

## FAMILY SELECTION IMPROVES THE EFFICIENCY AND EFFECTIVENESS OF SELECTING ORIGINAL SEEDLINGS AND PARENTS

By

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### Abstract

FAMILY selection has been used in several sugarcane breeding programs for many years, and has been shown to be superior to individual selection (also known as mass selection), in terms of gains from selection, resource efficiency, and cost of operation. Other breeding programs have expressed interest in family selection, but the technique has not been widely adopted for logistical reasons. Suggestions for overcoming the constraints to family selection are made. Family selection has also been shown to provide a superior method for estimating the breeding value of parent clones. Objective data on the performance of families provides invaluable information on the breeding performance of parent clones. Best Linear Unbiased Predictors (BLUPs) can be estimated for a range of traits from the results of family selection trials, and these are estimates of breeding value. In Australia, current research is aimed at improving the BLUP estimates by combining data across all selection programs, including family × environment interactions, and partitioning the genetic effects of each parent into additive and non-additive genetic effects.

### Introduction

Family selection is used in the Australian and West Indian sugarcane breeding programs (Cox and Hogarth, 1993; Kennedy and Bellamy, 1997) and a modified version of family selection is used in Brazil (Bressiani *et al.*, 2005), Colombia (Victoria, pers. comm.) and Argentina (Issa Joya, pers. comm.). The potential of family selection to be more efficient than individual selection at the original seedling stage of selection was first identified by Hogarth (1971). However, at that time, family plots had to be cut and weighed manually, and the cost was prohibitive.

When mobile weighing equipment was developed in Australia (Hogarth and Mullins, 1989), there was an opportunity to assess the benefits of family selection, and several research projects were conducted. There has also been interest in family selection in other countries such as Indonesia (Sukarso, 1986), Cuba (Ortiz and Cabellero, 1989), South Africa (Bond, 1989), Hawaii (Wu and Tew, 1989), Florida (Tai and Miller, 1989) and Louisiana (Chang and Milligan, 1992a, b). However, family selection has not been widely adopted and this may be because suitable harvesting and weighing equipment is not available. In this paper, we suggest methods that could be used to implement family selection without such equipment.

Cox and Hogarth (1993) showed that the most efficient method of family selection was likely to be based on the performance of families in replicated plant crop trials, followed by within-family selection in the first ratoon crop. McRae *et al.* (1993) and Cox *et al.* (1996) presented further

evidence that a combination of family and individual selection was likely to be more effective than family selection alone. Jackson *et al.* (1995) reviewed family selection in sugarcane and described its implementation in Australian regional selection programs. Family selection in Australia has proved to make better use of available resources and is less costly than individual selection in original seedlings.

Family selection is not just an effective method for selecting original seedlings; results from family selection trials can also be used to estimate the breeding value of the parent clones that produced the families. Stringer *et al.* (1996) and Barbosa *et al.* (2004, 2005) studied Best Linear Unbiased Predictors (BLUPs) of parental performance estimated from family selection trials. BLUPs are estimates of breeding value, which is the additive genetic component of the genotype. Stringer *et al.* (1996) showed that BLUPs were more effective than the empirical algorithm previously used by BSES (Hogarth and Skinner, 1986, 1987). Superior combinations were identified with less information so that a reduction in the generation interval is possible. Hence, since the early 1990s, BLUPs have been used to select parents for cross pollination in Australia. Until recently, data from each selection program were analysed separately and genotype $\times$  environment interaction for the families and parents was not considered. Current research by Atkin *et al.* (2009) and Atkin *et al.* (personal communication) is aimed at improving the breeding value estimates by combining data across all selection programs, including family $\times$  environment interactions and partitioning the genetic effects of each parent into additive and non-additive genetic effects.

In this paper, we will examine the theoretical basis for using family selection, examine the results of some family selection trials, suggest how family selection could be implemented without mobile weighing equipment, and discuss recent advances in the selection of parent clones and the adoption of a new genetic evaluation system.

### **The theoretical basis for family selection**

At the original seedling stage of selection, each genotype is represented by only one plant. The phenotype of that plant depends on its genotypic value and the effect of the micro-environment in which the plant is grown. The environmental effect includes the effect of competition between plants, and Skinner (1961) showed that competition can have a highly significant effect on selection efficiency. The relative importance of the genotypic and environmental effects can be determined by conducting quantitative inheritance studies.

