, its NMGYOT increasing from 8.1 in the plant crop to 12.3 in the ratoon crop. This illustrates the value of multiple standards in weighed trials. Standard varieties are supposed to reduce interactions. The multiple standards did this but the single standard (Q113) tended to increase them.

A comparison of pure family selection with the standard mass selection system is proposed at Meringa. Each system would occupy half the seedling area. Family selection would use single seedlings, with selection based on

visual grade of the whole plot. Numbers of advanced selections would be used to decide between the two systems. If numbers were approximately equal, pure family selection would be adopted, because it is less expensive than the standard system.

List of abbreviations.

The following abbreviations are used in this report:-

Crops

P Plant crop

R Ratoon crop

PR Mean of both crops = $(P+R)/2$

(lower case, p,r,pr may be used in Figures and Tables)

Trials

Ts Seedling trial e.g TsR = ratoon crop of the seedling trial

Te Evaluation trial

Tm Mass selection trial

Types (Trial Ts)

Bs Bunch-planted original seedlings = bunch seedlings

Ss Single-planted original seedlings = single seedlings

Types (Trial Te)

Re Random = unselected Ss

Be Bunch = result of modified mass selection in Bs

Se Single = result of modified mass selection in Ss

e.g. RePR = the average over both crops of the random type in the evaluation trial.

Statistical terms

AOV Analysis of variance

CV Coefficient of variation

DF Degrees of freedom

F Variance ratio

RCB Randomized complete blocks

Statistical significance

$P < 0.05$, * significant(ly) ($P \leq 0.05$)

$P < 0.01$, ** highly significant(ly) ($P \leq 0.01$)

\geq (is) greater (or \leq , less) than (not significant)

$>$ (is) significantly greater (or $<$, less) than

$>>$ (is) highly significantly greater (or $<<$, less) than

In some cases $>$ or $<$ is used as a general term for significance, including $>>$ or $<<$

Section numbers # e.g. #3.1 = Section 3.1

1. INTRODUCTION

An experiment conducted at Meringa from 1976-79 (Skinner, 1980, 1982) showed that family selection was more effective in sett-planted trials than in original seedlings. It was more effective in R than in P crops of sett-planted trials. It indicated that selection in bunch plantings could be improved by preceding mass selection with family selection based on number of stalks and brix. The bunch- and single-planted trials were adjoining but separate. The general mean for tonnes cane per hectare was higher in the bunch trial. It was desirable to determine whether this was caused by soil variation, or natural selection within bunch-planted families. The experiment did not give a clear estimate of the value of bunch and single planting for family selection. Problems occurred because variances of families were not measured in the seedling and evaluation trials.

The present experiment was designed to provide a better estimate of the relative efficiency of bunch (Bs) and single (Ss) seedlings for family selection. It included selection in P and R crops in both the seedling (Ts) and evaluation (Te) trials, as well as the P crop of a mass selection (Tm) trial.

A list of abbreviations used in this manuscript is given above.

2. MATERIAL AND METHODS

The experiment was conducted on the Meringa Experiment Station. Twenty-four families (12 proven and 12 experimental, Table 1) were compared using Bs and Ss seedlings planted in 1980. The families were planted in a Te trial in 1981, using selections from Bs and Ss seedlings, as well as random seedlings. A third (Tm) trial planted in 1982 compared equal numbers of selections from the P and R crops of the Ss seedlings. It included random seedlings, to provide a direct estimate of gains from mass selection.

Times of planting, selection and harvest of the three trials are shown in Table 2. Plot shape and size are illustrated in Figure 1. Characters recorded during selection and harvest, or computed later, are listed in Table 3.

2.1 Seedling trial.

A randomized complete blocks design was used, with 3 replications. The experiment contained a total of 10512 seedlings, 7920 Bs and 2592 Ss.

Each Bs plot was one-sixth the area of the Ss plot. Six Bs families were allotted at random to a main plot. With 24 crosses, bunch planting occupied 4 random main plots in each replicate. Thus there were 28 main plots per replicate, 24 occupied by the 24 Ss families, and 4 occupied by the 24 Bs families.

The P crop of the Ts trial provided planting material for the Te trial. Material of three types (Re, Be, Se) was provided for each family. For the Re type, planting material was cut from random Ss seedlings in only one replicate (No. 3 = M). The Be and Se types consisted of selections from the Bs and Ss seedlings respectively. A modified form of mass selection was used, the best nine selections being taken from each plot. This differs

from normal mass selection which is made without any reference to families. One family may provide more than nine selections per plot, and some families provide none.

The nine best seedlings were selected from each plot of Bs and Ss seedlings. The three seedlings with highest visual NMG in each plot were allotted to level 1 (L1), the intermediate three to L2 and the remainder (ranked 7th, 8th and 9th) to L3. If a clone of the Re type was selected in the Ss seedlings, it was planted in Re as well as Se plots.

Selection data were taken for each plant of the standard commercial variety (Q82) in both P and R crops. Each plant was weighed at harvest.

Net merit grades were allotted independently to each crop. That is, no data from the P crop were available to the selectors when grading the R crop.

The truncation points for Visual NMG in each crop were adjusted so the total number of selected Ss seedlings was the same for P and R crops. In the crop (P) with the larger number of selections, selections were eliminated from the borderline group by using random numbers. All selections, including the eliminated class, were planted in the Tm trial. Random seedlings were included as a control.

2.2 Evaluation trial.

The Te trial used a randomized complete blocks design with 3 replications x 76 plots per replicate. The 76 plots consisted of 24 families x 3 types (Re, Be, Se) plus three standard commercial varieties (Q82, Q90, Q113). Two plots of Q113 were planted in each replicate. Omission of the standard commercial varieties gave a factorial design with 3 types x 24 families x 3 replications. The Be and Se types also provided a split-plot design with a factorial design (2 types x 24 families) on the

main plots and three selection levels (L1, L2, L3) as subplots. The selection levels from each family were allotted at random to each row of the 3-row plot.

For the Re, Be and Se types, different clones were planted in each replicate, giving a total of 27 clones from each family for each type. Summed over the three types, the number of clones from a family was 81 or less, depending on whether the random seedlings were also selections.

2.3 Mass selection trial.

Material planted in this trial consisted of 5 classes (A - E):

| | Clones |
|--|--------|
| A. Selected in P crop, also selected in R | 176 |
| B. Selected in P crop, rejected in R | 216 |
| C. Rejected in P crop, selected in R | 216 |
| D. Surplus for crop (= P) with higher natural rate | 29 |
| E. Random | 243 |
| | — |
| Total | 880 |

Class E is a random sample of all Ss seedlings in the original seedling trial, no attempt being made to sample equal numbers from each cross. This group includes some clones which were also in the other classes (e.g. CE). In this example the clone would provide information for class C as well as class E.

No formal randomization was used in the Tm trial. The selections were planted in the trial in family groups. These groups were in the order collected from the Ts trial. The Ts trial was replicated, and this would provide effective replication in the Tm trial, despite the absence of formal control of replication and plot size. This would improve the

reliability of means, without providing data suitable for analysis of variance.

2.4 Statistical analysis.

Most statistical analysis was carried out using GENSTAT software, MSUSTAT software being used for paired t-tests and chi-square tests. Numerous programs were written in Turbo Basic and Fortran. These programs performed analyses not available in the commercial software. They also prepared data files in a form suitable for analysis, and checked for errors in manually entered data. Some programs prepared the larger tables in the report. Some combined statistical analysis and preparation of tables in a single program.

Standard analysis of variance was conducted for the Ts and Te trials. This included RCB analysis for both trials, and factorial and split-plot analyses in the Te trial. Methods and models followed those described by Steel & Torrie (1980).

Combined analyses over P and R crops were conducted in both of these trials. Split-plot and split-block designs were used for the analyses, results being presented for fixed and random models. The mathematical models and expected values for the mean squares are shown in Table 4 for the split-plot design and in Table 5 for the split-block.

Correlation matrices were computed for all characters in the Ts and Te trials. Genotypic, phenotypic and environmental correlations were computed for the most important characters in each trial.

Multiple regression analyses were performed, to show the extent to which performance of families in the Te trial (Y) depended on performance in Bs (X1) or Ss (X2) seedlings. A similar analysis tested P (X1) and R (X2) seedling crops.

Multiple regression analyses predicting Te trial performance from several important seedling characters, were computed using Genstat with automatic selection of co-variables. The "worst" and "minimise" directives, which correspond to methods known as backward elimination and stepwise regression (Draper and Smith, 1981) were used. Elimination or addition of co-variables ended when there was no further reduction in the residual mean square. Co-variables were also chosen manually for some analyses.

T values ($t = \text{estimated regression coefficient} / \text{standard error of this estimate}$) were presented instead of regression coefficients. They provide a standard estimate which can be used to compare different characters. Such comparisons were more important than the actual regression coefficients.

Efficiency of a multiple regression equation was expressed by the *percentage variance accounted for*, provided by GENSTAT regression analyses. This is the difference between residual and total mean squares in the regression AOV, expressed as a percentage of the total mean square. It is not quite the same as R^2 , the squared coefficient of multiple correlation, which gives a similar ratio for sum of squares.

Lateral competition was analyzed in Ss seedlings in the Ts trial, and in the Te trial. Weight of cane (kg), number of stalks per row, and weight per stalk were analyzed in the Te trial. Weight could not be analyzed in the Ts trial because weight of planting material removed was recorded on a plot basis instead of separately for each row. Only number of stalks per row was analyzed in the Ts trial.

AOV was conducted on the quantity "sum of border rows minus twice middle row" ($A+C-2B$). This does not provide a very sensitive measure of lateral competition. Error variance is probably inflated because the formula doubles the value of the middle row. A more sensitive measure was obtained by analyzing each row separately. Higher variance ratios (F

values) in the border rows (A or C) than the middle row (B) would indicate competition. Genotypic, phenotypic and environmental correlations between rows A, B and C were also computed. Higher correlations between the border rows (A vs C) than with the middle row (B vs A or B vs C) would indicate competition. Without competition, the latter correlations are expected to be higher than A vs C because rows A and C are further apart in the field.

In addition to standard competition AOV, factorial AOV for competition was conducted in the Te trial. Characters analyzed were weight of cane (kg), number of stalks per row, and weight per stalk. The factors were types (Re, Be and Se) and families. Differences in competition between types would indicate selection for competitive ability as well as true yield, when modified mass selection was conducted in Bs and Ss seedlings.

Theoretical gains from selection, for families reproduced clonally, were computed using the methods outlined in Table 6.

Realized gains from selection (G) were calculated by measuring the performance, in the Te trial, of the best 12, 6, and 4 of the 24 families in the Ts trial. This gave selection rates of 50, 25 and 17 per cent. The selection differential (D) was the difference between the mean of the best families and the general mean in the Ts trial. Realized heritability of family means was calculated as G/D . Theoretical gains were also computed in the Te trial and compared with realized gains in the Ts trial. The latter method is unorthodox, because the Ts trial was planted before the Te trial. However, it provided additional information.

Significance of differences between groups (e.g. Bs, Ss seedlings) for realized gains from selection were tested using paired t-tests. Tests were based on all observations, with evaluation using number of selections, or NMGYOT. Selection based on any character was regarded as an observation, selection in each crop being treated as a separate observation. Thus the t-

tests were based mainly on correlated responses rather than direct responses. The analyses were made on gains expressed as per cent of the mean for each Te character. An arcsin transformation was used before analysis, means being reconverted to per cent for presentation in tables.

Significance of differences between groups of correlations (e.g. P vs R crops) was tested by AOV. For example, a factorial AOV was used, with crops (P, R, PR) and types (Re, Be, Se) as factors. The correlations were transformed using Fisher's Z transformation (Snedecor, 1962, page 175), to give normal distributions. Each character in one of the trials (e.g. TCH in the Ts trial) was regarded as a replicate. Characters in the other (e.g. Te) trial were treated as normal characters for analysis. Analysis of absolute values, to eliminate negative values, was tested. It was rejected because it produced abnormal distributions of the Z values.

In 1990, cross ratios were computed using all series available since 1979, except the 80N series used in the experiment. This estimate of family value was completely independent of the experiment. It was used to estimate the value of treatments in the experiment.

3. RESULTS AND DISCUSSION

Mean values, in order of key numbers, are given for each family of Bs and Ss seedlings in Table 7. Sorted values for these means are given in Table 8. These means are based on all three replicates (KLM) of the Ts trial. Similar mean values, based on the two replicates (KL) which did not provide propagation material for the Te trial, are given in order of key numbers in Table 9.

Mean values for the Te trial, in order of key numbers, are given in Tables 10 (Re type), 11 (Be) and 12 (Se).

These tables of family means provided basic data for analyses presented below, including correlations, regressions and gains from selection.

3.1 Seedling trial.

There was a large amount of genetic variation among families in the Ts trial, especially in Ss seedlings. In Bs seedlings, variance ratios (Table 13) are significant or highly significant for all characters in the R crop. In the P crop, only hardness and appearance grade are not significant. Over both crops, only hardness is not significant, all other characters being highly significant.

