

## **EARLY GENERATION SELECTION OF SUGARCANE FAMILIES AND CLONES IN AUSTRALIA: A REVIEW**

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### **ABSTRACT**

Sugarcane breeding programs typically commence by evaluating a large number of seedlings derived from true seed. Individual clone (mass) selection applied at this stage of the program has been shown to be inefficient because of lack of replication and the associated confounding effects of the environment. In Australia, the introduction of mobile weighing machines made it possible to implement family selection. Several research projects demonstrated that family selection, when followed by individual clone selection, was superior in terms of genetic gain and more cost effective than either family or individual clone selection alone. This combination of family and individual clone selection is now used routinely in all the Australian programs. Families are evaluated using replicated plots for cane yield (mechanically harvested and weighed) and sucrose content in the plant crop. Individual clones are selected, based mainly on visual appraisal for cane yield, from selected families in the first ratoon crop. Family selection is usually liberal with about 30 – 40 % of families selected. More clones are selected from the best families with progressively fewer clones being selected from the moderate to average families. The availability of objective family data makes it possible to estimate the breeding value of parents using the Best Linear Unbiased Predictors (BLUP). This information is used to retain or drop parents from the crossing program and to plan better cross combinations.

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### **INTRODUCTION**

Although sugarcane is grown commercially as a clone, sugarcane breeding programs typically commence by evaluating large numbers of seedlings derived from true seed. Sugarcane breeders have traditionally employed intensive selection of individual seedlings or seedling bunches to select clones at this stage. Selection is usually subjective, based on visual appraisal for cane yield. Some programs also consider sucrose content, which is indirectly measured as

Brix (% soluble solids w/w in the juice) using a hand-held refractometer, in their selection criteria. Although satisfactory gains have been achieved using individual seedling selection, it is not efficient (Hogarth et al., 1997; Skinner, 1971). The lack of replications, competition effects among seedlings and, because individual clone selection is labor intensive and expensive, all contribute to reduce selection efficiency.

Research in Australia revealed that family selection would be superior to individual seedling selection at this stage (Hogarth, 1971). Family selection is particularly useful for traits with low heritability because, unlike clones, families can be replicated across years and sites, thereby improving estimates of family means as well as aiding in the identification of stable families (Jackson and McRae, 1998; Falconer and Mackay, 1996). Because sugarcane is exploited commercially as a clone, the rationale for family selection is not to produce superior families with commercial value but rather to identify families with a higher frequency of superior clones. Family selection makes it possible to focus selection for superior clones (individual clone selection) on the best families, because the probability of finding superior clones at later stages of the program is highest within these families (Cox and Hogarth, 1993). An added advantage of family selection in sugarcane is that family data can be used to infer the breeding value of parents based on progeny performance (Balzarini, 2000; Cox and Stringer, 1998; Stringer et al., 1996; Chang and Milligan, 1992a, b).

In the 1970s, families still had to be cut and weighed manually; therefore, the cost of implementing family selection was prohibitive at the time. With the development of mobile weighing machines in Australia, it became possible to investigate the advantages of family selection in more detailed experiments and under different geographical and environmental conditions (Hogarth and Mullins, 1989). Following results from these experiments, the Australian programs were redesigned to include family selection at this early (seedling) stage (Cox and Hogarth, 1993; Hogarth and Mullins, 1989). In this report, we share some of our experiences with family selection in Australia. We briefly review some of the experiments that led to the redesign of the Australian programs and further examine the impact of family selection on other aspects of the selection program. In particular, we reveal how family selection has contributed positively to the selection of parents and crosses and to population improvement. In this paper, as in other sugarcane breeding papers, the phrase family selection is used in some instances as an all encompassing one to describe the selection of families and clones within families.

## **Family selection in Australia**

### *Sugarcane growing regions and family selection experiments*

In Australia, sugarcane is cultivated over a 2100 km stretch from northern New South Wales (approximately 30°S) to northern Queensland (approximately 17°S), with the actual hectareage spread unevenly across this distance (Figure 1). Additional hectareage is emerging in the Ord river basin. The Bureau of Sugar Experiment Stations (BSES) operates five separate sugarcane selection programs in Australia, which are separated into regions by latitude (Hogarth and Mullins, 1989) and are strategically located in the major sugarcane-growing regions. Each selection program operates independently, but family selection is a common feature in the early

stages of all the programs (Table 1). The number of seedlings and clones planted and selected at each stage, varies in the different programs.