Skinner *et al.* (1987) showed that the degree of genetic determination (or heritability in the broad sense) for yield of cane at the original seedling stage was 0.17 or less (often much less) on an individual basis, but increased up to 0.75 on a family basis. This means that, on an individual basis, most of the variability among phenotypes is due to environmental effects. Consequently, selection for yield of cane on an individual basis will be largely ineffective in original seedlings. On the other hand, when families are weighed, most of the variability among families is due to genetic effects, so that the better families can be selected effectively.

When selected clones from the best families are planted into larger plots, the environmental effect is reduced relative to the genetic effect, and selection of individuals becomes more reliable.

It is important to recognise that most sugarcane traits are not inherited perfectly additively, especially cane yield, which is controlled about equally by additive and non-additive inheritance (see, for example, Hogarth (1987)). The implications of this are that parent clones can be selected for high sugar content or disease resistances based on the phenotypes of the parent clones but selection of parents for cane yield is much less reliable. As cane yield is a very important character, a strategy needs to be developed to maximise the chance of identifying families with high cane yield potential. The strategy developed in Australia is to plant as many experimental families as possible but relatively few seedlings are planted from each family (usually about 80 seedlings).

When the families are weighed in the plant crop, high yielding families are identified and, assuming their performance is satisfactory for other characters, these families are repeated in subsequent years in greater numbers. This maximises the chances of identifying high yielding families without wasting precious resources on planting a large number of seedlings from families that do not perform well.

### **Results from family selection research trials**

McRae *et al.* (1993) found that both individual and family selection were effective in an experiment conducted in the Burdekin region of Australia. In this experiment, the trial was planted later than commercial planting and the plant crop was poorly grown. They found that selection of families from the well-grown ratoon crop was more effective than family selection in the poorly-grown plant crop.

Nevertheless, both individual and family selection from the plant crop were effective, and the best method was combined family and within-family selection. That is, individual genotypes are only selected in the best families identified by family performance in the plant crop. In view of the experimental results, families are now planted in the Burdekin at the same time as commercial planting so that 'normal' crops are grown.

Cox and Hogarth (1993) and Cox *et al.* (1996) studied combinations of family and within-family selection in two experiments at the Bundaberg Experiment Station in Australia. They obtained gains of 3.4% and 5.3% from individual selection and gains of 9.7% and 12.9% respectively from a combination of family and within-family selection. Thus, combined family and within-family selection was about 2.5 times better than individual selection alone.

### **Family selection procedure**

Approximately 300 full-sib families are planted in each of the four regional selection programs in Australia. We aim to plant 80 seedlings per family in four replications of 20 seedlings. For each replicate, the seedlings are spaced at 50 cm in a single row of 11.4 m. If there are insufficient seedlings, there may be only two replicates from some families.

Typically, selection in family trials is a combination of family and within-family selection. Family selection is undertaken in the plant crop by assessing the performance of each family for cane yield, sugar and fibre content, and then concentrating selection efforts on the best performing families.

Only families in the top 40% undergo further selection in the ratoon crop, while poorer families are discarded as whole units. In addition, the numbers of individuals selected from within these top families depend on their performance in the plant crop. For example, 32 out of 80 individuals may be selected from the best 10% (i.e. 40% of individuals per family), 24 from the next 10%, 16 from the next 10%, and 8 from the next 10%. This means that the best families are selected at the highest rate.

### **Family selection without harvesters or mobile weighing equipment**

A number of breeding programs worldwide have expressed interest in family selection, but have been unable to implement it due to problems with harvesting and weighing the plots. There are two possible methods to overcome this problem, depending on the resources available.

#### **Method when cane is cut manually**

If cane is cut manually and the cutters can be relied on to identify plots, it is suggested that families be planted in two replicates of 45 seedlings. However, three-row plots should be used rather than single-row plots. At harvest, the cane cutters can load the cane from the three-row plot of cane into one bundle for easy weighing. Weighing can be done either mechanically using a grab with scales or manually with a boom and grab. Before the advent of mechanical harvesting and weighing, replicated trials in Australia were cut manually and weighed by using a boom and grab.

### **Method when cane is cut mechanically**

If cane is cut mechanically or the cane cutters can not be relied on to identify the ends of plots reliably, it is suggested that four replicates of single-row plots could be used as in Australia. To weigh the plots, the sampling method developed by Hogarth and Skinner (1967) could be used. Using this method, all the stalks in the plot are counted, and 40 stalks are cut from each plot. This 40-stalk sample would be weighed, and the plot weight estimated from the total number of stalks and the weight per stalk. By cutting 40 stalks from each plot, a path is cut through the trial allowing easy access of weighing equipment through the trial. A similar method was used in Australia for replicated trials when mechanical harvesters replaced manual cane cutters but before the development of mechanical weighing systems.

