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Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods *

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Summary. A quick, accurate method to determine the potential of a sugarcane (*Saccharum* spp.) cross to produce elite progeny is needed for maximizing genetic gain. Development of a practical cross appraisal method was initiated by evaluating 1,800 progeny from 15 crosses among 23 parents at two intrarow plant spacings (41 cm and 82 cm). Plant spacing was examined for its affect on stool weight variability. The goals were to identify the most reliable and/or easily obtained cross appraisal statistic and to determine the earliest breeding program stage and crop to collect these statistics. Three tests, on plant cane (PC) and first ratoon (FR) single stool seedlings and clonal plant cane plots, were conducted. Four statistics, the family mean, the estimated elite proportion (PROB), the observed elite proportion, and the best linear unbiased predictor (BLUP) were estimated and examined for each cross. These statistics were strongly correlated within each test ($0.69 \leq r \leq 1.00$). Family worth estimates based on single stool data were moderately correlated (ca. range $0.5 \leq r \leq 0.7$) to the family worth estimates based on clonal plots.

The research suggested that the potential of a cross to produce elite progeny for a trait could be accurately predicted by the cross mean of that trait. Data for the mean were the most easily obtained and, hence, would be the most practical family appraisal statistic to use in a breeding program. Correlations of statistics among the PC and FR seedlings and the clonal plots showed that the PC estimates of Brix, stalk weight, and its components, stalk length and stalk diameter, could be used for cross appraisal. Genotypic selection by the Louisiana Sugarcane Variety Development Program (LSVDP) occurs among the FR seedlings. FR stalk number and PC Brix and stalk weight data could be used to perform family selection prior to the currently practiced individual plant selection. The benefits of family selection to the LSVDP were demonstrated by the expected genetic gains for two selection scenarios. The gains were consistently larger for an initial 50% family selection and subsequent 20% individual selection than they were for simple individual selection at a 10% selection intensity. Our research also suggests that the use of a wider intrarow spacing may improve the ability to discern among seedlings due to its enhancement of stool weight variability.

Key words: Sugarcane – Cross prediction – Univariate normal probability – Best linear unbiased predictor – Family selection

Introduction

One of the major challenges confronting plant breeders is the choice of parental combinations. Sugarcane (*Saccharum* sp. hyb.) is a polyploid, highly heterozygous, clonally propagated crop. In Louisiana, the photoperiod of sugarcane genotypes, planted 1 year in advance, must be manually manipulated for 3 months using a cart and trolley system of heated photoperiodic bays and crossing houses to induce flowering for the production of crosses. Results by Milligan (1988) and Miller (1977) have indicated the importance of nonadditive genetic variance in determining the desirability of a sugarcane cross. Desirable crosses are commonly remade or replanted to successfully yield commercial cultivars. The costs and limitations of the crossing system and the importance of nonadditive genet-

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ic variance increase the need for an accurate and efficient cross appraisal system to maximize the genetic gains of the breeding program. Many sugarcane breeding programs worldwide appraise crosses by the percentage of the original seedlings planted that are selected and replanted in more advanced stages of testing. This empirical method requires several years to estimate. A faster measure of cross potential could be used to concentrate selection efforts on the most elite families and more effectively direct the production of the best crosses.

A number of statistics have been used to predict family performance. Brown et al. (1988) used the estimated probability (PROB) of elite progeny from a potato (*Solanum tuberosum* L.) cross to evaluate the potential to produce elite progeny. The PROB was the normal probability to exceed a target value calculated with the family mean and variance. In potatoes and tobacco, this PROB has been reported to be a useful predictor of elite progeny (Jinks and Pooni 1976; Caligari and Brown 1986; Brown et al. 1988; Brown and Caligari 1989). As early as 1962, George (1962a) proposed a similar concept to use the mean and estimated genetic variance (or phenotypic standard deviation) for calculating the theoretical number of seedlings of a sugarcane cross that would give a reasonable chance of producing a commercial variety. Coleman et al. (1962) suggested the percentage of superior sugarcane plants for each measured character in a cross could be used as the probability of obtaining elite progeny for that character, and frequency distributions could be used in evaluating parents and crosses. These earlier concepts were not seriously considered until Jinks and Pooni (1976) proposed normal probability prediction of the properties of recombinant lines. In their research, the family mean and additive genetic variance were used. It was found that in potato cross prediction the phenotypic standard deviation could replace the genetic variance in the estimation of PROB (Caligari and Brown 1986; Brown et al. 1988).

BLUPs (best linear unbiased predictor) have been used to estimate the breeding value of a sire to maximize gains in animal breeding (Henderson 1984) and have been suggested for use in plant breeding (Bridges 1989). BLUPs enable the integration of genetic information from relatives to theoretically improve the accuracies of the estimated family potential and provide insight into the future performance of the family. A simple statistic is the mean performance of a cross's progeny. Work by Caligari and Brown (1986) have shown that the family mean gives a good indication of potato cross potential. In Mauritius, mean performance also seemed to be a useful guide to the worth of sugarcane families when differences between crosses were large (George 1962b). The differences between the means of the families were often sufficiently reliable to permit the choice of the family with the highest mean expression.