Several family selection experiments have been carried out under different geographical and environmental conditions in Australia (Jackson et al., 1995a, b; McRae and Jackson, 1995; McRae et al., 1993; Cox et al., 1996; Hogarth et al., 1990; Hogarth, 1971). But, the best set of experiments to use in illustrating the benefits of family selection was carried out in the Burdekin region (Ayr, Figure 1) where the growing conditions have been described as unfavorable to selection (Jackson et al., 1992; Pollock, 1982). In this region, sugarcane is grown under irrigation, which results in large and frequently lodged crops. Because individual clone selection is impractical under such conditions, the practice was to restrict crop growth by minimizing irrigation and fertilizers to prevent lodging and enable individual clone selection. However, because the crop growth potential was not realized under such conditions, this probably had a negative impact on selection response because visual estimation of cane yield was poorly correlated with actual cane yield in heavily lodged crops (Jackson et al., 1992; Pollock, 1982). Indeed, in an experiment conducted by Hogarth et al. (1990), neither family selection nor mass selection was effective under conditions that restricted crop growth. The selection conditions (environments) were probably atypical of the target environment. Furthermore, under conditions of restricted crop growth, misleading information on family performance would probably lead to inappropriate parents being selected for crossing, thereby, impeding future selection progress (Kimbeng et al., 2000).

An experiment was conducted in which lodging was experienced as a result of letting it grow to its full potential (Kimbeng et al., 2000). One hundred full-sib families were evaluated in single-row plots, replicated four times with 20 seedlings per family plot. Family plot data were collected in the lodged plant crop using mobile weighing machines as described for a Stage 1 trial (see Table 1). In the young first ratoon crop, prior to lodging, three clones were visually selected, and another three clones were taken at random from each family plot. These clones were each planted to a single-row, 10-m plot in a split-plot arrangement and replicated into four randomized complete blocks. Whole plots were assigned to families and sub-plots to selection methods (random vs. selected) for a total of six clones per plot. First clonal stage data were collected in the plant and first ratoon crops as described for a Stage 2 trial (Table 1).

Figure 2 shows the percentage of elite clones (clones with Net Merit Grades, NMG > 9.0; see Table 1 for description of NMG) in Stage 2 with respect to the selection strategy used in Stage 1 for the top 40% of families. Essentially, the results showed that family selection could be effective even under lodged conditions. This is evident from the performance among random clones, which was generally higher among the top NMG families and decreased progressively in the poorer NMG families. Visual selection in the young first ratoon crop was also effective in identifying elite clones within families, as evident from Figure 2 and the significant effect of selection method (random vs. selected, 1df) in the ANOVA (data not shown). Also, the effectiveness of visual selection was consistent across families as indicated by the lack of significant family by selection method interaction in the ANOVA (data not shown). Family selection in the plant crop followed by individual clone selection in the first ratoon crop was superior to either family or individual clone selection. Similar results were found in a simulation study that modeled family by environment interactions, genotypic correlations

between the selected trait and sugar yield, among family variance, total variance and cost of selection (Jackson et al., 1995b). The authors reported superior genetic gain and cost effectiveness for combined family and individual clone selection compared to either family or individual clone selection in most cases. Family selection was also superior to individual clone selection in most cases. Individual clone selection was superior only in cases where there was both a small proportion of among-family variance and a high genetic correlation between the selected trait and sugar yield.

Any form of family selection, however, would have to be liberal because some clones have been found to perform better than expected on the basis of their family performance in seedling trials (Kimbeng et al., 2000; Hogarth et al., 1990). Furthermore, although an overall increase in family mean is desirable, the ultimate goal for sugarcane breeders is to select the best-yielding clone(s). Cox et al. (1996) suggested that only the top 30 to 40% of families be targeted for routine individual clone selection. He contends that after intentionally selecting clones from the moderate NMG families (50 – 70 %) for a number of years, not a single clone from this category progressed to the advanced stages (Cox, Personal Communication). Kimbeng et al. (2000) also found the highest percentage of elite clones within the top 30 to 40% of families (and see Figure 2). Kimbeng et al. (2001a, b; 2000), however, found evidence that elite clones could be selected from the moderate to low NMG families. They found some outstanding clones among moderate NMG families, especially those that had high CCS but low TCH and vice versa. According to Kimbeng et al. (2001b), the time required to select individual clones from these relatively poor families should not be a limiting factor in a field operation, because these plots can be predetermined using the plant crop family data. In central Queensland, each row is harvested immediately after individual clone selection, giving the selecting crew equal access to all rows and clones during selection.

A major practical benefit of family selection is that it allows genetic material to be evaluated across locations and years, which aids in the identification of stable families (Jackson and McRae, 1998). This is particularly useful in situations where family by environment interaction is important. In the Burdekin region (Ayr, Figure 1), McRae and Jackson (1995) did not find significant interactions between family and any of the environmental factors, namely soil types, management practices and crop cycle that they evaluated. Based on these findings, in this region, families are evaluated only in the plant crop and at one location (the breeding station) as described in Table 1. Significant family by environment interactions were found in the Herbert region (Ingham, Figure 1) (Jackson et al., 1994). However, Jackson et al. (1995a) and Jackson and Galvez (1996) later found that soil nutrient status was the principal cause of the interactions. Soil nutrient status is a predictable and repeatable source of genotype by environment interaction (Allard and Bradshaw, 1964) that was easily corrected. In southern Queensland, Bull et al. (1992) reported significant family by location interaction. When resources are not a constraining factor, families are evaluated at more than one location in this region.