### **Estimation of breeding value of parents**

Hogarth and Skinner (1986, 1987) developed an empirical method for evaluating the breeding potential of a parental clone based on agronomic performance called Net Merit Grade (NMG), disease resistance status, and selection rates from crosses involving that parent. This method was an improvement on the previous intuitive method, but the correlation between predicted performance and actual performance of crosses was only about 0.40–0.50. A major problem with the method was that the most important data about the performance of parent clones were the selection rates from families involving the parents. The most useful selection rate data were the rates from advanced stages of selection, so that it took many years (often at least 10 years) to obtain good data on new parent clones.

When Stringer *et al.* (1996) developed their method for estimating breeding values based on BLUPs, the correlation between predicted and actual performance improved. Furthermore, useful data were obtained as soon as the plant crop of family selection trials was harvested, so that useful parent clone performance data were available many years sooner. Cox and Stringer (1998) reported on BLUP estimates, based on NMG, for parents of families harvested from 1993 to 1996, which were correlated with actual family performance in 1995, 1996 and 1997. For 81-172 families with BLUP estimates for both parents, the correlations were 0.62–0.65 compared with 0.45–0.50 for the previous system for estimating breeding value. It should be emphasised that the BLUP estimates were often based on results of a single family selection trial whereas the previous breeding values were estimated from many years of selection data.

The NMG system for assessing clonal performance was described by Skinner (1967) and is based on tonnes cane per hectare (TCH), CCS (sugar content), fibre percent and visual appearance grade. Clones (or families) are compared with standard clones (or families), and a bonus is given if the CCS is higher than the standard CCS and a penalty is applied if fibre content is higher than the standards' fibre. When BLUPs were first used to estimate breeding value of parent clones, the NMG of a family was calculated by comparing family performance with the mean of several standard (proven) families.

### **Problems with the NMG system**

The problems with the NMG system and how to overcome them were detailed by Stringer *et al.* (2009). The issues will be described briefly in this paper.

The traditional genetic evaluation system relied on NMG and independent evaluation of clones for disease resistance and sugar quality. The system was inefficient because:

- Weightings of the different traits of importance in a cultivar did not reflect their true economic value. For example, NMG was highly correlated with TCH, so there was greater emphasis on selection for high TCH relative to high CCS. This was effective in maximising sugar yields, but high TCH clones have higher production and harvesting costs and produce a lower economic return for the whole industry than is possible with clones using optimal economic weightings for all traits.

- NMG did not incorporate disease resistances which were assessed independently for selection purposes. This is not as effective as index selection.
- NMG did not use inherent genetic correlations between traits and environments, even though many clones were tested at multiple sites and regions. An analysis that combines all trial results will produce a superior assessment of the true genetic value of a clone.
- NMG did not take account of variable data quality across trials and traits. BLUPs can overcome this problem.
- Breeding values predicted using BLUPs on data collected from family selection trials did not use pedigree information to calculate a NMG score.

### **The improved Genetic Evaluation System (GES)**

The improved system is based on the theory of selection index (Hazel, 1943; Smith, 1936). A selection index considers all traits of economic importance and weights those traits with an appropriate economic weight. Economic weights were derived from a model developed by Wei *et al.* (2006) who obtained information from a consultative group consisting of a range of industry experts. Income and cost structures for the entire production, processing and marketing chain were used in the model by linking the incomes and costs with sugarcane traits. By changing one unit of a trait while holding other traits constant, the change in cost of producing one tonne of sugar became the economic weight of the trait. The economic importance of a disease was determined by its risk factor or potential damage. Cane yield loss was assumed to be the only damage caused by a disease with no effect on CCS.

It is also necessary to predict breeding values (BVs) of parent clones, which is achieved by using the statistical software ASReml (Gilmour *et al.*, 2006). Until recently, the approach involved analysing each trial separately to identify outliers and site specific spatial variation as defined by Gilmour *et al.* (1997). Ten years of data were then combined with pedigree information on each parent within a region. A mixed model approach with a biparental genetic model (Henderson, 1984; Mrode, 2005) was used to obtain BLUPs for each parent. This approach was limited by not considering genotype $\times$  environment interaction for the families and parents. In a recent approach developed by Atkin *et al.* (2009) to use family data more efficiently, data from all four selection programs are now combined to exploit genetic variances and covariances between trials and regions (Atkin *et al.*, personal communication). Additionally, the genetic effects of each parent are partitioned into additive and non-additive genetic effects (Costa e Silva *et al.*, 2004). By using all available information from family trials and genetic correlations across regions, more reliable estimates of BV of parents are obtained.