The LSVDP plants its seedlings 41 cm apart within the row. Progeny of certain crosses commonly crowd each other, thereby inhibiting a genotype's ability to tiller. Lyrene et al. (1977) reported that the poorest tillering clone in a spaced test produced far more tillers per primary bud than the best tillering clone under high density conditions. His work suggested that selection of vigorously tillering clones among spaced stools could distinguish cultivars that produced above average stalk populations in competitive plantings. He hypothesized that wider intrarow plant spacing may increase the tillering variability of certain families. Increased variability among a progeny population could enhance the ability to identify those genotypes with high tillering ability.

The objectives of the study reported here were to identify the most practical statistic by which to accurately predict the potential of a cross to produce elite progeny and to verify if single, stool-based familiy appraisal estimates for cane yield can predict the cane yield potential based on clonal plot data. An additional goal was to determine the effect of intrarow plant spacing on cross variability.

Materials and methods

Sugarcane seedlings were planted in mid-April, 1989. A total of 120 progeny from each of 15 biparental crosses among 23 parents were randomly chosen and grown at the St. Gabriel Research Station, St. Gabriel, La. A randomized complete block (RCB) design with three replications and two intrarow plant spacings (the standard, 41 cm, and double spacing, 82 cm) were used. Each plot consisted of two rows (1.83 m apart) with 10 plants in each row. Additional plants were included to buffer the test plants and to equalize plot size. To appraise the relationship between single plant or single stool-based cane yield estimates and clonal plot cane yield estimates, two stalks from each of 60 progeny from each cross were randomly harvested and planted (1.83-m single row plots with 1.83-m interrow spacing and a 0.61-m plot alley) in November, 1989. The progeny were planted at random in a RCB design using three blocks.

Data were collected on Brix (% soluble solid w/w in the juice), stalk number, stalk diameter, and stalk length from plant cane seedlings in the fall of 1989 and from first ratoon seedlings (stools) in the fall of 1990. First clonal (FC) data were collected in the fall of 1990. The test encountered considerable johnson grass (*Sorghum halepense* L.) pressure, a record freeze in December, 1989 (<0 °C for 72 h), and a wet winter (November, 1989 to March, 1990, 32% rainy days with a total precipitation of 881 mm). Several plants died but 1,352, 1,228, and 449 plants or plots survived in the PC, FR and FC tests, respectively.

The stalk length was measured from the stalk base to the first visible dewlap (leaf collar) of the tallest stalk in each stool. The mid-stalk internode diameter and Brix of three stalks were measured by caliper and hand refractometer, respectively. Assuming the stalk was a perfect cylinder with a specific gravity of one, we estimated the stalk weight as:

$$\text{Stalk weight} = p \pi r^2 L$$

where the density $p = 1.0\ \text{gm cm}^{-3}$, r = stalk radius, and L = stalk length. Stool weight was estimated as stalk weight times stalk number per stool. Plot weight was calculated as stalk weight times stalk number per plot. A similar technique of plot weight estimation in South Africa gave a rapid assessment of yield in trials and showed a good correlation with actual yield (Bond 1977).

The probability (PROB) to exceed a target value assumed a normal distribution for the observations in this study and was estimated using the Z parameter for normal probability (Steel and Torrie 1980) as:

$$\mathrm{PROB} = \mathrm{Prob}\,(\mathrm{Z} > (\mathrm{target} - \bar{\mathrm{X}}_i)/\mathrm{s}_i)$$

where the $\bar{X}_i$ and s_i were the full-sib family mean and standard deviation, respectively, of family *i*. Acceptable target values were chosen to distinguish the family potential of producing elite lines. A SAS function, PROBNORM (SAS 1985a), was used to calculate PROB. The observed elite proportion (OBS) that transgressed the same target values as PROB was also calculated. For example, assume family *i* produced an average of 10 ± 2 stalks per square meter. Let the target be 13 stalks per square meter. Then

$$\mathrm{Z}_i = (13 - 10)/2 = 0.667$$

$$\mathrm{PROB}\,(\mathrm{Z} > 0.667) \approx 0.25$$

or about 25% of the progeny of family *i* should produce 13 or more stalks per square meter.

BLUPs have been adopted by animal breeders as a selection index of sire breeding value (Henderson 1982, 1984). BLUPs may use genetic and environmental variances and covariances in their calculations. This enables the use of genetic information from relatives and the ability to adjust for environmental factors, and is theoretically the most dependable predictor. The genetic variance-covariance matrix used in this study was derived from an analysis among full-sib families. The family variance was:

$$\sigma^2_{\mathrm{fs\,family}} = 1/2\,\sigma^2_{\mathrm{a}} + 1/4\,\sigma^2_{\mathrm{d}} + 1/4\sigma^2_{\mathrm{aa}} + 1/8\,\sigma^2_{\mathrm{ad}} + 1/16\,\sigma^2_{\mathrm{dd}} + \ldots$$

where σ^2_a was the additive variance, σ^2_d was the dominance variance, and σ^2_{aa}, σ^2_{ad}, and σ^2_{dd} represented types of epistatic variance (Becker 1984). The BLUPs calculated in this study incorporated genetic information from related crosses. The genetic information was weighted by the additive genetic relationship of relatives, and this was used to modify genetic variance estimates among the crosses. The genetic variance was biased upward by the nonadditive genetic variance. The degree of bias was unknown but could be substantial since Milligan (1988) found nonadditive variance constituted the major portion of the genetic variance of a similar population. The net effect of the bias would be to overextend the range of BLUP values, since BLUPs will regress toward the overall mean under low heritability situations. Since the bias was inflationary, the estimated heritabilities were likely inflated and, hence, the range of BLUP values was also so affected. In this study, the estimation of BLUPs for full-sib families generated broad genetic values rather than breeding values of crosses.