Competition among seedlings in a plot can affect selection response adversely if the appropriate intra-row spacing between seedlings is not used. Research under Louisiana growing conditions showed that genetic response was larger at a wider intra-row spacing of 82 cm compared to a narrower spacing of 41 cm (De Sousa-Vieira and Milligan, 1999). Intra-row

spacing varies among the Australian programs and is probably influenced by land availability and the size of the crop. For example, an intra-row spacing of 50 cm is used in central Queensland (Mackay, Figure 1), but in the Burdekin (Ayr, Figure 1), where they have access to irrigation and tend to grow bigger crops, the spacing is 60 cm.

*Appraisal of family selection using data generated from routine selection activities*

Any crop improvement program needs to be constantly monitored to ensure that the breeding and selection methods are operating at optimal levels. Retrospective analyses using data generated from routine selection activities can be particularly helpful in this effort because these data serve as footprints of the program's activities. Cox and Stringer (1998) analyzed the efficacy of early generation selection for the southern Queensland program (Bundaberg, Figure 1) using data from the selection database. In this analysis, all the clones that were advanced to Stage 3, based on their performance in Stage 2, were categorized according to the families from which they were derived in Stage 1 (see Table 1 for a detailed explanation of Stages). The results showed that selection rates for clones derived from Stage 1 families were low (3.8 %) for low NMG families (< 10), were similar for families with NMG 10 to < 13 (6.9% - 7.6%) and were quite high for the highest NMG category (13.6 %) (Table 2). It appears, during selection of clones in the first ratoon crop, selection intensity, which is normally higher for the poorer NMG families, more than compensated for the poor family performance. This explains the similar selection rates of clones from Stage 2 to Stage 3 for families with NMG 10 to < 13 (6.9% - 7.6%). Thus, selection intensity can be a major driving force to increase genetic gain. The authors suggested that genetic gain could be improved by planting larger numbers of clones (in extra plots) of the better families and increasing individual selection intensity for these families. In this case, the extra plots would be selected in the plant crop without having to wait for more data. This strategy combines the strengths of the family selection and proven cross methods.

An analysis similar to that of Cox and Stringer (1998) was performed for the central Queensland program (Mackay, Figure 1) using a much larger data set (Kimbeng et al., 2001a). The results, with respect to selection among families, were similar to those reported by Cox and Stringer (1998); selection rates were higher for the top NMG families and comparatively lower for the poor NMG families. However, a bias with this type of analysis is that the high NMG families were originally represented by more clones in Stage 2 compared to the poor NMG families. Therefore, no conclusion could be drawn with respect to the selection of clones within families. In an attempt to overcome this bias, Kimbeng et al. (2001a) divided the selection rate (Stage 2 to 3) by the percent of clones evaluated in Stage 2 for each NMG category. In this analysis, the selection rate was taken to represent the realized response and the percent of clones evaluated in Stage 2 represented the potential response. The results from this analysis revealed that although family selection was effective in identifying those families that harbor a greater proportion of elite clones, selection of clones within families was not efficient, especially for the high NMG families. Kimbeng et al. (2001a) observed that in central Queensland, the top NMG families did not undergo the strict appraisal process used for the lower NMG families and as a result more clones are advanced than is actually necessary. More clones are usually earmarked for selection from the high NMG families. Because the NMG formula awards a bonus for high sucrose content, there is a tendency not to Brix clones within the top NMG families because of the perception that most of the clones are high in sucrose content. The reverse is true for the low NMG families, where almost every clone is subjected to a Brix test before selecting a few. The

analysis, unfortunately, could not accurately account for what happened in the average to poor families. These families had either been discarded or had already undergone very stringent selection. The breeder could be discarding potential clones if the selection intensity applied to these families is more intense than necessary. Although differential selection rates are used within families, whereby more clones are selected out of the best families (top 10 %), with progressively fewer clones being selected from the 20 to 40% of families, the number of clones selected from these families is currently not based on any objective data. Based on the available resources, only a finite number of clones can be evaluated in Stage 2 trials and, for family selection to be efficient, selection of clones within families would have to be optimized. In central Queensland, the resources allocated to Stage 2 trials can accommodate only about 10% of clones from Stage 1.