The value $(R - P)/2$ estimates the importance of the linear regression of families on crops. A significant value shows a significant families x crops interaction. For the Bs seedlings it is not significant for the main characters (TSH and NMGYOT). It is significant only for TCH, appearance grade, and KG/STALK. For Ss seedlings (Table 14) this interaction is significant, or highly significant, for all important characters.

For all characters, including number of selections (Table 15), F values are higher for Ss than for Bs seedlings. This is not due to reduced genetic variation, but rather to increased environmental variation, in Bs seedlings. Coefficients of variation are about 50 per cent higher in bunch planted plots (Table 16), the ratio for bunch/single ranging from 1.1 to 2.3.

As expected, environmental variation is higher in Bs seedlings. The single-row Bs plots were only one-sixth the size of the 3-row Ss plots. The project was designed to provide results which could be applied to practical situations. This meant that Bs and Ss seedlings were not compared in plots of the same size. In practice, Bs seedlings occupy a smaller area than Ss seedlings. The proven cross system used by BSES is based mainly on biparental crosses. The number of seedlings produced is a limiting factor when such a system is combined with bunch planting. This is important in Queensland where seed setting is poorer than in some other countries. The

Ts trial contained 108 Ss seedlings per family compared with about 330 Bs seedlings. These numbers approximate the relative numbers used in practice with each system.

Bunch planting was developed in Hawaii where seed setting is better than in Queensland. Even so, the Hawaiian system relies on polycrosses (melting pots) to provide enough seedlings for the system. Such a system exploits general combining ability. A proven cross system such as that used by BSES exploits specific as well as general combining ability. The system involves discard of many seedlings from inferior or experimental crosses, before seedlings are planted in the field. Total seedling production by BSES would be sufficient for fairly extensive bunch planting. However, the need for selection before planting makes seedling production a limiting factor when bunch planting is used. Seedling production would also be a limiting factor with pure family selection. This made it necessary to use much smaller plots for Bs compared with Ss seedlings.

In the old experiment (Skinner, 1980, 1982), the general mean for tonnes cane per hectare was higher in the Bs seedlings. In the present project $Ss \geq Bs$. There is no real difference in productivity of unselected Bs and Ss seedlings. The higher yield in the old experiment was evidently due to the Bs seedlings being planted in more productive soil. The bunch and single trials were adjoining but separate in the old experiment.

The number of missing Ss seedlings shows significant differences between families (Table 14). There are variations in the number of misses for different characters presented in the table. However, the misses mainly involve the same seedlings. The general mean is lower for Visual NMG misses than for other characters. It was possible to give a grade to a seedling which was too poor for provide a brix or other measurement. The number of misses shows significant genetic variation. This may be a false effect. A

whole family may suffer an environmental effect in the seedling flats, or on the seedling benches, where there was no systematic replication. This would be shown as a genetic effect in the field trial.

There are some significant differences between families for within-family variance for stalks, brix, and visual NMG (Ss seedlings, Table 14). Thus the data may provide some information on the relative importance of means and variances for evaluation of families.

The proven cross system is based mainly on selection rate. It is not clear whether selection rate is preferable to means (TSH or NMGYOT) which can be measured more objectively, using weighing machines. Up to the present, it has been the main character available for selection of families. Despite larger environmental variation (Table 16) selection rate may be better. It is based on within-family variances as well as means, and may provide a better estimate of the superior varieties in a family. There are highly significant differences between families for selection rate (Table 15). The normal truncation point is about 8.0 (SEL8). A lower truncation point (SEL7) gives higher F values. A higher truncation point (SEL10) gives lower F values, and there are no significant differences in the P crop. There are highly significant interactions between families and crops, as shown by $(R - P)/2$, with truncation points of 7 and 8. This does not occur with severe selection (SEL10). Interactions are probably present for SEL10. They could not be detected because of the environmental variation which resulted in no significant differences between families in the P crop.

A combined analysis over P and R crops, confirms the importance of family x crops interactions in Ts seedlings. The F ratios (CrossxYear, AB) are similar to those for $(R-P)/2$, for Bs (Table 17) as well as Ss seedlings (Table 18). Differences between years are highly significant for the

harvest characters TCH, CCS, TSH, and NMGYOT for Ss seedlings. They are significant for all except CCS for Bs seedlings (modified split plot, random model, Tables 17 and 18). For Ss seedlings, within family variances show large and highly significant differences for years. Cross x years interactions are significant or highly significant.

3.11 Correlations in the seedling trial.

Phenotypic correlations between characters in Bs and Ss seedlings are shown in Table 19. Genotypic correlations are shown in Tables 20, 21 and 22.

3.111 Correlations between plant vs ratoon crops.

Genotypic correlations between P and R crops are fairly similar in Bs and Ss seedlings (Table 20). Environmental correlations are higher in Ss than in Bs seedlings. This results in higher phenotypic correlations. However, this effect is not significant for the main characters TSH and NMGYOT. Correlations are lowest for KG/STALK.

3.112 Correlations involving weight per stalk and number of stalks.

Bs seedlings show very little correlation between number of stalks and weight per stalk (KG/STALK, Table 21). Ss seedlings show a slight negative correlation in the P and a fairly strong negative correlation in the R crop. This is due to a negative genotypic correlation (-0.78^{**}) in the R crop. A negative correlation is expected because both components depend on the total energy fixed by the plant.

The size of this negative correlation depends on the extent to which both components develop at the same time. The period between planting to the field, and filling of the drills with soil, is less for potted

seedlings than for crops planted using cuttings. This may limit changes in stalk populations in the P seedling crop, most energy stored later in the season being used to increase weight per stalk. This would result in low or zero correlations between number of stalks and weight per stalk. They would not compete with one another for energy. The stalks which will survive may be decided much earlier in Bs than Ss seedlings, because of the very close spacing. This would make number of stalks independent of weight per stalk in Bs seedlings.

An environmental effect which occurs in all replicates of a trial, will influence the genotypic rather than the environmental correlation. Such environmental effects are detected as genotype x environment interactions. Thus the size of a genotypic as well as an environmental correlation shown by the same population, may differ in different locations or years. It is probably safe to assume that all typical populations can show strong negative correlations between number of stalks and weight per stalk. Whether such a capacity is expressed depends on factors such as genotype x environment interactions, and probably on the planting method used for seedling populations.

Number of stalks shows medium to high correlations with TCH in Bs and Ss seedlings. The genotypic and phenotypic correlations are highly significant. The environmental correlations are lower, but are significant in both crops, except BsP seedlings. Bs and Ss seedlings, and P and R crops, have fairly similar correlations between number of stalks and TCH.

Environmental correlations with TCH are much higher for weight per stalk than for number of stalks (Table 21). For weight per stalk they range from 0.73** to 0.87**. Bs seedlings have a moderately high (0.6**) genotypic correlation between weight per stalk and TCH in the R crop. They have a very high genotypic correlation (0.9**) in the P crop, resulting in

a high (0.9^{**}) phenotypic correlation. Ss seedlings have a genotypic correlation of 0.55^{**} in the P crop. It is slightly negative (-0.15) in the R crop. In the SsR crop, there is a slightly negative genotypic correlation, combined with a high positive environmental correlation. The resulting phenotypic correlation for family means is close to zero (0.05 , KG/STALKr vs TChr, Table 21).

Correlations for number of stalks vs CCS are close to zero for Ss seedlings. They are low for Bs seedlings, but the phenotypic correlations for means are high enough to be highly significant in both crops. There are positive genotypic correlations between CCS and weight per stalk in Bs and Ss seedlings. They are significant only for the SsP and BsR seedlings (Table 21). However, they are high enough to produce highly significant phenotypic correlations, despite low negative environmental correlations in three of the four cases.

Genotypic and phenotypic correlations between number of stalks and NMGYOT range from 0.48^{**} to 0.69^{**} . These correlations are slightly higher in Bs than Ss seedlings.

Correlations with NMGYOT are higher for weight per stalk than for number of stalks in both crops of Bs seedlings. This also occurs for the SsP seedlings. However, the genotypic correlation between KG/STALK and NMGYOT in Ss seedlings falls from 0.64^{**} in the SsP crop to about zero in the SsR crop. Because of this the phenotypic correlation falls from 0.615^{**} in the SsP crop to 0.1 in SsR, despite an environmental correlation of 0.715^{**} (Table 21).

Weight per stalk is a very important selection character for mass selection in bunch nurseries. Only one stalk is available from each clone for selection. No selection can be made for number of stalks, and it is too costly to measure the sugar content of each stalk. The above discussion

shows that the correlations favour Bs more than Ss seedlings. The expected negative correlation between number of stalks and weight per stalk does not occur. This removes a barrier to progress from selection based on weight per stalk in Bs seedlings. The positive correlation between weight per stalk and CCS partly compensates for the absence of selection for sugar content in bunch nurseries. The favourable correlations are likely to make mass and family selection in Bs seedlings more effective than expected compared with Ss seedlings. They may partly compensate for the disadvantage of the much smaller plot size used in the experiment for Bs compared with Ss seedlings.

The correlations between weight per stalk and NMGYOT in Ss seedlings, show a marked interaction with crops. The genotypic and phenotypic correlations fall from 0.64** and 0.62** in the P crop to about zero in the R crop. The strong environmental correlation in the R crop is likely to hinder rather than help selection. These correlations are likely to make selection in ratoon seedlings less effective than expected.

3.113 TCH vs CCS.

There is no environmental correlation between TCH and CCS, the values ranging from -0.18 to +0.19 (Table 21). The genotypic correlation is 0.47* for SsP and 0.82** for BsR seedlings. Thus the high yielding families in the project tend to be above average for CCS. The families used in this project are not typical of all families, so far as this correlation was concerned. Berding and Skinner (1989) obtained a phenotypic correlation between variety means of -0.05 for 35 typical proven families. The true correlation for random experimental families is probably low but negative. The corresponding correlations in the present project range from 0.096 to 0.553, and three of them are highly significant. The absence of a

significant negative environmental correlation in the present project, is noteworthy. A negative correlation could be expected because the energy fixed by a plant may be used for growth or stored as sugar. However, the use of the alternative pathways is probably restricted in Queensland where there is a fairly distinct separation between the growing and ripening periods.

3.114 Correlations involving visual NMG of the whole plot.

Visual net merit grade of the whole plot is closely correlated with the yield characters TCH, TSH and NMGYOT. The correlations with CCS, TSH and NMGYOT increase when brix is included in the whole plot grade (NMGplot+BR, Table 21). The resulting phenotypic correlations with TSH and NMGYOT range from 0.82** to 0.85**, being similar in Bs and Ss seedlings in both crops. All have very low standard errors. These correlations are comparable to, but slightly higher than, those usually obtained at Meringa when weight of cane is estimated visually in three-row clonal plots. The genotypic correlations are higher than the phenotypic correlations, and approach 1.0. The estimates for Bs seedlings range from 1.0** to 1.1**. Those for Ss seedlings range from 0.88** to 0.92**. The environmental correlations are much lower, ranging from 0.22 to 0.57**. Because of the high genotypic and phenotypic correlations, visual net merit grade of the whole plot is promising. It must be seriously considered as a lower cost alternative to harvest characters such as NMGYOT, for family selection in Bs and Ss seedlings.

3.115 Correlations between mean and variance.

There are significant correlations between mean and variance (Table 22, first four items). These correlations are positive for visual NMG and

number of stalks, but negative for brix. For means, CCS was used instead of brix. In this Ts trial, a linear regression equation was used to predict CCS from brix, so it has exactly the same correlations. However, brix was the character measured in the field.

Genotypic, phenotypic and environmental correlations are all negative for brix. They are more marked in the P than in the R crop. However, the phenotypic and environmental correlations are highly significant in both crops. Negative correlations between mean and variance for brix have a physiological basis. There is some evidence indicating that effective selection over a long period raised sugar content to such a high level that it is approaching a physiological limit. This would reduce the variance of families high in sugar content.

The genotypic correlations between mean and variance are high, and highly significant, for visual NMG and number of stalks. Phenotypic and environmental correlations are also highly significant. Correlations are presented only for the R crop because of a lack of a significant variance component in the P seedling crop. The reason for the positive correlations between mean and variance for visual NMG and number of stalks is not known. However, it is beneficial for selection. Whether selection of families is based on means or selection rate, the positive correlations make it easier to select families high in both mean and variance. Such families are best for producing superior clones. The correlations make it easier to use means for family selection, ignoring variances. They may help explain why the use of selection rate, and the proven cross system based on it, has been so successful.

Berding and Skinner (1989) also obtained highly significant positive correlations between mean and variance for visual NMG and number of stalks, and highly significant negative correlations for brix. It is concluded that

these correlations are a normal feature of seedling populations.

3.116 Correlations involving number of selections in single seedlings.

Correlations between number of selections and NMGYOT (the main selection character for family means) are highest with SEL7, lower with SEL8, and lowest with SEL10 (Table 22). The genotypic correlations for SEL10 are not satisfactory in the P crop, having very high standard errors. For the phenotypic correlation, SEL10 << SEL8 in the P crop. For the R crop only, SEL7 >> SEL8. For SEL8, P >> R. The results clearly favour liberal selection (SEL7) in seedlings, especially in R crops. However, the standard selection rate (SEL8) is about equal to SEL7 in the P crop.