BLUPs were calculated using the mixed model equation:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{U} + \mathbf{e}$$

where **X**, **Z** were design matrices of fixed and random effects, respectively; $\boldsymbol{\beta}$ and **U** were parameter vectors of fixed and random effects, respectively; **e** was the residual error matrix; and **y** was the individual observation vector. The solution to the mixed model equation was shown by Henderson (1973, 1984) to be:

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \mathbf{b} \\ \mathbf{u} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$

where **b** and **u** were solutions to the mixed model equations; **b** was best linear unbiased estimator of fixed effects ($\boldsymbol{\beta}$); and **u** was the best linear unbiased predictor of random effects (**U**). Genetic (**G**) and environmental (**R**) variance-covariance matrices were obtained by REML methods (Proc Varcomp, SAS 1985b). The genetic variance of a cross for each trait was modified by the additive genetic numerator relationship matrix among the crosses (Henderson 1976) using a SAS IML program (SAS 1985c). Since in the study presented here we were interested in predicting the future performance of a family and were not concerned about the future records of blocks, the block effect was treated as a fixed effect while cross effects were considered random effects in model (1). Such a consideration had no effect on the BLUPs calculated. The initial model used was:

$$\mathrm{Y}_{ijk} = \mu + \beta_k + \mathrm{S}_j + \mathrm{C}_i + \mathrm{SC}_{ij} + \mathrm{e}_{ijk} \qquad (1)$$

where Y_{ijk} was the individual observation of family *i* in block *k* and intrarow spacing *j*, μ was the overall mean, β_k was the block *k* effect ($k = 1, 2, 3$), S_j was the intrarow spacing *j* effect ($j = 1, 2$), C_i was cross *i* effect ($i = 1, 2, \ldots, 15$), SC_{ij} was the cross by spacing interaction, and e_{ijk} was the residual.

Three additional reduced models were also considered:

$$\mathrm{Y}_{ijk} = \mu + \beta_k + \mathrm{S}_j + \mathrm{C}_i + \mathrm{e}_{ijk} \qquad (2)$$

$$\mathrm{Y}_{ik} = \mu + \beta_k + \mathrm{C}_i + \mathrm{e}_{ik} \qquad (3)$$

$$\mathrm{Y}_i = \mu + \mathrm{C}_i + \mathrm{e}_i \qquad (4)$$

The effects of model (1) not contained in models (2), (3), or (4) were pooled into the residual. For all traits the solutions of **u** for cross effects using the reduced models (2), (3), and (4) were found to be strongly correlated ($r \geq 0.98$) with that of the full model (1). For simplification, the reduced model (3) was adopted to estimate the BLUPs of a cross. The prediction could be written as:

$$\mathbf{w} = \mathbf{K}'\boldsymbol{\beta} + \mathbf{M}'\mathbf{U}$$

$$\text{BLUP of } \mathbf{w} = \text{BLUP of } \mathbf{K}'\boldsymbol{\beta} + \mathbf{M}'\mathbf{U} = \mathbf{K}'\mathbf{b} + \mathbf{M}'\mathbf{u}$$

where $\boldsymbol{\beta}$, **U**, **b**, **u** were as defined previously, and **K**′ and **M**′ were estimable functions of fixed and random effects, respectively (Henderson 1984). For example, $\mathbf{K}' = \{1, 1/3, 1/3, 1/3\}$, $\mathbf{M}' = \{1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0\}$ are vectors for estimating the BLUP of the first cross averaged over three blocks.

Analysis of the effect of intrarow plant spacings on the family variability used the family standard deviation following the full model (1). In this model, Y_{ijk} was the family standard deviation of cross *i* in block *k* and intrarow spacing *j*. The block was considered to be random, while the other effects were considered to be fixed.