#### *Simulated selection to optimize family selection*

An experiment was carried out in central Queensland (Mackay, Figure 1) to investigate optimum selection intensities for family and individual clone selection (Kimbeng et al., 2001b). In this experiment, families (replicated family plots) and random clones within each family plot were assessed for various characteristics, including cane yield, sucrose content, visual grade and Brix in the plant crop of a Stage 1 trial (see Table 1 for explanation of a Stage 1 trial). These clones were evaluated in Stage 2 (first clonal stage) in the plant and first ratoon crops. Response to selection in Stage 1 was judged on the performance of corresponding clones in Stage 2. The main objective was to simulate optimum rates of combined family and individual clone selection in Stage 1. The simulations to determine optimum rates of combined family and individual clone selection in Stage 1 were performed using Microsoft Access Relational Database.

The results confirmed that while family selection was effective in identifying families with a high proportion of elite clones, it was more efficient when combined with visual selection (Table 3). The efficiency improved further when clones with good visual grade were subjected to a Brix test. Most of the efficiency arose from the fact that inferior clones were rejected on the basis of visual grade and Brix, and considerably fewer clones were evaluated in Stage 2. Given that only 10% of clones from Stage 1 can be accommodated in Stage 2 trials, this would represent about 240 clones in this study (Table 3).

Enforcing a strict selection for Brix led to the loss of a considerable number of elite clones. But, when the cut-off point for Brix was allowed to vary, depending on the visual grade, (for example a clone with low Brix is accepted when the visual grade is high), the number of elite clones that would have been discarded dropped dramatically, but one would have had to increase the number of clones evaluated in Stage 2. In practice, the decision to accept or reject a clone based on visual grade is much easier to make since that decision always equals to a yes (acceptable) or no (unacceptable) answer. Based on the results from the simulations, individual clone selection rates of 40, 30, 25 and 10% were optimum for family selection rates of 10, 20, 30 and 40%, respectively, when selecting families (based on NMG) in the plant crop and clones (based on visual appraisal) in the first ratoon crop. Individual clone selection based on Brix was best determined by taking into consideration the visual grade of the clone. These selection rates should be applied with some caution because they probably depend on the germplasm base and, as such, may differ in other programs. In Louisiana, for example, the best outcome was achieved with 75% family and 13% within-family selection, and the author contends that this was only slightly more efficient than mass selection (Zaubrecher, 1995). The author attributed this to the

narrow genetic diversity or low among-family variance (11%) in the Louisiana program. During the study period, only about 80 parents were used to make an average of about 300 biparental crosses in Louisiana, compared to 800 -1000 parents used to make about 2,500 crosses in Australia each year. The number of parents used in the Louisiana crossing program has increased to about 160, largely because of increased efficiency of floral initiation using the photoperiod facility.

### **Impact of family selection on other aspects of the breeding program**

#### *Selection of parents, crosses and population improvement*

A selection cycle in sugarcane usually involves a sequence of about four to six stages (Skinner et al., 1987). A selection cycle typically takes about 12-15 years to complete. The first stage is the only stage, after hybridization, to be planted with true seed. Subsequent stages are planted using vegetative propagation, and progressively fewer clones are selected and evaluated in the more advanced stages. During this 12 to 15 year period, no opportunities exist for sexual recombination or the creation of new genetic variation that the breeder can exploit. The breeder has to rely on the initial variation created during hybridization. Research that can predict the outcome of a cross would help the breeder to concentrate effort on the most profitable crosses, which in turn would substantially increase the chances of selecting elite clones. The selection of genotypes to use as parents, or crosses to plant, is one of the most critical decisions the sugarcane breeder has to make.

At the BSES, Hogarth and Skinner (1986) developed an algorithm for assessing the breeding value of parental clones that combined breeding information, agronomic data and disease ratings into a single index. The breeding information relied heavily on the percent of clones from a cross that are advanced to later stages. Crosses with high advancement rates (proven crosses), were usually replanted to large numbers of progenies, unduly increasing their odds of producing advanced clones to the detriment of experimental crosses. Furthermore, although the agronomic data and disease ratings combined information from both the parent and progenies, the method required several years to reliably estimate breeding value, and it is now known that individual clone selection in the early stages was not efficient.

BSES breeders recognized the limitations of this empirical approach and sought more efficient methods of estimating breeding value. But this effort was hampered by the lack of objective data on family or clonal performance, as early stage data were based on indirect measurements; that is, visual assessment to estimate cane yield and Brix to estimate sucrose content. Therefore, the availability of objective family data on both cane yield and sucrose content presented a unique opportunity to apply statistical approaches to the problem. However, the highly unbalanced nature of data sets generated from routine progeny evaluation trials precluded the use of statistical methods such as factorial (or North Carolina design II) (Comstock et al., 1949, Comstock and Robinson, 1948) and Diallel (Griffing, 1956; Hayman, 1954) mating designs.