For the phenotypic correlation between SEL8 and number of stalks, P > R. For SEL8 vs weight per stalk, P >> R. Despite some significant differences, correlations involving SEL8 are fairly similar to corresponding correlations for TSH and NMGYOT (Tables 21 and 22). This indicates that the grading system has a sound basis.

SEL8 and visual NMG of the whole plot, including brix, show similar genotypic and phenotypic correlations with NMGYOT (Tables 21 and 22). These correlations are all high, ranging from 0.76** to 0.92**, and correlations for SEL8 and visual NMG of the whole plot do not differ significantly from one another. Thus, if NMGYOT is regarded as the best measure of the value of families, SEL8 and NMGplot+BR are about equal. If SEL8 is regarded as the best measure, NMGYOT and NMGplot+BR are about equal, showing very similar genotypic and phenotypic correlations.

3.12 Competition analysis in the seedling trial.

Competition analysis for number of stalks shows no sign of lateral competition between families in either crop of the Ts trial (Table 23).

The standard measure of competition (A+C-2B) has no significant F values. They are about 1.0. Separate analysis of each row gives no indication of competition (Table 23). Indeed, the F values are higher in the middle than in the border rows in both crops. This appears to be due at least partly to lower error variance in the middle row. The CV is two per cent lower in the middle row than in either of the border rows.

Competition is expected to inflate error variance as well as genotypic variance. Inflation of genotypic variance is often observed. Inflation of the error variance is usually small (Skinner, 1961). Competition may be responsible for the larger error variance in the border rows.

Correlations between rows give little or no indication of competition (Table 24). The phenotypic correlation for variety means, A vs C, is slightly lower than the other correlations in the P crop. It is slightly higher in the R crop. All genotypic correlations are close to 1.0 and, for genotypic correlations, have low standard errors. This again indicates no competition between families in either crop of the Ss seedlings.

Environmental correlations are not significantly different from zero, but all are slightly negative. Without competition, positive correlations are expected between adjoining rows. The results may indicate some environmental competition effects, but there is not enough evidence for a definite conclusion.

Number of stalks is a reliable character with high F values, even on a single row basis. The conclusion that competition was negligible for this character, is considered reliable. Skinner (1961) found a close correlation between competition measured by number of stalks and competition measured by weight of cane in clonal material. It is not certain that this applies in seedlings. Weight of cane could not be analyzed in the Ts trial.

3.2 Evaluation trial

Variance ratios are lower in the Te trial than in the Ts trial. However, they are still significant or highly significant for most characters. When Re, Be and Se types of a family are regarded as different treatments (Table 25) variance ratios are highly significant for all harvest characters.

3.21 Interaction of families and types with crops.

There are large differences between years, and family x years interactions are significant or highly significant for some characters. This is shown by separate analyses of the Re (Table 26), Be (Table 27), and Se (Table 28) types.

SEL7 and SEL8 show a significant cross x years interaction in Re and Be types, but not in the Se type. By contrast, SEL10 show a significant cross x years interaction in Se, but not in Re or Be. The interaction for visual NMG is stronger in Re and Be, than in Se. More liberal selection is expected to give results which correspond more closely to results for means. Tonnes sugar per hectare and KG/STALK show significant interactions in Se, but not in Re or Be. The reason for the differences between the interaction for Se, compared with Re and Be, is not known. All types show significant interactions for stalks and brix, and NMG variance.

For most characters, a combined analysis (Table 29) shows no significant interaction of years x types, or years x crosses x types. These interactions are significant only for hardness and NMG variance (years x types) and for NMG variance for years x crosses x types. Crosses x years interactions are much more important, being highly significant for several important characters. These included tonnes sugar per hectare, all selection rates, visual NMG, as well as brix, stalks and weight per stalk.

There is a fairly close correlation between CCS and brix, if both are measured at the same time. However there is no crosses x years interaction for CCS, despite a highly significant interaction for brix. Brix and CCS were both measured in early October in the P crop (Table 2). In the R crop, brix was measured at the time of selection early in August, before the cane was completely mature. CCS was measured at the time of harvest almost three months later. The cane was probably at about the peak of maturity at the time of harvest. Genetic variance for sugar content declines as maturity approaches, differences between clones and families being higher in less mature cane. This aspect probably explains the large interaction between families and crops (years) for brix and the lack of interaction for CCS.

The families x years interaction is not significant for NMGYOT, but it is highly significant for visual NMG. In both cases, the clones were compared with commercial varieties. However, clones were compared with a single variety (Q113) for visual NMG. They were compared with the mean of 3 varieties (Q82, Q90, Q113) for NMGYOT. Q113 performed poorly in the P crop. The NMGYOT for Q113 increased from 8.13 in the P crop to 12.26 in the R crop. Multiple standard varieties were introduced for weighed trials several years ago, to produce a more stable standard. The present experiment gives a good illustration of their value. Visual NMG is necessarily obtained using one standard variety. The use of a standard is designed to adjust for environmental variation and interactions. However, if the standard shows a marked variation or interaction, it can increase rather than reduce variation and interactions for new clones. Since the families x years interaction was highly significant for TSH and not for NMGYOT (Table 29), the multiple standards were effective in eliminating the interaction. The single standard (Q113) used for visual NMG was not effective for this purpose.

Because of the lack of interactions involving types, for most characters, the combined analysis gives larger variance ratios for families, compared with analyses for each type separately.

3.22 Family x types interaction.

There is no families x types interaction for the main characters in the Te trial. It is significant only for hardness variance (Table 29).

When each crop is analyzed separately, there are no significant family x types (Re, Be, Se) interactions in the P, R, PR or (R-P)/2 crops (Tables 30, 31, 32, 33). Selections from Bs or Ss seedlings give a ranking of families similar to that from random seedlings. However, a later analysis (#3.634) shows that important interactions were present, but were not detected by the analysis of variance.

3.23 Effect of modified mass selection in Bunch and Single seedlings

For the important characters, there are highly significant differences between types, in P, R and PR crops of the Te trial (Tables 30, 31, 32). For number of selections from the Te trial, there are significant or highly significant differences between types with the normal truncation point (SEL8) and with liberal selection (SEL7), but not with severe selection (SEL10).

Performance of Re, Be and Se types in the Te trial, provides an estimate of realized gains from modified mass selection in the Ts trial. For example, realized gains from selection in Bs seedlings are estimated by the difference (Be - Re). Realized gains estimated in the P, R and PR crops of the Te trial are shown in Tables 34, 35, and 36.

There are worthwhile and highly significant gains from mass selection in the Ts trial. In Ss seedlings, the realized gain for NMGYOT is about ten

per cent, with a gain of about 25 per cent for selection rate (SEL8). Liberal selection gives satisfactory gains, but severe selection (SEL 10) does not give a significant gain in any crop. The results favour normal or more liberal selection. They do not favour severe selection. A square root transformation ($\sqrt{X+0.5}$) was included in the analysis of selection rates, because of the small numbers involved. However, it is appropriate to use actual rather than transformed data when comparing relative gains. The gain in visual NMG from selection in Ss seedlings is about 8 per cent. The P and R crops give fairly consistent estimates, the gain from selection in Ss seedlings being 9.3**, 11.9** for NMGYOT and 25.6*, 22.9* for number of selections (SEL8).

Bs and Ss seedlings differ in selection efficiency (Table 37). Before the experiment was conducted, mass selection was expected to be much more effective in Ss than Bs seedlings. Each Ss seedling produces several stalks. Only one stalk is available for selection of each Bs seedling. Thus selection for weight of cane can only be based on weight per stalk in Bs seedlings. In Ss seedlings, weight per stalk and number of stalks are both available for selection. No selection for brix was made in Bs seedlings. In Ss seedlings, brix of each seedling was measured during selection. Thus Ss seedlings were expected to have the advantage of gains in sugar content, combined with additional gains due to selection of number of stalks per stool. This was expected to make gains in tonnes sugar per hectare, NMGYOT and number of selections, much higher when selection was made in Ss than in Bs seedlings.

In the experiment, selection in Ss seedlings did produce highly significant improvements in sugar content in all crops of the Te trial. It is considered that sugar content approaches a physiological limit, because of previous effective selection. This limits genetic variation, and the

gains which can be made from selection. The gain in sugar content is only about three per cent (Se - Re, Table 36). Selection in Ss seedlings gave a gain of about 5.5 per cent in tonnes cane per hectare. The gain in tonnes sugar per hectare, resulting from gains in tonnes cane and sugar content, is about 8.5 per cent.

Selection for weight of cane was expected to be less effective in Bs than in Ss seedlings. In fact, selection in Bs seedlings gave a gain of about 12.5 per cent in tonnes cane (Be - Re, Table 36), more than twice the gain in Ss seedlings, with $Be \gg Se$. This gives $Be > Se$ for tonnes sugar per hectare for the PR crop, and $Be \geq Se$ for NMGYOT and number of selections.

Number of stalks and weight per stalk are components of tonnes cane. Selection in Ss seedlings gave improvements of only about 1.5 per cent in number of stalks and 3.5 per cent in weight per stalk (Table 36). These improvements are not significant in either crop.

By contrast, selection in Bs seedlings gave a large improvement in weight per stalk (about 14 per cent**, Table 36). It gave a slight (1.5 per cent) reduction in number of stalks. This is not significant, and does not counteract the benefits from increased weight per stalk.

In Ss seedlings, the correlations with CCS are slightly lower for SEL8 than for NMGYOT, although the difference is not significant (Tables 21 and 22). NMGYOT gives the best available economic weight to sugar content. The emphasis given to sugar content when allotting visual NMG is not too high, on this economic basis. However, as discussed below (#3.3321), $TCH \gg NMGYOT$ in Ss seedlings, when correlated with important characters in the TePR trial. Thus the value of sugar content for both mass and family selection may be much lower than its economic value. This may occur because of the low genotypic variance for sugar content.

Modified mass selection gave a highly significant but small gain in

sugar content (3%**, Se - Re, Table 36). The emphasis given to sugar content may be too strong. It may have reduced the selection differential and hence the gain for weight of cane.

Earlier research (Anon, 1968) indicated that sugar content was very important for seedling selection. Since that time, the proven cross system has improved the average sugar content of seedling populations. The value of sugar content as a seedling selection character has probably declined. Too much emphasis on any character except NMG is expected to be harmful.

The present strong emphasis on sugar content in Ss seedlings may be harmful. The results indicate this, but do not give a clear conclusion. There may be some other undetected explanation for the highly significant inferiority of the Se to the Be type for weight of cane. The question of whether or not to measure brix of Ss seedlings is important. Use of brix is expensive, and may be harmful. It would become more expensive with more liberal selection. BSES must do more research to answer this question.

The above discussion has concentrated on gains from modified mass selection in Bs and Ss seedlings, estimated from separate analysis of each crop. Gains estimated from the combined analysis for families, types and crops are shown in Table 38, which corresponds to the variance ratios shown in Table 29. For harvest characters, including KG/STALK, the results are similar to those based on the analysis of PR, Table 36. For all other (selection) characters, the results differ to some extent. In Table 36, the means for PR were obtained for each clone, which occupied a 4-sett subplot. In the combined analysis (Tables 29 and 38) the means are the average of the whole plot values for the P and R crops. This produces different results for selection numbers and within-plot variances. However, the gains for the combined analysis are similar to the summary given for PR, Se - Be, in Table 37, except that the value for SEL8 is -2.8 instead of -2.3 per

cent.

3.231 Evaluation of modified mass selection using the middle row.

Gains from modified mass selection are smaller when they are evaluated using the middle row, instead of the whole plot in the Te trial (Table 39). The reduction occurs in both Bs and Ss seedlings. It is more serious in Ss seedlings. In 3-row plots there is a gain of about 5.5 per cent** for TCH in 3-row plots, compared with 1.4 per cent (not significant) when the middle row is used for evaluation (Se - Re, PR crop, Table 39).

Estimated gains from selection in Bs seedlings fall only by two per cent (from 12.5** to 10.4** per cent). The superiority of Be over Se increases from 7 per cent** in 3-row plots to 9 per cent** with evaluation using the middle row.

The middle row of a 3-row plot is guarded from lateral competition. The results in Table 39 provide a definite indication that gains from modified mass selection are over-estimated when three-row plots are used for evaluation. The border rows (rows A or C) of the 3-row plots gained from competition. This effect is more serious for Ss seedlings. This was not expected because the much closer spacing between seedlings would give much more intense competition in the bunch nursery. However a different type of competition may be involved. Ss seedlings are more typical of commercial crops so selected Ss seedlings may compete well in commercial plantings. This explanation involves the assumption that type of competition is much more important than the intensity of competition in Bs and Ss seedlings.

The results in Table 39 show that the excellent results from modified mass selection in Bs seedlings are not due to competition effects. The gain, Be>>Re and Be>>Se occurs with evaluation in the middle row, as well as in the whole 3-row plot.

These results strongly favour bunch planting. However, a later analysis (#3.6) showed that the value of modified mass selection and bunch planting was much less than the estimates given by mean values in this section.