Expected genetic gains of single traits from combined among- and within-family selections (GA_c) and simple mass selection (GA_i) were calculated following the formulas adopted by Loo-Dinkins et al. (1990):

$$\mathrm{GA_c} = \frac{\mathrm{k_f}\,\sigma^2_{\mathrm{gf}}}{(\sigma^2_{\mathrm{gf}} + \sigma^2_{\mathrm{fs}}\,\mathrm{t} + \sigma^2_{\mathrm{e}}/\mathrm{r\,t})^{1/2}} + \frac{\mathrm{k_i}\,\sigma^2_{\mathrm{gi}}}{(\sigma^2_{\mathrm{gi}} + \sigma^2_{\mathrm{fs}} + \sigma^2 + \sigma^2_{\mathrm{w}})^{1/2}} \qquad (5)$$

$$\mathrm{GA_i} = \frac{\mathrm{k_i}\,\sigma^2_{\mathrm{gi}}}{(\sigma^2_{\mathrm{gi}} + \sigma^2_{\mathrm{fs}} + \sigma^2 + \sigma^2_{\mathrm{w}})^{1/2}} \qquad (6)$$

$$\sigma^2_{\mathrm{e}} = \sigma^2_{\mathrm{w}}/\mathrm{n} + \sigma^2$$

$$\mathrm{GA\%} = 100\,\mathrm{GA}/\text{general mean}$$

where in equation (5), $k_f = 0.798$, $k_i = 1.400$ for 50% family selection intensity followed by 20% individual selection intensity (combined selection) in standard deviation units, respectively, and in equation (6), $k_i = 1.756$ for 10% mass selection intensity in standard deviation units. σ^2_{gf} and σ^2_{gi} were among- and within-family genetic variances, respectively. σ^2_{fs} was the family by spacing variance; σ^2_e was the error variance; σ^2_w and σ^2 were within-and among-plot variances, respectively. The number of individual plants per plot was represented by n, while t was the number of intrarow plant spacings, and r was the number of replications. The parameters of family selection and individual selection were estimated on a plot mean basis and individual plant basis, respectively. The selected families (50% of original families) were assumed to have the same genetic and environmental variances as the original population. Variances in formulas (5) and (6) were obtained by REML methods (Proc Varcomp, SAS 1985b). Expected genetic gains were divided by the general mean of each trait to allow relative comparison among traits.

Results and discussion

Analysis of variance of the family standard deviation of single traits suggested that the variance differed among crosses for all cane yield components and Brix in the PC (Table 1). Cross variance was significant for stool weight, stalk number, and stalk weight in the FR, and was significant for Brix in the clonal plots. Intrarow plant spacing significantly affected cross variance for stool weight in the PC and FR and also affected its stalk length (Table 2). The mean standard deviation of crosses for stool weight was larger in wider intrarow plant spacings than in narrow row plant spacings in both the PC and FR tests. Stool weight is the product of stalk weight and stalk number. Standard deviations of stalk weight for narrow and wide spacings were similar in both PC and FR, while stalk number showed a trend toward larger standard deviations at wide spacings than at narrow spacings for PC and FR. This was probably the reason for the difference between narrow and wide spacing standard deviations of stool weight. The standard deviation of stalk length was smaller at wide spacings than at narrow spacings. Breaux and Miller (1987) suggested that sugarcane seedlings must be spaced far enough apart within the row to be readily distinguishable from each other at selection time, but spacial constraints and the desire to use land for more tests may affect the final choice of intrarow spacing.

Table 1. Mean squares based on family standard deviation for plant cane and first ratoon seedlings and first clonal plots

Source	*df*	Stool weight (kg^2)	Stalk number [(stool^{-1})^2]	Stalk weight (kg^2)	Stalk diameter (cm^2)	Stalk length (m^2)	Brix (%^{2})
Plant cane seedlings							
Block	2	4.62	3.39	1.44	6.58	5.85	10.32
Spacing (S)	1	2.18*	0.30	4.56	4.58	21.87	1.29
Cross (C)	14	1.74**	1.20§	9.38**	9.37§	11.01§	5.67§
C × S	14	0.70	0.51	5.61	6.64	9.96	2.09
Error	58	0.54	0.70	3.77	5.53	5.91	3.22
First ratoon seedlings							
Block	2	4.44	0.71	12.25	1.93	1.54	2.97
Spacing (S)	1	19.62§	9.92	1.80	2.22	0.01	0.38
Cross (C)	14	13.87*	13.15§	16.79**	10.71	4.57	3.02
C × S	14	5.38	5.02	5.58	10.31	7.59	4.15
Error	58	6.86	7.45	5.25	6.64	4.90	3.86
First clonal plots							
Block	2	25.95	11.50	1.49	2.60	9.44	1.09
Cross	14	139.24	5.01	12.72	7.87	8.16	8.11**
Error	58	153.38	4.50	15.44	6.34	11.72	2.46

§,*,** Significant at 10%, 5%, and 1% probability levels, respectively

Table 2. Mean family standard deviation for narrow and wide intrarow plant spacing in plant cane and first ratoon seedlings

Spacing	Stool weight (kg)	Stalk number (m^{-2})	Stalk weight (kg)	Stalk diameter (cm)	Stalk length (m)	Brix (%)
Plant cane seedlings						
Narrow (41 cm)	2.25	2.82	0.26	0.33	0.40*	2.29
Wide (82 cm)	2.99*	3.25	0.25	0.34	0.37	2.35
First ratoon seedlings						
Narrow (41 cm)	6.03	6.18	0.29	0.32	0.36	2.41
Wide (82 cm)	7.35§	6.85	0.32	0.32	0.38	2.24

§,* Mean standard deviations are significantly different at the 10% and 5% level, respectively