The Best Linear Unbiased Predictor (BLUP), which was developed to estimate breeding value in animal breeding (Henderson 1975), can handle large, highly unbalanced data sets such as those generated in routine sugarcane progeny evaluation trials. The BLUP allows data from a diverse range of mating designs, relatives, and precisions to be combined into a single breeding

value for each trait and genotype (Balzarini, 2000). Chang and Milligan (1992a, 1992b) were the first to report that the BLUP was reliable in predicting the potential of a cross to produce elite progeny in sugarcane. They also found that the potential of a cross to produce elite progeny could be accurately predicted from the cross mean of that trait, and the cross mean was more readily obtained than the BLUP (Chang and Milligan, 1992b). These latter results were obtained using a balanced data set and were restricted to one stage of the breeding program. The real advantage of the BLUP over other statistical methods arises when highly unbalanced data sets, such as those generated from routine sugarcane selection trials, are analyzed across different stages of the program and include information about relatives (Balzarini, 2000; Stringer et al., 1996).

Using routine family appraisal data from the southern Queensland (Bundaburg, Figure 1) breeding program, Stringer et al. (1996) and Cox and Stringer (1998) compared the utility of the BLUP with that of an empirical method (Hogarth and Skinner, 1986) in predicting cross performance. The predictions were made by correlating the mean BLUP values obtained using data accumulated over several years up to a certain year, with the actual family mean values obtained in the following year. In other words, family mean plant crop data, in say 1995, were correlated with the corresponding mean BLUP values estimated using family data accumulated from, say 1992-1994. The empirical values were derived from at least ten years of data. These results showed that the BLUP method was superior to the empirical method in predicting cross performance (Table 4). Generally, the BLUP method requires less information (at least 1 year) compared to the empirical method (at least 10 years) and its power to predict cross performance increases as more data become available and is expected to increase even further when information on relatives is included in the model (Stringer et al., 1996). The robustness of the BLUP estimates depends largely on the availability of objective family appraisal data, albeit highly unbalanced.

Encouraged by the high predictive power of the BLUP analytical method, BSES breeders began to change their philosophy with respect to choice of parents and crosses. The BLUP was increasingly used to select parents and crosses, and to design new crosses. This led to a gradual increase in crosses involving newer parents. Use of historical parents began to decline, even when they were involved in 'proven crosses' (Cox and Hogarth, 1993). The new philosophy sought to achieve a much-needed balance between the short-term goals of producing elite sugarcane clones with the long-term need to continuously improve the base population. These issues needed to be considered simultaneously, because the repetitious nature of breeding for short-term needs was unlikely to provide the best results to accomplish long-term goals. For example, the hitherto strong emphasis on proven crosses in the BSES breeding program served the short-term need of producing elite varieties. However, it hampered efforts to broaden the genetic base of the breeding population, because only limited chances were available to evaluate experimental parents and crosses. Furthermore, it is well known among sugarcane breeders that the genetic base of cultivated sugarcane is very narrow, so concerted efforts had to be made to broaden the base population (Berding and Roach, 1987; Mangelsdorf, 1983).

Population improvement and base broadening efforts at the BSES encompass the rapid introduction of superior clones from advanced stages of the selection program as well as superior germplasm from exotic crosses, and international and national programs (inter-station exchange),

into the crossing program (Cox and Hogarth, 1993). In other instances, population improvement involved recurrent selection for specific traits, for example high early sucrose content (Cox et al., 1994; Cox et al., 1990) to provide suitable parents for the variety development crossing program. The availability of sound, objective data on family performance coupled with robust estimates of the BLUP, are crucial to the success of population improvement efforts.

The implementation of this new effort was assessed for the southern BSES program by evaluating the relative performance of families derived from crossing new versus old parents. The analysis used four years of routine family appraisal data in which parents were arbitrarily categorized as old (O), medium (M), or new (N) if the seedling parent had a year prefix < 65, 65-74, or > 74, respectively (Cox and Hogarth, 1993). The crosses were designated O×O, O×M, O×N, M×M, M×N, or N×N (Table 5). Although the small sample size of the N×N crosses precluded a reasonable assessment of this group of crosses, the overall results point to the inferior performance of old parents compared to the relatively new ones. Old parents performed poorly even when used in combination with relatively new parents, compared to crosses between relatively new parents. These results justify the continuous use and rapid recycling of parents in the breeding program. Again, data accumulated from family evaluation trials are crucial to the successful implementation of this policy.