3.24 Reduction of genetic variance during selection.

Within family variance for Brix was reduced by selection in Ss seedlings, and NMG variance was reduced by selection in both Ss and Bs seedlings. The reductions are significant or highly significant in the R and PR crops (Tables 35 and 36). Only log variances are significant in the P crop (Table 34). Families in this crop do not differ significantly in variance. These results are for phenotypic values, but the variance component is genotypic.

Successful selection is accompanied by a reduction in genetic variance. The reductions in variance show a partial correspondence with the effectiveness of selection. However, brix variance is reduced by selection in Bs seedlings. No selection was made for brix in Bs seedlings, and there was no response. The effect is only significant for log brix variance and only in the P crop (Table 34), but the results are consistent enough to indicate a real effect. If so, it represents a correlated response to selection.

In the R crop, brix variance was reduced ($P < 0.01$) by selection of Ss seedlings (Table 35). This occurred even though the families did not differ significantly in brix variance (Table 31).

Within-plot variances show considerable environmental variation, and are sometimes not significant for families. However, reduction in variance due to successful selection is shown in the experiment. This may be an important aspect of selection. Modified mass selection within families reduced variance within families. Selection of better families using the

proven cross system, is expected to reduce genetic variance among families. Too much reduction in variance will inhibit gains from selection.

Superficially, reduction of variance due to selection may not seem important, because the reduction is due to the discard of inferior clones or families. This theory is faulty. Two aspects are involved, selection of clones for use as commercial varieties and their selection as parents.

For selection of clones, the highest average gains from one stage of selection in original seedlings are usually obtained by very severe selection. However, this does not result in maximum production of commercial varieties. The performance of a clone is partly due to its genetic value and partly to an environmental component. In original seedlings the environmental component influences about 80 per cent of the performance (Skinner *et al*, 1987). The reduction in genetic variance due to selection is accompanied by rejection of many clones with high genetic values and negative environmental effects. With severe selection, some of these discarded clones are likely to be superior commercially to those selected.

Some of the selected clones are also selected as parents. In addition to environmental effects, their value as parents is strongly influenced by transgressive segregation (Skinner, 1981) and heterosis. Phenotypic value, on which selection of clones must be based, gives a poor estimate of breeding value. When genetic variance is reduced by selection, the best parents are likely to be in the discarded group. This happens despite the general tendency for selection to produce superior parents. It occurs because the number of clones is very much higher in the discarded than in the selected group. Selection is not efficient enough to detect many of the superior clones.

Up to the present, BSES has depended on the use of many crosses, combined with extensive use of foreign parent varieties, to maintain

genetic variance. However, even world-wide genetic variance is limited. It is desirable for BSES to increase genetic variation deliberately, to counter the automatic erosion of genetic variation caused by effective selection. More systematic use of the wild cane program is the most promising avenue.

3.25 Selection levels.

F values and means for split-plot analysis of variance, with families as main plots and selection levels as subplots, are presented in Tables 40, 41 and 42 for the P, R and PR crops of the Te trial. These tables also include F values for RCB analysis at each level. Differences between levels, and their statistical significance in the split-plot analysis, are presented in Tables 43, 44 and 45 for the P, R, and PR crops. A summary for characters showing significant differences between types is given in Table 46.

Cross x levels interactions are not significant for any character in the P or R crops. They are significant only for hardness in the PR crop. There are significant differences between families for most characters, and between levels for a few characters. There is little or no tendency for some families to be more successful than others with liberal or severe modified mass selection.

For Be, there are highly significant differences between levels for weight per stalk in all crops (Tables 40, 41 and 42). This was the character selected most effectively in Bs seedlings. In most populations, there is a negative correlation between number of stalks and weight per stalk. This correlation did not have much effect on whole plots. Selection increased weight per stalk by 14 per cent, and the negative correlation reduced number of stalks by only 1.5 per cent (Table 36). However, the

negative correlation had more effect when selection levels were considered. Weight per stalk is highest at L1 and lowest at L2, in all crops (Be, Tables 43, 44, 45). $L1 \gg L2$ in all crops (Table 46), $L1 > L3$ in the P and PR crops, and $L2 < L3$ in the R crop. The low weight per stalk for L2 was probably produced by the negative correlation between number of stalks and weight per stalk. The number of stalks is highest in L2 and lowest in L1, with $L2 > L1$ in the R and PR crops, and $L1 \leq L3$ in both crops. Clones with very large stalks (L1) probably lack the capacity to produce many stalks. The intermediate group (L2) was more adaptable. This does not explain why L3 has larger stalks than L2. The smaller stalks did not reduce the yield of L2. For TCH, $L1 \geq L2 \geq L3$. All three levels have larger stalks and more tonnes cane per hectare than selections from Ss seedlings. However, no test of significance was applied to this difference in this group of tables.

In the Se type, more characters show significant differences between levels. All significant differences are in the order expected from effective selection, $L1 > L2 > L3$ for means and $L1 < L2 < L3$ for within family variances. Visual NMG (and SQRNMG) are the only characters showing significant differences in both crops (L1-L3, Table 46). For brix, $L1 \gg L3$ in the P and PR crops. The effective within-plot selection for brix was accompanied by large reductions in within-family variance, with $L1 \ll L3$ and $L1 < L2$ in the R and PR crops. As discussed above, effective selection is accompanied by reductions in genetic variance. The results for levels show that this reduction becomes more serious as selection becomes more severe.

Although significant differences have been emphasized, most characters do not show significant differences between levels. Lack of significance is partly due to environmental variation. The results for each level are based on single-row plots which are too small to give accurate results. However, if selection is made more severely, after an optimum level is reached, less

response is expected.

The variance ratios for RCB analysis (Tables 40, 41, 42) show changes in discrimination between families with different levels of selection. Although the pattern is not clear or consistent, there is some tendency for better discrimination at L3. This level contains normal selections from good families, but normal selections are confined to L1 in poor families.

Variance ratios for split-plot analysis of variance, with 24 families x 2 types (Be, Se) as a factorial on the main plots and levels as subplots, are shown in Tables 47 and 48 for the P and R crops. Table 49 shows similar F values for PR and $(R-P)/2$. Means for both types are also shown in these tables for each level.

Interactions of cross x level and cross x type x level are not significant for any character in any crop. Type x level interactions are significant for brix in all crops, but are not significant for any other character in any crop. Interactions for cross x type are significant only for Visual NMG and hardness variance in the P crop, brix and hardness variance in the R crop, and only for hardness variance in the PR crop.

3.26 Correlations in the evaluation trial.

Phenotypic correlations based on family means are presented for the Re, Be and Se types in Tables 50 (TeP), 51 (TeR), and 52 (TePR). Similar correlations are presented for all crops of each type separately in Tables 53 (Re), 54 (Be) and 55 (Se). Correlations for each crop of each type are shown for harvest characters in Table 56. Correlations for the mean over all three types are in Table 57. Correlations based on plot values are shown for all types in Table 58.

Genotypic, phenotypic and environmental correlations for the Re type are shown in Table 59. Similar correlations between mean and variance are

given in Table 60, for Re, Be, and Se types. These correlations are for means of 24 families. Correlations for family means for all three types (Re+Be+Se, 72 treatments) are also included in this table. Correlations for the three types, and Re+Be+Se, are compared in Table 61. Correlations between P and R crops are given for each character in Table 62.

3.261 Correlations between mean and variance in the evaluation trial.

F values for within-family variances are positive but not significant for several characters. This occurs for stalks variance for the Be type in the R and PR crops (Tables 31, 32, 60). Despite this, this character shows a positive ($P < 0.01$) phenotypic correlation between mean and variance in these crops, although the genotypic correlation is not significant (Table 60). The phenotypic correlation is positive ($P < 0.01$) for visual NMG in the R crop, for all three types. The genotypic correlation is significant for the Re type. The phenotypic correlations are highly significant for the Re and Be types. However, the F values are not significant for within family variance for these types in the R crop. The results indicate that analysis of variance may not be very effective in detecting real differences in within-family variance.

Brix shows negative correlations between mean and variance. Phenotypic and environmental correlations are significant or highly significant in all cases in which they could be computed. All genotypic correlations are negative but had large standard errors, and are not significant.

Hardness shows positive correlations between mean and variance. Phenotypic correlations are highly significant in the P crop, and in some cases in R. Genotypic correlations are highly significant for the Re and Be types, and for Re+Be+Se, in the P crop. Environmental correlations are low for hardness, and in most cases are not significant.

As in the Ts trial (#3.115, Table 22), there are significant or highly significant correlations between mean and variance for number of stalks, visual NMG, and brix. In both trials the correlations are positive for visual NMG and number of stalks, and negative for brix. The Te trial results indicate that these correlations are normal for clonally reproduced material as well as for seedlings. However the correlations for visual NMG and number of stalks are lower in the clonal material. This may be due to the small number of significant within-family variances. However, it leaves open the possibility that the within-family variances which have been measured are mainly due to competition between clones within each family. The Te trial used larger plots (4-plant versus single plant) for each clone. The correlations between mean and variance may disappear, or may be significant but different, if large plots were used for each clone. Experiments to test this hypothesis would be expensive. The present results leave doubts about the correlations in clonal trials using larger plots. However, a factor other than competition may be responsible. The number of clones per family in the Te trial (27) may be too small to give a reliable estimate of within-family variance. This would account for the lower correlations and the small number of significant differences.

3.262 Correlations between Plant vs Ratoon crops in the evaluation trial.

Genotypic correlations between P and R crops, for the same character (Table 62) are expected to be biased (increased in a positive direction) by common environmental effects in P and R crops of the same plot. However, comparisons can be made between different characters.

Genotypic correlations are high ($P < 0.01$) for harvest characters. CCS of the Re type was an exception, the correlation not being significant because of the high standard error in the R crop. Other correlations for CCS, and

all correlations for fibre, are close to 1.0.

Selection characters show a wide variation in the genotypic correlations. The correlations are fairly high ($P < 0.01$) for stalks and hardness. Correlations are significant for brix only in Se seedlings, for visual NMG of Re and Se types, for SEL7 in the Se type, and SEL10 in the Be type (Table 62). None of the genetic correlations between P and R crops are significant for the normal selection rate (SEL8). In the Re type the genotypic, phenotypic and environmental correlations for SEL8 are approximately zero. This shows a very large interaction with crops or years for this character.

3.263 Correlations in the random type.

Correlations involving CCS have very large standard errors in the R crop of the Re type (Table 59). This does not happen in the P crop for this type, or for the Be and Se types in either crop. Nor does it happen for brix in the R crop of the Re type.

The environmental correlation for KG/STALK vs STALKS is negative ($P < 0.01$) in the P crop and zero in the R crop of the Re type (Table 59). The phenotypic correlation is stronger (more negative) in the P than in the R crop. In the Ts trial, environmental correlations are about zero in both crops (Ss seedlings, Table 21). As expected, genotypic and phenotypic correlations are negative in the Te trial.

The environmental correlations between number of stalks and NMGYOT are fairly similar in all crops (Table 59). For the phenotypic correlation R >> P. Although the genotypic effect is not significant, the highly significant phenotypic difference has a genetic basis. The environmental correlations are similar in both crops. The genotypic and phenotypic correlations for stalknumber, PR crop, are much higher with NMGYOT, R crop than with

NMGYOT, P crop. In this comparison, the genotypic difference is significant, and the phenotypic difference is highly significant.

Correlations between number of selections (SEL8) and NMGYOT are fairly similar in P and R crops (Table 59). This is unexpected because there are moderately high ($P < 0.01$) correlations between P and R crops for NMGYOT, but a zero correlation for SEL8. There is a fairly close correlation between visual NMG and SEL8 in both crops. However, the correlation between P and R crops is higher for visual NMG than SEL8. The genotypic correlation between P and R crops is about zero for brix, and the phenotypic correlation is highly significant but low (0.206 ± 0.067 , Table 59). By contrast, the phenotypic correlation between crops for CCS is quite high (0.85^{**}). The contrast between SEL8 and NMGYOT, may be partly due to the different behaviour of brix and CCS over the two crops. However, the marked interaction between the standard commercial variety with the two years (crops) is probably a more important factor.

SEL8 is based on visual NMG, but they differ in behaviour over the two crops. This is probably due to differences in within family variances in the two crops. In the Re type, within family variance for visual NMG has a negative genotypic estimate in the P crop (Table 30). The estimate is positive but not significant in the R crop (RCB, Re, Table 31). Despite this, variance for visual NMG has a fairly high genotypic correlation with its mean (0.8^* , Re type, R crop, Table 60), and a highly significant phenotypic correlation. There is a clear difference between the behaviour of the mean (visual NMG) and the variance over the two crops.

3.264 Factorial analysis of phenotypic correlations.

Factorial AOV of the correlations for family means in the Te trial (Tables 50 and 51), is summarized in Table 63. There were 15 replicates,

consisting of five harvest characters (Fibre, TCH, CCS, TSH, NMGYOT) for the three types. The means thus show average correlations (expressed as Z values), over several characters.

There are no significant differences between the Re, Be and Se types. The characters x types interaction is not significant. The type x crops interaction is not significant. However, a highly significant interaction is present but was not detected. Separate factorial analyses for each type shows differences ($P < 0.01$) between crops for the Re and Se types. However, there is no sign of such a significant difference for the Be type.