Table 3. Correlation of the observed elite proportion, the full-sib mean, the predicted elite proportion, and best linear unbiased predictor among plant cane and first ratoon seedlings and the first clonal plots for stool weight

	PC			FR				FC			
	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP
PC[a] OBS[b]	0.91**	0.95**	0.88**	0.65**	0.78**	0.70**	0.78**	0.59*	0.54*	0.54*	0.52*
PC MEAN		0.91**	0.98**	0.80**	0.87**	0.83**	0.87**	0.54*	0.59*	0.56*	0.58*
PC PROB			0.89**	0.57*	0.70**	0.64**	0.69**	0.55*	0.51§	0.49§	0.53§
PC BLUP				0.79**	0.85**	0.82**	0.87**	0.48§	0.56*	0.51§	0.58*
FR OBS					0.94**	0.92**	0.93**	0.52*	0.57*	0.52*	0.52*
FR MEAN						0.97**	0.99**	0.56*	0.62*	0.57*	0.57*
FR PROB							0.96**	0.50§	0.57*	0.51§	0.53*
FR BLUP								0.55*	0.61*	0.55*	0.57*
FC OBS									0.85**	0.90**	0.79**
FC MEAN										0.97**	0.98**
FC PROB											0.93**

§, *, ** Significant at 10%, 5%, and 1% probability level, respectively

[a] PC, Plant cane seedling; FR, first ratoon seedling; FC, first clonal plot

[b] OBS, Observed elite proportion; MEAN, full-sib family mean; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

Skinner et al. (1987) showed that in small plots competition may inflate the phenotypic, genotypic, and error variances. A high-yielding commercial variety requires satisfactory stalk number, stalk diameter, and stalk length. The enhancement of stool weight variability by increasing the intrarow plant spacing should facilitate selection for high-yielding genotypes.

In Louisiana, single stool selection is performed on first ratoon seedlings in early September, about 17 months after planting, to allow for natural selection for winter hardiness and to consistently produce stalks of sufficient planting size. The important traits included in the early selection stages are cane yield components (stool weight, stalk number, stalk weight, stalk diameter, stalk length), juice quality (Brix, juiciness-pith), stalk solidness (tube), vigor, and disease resistance.

Although seedling selection occurs during September, stalk number can be accurately recorded in August while stalk weight and sucrose content continue to increase through November. Thus, the seedling stage potentially permits two stalk number recording seasons and one (PC) stalk weight and sucrose content data collection seasons prior to single stool selection.

Stool weight values of both the PC and FR seedlings tests were moderately correlated ($0.48 \leq r \leq 0.62$) to the clonal plot values (Table 3). Since sugarcane is a clonally propagated crop, the data collected from the FC test were assumed to be the most accurate measures of family cane yield values. Since we were interested in a quick evaluation, if PC or FR data were correlated to FC data, PC or FR data may suffice to estimate family yield potential. The correlations among tests seemed adequate to support the contention that family cane yield estimates based on single stool evaluations were worthy statistics for family cane yield appraisal. The MEAN and the BLUP displayed slightly stronger correlations between tests than did OBS and PROB. MEAN in the PC strongly correlated with statistics in the FR ($0.80 \leq r \leq 0.87$), but correlations were lower between the PC and the FC tests ($0.54 \leq r \leq 0.59$). MEAN values in the FR also moderately correlated with statistics in the FC ($0.56 \leq r \leq 0.62$). The mean family value is the easiest statistic to collect and appears to be a reasonable predictor of cross worth for stool weight.

The correlations among tests for stalk number were variable and poor between the PC and the FC tests ($0.04 \leq r \leq 0.46$), but moderately strong between the FR and the FC tests ($0.42 \leq r \leq 0.66$) (Table 4). The genetic variability of this trait, the potential for improvement by selection, and its stronger correlation to cane yield than stalk weight suggests that stalk number is the most important component of cane yield (James 1971; Milligan et al. 1990). Correlations of PC values with FR or FC values were better for MEAN and BLUP statistics than for OBS or PROB statistics. Thus, the best estimates were obtained in the FR. Since accurate stalk counts can be made in August before the normal FR single stool selection occurs in September, it would allow selection among families for stalk number before selection among stools.

Stalk weight was significantly correlated between tests, with higher values between the PC and FR tests ($0.61 \leq r \leq 0.89$) and between the FR and FC tests ($0.63 \leq r \leq 0.73$) (Table 5) than between the PC and FC tests ($0.45 \leq r \leq 0.75$). The rather strong correlations between PC and FR, as well as between FR and FC, suggested that stalk weight could be either evaluated late in the PC

Table 4. Correlation of the observed elite proportion, the full-sib mean, the predicted elite proportion, and best linear unbiased predictor among plant cane and first ratoon seedlings and the first clonal plots for stalk number