Apart from evaluating parental performance, the population from which families and clones are selected (Stage 1, see Table 1) and the population of clones immediately following family and clonal selection (Stage 2, see Table 2) are also constantly monitored. This is to ensure that these populations are not adversely affected as a result of adopting family selection measures (for example, the BLUPs to select parents; the rapid recycling of newer parents including overseas clones). The performance of seedling populations (Stage 1) from 1993 to 2000 in southern Queensland depicts an overall gradual improvement in NMG at the rate of 0.02 units per year. Cane yield was a major driving force of this improvement [ $TCH = 0.02Year + 0.58$ ;  $R^2 = 0.70$ ], compared to sucrose content [ $CCS = -0.002Year + 0.93$ ;  $R^2 = 0.03$ ]. Heritability, estimated on an entry-mean basis using replicated family plots (Stage1), was higher for cane yield, 64%, compared to sucrose content, 48% (Kimbeng and McRae, 1999). Cane yield may, therefore, be more influential in determining among-family differences in seedling populations (Stage 1 trials) compared to sucrose content.

Within the same period, the NMG of clones (Stage 2) immediately following family and clonal selection improved on average by 1.58 units per year (Figure 4). The NMG of the top 10% of the mean, which constitutes most of the clones advanced to the next stage, improved on average by 2.02 units per year. Contrary to the seedlings, population improvement in the clones was driven more by improvements in sucrose content [ $CCS = 1.0Year + 89.92$ ;  $R^2 = 0.63$ ] than by cane yield [ $TCH = 0.11Year + 81.73$ ;  $R^2 = 0.005$ ], which is consistent with well-established expectations. In Stage 2 trials, large numbers of clones are evaluated in unreplicated, single-row plots. Cane yield is more adversely affected by the lack of replication and competition effects among clones in small plots compared to sucrose content (Jackson and McRae, 2001; McRae and Jackson, 1998; Hogarth, 1977). Kimbeng et al. (2001a) reported correlation coefficients that were always higher in magnitude for sucrose content compared to cane yield between clones in Stage 2 (single-row, unreplicated) and Stage 3 (2 replicates, multiple locations, 4-row plots) trials. Even in replicated clonal plots, the degree of genetic determination was five fold higher

for Brix compared to cane yield (Hogarth, 1977). Sucrose content is a more influential trait than cane yield in determining among clone differences in Stage 2 trials. The BSES is now routinely using spatial analysis, with the model also adjusting for intergenotypic competition, to improve estimates of cane yield in Stage 2 trials (Stringer and Cullis, 2002a, b). Research is underway to test the selection system proposed by Jackson and McRae (2001) in which, clones are evaluated in replicated 5-m plots with selections geared more towards sucrose content (measured objectively) and liberal for cane yield (measured as visual yield).

## CONCLUSIONS

Several research and simulation studies have shown that combined family and individual clone selection is a practical and cost-efficient method of selection in early stage sugarcane trials. Family selection is very practical under lodged conditions and is especially suited to mechanical harvesting. Family selection, based on the plant crop data, is useful in identifying those families that harbor the highest proportion of elite clones. This makes it possible to focus selection for superior clones (individual clone selection) on the best families. Adopting family selection in early stage trials has positively affected other aspects of the selection program. For example, the availability of objective data on progeny performance presented the opportunity to generate robust estimates of the breeding value of parents involved in crosses. This allowed for a more rapid recycling of elite parents into the crossing program than was previously possible with the proven cross method. The population from which families and clones are selected and the population of clones immediately following family and clonal selection showed an overall gradual improvement indicating that these populations were not adversely affected by the adoption of family selection. Taken together, this can only lead to an improvement in the overall efficiency of the selection programs.

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**Table 1.** The activities of the first two stages of a typical BSES sugarcane selection program

Year	Stage/ Crop	Operation <sup>†</sup>
1	Stage 1	<b>Seedling stage planted:</b> Full-sib families x 5 replicates x 20 seedlings/replicate.
2	P	<b>Family performance data collected:</b> Sucrose content (CCS) is estimated using eight stalks, one from each of eight randomly chosen stools in a plot. Cane yield (TCH) is estimated on a family-plot basis using mechanical harvester and mobile weighing tipper. The selection index, net merit grade (NMG), is calculated using CCS, and TCH data. NMG expresses family performance relative to that of standard families or proven crosses, which are adjusted to a mean of ten. The NMG formula penalizes families with poor appearance grade and awards a bonus for high sucrose content.
3	1R	<b>Clones selected from best families:</b> Individual clone selection is based on visual appraisal for yield and appearance grade and on Brix (% soluble solids w / w in the juice) measured using hand held refractometers.
	Stage 2	<b>First clonal stage planted:</b> Single-row, single replicate, 10-m plots.
4	P	<b>First clonal stage data collected and top 30% of clones selected as “tentatives”:</b> CCS is estimated using two random stalks in a plot. TCH is estimated for each clone using mechanical harvester and mobile weighing tipper. The selection index, NMG, is calculated using CCS and TCH data.
5	1R	<b>Data collected on “tentatives” and the top 20% selected:</b> CCS estimated using two random stalks in a plot. TCH is estimated for each clone using mechanical harvester and mobile weighing tipper. NMG is calculated using CCS and TCH.