Error mean squares are fairly high, CV being about 75 per cent. This indicates there are large interactions between the treatments and the harvest characters used as replicates. This is to be expected, because the selection characters used as treatments show a highly significant interaction with crops. Despite the variation, the analysis gives highly significant differences. It was conducted because it was suspected there were differences between the Re, Be and Se types. No conclusion could be drawn by inspecting the correlations. The analysis gives a clear conclusion that these types have similar average correlations.

Average correlations are higher ($P < 0.01$) in the R crop. There is a highly significant characters x crops interaction. SEL10 and STALKS have significantly higher correlations in the R crop. Weight per stalk has higher ($P < 0.01$) correlations in the P crop.

3.27 Competition analysis for the evaluation trial.

3.271 RCB analysis for weight of cane.

No competition between families was detected in the Te trial by normal competition analysis for weight of cane (Table 64). There are no significant F values for A+C-2B, the highest F value being 1.1. Separate

analysis of each row did not detect competition. For separate analysis of the Re, Be and Se types ($n = 24$) there are three highly significant F values in row A, three significant in the middle row, and three significant in row C. For the Re type, the only significant difference is in a border row (C), but the F values for row B are about intermediate between A and C. For Re + Be + Se (72 treatments) the only F value which is not significant is for a border row (C, 1.3, Table 64).

In the Be and Se types, three selection levels were allotted at random to rows A, B, and C. The random allotment would avoid bias in the means for each row, but the treatment effects might increase the error variance. This did not occur. There is no tendency for the CV to be higher in the Be and Se compared with the Re type (Table 64). In the middle row, protected from lateral competition, the CV is highest in the Re type in all crops. However, the difference is too small to be significant.

The single-row plots (rows A, B and C, Table 64) were too small to be effective. Only one-third (9/27) of the F values for Re, Be and Se are significant. CV ranges from 17 to 26 per cent, most (15/27) of them being higher than 20 per cent. With 3-row plots, CV ranges from 11 to 16 per cent. All of the F values are significant, 7/9 being highly significant. With 72 treatments, 8/9 of the F values for single rows are highly significant. However, none of them is above 2.0. All three are 3.0 or higher in 3-row plots. There are real differences between families. Single-row plots often do not detect these differences, because of excessive environmental variation.

If results such as those in Table 64 had come from larger 4-row instead of 3-row plots, they would provide a definite conclusion that competition was absent or negligible in both crops of the Te trial. The two middle rows of the 4-row plots would have provided a more reliable basis for estimating

competition. For rows A+C, 10/12 F values were significant or highly significant. Since there was no competition, this result shows that the two middle rows of a 4-row plot would be reliable. They could be used to estimate correlations and realized gains from selection, if competition was detected in the border rows. The middle row of the 3-row plot used in the Te trial, is not reliable enough for this purpose.

The poor reliability of all single-row plots casts some doubt on the reliability of the competition analysis. Instead of providing a definite conclusion that competition was negligible in the Te trial, only a tentative conclusion can be drawn. However, the competition analysis does strongly indicate that competition was not important in either crop of the trial.

3.2711 RCB analysis for number of stalks and weight per stalk.

Competition analysis was also conducted for number of stalks per row (Table 65) and weight per stalk (Table 66). As occurred for weight of cane, no competition between families was detected for number of stalks or weight per stalk.

For number of stalks, the Te trial (Table 65) is much more variable than the Ts trial (Table 23). For single rows, CVs range from 9 to 12 in the Ts trial compared with 15 to 24 per cent in the Te trial. F values in the Ts trial range from 4.7** to 9.4**, compared with 1.0 to 3.9** in the Te trial. All 9 values are highly significant in the Ts trial. By contrast, 7 of the 9 values in the Re type are not significant. The lower F values in the random type are probably due to the larger amount of environmental variation, not to a change in genetic variation. The same families are in both trials. The variation shown in the Te trial is fairly typical, the seedling trial being less variable than usual.

3.272 Factorial analysis of competition shown by weight of cane.

The standard competition analysis showed no competition in the Te trial. However, a factorial analysis, with types and families as factors, does give a clear indication of competition (Table 67). The single row plots (rows A, B, or C) were too small to give reliable results for RCB analysis (Table 64) but they give significant or highly significant results for the two factors in all rows in both crops. For types, F values range from 3.9* to 9.3**. Means for types are each based on 24 families (72 plots), so are expected to be fairly reliable. F values for families range from 1.8* to 4.0**, fairly similar to those for 3-row plots with RCB analysis (Table 64). There are no significant families x types interactions, so the single rows averaged over the three types are about as accurate as a 3-row plot for one type.

In each crop, and in the average of both crops, the middle row (B, Table 67) gives highly significant differences. Be is superior to both Re and Se. That is, the superiority of the Be type is real, and not due to competition. In the middle row, the Se type does not differ significantly from the Re type, and is only one or two per cent better than it.

Means expressed as per cent of the Re type (Table 67) show that the border rows (A or C) give inflated estimates for both the Be and Se types. The inflation is higher in the Se than the Be type. Rows A+C show a similar effect. There is a moderate effect on the standard 3-row plot (A+B+C).

There is little doubt that this inflation of values in the border rows is due to competition. The gain is at the expense of the Re type. Se gains more than Be from this competition. Thus the superiority ($P < 0.01$) of Be over Se (middle row) disappears in the border rows in all cases, except the R crop of row C (Table 67). Se is only about one per cent above Re (not significant) in the middle row. It becomes higher ($P < 0.05$) than Re in the

border rows for the average of both crops, and for the P crop of row C. $Se > Re$ in all crops, for A+C and A+B+C. Thus there is a clear indication of competition in all plots with border rows, including the standard plot (A+B+C).

The per cent figures in Table 67 demonstrate the presence of competition. However, they over-estimate the amount of competition. They are calculated as per cent of the Re type for each row. The mean values for the Re type are reduced by competition in the border rows. For the R and the PR crop, the mean for the Re type is lower in the border rows than in the middle row. The reduction over both crops is about 2.5 per cent, when calculated by expressing each row as per cent of the general mean.

Despite the small plot size, the middle row provides the best estimate of true yield free from competition. The estimates of gain from modified mass selection are 10 per cent for selection in Bs seedlings, and about one per cent for selection in Ss seedlings. The estimate for Ss seedlings is surprisingly low. It is probably too low, but it is the best estimate provided by the project. Gains from modified mass selection are clearly and significantly higher in Bs than in Ss seedlings.

The demonstration of competition effects in Ss seedlings has important implications. The competition effect occurs because clones in the border rows gain from competition, mainly at the expense of the Re type. Each border row is subject to only half the lateral competition which would occur in a single-row plot. Short single-row plots would also suffer considerable end competition. Thus, when selected Ss seedlings are planted in single-row plots, together with random clones as controls, strong competition is likely. This procedure was followed in the T_m trial in this project, and it has been done in other experiments. Because of competition, the method is likely to give inflated estimates of realized gains from mass

selection, and inflated estimates of broad sense heritabilities.

No competition was detected by the normal RCB competition analysis (Table 64). It was detected by the factorial analysis (Table 67). Lateral competition measured by the difference between the middle and border rows of each plot (A+C-2B) gives no significant differences in either analysis. There is no significant difference between types for this measure (Table 67). Mean values for row B compared with rows A and C, and changes in significant differences between types when these rows are analyzed, show there were real differences between the types, due to competition. The measure A+C-2B is not sensitive enough to detect the amount of competition (about six per cent) which occurred. Although the factorial analysis shows a tendency for F values to be higher in the border rows (A or C) than in the middle row (R and PR crops, Table 67) it is not very marked. The main indication of competition in the factorial analysis is provided by the analysis of types. This method was not used in the RCB analysis, which deals mainly with behaviour of families within each type.

3.2721 Factorial analysis for stalks and weight per stalk.

Factorial analysis of competition shown by number of stalks (Table 68) shows no significant differences between types, and no indication of competition for this character. Factorial analysis for weight per stalk (Table 69) gives highly significant differences between types and families. As with weight of cane (#3.272) there are definite indications of competition between types, but no evidence of competition between families. For weight per stalk the competition effect is stronger (about 6 per cent) in Be than Se (about 4.5 per cent). The competition effects are stronger for weight per stalk than weight of cane. This is shown by inflation of the F ratios for types in rows A and C compared with row B.

Competition between types for weight of cane was due to competition effects on weight per stalk and not number of stalks per row. This differs from research by Skinner (1961). He found that competition between clones shown by weight of cane was due to number of stalks and not weight per stalk.

The Be type shows slightly more competition than Se for weight per stalk. It is reasonable to conclude that competition between clones was an important factor in both Bs and Ss seedlings. Modified mass selection involves the selection of clones which were above average in competitive ability, as well as true yielding ability.

3.273 Correlation between rows.

Although the RCB analysis (#3.271) gave no indication of competition, correlations between rows A, B and C indicate competition in the R crop in the Se type. The phenotypic correlation for means is higher ($P < 0.01$) for A vs C than for B vs A or B vs C (R crop, Se type, Table 70). Without competition, the correlations are expected to be higher with row B, because rows A and C are further apart in the field. The correlations give no indication of competition in the P crop of the Se type. Indeed, the correlation is higher ($P < 0.01$) for B vs C than for A vs C.

The single-row plots were too small to give reliable results for AOV (Table 64). As a result, estimates of genotypic correlations are of little value. Most have very high standard errors. This gives a marked contrast with a similar analysis for number of stalks in the Ts trial (Table 24). In that trial the genotypic correlations are close to 1.0, have low standard errors, and are all highly significant. Number of stalks per row in the Ts trial is much more reliable than weight of cane per row in the Te trial. In the Te trial, there are only two correlations with significant F values for

both X and Y (Table 70, Be type, row A vs row B, P and PR crops). In both cases, the genotypic correlation is highly significant.

Two of the genotypic correlations could not be computed for the Be type in the R crop, because of F values less than 1.0 for row C. However, for the P and PR crops in the Be type, the phenotypic correlation is higher for row A vs row C than for B vs A or B vs C. This indicates competition in the Be as well as the Se type. The difference between A vs C and B vs C is significant in the P crop, and highly significant for PR.

There is no tendency for the correlation A vs C to be higher than B vs A or B vs C in the Re type. The correlation A vs C was slightly (not significantly) lower in all crops, as expected without competition. The factorial analysis (Table 67) shows that the Se and Be types gained from competition at the expense of the Re type. Thus the Re type was affected by competition but the correlations indicate that this type did not show competition. This indicates that the competition effect on the Re type was passive and environmental. Because of this, three-row plots of the Re type are expected to give reliable evaluation of realized gains from family selection, and of correlations between family means. This is expected, despite some reduction in the general mean, and probably some increase in the error variance, due to competition effects from the Be and Se types.

In the Se type, most of the environmental correlations are not significant. However, there is a tendency for positive correlations between A vs C, and negative environmental correlations between B vs A and B vs C. The environmental correlation A vs C is higher ($P < 0.05$) than B vs C in the P and in the R crop (Table 70, Se type). This shows an environmental competition effect. Without competition, environmental correlations between B vs A and B vs C are expected to be positive, and higher than A vs C. Row B adjoins rows A and C in the field.

3.274 Competition effects, general.

There was no competition between families in Ss seedlings, so far as this can be measured by number of stalks (#3.12). However, the results discussed below show there was intense competition between clones. Berding and Skinner (1989) also found intense competition between Ss seedlings. It is an important factor in seedling selection. Selected clones owe their superior performance partly to true yield, but also partly to competitive ability.

The standard analysis of variance for competition gives no indication of competition between families in the Te trial. However, correlations between rows of the 3-row plots indicate that competition did occur in the Se type in the R and PR crops. It also gives some indication of competition in the Be type in all crops (Table 70, #3.273). This competition between families is a selection effect. It is associated with competition effects on the Be and Se types, generated by modified mass selection. Correlation between rows gave no indication of competition between unselected families (Re) in the Te trial.

A factorial analysis of variance, with types and families as factors (#3.272, Table 67) gives a clear indication of competition. The competition is expressed by differences between types, not by differences between families within types. It was produced by modified mass selection of individual seedlings, not by selection of families.

Competition in the Te trial inflated the estimated gains from modified mass selection in both Bs and Ss seedlings. This is shown by gains from modified mass selection estimated using the middle row instead of the whole 3-row plot in the Te trial (Table 39, #3.231). Gains are over-estimated more seriously when selection was made in Ss compared with Bs seedlings.

Middle row analysis indicates that gains in true yield from modified mass selection were negligible in Ss seedlings, the estimated gain being only about one per cent.

The middle row was not reliable enough to be used for the main evaluation work. The whole 3-row plot provides the best available basis for routine evaluation of the results. However, the estimates it provides for realized gains from modified mass selection, are inflated to some extent by competition. Gains from competition have been demonstrated for the Be and Se types. This automatically involves some loss from competition in the border rows and hence the whole plots of the Re type. Despite this, 3-row plots of the Re type are expected to provide satisfactory estimates of realized gains from family selection, and correlations between the Ts and Te trials.

Bias in estimated gains, due to competition, is likely to be much less for family than for mass selection.