	PC			FR				FC			
	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP
PC[a] OBS[b]	0.82**	0.87**	0.81**	0.60*	0.70**	0.72**	0.68**	0.04	0.24	0.15	0.28
PC MEAN		0.85**	0.98**	0.73**	0.80**	0.80**	0.76**	0.28	0.42	0.31	0.44§
PC PROB			0.82**	0.48§	0.53*	0.53*	0.51§	0.05	0.17	0.08	0.26
PC BLUP				0.78**	0.81**	0.82**	0.79**	0.28	0.44§	0.30	0.46§
FR OBS					0.92**	0.88**	0.93**	0.42	0.59*	0.51§	0.51§
FR MEAN						0.99**	0.99**	0.52*	0.66**	0.58*	0.56*
FR PROB							0.98**	0.47§	0.60*	0.52*	0.50§
FR BLUP								0.51§	0.65**	0.59*	0.53*
FC OBS									0.70**	0.86**	0.53*
FC MEAN										0.85**	0.95**
FC PROB											0.70**

§,*,** Significant at 10%, 5%, and 1% probability levels respectively

[a] PC, Plant cane seedling; FR, first ratoon seedling; FC, first clonal plot

[b] OBS, Observed elite proportion; MEAN, full-sib family mean; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

Table 5. Correlation of the observed elite proportion, the full-sib mean, the predicted elite proportion, and best linear unbiased predictor among plant cane and first ratoon seedlings and the first clonal plots for stalk weight

	PC			FR				FC			
	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP
PC[a] OBS[b]	0.92**	0.95**	0.89**	0.79**	0.64**	0.68**	0.61*	0.60*	0.50§	0.55*	0.45§
PC MEAN		0.76**	0.98**	0.87**	0.76**	0.76**	0.74**	0.72**	0.63*	0.69**	0.59*
PC PROB			0.93**	0.89**	0.80**	0.82**	0.77**	0.60*	0.54*	0.58*	0.51§
PC BLUP				0.89**	0.80**	0.80**	0.80**	0.75**	0.69**	0.75**	0.67**
FR OBS					0.94**	0.97**	0.91**	0.73**	0.71**	0.73**	0.69**
FR MEAN						0.98**	0.98**	0.60*	0.65**	0.66**	0.65**
FR PROB							0.95**	0.64**	0.66**	0.67**	0.66**
FR BLUP								0.63**	0.70**	0.70**	0.71**
FC OBS									0.92**	0.95**	0.91**
FC MEAN										0.99**	0.99**
FC PROB											0.98**

§,*,** Significant at 10%, 5%, and 1% probability level, respectively

[a] PC, Plant cane seedling; FR, first ratoon seedling; FC, first clonal plot

[b] OBS, Observed elite proportion; MEAN, full-sib family mean; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

season (November) or evaluated at the same time as stalk number in the following summer (August) in order to estimate the cane yield potential of the families. This would allow selection among families for high cane yield before singles tool selection occurs in September. Thus, efforts could concentrate on the high-yielding families to enhance selection for high-yielding genotypes.

Stalk diameter and stalk length are components of cane yield and of stalk weight (Kang et al. 1983). Milligan et al. (1990) reported that stalk diameter was more important than stalk length in determining stalk weight. Stalk weight is not typically measured at early selection stages. Instead, stalk diameter and stalk length are subjectively appraised to estimate stalk weight. Gravois et al. (1991) suggested that when the breeding objective was an increase in stalk weight, stalk diameter should be slightly emphasized over stalk length. Correlations for stalk diameter were moderately strong between PC and FR statistics ($0.42 \leq r \leq 0.65$) and between PC and FC ($0.55 \leq r \leq 0.79$), with the exception of FC OBS ($r = 0.45$) (Table 6). The results suggest that the assessment and prediction of future family performance for stalk diameter could be made in the PC.

Correlations of stalk length between the PC and FR seedlings were rather strong ($0.60 \leq r \leq 0.72$) and better than those found for other combinations of tests

Table 6. Correlation of the observed elite proportion, the full-sib mean, the predicted elite proportion, and best linear unbiased predictor among plant cane and first ratoon seedlings and the first clonal plots for stalk diameter

	PC			FR				FC			
	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP
PC[a] OBS[b]	0.85**	0.97**	0.84**	0.42	0.52*	0.48§	0.52*	0.45§	0.55*	0.60*	0.55*
PC MEAN		0.91**	0.98**	0.48§	0.51§	0.45§	0.55*	0.70**	0.69**	0.74**	0.69**
PC PROB			0.91**	0.59*	0.64**	0.62*	0.65**	0.57*	0.68**	0.72**	0.68**
PC BLUP				0.50§	0.55*	0.49§	0.63*	0.72**	0.74**	0.79**	0.76**
FR OBS					0.90**	0.97**	0.85**	0.24	0.50§	0.50§	0.53*
FR MEAN						0.89**	0.95**	0.24	0.55*	0.53*	0.59*
FR PROB							0.83**	0.20	0.47§	0.47§	0.51§
FR BLUP								0.34	0.64*	0.64**	0.70**
FC OBS									0.88**	0.91**	0.86**
FC MEAN										0.97**	0.99**
FC PROB										1.0	0.98**

§,*,** Significant at 10%, 5%, and 1% probability level, respectively

[a] PC, Plant cane seedling; FR, first ratoon seedling; FC, first clonal plot

[b] OBS, Observed elite proportion; MEAN, full-sib family mean; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