<sup>†</sup> See Skinner (1967) for a more detailed explanation and calculation of NMG; the procedure to estimate CCS is outlined in a BSES (1984) publication.

**Table 2.** Selection rates, from Stage 2 to 3, of clones derived from different net merit grade (NMG) classes in Stage 1.<sup>†</sup>

Stage 1 NMG	No. of families selected in Stage 1	No. of clones selected Stage 1 to 2	% of clones selected Stage 1 to 2	No. of clones selected Stage 2 to 3	% of clones selected Stage 2 to 3	% of Stage 1 clones selected to Stage 3
9.0-9.9	19	53	2.7	2	3.8	0.11
10.0-10.9	54	379	7.0	26	6.9	0.48
11.0-11.9	36	486	13.5	36	7.4	1.00
12.0-12.9	18	304	16.9	23	7.6	1.28
= 13.0	11	191	17.4	26	13.6	2.36
Total	138	1413	10.2	113	8.0	0.82

<sup>†</sup> See Table 1 for a description of NMG and selection Stages.

**Table 3.** Gain from different selection strategies in Stage 1 as measured by performance in Stage 2.<sup>†</sup>

Selection strategy <sup>‡</sup>	Appraised Stage 1	Evaluated Stage 2	With NMG > 9.0 Stage 2 <sup>§</sup>	Gain, %
	.....No of clones.....			
Individual clone	2444	340	51	15.0
Family (F)	944	944	88	9.3
F + Visual grade	944	360	54	15.0
F + Visual grade + Brix	944	240	43	17.9

<sup>†</sup> See Table 1 for explanation on Stages of selection and NMG.

<sup>‡</sup> Only the top 40% of families are shown here.

<sup>§</sup> Clones with NMG > 9.0 are considered to be elite clones and are selected to the next stage.

**Table 4.** Correlation coefficients (r) between net merit grade (NMG) and Best Linear Unbiased Predictor (BLUP), and between NMG and empirical method among crosses in sugarcane. <sup>†</sup>

No. of families	Year(s) of data used to estimate BLUP values	Year of data used to estimate NMG values	r (NMG vs BLUP)	r (NMG vs Empirical method) <sup>‡</sup>
81	1992-93 (2)	1994	0.62	0.45
97	1992-94 (3)	1995	0.63	0.50
173	1992-95 (4)	1996	0.65	NA

<sup>†</sup> See Table 1 for explanation on NMG.<sup>‡</sup> At least 10 years of data used to estimate empirical mean values.**Table 5.** Mean net merit grade and standard deviation for families derived from parents arbitrarily categorized as old (O), medium (M), or new (N). <sup>†</sup>

Family category	No. of families	Net merit grade <sup>‡</sup>
OxO	21	5.31 ± 1.30 c
OxM	135	6.38 ± 1.47 b
OxN	22	6.17 ± 1.47 b
MxM	83	7.07 ± 1.74 a
MxN	30	7.05 ± 1.55 a
NxN	2	5.91 ± 1.42 abc

<sup>†</sup> Parents were arbitrarily categorized as old (O), medium (M), or new (N) if the seedling parent had a year prefix < 65, 65-74, or > 74, respectively; data averaged over four years.<sup>‡</sup> See Table 1 for explanation on NMG. NMG was calculated relative to standard clones in the trial. Usually, proven crosses are used as standard families.<sup>§</sup> Means followed by different letters are significantly different (P > 0.05); the NxN group had too few families to permit any reasonable comparison.



Figure 1. The shaded portions show areas where sugarcane is cultivated in Australia. The breeding stations operated by the BSES are located at Meringa (south of Cairns), Ingham, Ayr, Mackay and Bundaberg.

Figure 2. Percentage of elite Stage 2 clones resulting from different selection strategies in Stage 1. See Table 1 for explanation of selection stages and NMG.