3.3 Correlations between the seedling and evaluation trials.

Correlations between family means in the Ts and Te trials are given in Tables 71, 72, 73, 74 and 75.

3.31 Factorial AOV of correlations.

Factorial analysis of variance of the correlations in Tables 71, 72 and 73, with two crops (P, R) and four types (Re, Be, Se, and mean of the three types) in the Te trial as factors, is summarized in Table 76. RCB analyses of the correlations in Tables 74 and 75 are summarized in Table 77. Separate analyses were carried out for each character in the Te trial. The replicates were the characters in the Bs and Ss seedlings. The mean values for each crop and type thus show average correlations (expressed as Z values) over a wide range of characters.

Tables 76 and 77 were further condensed by using them as data files for paired t-tests (Table 78). TeR >> TeP crop, whether variances were included or omitted.

Correlations for the mean type and the Re type are about equal, and do not differ significantly in any comparison in Table 78. Re > Se > Be and Me >> (Be, Se) in all comparisons with variances omitted.

There are very few significant interactions between the Re, Be and Se types. The mean of the three types was expected to give a better estimate of the value of each family than that provided by any one type. Because of this, it was expected to give higher correlations with the Ts trial. The results in Table 78 show that this did not happen. The mean is no better than the Re type, on average. The estimate of family value provided by the Re type, cannot be improved by including the Be and Se types.

Correlations involving within-family variances differ from those for other characters. They should not be included with other characters when

average trends are being considered. This is obvious for brix variance which shows a negative correlation with brix mean, and negative correlations with other characters. Furthermore, families do not differ much for within-family variance in the Te trial, variance ratios often being not significant.

Omission of within-family variances (Table 78) gives higher correlations. It increases the difference between the Re, Be and Se types, and gives more highly significant differences. It is difficult to draw general conclusions about average correlations involving within-family variances. There are only a small number of characters in this group. Differences between families are fairly small. Variances tend to be correlated with means, and these correlations differ in sign. Brix shows negative correlations between mean and variance, and visual net merit grade shows a strong positive correlation between mean and variance in the Ts trial. For variances, the Be type had higher average correlations than the Re type (Tables 76 and 77). This is the opposite of the results shown by family means.

3.311 Interaction between crops and types in the evaluation trial.

Interactions between crops and types in the Te trial are highly significant for most characters (Table 76). The only characters not showing significant interactions are TCH, TSH, SEL7, SEL8 (TsR and TsPR crops only), and Brix. Interactions are highly significant for CCS, but not for brix. In the Te trial, normal analysis of variance gives no families x years interaction for CCS, despite a highly significant interaction for brix (#3.21, above). This appears to contradict the present result, but confirms that brix and CCS show different interactions with crops in the Te trial. This is probably related to differences between the time of

selection and harvest.

For correlations (Table 76) the interaction for CCS is shown mainly by higher correlations in the P crop for Re and in the R crop for Se. ReP >> SeP but SeR >> ReR.

The interactions are different for different characters. That is, there are interactions between characters, crops and types in the Te trial. For crops, tonnes cane and tonnes sugar do not differ significantly. For NMGYOT, P > R. For most selection characters, including selection rate and visual NMG, R >> P. In this case, CCS is a fairly typical harvest character, with P ≥ R. Although brix and CCS estimate the same property, brix behaved as a typical selection character, with R >> P.

For most characters, differences between the Re, Be and Se types do not show marked changes in significance when P and R crops are compared. However, for some characters they change enough to produce highly significant interactions. For visual net merit grade Be << (Re, Se) in the P crop, but there are no significant differences in R. The interaction for NMGYOT is different from that for visual NMG. For NMGYOT, BeP >> BeR, but this does not occur for Re or Se.

Interactions for normal selections (SEL8) are significant only for the TsP crop. In that crop, Se >> (Re, Be) in the TeP but not in the TeR crop. For Re and Be, TeR >> TeP, but this effect is not significant for Se.

3.312 Seedling crops.

For most characters (12 out of 15, general mean, Table 76) correlations are higher in the TsR than the TsP crop. This does not occur for CCS, fibre, or brix. Furthermore, for the main characters (TSH, NMGYOT, SEL8) in the Re type, correlations are about equal in the TsP and TsR crops. Brix variance was omitted from this comparison because it shows negative

correlations. However, brix variance correlations are higher in absolute terms (that is, more negative) in the R crop. There is not much difference between P and R for CCS, fibre and brix. Thus, rather than interactions, the general means show a strong tendency for higher correlations in the TsR than in the TsP crop.

The TsP and TsR crops give fairly similar results for comparisons of crops and types in the Te trial, for most characters. Normal selection rate (SEL8) shows highly significant crops x types interactions in the TsP crop, but no interaction in the TsR crop. However, this is an exception, a general inspection of Table 77 emphasizing agreement between TsP and TsR crops, rather than interactions. This general impression is probably correct. However, interactions may have been found more important than expected, if the analysis of variance had been structured to estimate and test them.

3.32 Correlations for important characters.

Correlations for the more important selection and harvest characters are summarized in Table 79. This table shows correlations for the same character in each crop of the Ts and Te trials.

3.321 Average correlations.

3.3211 Types in the evaluation trial.

Average correlations are highest in the Re type. They are lowest for the Be type, the Se type being intermediate (Table 79). Re >> Be in all four combinations of P and R crops of the Ts and Te trials. SeR >> BeR for both crops of the Ts trial. Re > Se only in the TsP crop evaluated in the TeP crop. Correlations for the mean $(Re+Be+Se)/3$ are similar to Re for all crops except R seedlings evaluated in the TeP crop. In this case the mean

>> Re, Be and Se types.

3.3212 Crops.

There are no significant differences between crops when the Re type is used for evaluation (Table 79). By contrast, there are some highly significant differences between crops evaluated in other types. In the Be and Se types, and in the mean of the three types, correlations are higher in the R than in the P original seedlings. R seedlings with evaluation in P or R crops, give correlations which were higher ($P < 0.01$) than those from the TsP crop evaluated in the P crop. For the R crop of the Te trial, SsR > SsP. Better estimates of family means are provided by R than by P seedlings, if the families are evaluated using selections from Bs and Ss seedlings. This superiority of TsR crops does not have any obvious practical application, because it does not occur in the Re type which has higher correlations.

Reduced correlations in the Be and Se types, and higher correlations in R crops when Be and Se types were used for evaluation, are both selection effects. Higher correlations for R seedlings may occur because selection was made in the TsP and not in the TsR crop.

3.322 Correlations for each character.

For NMGYOT, correlations for all crop combinations of Bs and Ss seedlings are fairly similar, when Re seedlings are used for evaluation. No combination gives higher correlations than P seedlings evaluated in the TeP crop. Marked interactions with crops occur for the other main selection character, SEL8. Correlations in P seedlings are much lower when evaluated in TeP (0.17, Table 79) than in TeR (0.73). By contrast, R seedlings give slightly higher correlations when evaluated in P (0.56) than in R (0.34).

These results are fairly similar to those obtained for realized gains from selection, this interaction for SEL8 being discussed in more detail in that section (#3.414).

Number of selectable stalks in the Bs nursery was recorded only in the P crop. It gives fairly low correlations, especially with R evaluation where it has much lower correlations than those for Ss seedlings.

Visual net merit grade, the main character used for selection of small plots such as Ss seedlings, gives satisfactory correlations, comparable with those for NMGYOT. Number of selections (SEL8) is based on visual net merit grade of each seedling. However, the latter shows less interaction with crops. For both SEL8 and VisNMG, the highest correlation occurs for P seedlings evaluated in TeR (0.73, 0.74). P seedlings evaluated in the TeP crop give a much lower correlation for SEL8 (0.17) than for VisNMG (0.51).

3.33 Important Ts characters vs the three main characters in the Te trial.

Correlations for important characters in the Ts trial with TSH, NMGYOT and SEL8 in the Te trial, are given in Tables 80, 81, 82 and 83. These tables indicate the value of each Ts character for selection of families. Tables 80 and 81 show correlations for P or R crops in the Ts and Te trial. Tables 82 and 83 show only correlations for the TePR crop, but include separate correlations for P, R, and PR crops in the Ts trial. Actual correlations are shown in Tables 80 and 82. Tables 81 and 83 show the results of analysis of variance using correlations in Tables 80 and 82, respectively, as data. The three characters in the Te trial were treated as three replicates. A factorial analysis was conducted with Ts characters, Ts types (Bs, Ss), Te trial types (Re, Be, Se, mean), and crops as factors. Correlations were converted to Z values for analysis of variance. Z values are presented in Tables 81 and 83 whereas correlations are presented in

Tables 80 and 82. The analysis shows highly significant variance ratios for a number of factors and interactions.

3.331 Crops.

Tables 80 and 81 are especially suitable for the study of crop effects in both trials, so discussion of these tables will concentrate on this aspect. Results for other factors will be mainly based on Tables 82 and 83.

There are large ($P < 0.01$) differences between crops in both trials (Ocrop, Ecrop, Table 81). Ts characters show highly significant interactions with crops in both the Ts and Te trials (Ochar.Ocrop, Ochar.Ecrop). Ts types (Bs, Ss) do not interact with crops in either trial. Te types show a highly significant interaction with Ts crops and a significant interaction with Te crops (Etype.Ocrop, Etype.Ecrop).

3.3311 Main effects of crops.

The Z values show $R \gg P$ in both the Ts and Te trials (Ocrop, Ecrop, Table 81). Superficially, this favours R selection in original seedlings. However, interactions must also be considered.

3.3312 Interaction between crops and evaluation types.

For Te types, interactions are less marked with Te than with Ts crops. $TeR > TeP$ in all types, the superiority being significant in Be and highly significant in all other Te types (Etype.Ecrop, Table 81).

There is a marked interaction between Ts crops and Te types (Table 81, Etype.Ocrop). For the Re type, $TsP \geq TsR$ crop. By contrast, $R \gg P$ for the Be, Se and mean types. There is a marked difference between the Re and the selected types, and the selected types dominate the mean. When there are significant interactions, average values do not give clear conclusions.

3.3313 Interaction between crops and seedling types.

Bs and Ss seedlings do not differ in average effects, and give similar results in both crops in the Ts and Te trials (Otype; Otype.Ocrop, Otype.Ecrop, Table 81). However, there is a large second order interaction (Otype.Ocrop.Ecrop, $F = 14.0^{**}$). Bs > Ss when the same crop is involved in both trials (both P or both R). Ss ≥ Bs when different crops are involved in the two trials.

3.3314 Interaction between original seedling characters and crops.

The highly significant interactions between Ts characters and crops (Ochar.Ocrop, Ochar.Ecrop, Table 81) are produced mainly by atypical results for weight per stalk. It is the only character having P > R. This occurs in both trials. In the Te trial, all other characters have R >> P. In the Ts trial, TCH, TSH, NMGYOT and NMGLOT have R >> P. Thus, for the most important characters, the R crop gives significantly higher correlations in both trials. Interactions between characters, Te type and crops are not significant in either trial (Ochar.Etype.Ocrop, Ochar.Etype.Ecrop, Table 81). This would confirm the higher correlations in R than in P cane in both trials. However, for the Re type, TsP>TsR (#3.3312).

ReR >> ReP for NMGLOT, CCS and STALKS. ReR > ReP for TSH and NMGYOT (Ochar.Etype.Ecrop, Table 81). However, in the Ts trial, only one character shows a significant difference for the Re type. For weight per stalk TsP >> TsR (Ochar.Etype.Ocrop, Table 81, $0.37 >> 0.12$). None of the characters in the Re type shows TsR > TsP.

Thus, although average correlations are much higher in the R crop in both trials, the following conclusion is drawn for the Re type. For the main characters, TeR > TeP. However, correlations are about equal in both

crops of the Ts trial. There is a strong selection effect, selected Ss and Bs seedlings showing significantly higher correlations in the TsR trial. This selection effect dominates the mean which also shows significantly higher correlations in the TsR crop. Since it does not occur in the Re type, higher correlations in the TsR crop are a selection effect rather than a crop effect. Correlations may be lower in the TsP trial because the Be and Se types were selected in that trial. Such an effect does not provide any support for the use of R seedlings. If selection had been made in the TsR crop, the selections may have shown TsP > TsR.

3.3315 Effect of crops on error variance.

The analysis in Table 81 has a higher ($P < 0.01$) error variance than that in Table 83 :-

| | Table 81 | Table 83 |
|-------------------|----------|----------|
| DF | 527 | 370 |
| Error mean square | 0.02235 | 0.01189 |
| General mean | 0.4978 | 0.5729 |
| CV | 30 | 19 |

The main difference between the two analyses is the use of separate TeP and TeR crop results for Table 81 compared with TePR for Table 83. The larger error in Table 81 is probably produced by a large interaction between the treatments and the three Te trial characters used as replicates in the analysis. Examination of the original correlations in Table 80 confirms this. For example, for NMGYOT in Ss seedlings evaluated using the Re type, evaluation using SEL8 gives correlations which differ considerably from those given by TSH and NMGYOT:-

| Ts | P | | P | |
|--------|------|------|------|------|
| Te | P | R | P | R |
| TSH | 0.69 | 0.65 | 0.67 | 0.69 |
| NMGYOT | 0.67 | 0.59 | 0.67 | 0.67 |
| SEL8 | 0.26 | 0.75 | 0.45 | 0.66 |

The correlations with the Te characters TSH and NMGYOT are fairly similar for all crops, and do not differ significantly. For the TsP crop, the correlation with the Te character SEL8 is significantly higher with evaluation in R compared with P.