Table 7. Correlation of the observed elite proportion, the full-sib mean, the predicted elite proportion, and best linear unbiased predictor among plant cane and first ratoon seedlings and the first clonal plots for stalk length

	PC			FR				FC			
	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP
PC[a] OBS[b]	0.89**	0.93**	0.89**	0.66*	0.62*	0.67**	0.60*	0.30	0.50§	0.53*	0.39
PC MEAN		0.87**	0.97**	0.61*	0.60*	0.65**	0.61*	0.47§	0.61*	0.62*	0.47§
PC PROB			0.92**	0.72**	0.58*	0.70**	0.64**	0.41	0.54*	0.58*	0.49§
PC BLUP				0.67**	0.65**	0.71**	0.69**	0.53*	0.67**	0.69**	0.57*
FR OBS					0.78**	0.94**	0.74**	0.17	0.27	0.28	0.26
FR MEAN						0.86**	0.94**	0.31	0.50§	0.49§	0.50§
FR PROB							0.80**	0.29	0.40	0.41	0.39
FR BLUP								0.40	0.57*	0.56*	0.58*
FC OBS									0.95**	0.94**	0.94**
FC MEAN										1.00**	0.96**
FC PROB											0.96**

§,*,** Significant at 10%, 5%, and 1% probability level, respectively

[a] PC, Plant cane seedling; FR, first ratoon seedling; FC, first clonal plot

[b] OBS, Observed elite proportion; MEAN, full-sib family mean; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

(Table 7). The MEAN and the BLUP produced stronger correlations among tests than the OBS and the PROB. Therefore, the prediction of stalk length could be made in the PC. The stalk diameter and stalk length data in the PC could also be combined to predict stalk weight of the family.

Correlations between tests for Brix were all moderately strong, being stronger with the MEAN and the BLUP statistics than with the OBS and PROB statistics (Table 8). Brix is the single most important factor determining sucrose content (Gravois et al. 1991; Milligan et al. 1990). On the basis of the results of this work, estimation of the potential of a family to produce high sucrose genotypes could be made late in the PC year.

Crosses may vary in their variance for certain traits (Table 1). This suggests that the data collection process to estimate family variances for the calculation of PROBs and BLUPs should be worth while since this information should enhance selection among families. The strong correlations among the OBS, MEAN, PROB, and BLUP statistics within a test do not, however, support this contention (Tables 3–8). The predicted cross potential was similar, regardless of the statistical methods used. Caligari and Brown (1986) also found little difference between

Table 8. Correlation of the observed elite proportion, the full-sib mean, the predicted elite proportion, and best linear unbiased predictor among plant cane and first ratoon seedlings and the first clonal plots for Brix

	PC			FR				FC			
	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP	OBS	MEAN	PROB	BLUP
PC[a] OBS[b]	0.92**	0.96**	0.91**	0.38	0.44§	0.44§	0.40	0.59*	0.61*	0.63*	0.54*
PC MEAN		0.88**	1.00**	0.51§	0.65**	0.58*	0.61*	0.57*	0.70**	0.58*	0.63*
PC PROB			0.87**	0.38	0.40	0.41	0.37	0.61*	0.55*	0.59*	0.47§
PC BLUP				0.50§	0.65**	0.58**	0.62*	0.54*	0.70**	0.57*	0.63*
FR OBS					0.85**	0.98**	0.82**	0.56*	0.53*	0.52*	0.52*
FR MEAN						0.87**	0.99**	0.56*	0.72§	0.57*	0.69**
FR PROB							0.86**	0.56*	0.58*	0.54*	0.57**
FR BLUP								0.50§	0.70**	0.54*	0.68**
FC OBS									0.83**	0.96**	0.83**
FC MEAN										0.91**	0.99**
FC PROB											0.91**

§, *, ** Significant at 10%, 5%, and 1% probability level, respectively

[a] PC, Plant cane seedling; FR, first ratoon seedling; FC, first clonal plot

[b] OBS, Observed elite proportion; MEAN, full-sib family mean; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

Table 9. Expected genetic gains (GA) for yield components from combined among- and within-family selections and simple mass selection

Trait	Plant cane selection method			First ratoon selection method		
	50% family then 20% individual		10% individual	50% family then 20% individual		10% individual
	GA%[a]			GA%		
	Reps[b]	No reps	No reps	Reps	No reps	No reps
Brix	5.6	4.6	2.8	7.0	6.1	3.8
Stalk diameter	3.5	2.6	1.2	1.7	1.1	0.4
Stalk length	5.4	3.5	1.6	8.9	7.2	4.5
Stalk weight	11.9	8.8	5.5	11.7	9.6	5.6
Stalk number	11.8	8.6	4.9	13.0	10.0	4.5
Stool weight	15.4	9.0	5.3	16.9	13.5	7.2

[a] Reps refers to two spacings and three replications; no reps refers to selection among unreplicated families and genotypes

[b] GA expressed as a percentage of the overall mean

the mean and the PROB in predicting family performance. The high correlations between the observed (OBS) and predicted proportions of elite progeny (PROB) suggest that the assumption of normality was valid.