To determine the best families, seven years' data from each region are combined, excluding pedigree information. Data are analysed using a mixed model to partition individual family effects, and regions are assumed to be independent. BLUPs for each family within each region are estimated.

The Economic Breeding Value (EBV) of a parent clone is estimated from a selection index that incorporates the genetic effects and the economic weightings. The index is optimised to give estimates that have the most relevance for commercial production of sugarcane.

### **Conclusions**

Family selection has been used in the Australian sugarcane breeding program for almost 20 years. There is a strong body of evidence to show that a combination of family and within-family selection is more effective (greater genetic gains) and more efficient than individual selection alone. In recent years, there have been major improvements to the way family selection is used in the BSES-CSIRO Joint Venture variety improvement program. We have replaced NMG with a new

selection index for estimating both the genetic value of families and the breeding value of parents, which uses economic weights of the various traits in a sugar production system and the best genetic estimates. This is part of an improved genetic evaluation system. We have also greatly improved methods of analysis by accounting for spatial variation, combining all data (over years and locations) and, for parents, partitioning the genetic effects into additive and non-additive genetic effects.

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## LA SÉLECTION FAMILIALE AMÉLIORE L'ÉFFICIENCE ET L'EFFICACITÉ DE SÉLECTION DES PLANTULES ORIGINALES ET DES PARENTS

Par

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**MOTS CLÉS:** Sélection Familiale, Plantules Originales, Sélection Parentale.

### Résumé

LA SÉLECTION familiale a été utilisée dans plusieurs programmes d'amélioration variétale depuis de nombreuses années, et s'est avérée supérieure à la sélection individuelle (également connue comme la sélection massale) en termes de gains en sélection, utilisation des ressources et coûts de l'opération. D'autres programmes d'amélioration variétale ont exprimé un intérêt pour la sélection familiale, mais la technique n'a pas été largement adoptée pour des raisons de logistiques. Des suggestions pour surmonter les contraintes de la sélection familiale sont faites. La sélection familiale a également démontré qu'elle peut fournir une méthode supérieure pour estimer la valeur génétique des parents. Les données objectives sur la performance des familles peuvent fournir des informations inestimables sur la performance des géniteurs. 'Best Linear Unbiased Predictors' (BLUP) peuvent être estimés pour une gamme de caractères à partir des résultats des essais de sélection familiale, et représentant des estimations de la valeur des parents. En Australie, la recherche actuelle a pour but d'améliorer les estimations du BLUP en combinant des données provenant de tous les programmes de sélection, y compris les interactions famille x environnement, et en décomposant des effets génétiques de chaque parent en effets génétiques additifs et non-additifs.

## LA SELECCIÓN FAMILIAR MEJORA LA EFICIENCIA Y EFICACIA DE SELECCIÓN INICIAL DE LAS PROGENIES Y PROGENITORES

Por

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**PALABRAS CLAVES:** Selección Familiar, Progenies Iniciales, Selección Parental.

### Resumen

LA SELECCIÓN familiar ha sido usada en varios programas de mejoramiento de caña de azúcar por varios años, mostrando ser mejor que la selección individual (conocida también como selección masal), en términos de ganancia por selección, eficiencia de uso de recursos y costos de operación. Aunque otros programas de mejoramiento han expresado interés por el uso de la selección familiar, esta técnica no ha sido usada mayormente por razones logísticas. Algunas sugerencias para sobrepasar los obstáculos del uso son sugeridas. La selección familiar también ha mostrado ser superior para estimar el valor genético de los parentales como una información objetiva sobre el comportamiento de las familias y la capacidad de cruza de los clones parentales. Las mejores predicciones lineales no sesgadas (BLUPs) pueden ser estimadas para un rango de caracteres desde los resultados de los ensayos de selección familiar, que a su vez son los estimados del valor genético. En Australia, actualmente los experimentos están encaminados a mejorar los estimados de BLUP, combinando datos de todos los programas de selección, incluyendo las interacciones familia× ambiente, separando los efectos genéticos de cada progenitor entre los efectos aditivos y no-aditivos.