3.332 Correlations based on the mean of both crops in the evaluation trial.

As discussed above (#3.3315), analysis of correlations in the TePR trial (Table 83) has lower error variance than that for the separate P and R crops (Table 81). Correlations are higher for the PR crop, the general mean being 0.5729 in Table 83 and 0.4978 in Table 81. Variance ratios are higher, except those involving Ts crops. Two interactions involving original Ts characters and types (Ochar.Etype and Ochar.Otype.Etype) are not significant in Table 81 but highly significant in Table 83.

The interaction between Ts crops and the Re versus the other Te trial types is even more marked in Table 83. In the Re type, TsP >> TsR crop. In all other types TsR >> TsP (Ocrops.Etype). However, the individual correlations for the Re type (Table 82) show that TsP and TsR crops are about equal for the main characters TSH, NMGYOT, and NMGPLOT.

3.3321 Characters.

The important characters TCH, TSH, NMGYOT, NMGPLOT, have fairly high correlations between the Ts and Te trials. Z values range from 0.70 for

NMGYOT to 0.75 for TCH (Table 83). Surprisingly, TCH >> NMGYOT. The individual correlations for each replicate (Table 82) show that, for Ss seedlings, TCH is higher than NMGYOT for evaluation using TSHpr and SEL8pr. The correlations are equal for NMGYOTpr. It is not clear why TCH gives higher correlations than NMGYOT. Tonnes cane dominates the evaluation of families. Nothing was gained by measuring sugar content, fibre and non-yield characters in original seedlings. Furthermore, visual net merit grade of the whole plot (NMGLOT, Z = 0.73, Table 83) is about equal to TCH. For evaluation of families, nothing was gained by weighing the Ts trial. Provided experienced selectors are available, rapid visual grading is as good as weighing, and much more efficient when costs are considered. The increased objectivity and precision which are expected from mechanical harvesting, weighing, and laboratory processing of samples, are an illusion at the original seedling stage. However, cross ratio analysis (#3.94) showed NMGYOT to be the most efficient character for family selection in bunch seedlings.

3.3322 Types.

The Bs and Ss types do not differ significantly. There are marked differences between the Te types, with Re>>Se>>Be (Table 83). The mean of the Re, Be and Se types is equal to the Re type. The mean is based on 72 plots per replicate in the Te trial, compared with 24 for the Re type. Despite this, nothing is gained by including the Be and Se types in the mean. Without any increase in the correlations, the mean type is of little value. As discussed above, the mean is dominated by the selection types (Be, Se) and this produced biased results in some cases.

There are marked differences between Te types, for correlations between the Ts and Te trials. This contrasts with the lack of any significant

difference between these types, for correlations within the Te trial (#3.264, above).

3.3323 Crops.

TsR >> TsP, but interactions make it difficult to apply this result. It does not apply to the Re type, so it does not apply to the normal selection situation. Interactions between types and crops are fairly similar to those discussed above for Table 81 (#3.3312, #3.3313). The interaction between original Ts crops and Te types is even stronger in Table 83. For the Re type, TsP >> TsR (Etype.Ocrop, Table 83). This difference is present but not significant in Table 81. However, the same general conclusions are given by both tables.

3.3324 Interactions.

Bs and Ss seedlings have similar correlations for NMGYOT ($Z = 0.70$, 0.69 , Ochar.Otype, Table 83). Ss > Bs for TCH, TSH, and NMGLOT. Bs >> Ss for CCS and weight per stalk. The higher correlation for CCS in Bs may be due to a lack of selection in the Bs nursery. However, the higher correlations for weight per stalk in Bs seedlings do not fit the theory that selection reduces correlations. Weight per stalk is one of the main selection characters in Bs seedlings, and selection for it was effective.

For Bs seedlings, the Z values for TCH (0.69), TSH (0.71) and NMGYOT (0.70) were similar. The Z value for NMGLOT (0.64) was significantly lower. For Ss seedlings, Z values for TCH (0.80), TSH (0.77) and NMGLOT (0.82) are higher ($P < 0.01$) than that for NMGYOT (0.69).

Ts and Te types show strong interactions. The Bs and Ss types both show the same differences between Te types (Re >> Se >> Be, Otype.Etype, Table 83). For the Re type, Ss >> Bs seedlings but, for the Be type, Bs >> Ss.

Interactions between Ts characters and Te types are not significant in Table 81 but highly significant in Table 83. The main ranking (Re >> Se >> Be) was maintained for most characters (Ochar.Etype, Table 83). For TSH and NMGYOT, Ss >> Bs in the Re type. By contrast, in the Be type Bs > Ss seedlings for these characters (Ochar.Otype.Etype, Table 83). For NMGLOT Ss >> Bs seedlings in the Re and Se types, but it is also (not significantly) higher in the Be type. For CCS and weight per stalk, Bs >> Ss seedlings in all Te trial types.

3.333 Factorial AOV for each type separately in the evaluation trial.

The marked interactions between characters, crops and types made it difficult to draw general conclusions about average correlations for the factors analyzed. Interactions involving the Re, Be, Se and mean types in the Te trial are especially serious. The types produced by selection (Be, Se) give significantly different results from the Re type. The selection types tend to dominate the mean which thus gives results which sometimes differed significantly from the Re type. General conclusions about normal selection in original seedlings must be based on the Re type. The Be and Se types are mainly of interest because of the marked selection effects they show when used for evaluation. They may have practical applications for the second stage of selection, but not for the original seedling stage.

Separate factorial AOV was conducted for each Te type separately. This gave results for the Re type, free from interactions with other types. It also avoided the possibility of unequal error variances for types. The results for the Re type, for correlations based on separate TeP and TeR crops, are presented in Table 84. This table is related to Tables 80 and 81. Similar results for the TePR crop are presented in Table 85 (related to Tables 82, 83). These tables also show F ratios for separate analyses of

the Be, Se and mean Te types.

As happened with analyses involving all types, error variances are much higher for separate Te crops than for the TePR crop (Table 86). In all four Te types, the difference is highly significant. There are no significant differences between the error variances for the four types in the TePR crop (Table 85). There are significant differences between the types if separate Te crops are used in the analysis (Tables 84 and 86). In Table 84, the error mean square for the Se type is lower ($P < 0.01$) than that for any other type (including Re), and $Be > Re$.

The assumption of equal error variance for all treatments is violated by the Te types in Table 81, but not in Table 83. It is possible that error variances may not be uniform in either table. Unequal error variances may occur for factors other than Te types. Verification of this assumption for each factor would require a lot of additional analysis. The analyses are accepted, but some caution is necessary when drawing conclusions. Some of the main conclusions are so marked that they are not likely to be altered by heterogeneity of error variances.

It is not known why the error variance is lowest for the Se type in Table 84. Error variance was expected to be higher in the Re type than in other types, because it included very poor clones. It has a higher ($P < 0.01$) variance than the Se type. However it has a significantly lower variance compared with the Be type (Table 86). There does not seem to be any consistent tendency for selection to change error variances. Differences between error variances disappeared when correlations for the PR crop were used (Table 85).

The Se type has a lower error variance than any other type in Table 84. However, this does not give more significant F values. The Re type has the smallest number of significant F values in Table 84. The F value for Ts

crops is highly significant for all types except Re. Lack of significance for this factor in the Re type is apparently due to the large error variance. It is highly significant for all types in Table 85. In both tables, Ts type is not significant in the Se or mean types. It was highly significant in the Re and Be types. The reason for it is not known. The F values for the different types in Tables 84 and 85 show no obvious selection effects.

The main results from separate analysis of the Re type (Tables 84, 85) are:-

Characters. Correlations are significantly higher for TSH and NMGLOT than for NMGYOT (Table 85). For Ss seedlings, correlations are higher ($P < 0.01$) for TCH, TSH and NMGLOT than for NMGYOT (Ochar.Otype, Table 85).

Types. Ss >> Bs seedlings. This occurs for the main characters TCH, TSH, NMGYOT and NMGLOT. For weight per stalk and CCS, Bs >> Ss seedlings (Otype.Ochar, Table 85). Overall, the correlations indicate that family selection would be more efficient in Ss than in Bs seedlings. However, the correlations for the main characters are highly significant and fairly high in Bs seedlings. For example, for NMGYOT the correlation is 0.62 ($Z = 0.73$) for Bs seedlings, compared with 0.70 ($Z = 0.87$) for Ss seedlings. The correlations indicate that family selection would be fairly effective in Bs seedlings, although less effective than in Ss seedlings.

Seedling crops. TsP >> TsR crop (Table 85 only). However, this is due to CCS and weight per stalk. The main selection characters do not differ significantly for crops (Ochar.Ocrop, Table 85), except that NMGLOT has a significantly higher correlation in R seedlings. Ts crops showed no tendency for R correlations to be higher than P, for TCH, TSH, or NMGYOT. Overall, the results do not support to the use of R original seedlings.

Evaluation crops. TeR >> TeP crop (Table 84). The only character with TeP >

TeR is weight per stalk (Ochar.Ecrop, Table 84). $TeR > TeP$ for CCS, TSH, NMGYOT, STALKS, and NMGLOT. In the original experiment selection efficiency was higher in the R than in the P crop of the Te trial. Both experiments thus show higher selection efficiency in R than in P clonal trials. Results from the present experiment show that this does not apply to original seedlings.

3.34 Multiple regression analysis.

3.341 Choice of Y and X variables.

Family selection in original seedlings must be evaluated using the Re type. Initially, it was thought that a more accurate evaluation might be obtained by using the mean of the Re, Be and Se types. However, the above analysis (#3.3322) clearly shows that the mean is not suitable. The mean does not give higher correlations than the Re type. It is biased by marked selection effects shown by the Be and Se types. More reliable results are given by the TePR crop (#3.3315), than by analysis of each crop as a separate factor. Therefore, evaluation of seedling selection should be based on RePR.

Number of selections (SEL8) and NMGYOT are the logical characters to use in the Te trial. Both must be included because there is no basis at present for choosing one in preference to the other. NMGYOT is attractive because it is the character used to select clones in weighed trials. However, it does not have an obvious advantage over SEL8 for evaluation of families.

The value of families depends not on their mean values, but on the number of superior clones they produce. There may be differences in within-family variances and in the shapes of distributions. Because of this, SEL8 may give a better estimate of the number of superior clones in a family,

despite higher error variances. Furthermore, the present proven cross system is based on this character. No problem arises if the two evaluation characters agree. If they do not agree, results for each must be considered when drawing conclusions. TSH is a third character which may be considered for evaluation. It does not include the non-yield characters included in NMGYOT but it is the most important completely objective commercial character. The choice of the dependent (Y) variables for multiple regression analyses is easily made, namely SEL8, NMGYOT and TSH.

The choice of independent (X) variables cannot be made on theoretical grounds. It must include all characters which show high correlations with the Y variables. All the characters in Table 80 (and 82) were included as X variables, plus net merit grade of the whole plot, omitting brix.

3.342 Choice of multiple regression equations.

The main Ts characters show fairly close correlations with one another. They also show fairly similar correlations with the Te characters. This made it difficult to choose optimum X variables for the multiple regression equations. There was no obvious manual choice, so they were chosen automatically. Two methods were used, stepwise regression and backward elimination (Draper and Smith, 1981).

Backward elimination (Table 87) does not give satisfactory equations. Too many X variables are left in the equations. About 50 per cent of the variables have negative coefficients, although their simple correlations are positive. The most successful X variables are TCH with 9/14 positive T values, TSH (8/10), and net merit grade of the whole plot, including brix (7/9). In this case, success is based on the number and proportion of positive correlations. The equations probably use negative X variables to allow for environmental variation. In such cases the equations are

successful, but the characters involved are not, according to the present definition. KG/STALK, with 13/16 negative values, is also regarded as a successful character. In this case the negative correlation may have a biological basis. The least successful character is, surprisingly, NMGYOT, with 3/14 positive T values.

Stepwise regression (Table 88) produces better multiple regression equations, with fewer X variables. The equations account for less of the variance, but the reduction is reasonable, considering the reduced number of variables in each equation. There are a few high negative T values for characters expected to show positive correlations. The equations in Table 88 are not very consistent. With closely correlated X variables, one may be included or omitted, or given a negative instead of a positive coefficient, due to a small non-significant difference from another X variable. In some cases, the stepwise procedure did not proceed beyond the first step, the minimum residual being obtained using the character showing the highest simple correlation.