With the exception of stalk number, it was generally observed that single stool data collected in the PC seedlings were as well correlated to clonal plot data as the FR seedling data. Since these measures are types of repeatability estimates, it would be expected that heritability estimates may be similar. Estimates of heritability for sugarcane traits have been widely reported (Milligan 1988). Broad-sense heritabilities of yield components based on an individual plant were generally low (Skinner et al. 1987). However, the heritabilities on a family basis were generally higher for most traits, indicating that family selection could be effective (Skinner et al. 1987; Milligan 1988). Our findings, although biased upward due to genotype × environment interaction being confounded with the genetic value estimates of the crosses, were concordant with these reports and suggest that selection among families could be effective.

Skinner et al. (1987) suggested that by using a combination of family as well as individual selection it is possible and desirable to include low heritability characters when selecting among original seedlings. Comparisons of the expected genetic gains for the yield components between combined among- and within-family selection, and simple individual selection showed that the gains expected from selection among families for the top 50% followed by 20% individual genotype selection within elite families were larger than those from simple mass selection of the best 10% (Table 9). Although family replication improved the expected gains, most of the gains were made by the incorporation of family selection. Hallauer and Miranda (1981) pointed out that the expected genetic gains from combined selection were usually higher than those from mass selection alone when selection intensities were comparable because family selection increased the heritability of the trait under selection. A similar finding has also been reported in winter wheat (Abdalla et al. 1989). Hogarth et al. (1990) also reported that family means were more useful than within-family variances for the selection of sugarcane families capable of producing superior commercial clones. They suggested the use of the family mean for combined family and individual genotype selection within elite families for a sugarcane breeding program.

Results from this study suggested that a combination of plant cane and first ratoon seedling data for cross prediction could be used to direct crosses to be remade or replanted, and to eliminate inferior crosses before single plant selection. Percentage advancement values require about 4 years to estimate in the LSVDP. The use of an objective cross appraisal method in the seedling stage should improve the effectiveness of the breeding program by shortening the appraisal time by about 2 years.

In most predictions, the MEAN for traits was as well-correlated between tests as was the BLUPs. The average correlation coefficients among tests for OBS, MEAN, PROB, and BLUP were not statistically different ($r = 0.48 \pm 0.21$, 0.64 ± 0.18, 0.52 ± 0.19, and 0.66 ± 0.16, respectively), which suggests that the MEAN was equal to the predictive value of the BLUPs in this study. Since heritabilities of the traits were low, the adjustments to the family mean for information from relatives in the BLUP calculations were minor. Thus, the BLUP and MEAN were effectively the same. In North Queensland, the MEAN was found to be of greater importance than within-cross variability in determining the importance of a cross (Hogarth 1971). The high correlations between the MEAN and the PROB estimates were consistent with Hogarth (1971). Estimations of PROB and BLUP need individual plant data and the calculations of parameters such as the standard deviation, the Z value, genetic and error variances, and may require substantial computer power. In practice, it is easier to obtain the MEAN than the PROB or the BLUP, since individual plant data need not be collected.

The results suggest that the OBS from a adequate sample size could also be used to give an equally accurate prediction of cross potential. Brown et al. (1988) reported similar observations. Wu et al. (1978), substantiated by Pollock (1980), showed that a sample size of 40 or smaller was sufficient for the estimation of sugarcane family variance or mean. This study used more than 70 progeny in the PC, more than 60 progeny in the FR, and about 30 progeny (plot basis) in the FC for each cross. The high correlation between OBS and PROB estimates suggested that the sample size was sufficient in all these tests for family evaluation.

Our results support the use of mean stool data to predict the potential of a family to produce elite progeny. There appears to be no compelling reason to use more sophisticated statistics or no need to use clonal data for family prediction. The correlations between different seedlings tests were generally strong enough to suggest that the prediction of a cross's potential for Brix and stalk weight could be made in plant cane seedlings. The gathering of only mean data eases data collection since information could be collected on a plot basis. Lyrene et al. (1977) suggested that the collection of mean data from replicated plots could reduce the effect of field variation.

Our study involved three tests (PC, FR, FC) over 2 years at one location. In sugarcane, cross by environment interaction (CE) has been reported (Hogarth and Bull 1990; Milligan and Legendre 1991), and has been suggested that CE is important for many traits (Milligan and Legendre 1991) in the Louisiana breeding environment. In Australia, it has been shown that rankings of families are affected by the interaction, but cross by crop-year interaction is less important (Hogarth and Bull 1990). Tai and Miller (1989) reported that cross performance could be affected by environmental influences and suggested that the multi-site or multi-year testing of crosses would be more effective to predict sugarcane cross potential. Multi-site testing of crosses on a full scale (200–300 crosses/year) is not feasible for the LSVDP. A replicated full scale test each ear for all crosses planted in the routine selection program is proposed instead. Since clonal selection is seeking the best genotypes, a cross interacting favorably with a particular year's environment may produce such genotypes. If the cross fails the following year, it would be dropped. This compromised system would favor adapted crosses, but would not eliminate them as quickly as multi-site testing would.

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