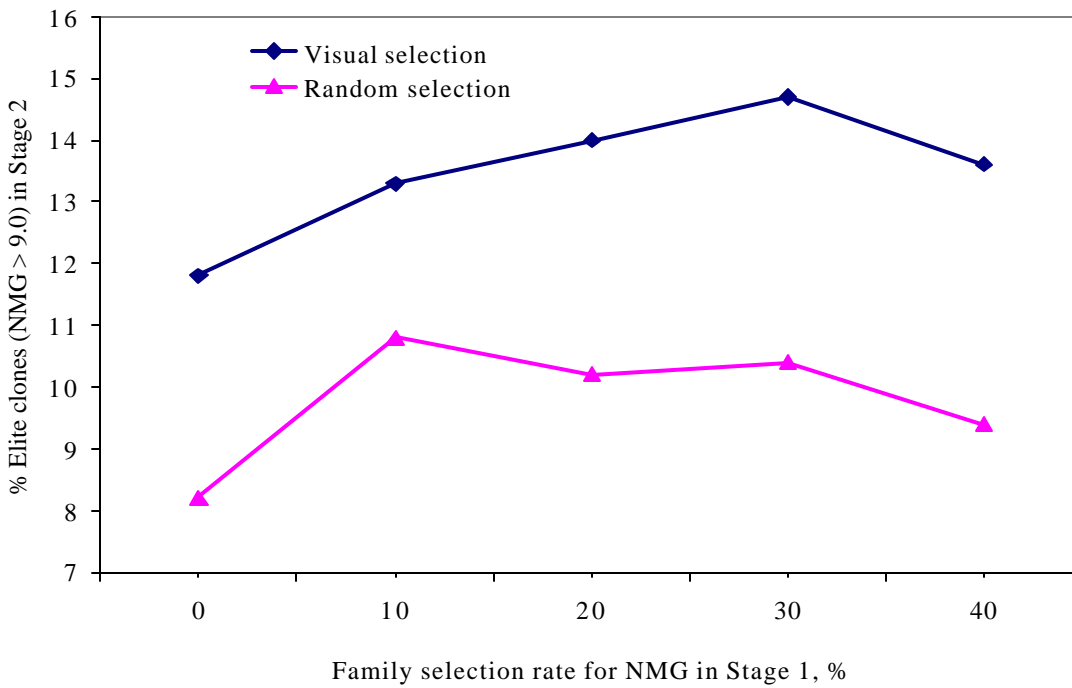


Figure 3. Population improvement in sugarcane: performance (NMG) of seedlings (Stage 1) relative to the cultivar Q151 from 1993 to 2000. See Table 1 for explanation of Stage 1 trials and NMG.

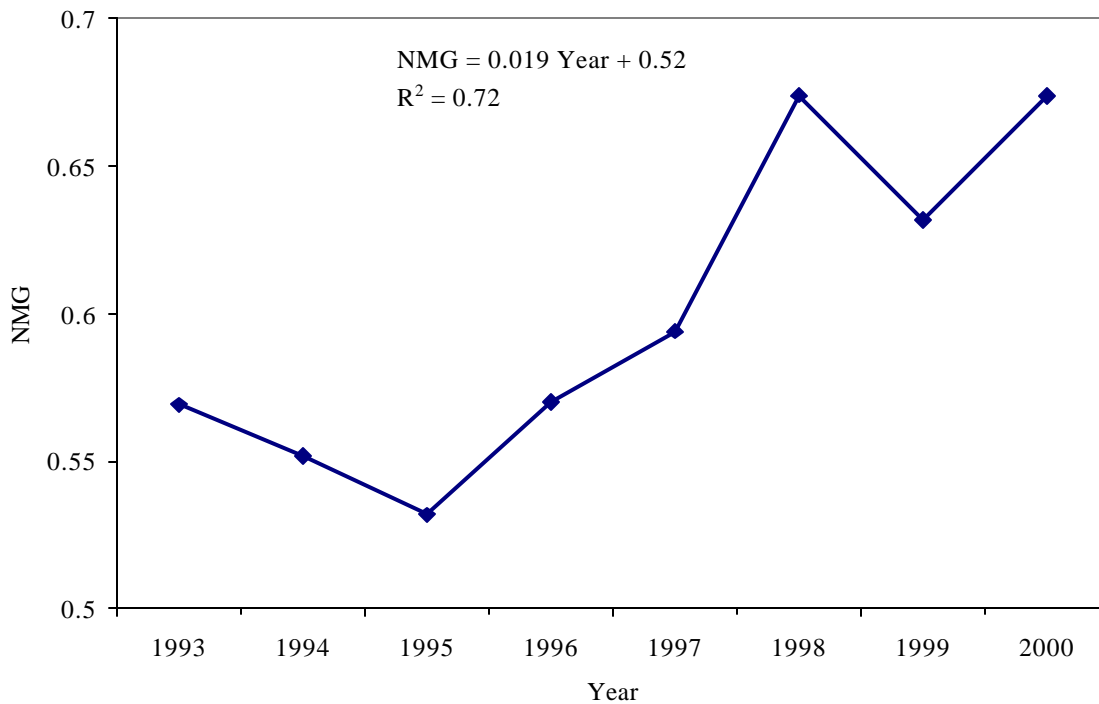


Figure 4. Population improvement in sugarcane: performance (NMG) of clones in Stage 2 relative to the cultivars Q141 and Q151 from 1994 to 2000. See Table 1 for explanation of Stage 2 trials and NMG.