Plot NMG including brix is the most successful character, with 12/12 positive T values. It is followed by TCH with 7/7 positive. Weight per stalk is also considered successful, with 6/6 negative values. TSH is not very successful (3/3 positive) and NMGYOT (3/5) is surprisingly poor. There is some agreement between these success ratings, and those obtained by backward elimination. The equation for SsPR (Table 88) with TSH for evaluation, is probably the most successful one. The two X variables (TCH and Plot visual NMG including brix) both have positive coefficients, and account for 78.5 per cent of the variance. Considering that different years and trials are involved, this equation gives good prediction. The highest prediction is given for the R crop (SsR, $Y = TSH$, 83.3%). Three X variables are involved, namely TSH, NMGYOT and Plot visual NMG including brix. All

three have highly significant coefficients, one (NMGYOT) being strongly negative.

Some promising sets of X variables were selected from Table 88 and applied to the same data. This was done to see if better equations than those obtained by stepwise regression could be obtained manually. It would also show if the equations became more consistent when the number of X variables was restricted. Results for the best two of the six selected sets are presented in Table 89. In most cases, prediction using the fixed sets is inferior to that obtained by stepwise regression (Table 88). There are a few minor improvements. The only worthwhile improvement is for SsPR, Y = TSH (Table 89). The "variance accounted for" increases from 78.5 to 82.7. The three X variables are those which gave the highest prediction equation in Table 88. There does not seem to be much room for improvement over the equations obtained by stepwise regression. However, the fixed sets perform fairly well over all sets of data. The stepwise equations in Table 88 account for more of the variance. However, the average superiority is fairly small, being four per cent over the first set and three per cent over the second set in Table 89. The range is (-2 to +12) over the first set, and (-4 to +8) over the second set. This is not a test of the stepwise over the manual method, because the manual method used sets of variables chosen from the stepwise analysis. However, it shows that a suitable fixed set of two or three X variables is consistent enough to give fairly satisfactory results over different sets of data.

Although the equations for the two fixed sets of X variables give fairly consistent results, the actual coefficients show wider fluctuations. For example, wide fluctuations are shown by the T values for TSH and NMGYOT in the equations used to predict TSH, when the P and R crops of Bs seedlings are compared (Table 89). However, there is some consistency in

the coefficients. All 18 of the coefficients for TCH are positive, as are 34/36 of those for Plot NMG+Brix. For TSH there are 15/18 positive coefficients. NMGYOT and KG/STALK both have 15/18 negative coefficients. The negative coefficients for KG/STALK are probably reasonable. However, the negative coefficients for NMGYOT are surprising, considering that it is one of the main characters in the project, and one of the three Y variables.

3.343 Bunch vs single seedlings.

The multiple regression equations in Tables 87, 88, and 89 show much better prediction of family means in Ss than in Bs seedlings. Multiple regression analysis for each of the four main characters, with Bs and Ss seedlings as the independent variables, confirm this (Table 90).

Prediction of TSH and NMGYOT is almost completely dominated by the Ss seedlings, Bs seedlings making a negligible contribution. The only case in which Bs was comparable with Ss is for NMGYOT vs NMGYOT in the TsP crop (Table 90, 1.25 vs 1.59). Prediction of number of selections is also dominated by Ss seedlings in all crops with TCH and TSH as X variables. This also occurs in R crops for all X variables. For P cane, with NMGYOT and NMGPlot+Brix as X variables, and number of selections as the Y variable, Bs and Ss seedlings are about equal, with Bs \geq Ss.

Overall, Ss is clearly superior to Bs. This indicates that family selection would be much more effective in Ss than in Bs seedlings.

3.344 Plant vs ratoon seedling crops.

Differences in efficiency of prediction are much less marked in different crops, compared with those between Bs and Ss seedlings. There are marked interactions with crops and the X and Y variables (Table 91). For

prediction of number of selections, P is clearly superior to R. One exception is Ss seedlings with selection based on NMGPlot, where R is clearly superior.

P is clearly superior to R for predicting all three Y variables when the X variable is number of selections. For prediction of NMGYOT, P is superior to R in Bs seedlings selected for TSH, NMGYOT AND NMGPlot. By contrast, R selection is superior for these characters in Ss seedlings. For prediction of TSH, R selection is superior in most cases. However, there are two important exceptions, namely selection based on NMGYOT in Bs seedlings, and number of selections in Ss seedlings.

Overall, the TsP and TsR crops seem to be about equally effective. There is no marked tendency for superior results in TsR compared with TsP seedlings.

For most characters, prediction using the multiple regression equations for each crop separately, is about equal to that using simple regression for the mean of both crops. This is surprising, considering that the multiple regression equations often use coefficients which differ considerably from the equal weight given to each crop when using PR.

3.4 Realized gains from family selection.

In this discussion, realized gains from selection are expressed as per cent of the mean for the character used for evaluation. This character is usually number of selections graded 8.0 or higher, or NMGYOT. Mean per cent values were computed using an arcsin transformation ($\arcsin \sqrt{\%}$), and reconverted to per cent for presentation. Unless otherwise specified, a selection rate of 25 per cent (6/24 families selected) is used for discussion.

3.41 Realized gains from selection in the seedling trial.

Family selection is effective. Large gains are achieved for a number of characters (Table 92).

3.411 Bunch seedlings.

Number of selectable stalks in the BsP crop gives gains of 24 per cent for number of selections (SEL8) from the TePR trial. It gives gains of 14 per cent for NMGYOT in the TePR trial. This result is important, showing that family selection in Bs seedlings is effective. It also shows that such selection can be based on selection rate. Skinner (1969) found that some worthless families, which produced large attractive stalks, gave high selection rates in Bs plantings. When replanted, the selections had attractive stalks, but a very small number of stalks per stool. The observations were repeatable, but were limited to a small number of families. Thus they did not provide a basis for general conclusions. However, it was thought that direct selection of families in Bs seedlings would not be effective, due to the negative correlation between weight per stalk and number of stalks per stool. The present results show that this opinion is wrong. Direct selection of families in Bs plantings, based on

selection rate, is effective.

Selection rate (number of selectable stalks) and weight per stalk are about equally effective in BsP seedlings. Each of these characters is about equal to NMGYOT which gives 27.3 per cent gain for SEL8 and 14.6 for NMGYOT (Table 92). Visual net merit grade of the whole plot is the most effective character in the P crop. It is about equally effective with brix included (B3GBp, 39.7, 14.6) or omitted (B3G_Bp, 36.6, 16.3) when grading the plot. These comparisons are made for the P crop. Because of an oversight, number of selectable stalks was not measured in the BsR seedlings.

When both crops are considered, the most effective character is visual net merit grade of the whole plot, including brix (Table 93). The results show that, if experienced selectors are available, there is no advantage in weighing Bs seedling plots. Although there would be no significant difference between the gains for graded and weighed plots, visual grading of plots is a rapid procedure which is much less expensive than weighing. Although inclusion of brix in the visual grade did not give a large improvement, the results show that it would be efficient to include it.

Although selection based on total number of stalks reduced CCS, selection based on all of the important characters improved CCS. This improvement occurred even for characters such as number of selectable stalks, weight per stalk, TCH and visual grade of the whole plot omitting brix (Table 92). Brix is not considered when selecting for these characters, so the gain in CCS is a correlated response to selection. Families which produce many heavy attractive stalks in the Bs nursery are above average in sugar content. However, families which produce a large total number of stalks tend to be below average for sugar content.

These results are as expected, considering the origin of commercial varieties. Most commercial varieties are complex hybrids resulting from

crosses between the noble species *Saccharum officinarum* and the wild species *Saccharum spontaneum*. The first cross is followed by backcrossing to *Saccharum officinarum*, and crossing between the commercial-type hybrids. *Saccharum officinarum* has higher sugar content, heavier stalks, and a small number of stalks per plant. *Saccharum spontaneum* transmits higher yield produced by numerous thin stalks, combined with very low sugar content. The results are as expected from this method of breeding. High sugar content is positively correlated with heavy stalks, but negatively correlated with number of stalks. Although this is a satisfying hypothesis, it can only be tentative. The sample of families in the project was limited in size (24) and not completely random. For this population, the hypothesis receives some support from correlation analysis. The genotypic correlation, as estimated from the phenotypic correlation with CCS in the Te trial is 0.5* for weight per stalk and -0.1 for number of stalks (RePR vs BsPR, Table 74).

3.412 Realized gains from selection in single seedlings.

As in the Bs seedlings, the most successful character in Ss seedlings is visual net merit grade of the whole plot, including brix (Table 93). Provided experienced selectors are available, visual grading is more efficient than mechanical harvesting and weighing of seedling plots. Severe selection (SEL10) tends to be inferior to more moderate selection. Selection rates differ for plr (selection of each seedling based on the mean over both crops) and pr in which the number of selections is the mean of the plot values over both crops. However realized gains are fairly similar, with pr slightly superior. With moderate selection, selection rate is about equal to NMGYOT. Family selection based on within-family variance for NMG is surprisingly effective. It is only slightly below selection

based on the mean NMG. Within family variance is not a practical selection character. However, it influences the choice between selection rate and means for family selection.

3.413 Efficiency of bunch vs single seedlings for family selection.

Gains from family selection were about equal in Bs and Ss seedlings. There were no significant differences between them. The most successful character was visual plot grade including brix (Tables 93 and 94). For this character, Ss seedlings are more efficient than Bs if selection is made in the PR seedling crop (Table 93). However, selection would normally be made in the TsP crop. In this crop, visual plot grade gave higher gains in Bs than Ss seedlings (Table 94). For selection based on NMGYOT, family selection is about equally efficient in Bs and Ss seedlings. For selection rate in the TsP crop (Table 94), with 25 per cent of the families selected, a larger realized gain is obtained by selection in Bs than in Ss seedlings. However, probably by chance, Bs selection is favoured by this selection rate. Ss is much superior to Bs with the other two selection rates. Considering all selection rates, Ss is superior to Bs, although the difference is not significant. Family selection in Bs seedlings, using selection rate, is much more effective than expected.

The project has provided new information which completely changes the previous opinion, that direct family selection was likely to be ineffective or harmful in Bs seedlings. Family selection is effective in Bs seedlings.

Bs seedlings have the advantage that they require only one-sixth of the seedling area. However, this is more than balanced by the disadvantage that they require three times the number of seedlings (330/108). BSES probably lacks the capacity to produce enough seedlings from good families, for family selection using bunch planting on all experiment stations. Added

seedling requirements for bunch planting may make it necessary to plant numerous seedlings from poorer families in the field. This would reduce progress from family selection in Bs compared with Ss seedlings.

This problem might be overcome by planting only three to five seedlings per bunch instead of ten. Unfortunately, it cannot be assumed that gains from family selection would be as large as those estimated in this project, if the number of seedlings per bunch was reduced. It would be necessary to carry out further research.

If pure family selection is adopted, it is important to choose the optimum planting system. It is not likely that either of the planting systems tested in the present project would be best for family selection. The standard Hawaiian bunch planting system, with about ten seedlings per bunch, was used. It requires too many seedlings to be efficient in Queensland. Seed setting is much poorer here, and biparental crosses are used as the main system. The single planting system was developed for mass selection, not for family selection.

Possible improvements for family selection include closer single planting, and bunch planting with reduced numbers of seedlings per bunch. Very close single planting is likely to make more efficient use of seedlings, than bunch planting with a small number of seedlings per bunch. Some seedlings die from competition in pots when bunch planted. Close single planting would avoid such losses, and reduce other losses from competition. The value of very close single planting would depend on the development of nursery and field techniques to handle large numbers efficiently. However, single planting at half the present spacing would be practical with the present techniques.

Gains from selection of 25 per cent of the families, using number of stalks and weight per stalk are as follows:-

| Crop selected | Realized gain (% of mean) over both crops for | | | | | |
|-----------------|---|-------|------|--------|------|-----|
| | Number selected (SEL8) | | | NMGYOT | | |
| | P | R | PR | P | R | PR |
| Stalk number Bs | -16.3 | 11.7 | 21.0 | -5.6 | 0.6 | 4.3 |
| Ss | 45.8 | 36.6 | 33.4 | 10.2 | 8.7 | 8.9 |
| Weight/stalk Bs | 27.3 | 5.6 | 14.9 | 14.6 | 3.0 | 4.4 |
| Ss | 33.5 | -13.0 | 21.1 | 11.0 | -1.4 | 8.9 |

Gains from selection are fairly small for BsPR. For both characters, gains are higher for selection of Ss compared with Bs seedlings. There is an indication of an interaction between Ts type and crops for each character. For stalk number, Bs seedlings give a negative gain from selection in the P crop and positive in R. Ss seedlings give a strong positive gain in both crops for number of stalks. For weight per stalk Ss seedlings give a strong positive gain from selection in the P crop, but a negative gain from the R crop. For both Bs and Ss seedlings, selection based on weight per stalk is much more effective in the P than in the R crop. The crop class (P,R) is likely to be responsible. P crops are produced from potted seedlings planted to the field later in the season than commercial crops. The method and time of planting may reduce the effect of competition on weight per stalk and number of stalks. It also reduces the negative correlation between number of stalks and weight per stalk (#3.112). This effect is not important in Bs seedlings, in which the correlation is about zero in both crops. However, the much stronger negative correlation in the SsR crop, combined with selection for number of stalks, probably produced the negative gain for weight per stalk in the SsR crop. The benefits from potted seedlings were not expected. They are likely to destroy any possible advantage of ratoon crops for selection of Bs and Ss seedlings.