Theor Appl Genet (1992) 84: 633–639

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

Y. S. Chang [1] **and S. B. Milligan** [2]

[1] Department of Plant Breeding, Taiwan Sugar Research Institute, Taiwan 70123, Taiwan
[2] Department of Agronomy, Louisiana State University, Baton Rouge, LA 70803, USA

Received September, 10, 1991; Accepted January 18, 1992
Communicated by A. R. Hallauer

Summary. Three bivariate statistical methods to predict the family potential to produce elite progeny were studied to improve the efficiency of a sugarcane (*Saccharum* spp.) breeding program. Progeny from 15 piparental crosses were evaluated in plant cane and first ratoon seedlings, and in clonal plant cane plots during 1989 and 1990. The bivariate predictions of Brix combined with cane yield components (stalk number, stalk weight, stalk diameter, stalk length, and stool weight) were investigated. The best linear unbiased predictors (BLUPs) and the sum of ranks based on family mean values of two traits (RANK) were repeatable among tests in the estimation of family potential. Bivariate normal probabilities (PROB) estimated with family means, phenotypic standard deviations, and genetic correlations generally demonstrated poor repeatability among tests. The three statistical predictions were compared with the progeny selection rate within the crosses through three selection stages. Predictions were not correlated to the selection rates of eight crosses with smaller initial progeny populations (<500 progeny). However, when the predictions were compared with the 7 of 15 families over which 1,000 progeny for each cross had been evaluated, the rankings based on BLUP and RANK bivariate predictions of Brix and stool weight identified the better crosses. PROB was inconsistent in this regard. Early selection work is highly subjective. We speculate that near-random selection occurs for stalk number at the initial selection stage and that the high selection rate at this stage ($\approx 5\%$) generates a first clonal population (10 to 25) that is too small to accurately base selection rates for stalk number. Larger initial progeny populations produce sufficiently large clonal populations (>50) to appraise crosses using selection rates. The study suggested that family evaluations for breeding programs can use bivariate predictions. The comparative ease of calculating the RANK estimate versus the BLUP along with the absence of any apparent loss of predictive value suggests that the RANK method would be the most suitable statistic to use for bivariate predictions.

Key words: Sugarcane – Joint prediction – Bivariate normal probability – Best linear unbiased predictors (BLUPs) – Family selection

Introduction

Chang and Milligan (1992) showed that univariate prediction of a trait could provide a fair estimate of the potential of a cross to produce elite progeny. In the breeding of new cultivars, however, more than one character at a time is usually considered. Pooni and Jinks (1978) proposed multivariate predictions for two or more characters. Joint prediction for multiple traits has been studied in *Nicotiana rustica* (Pooni and Jinks 1978), *Hordeum vulgare* (Powell et al. 1985; Thomas et al. 1986), and *Solanum tuberosum* (Brown and Caligari 1988). These predictions were based on estimations with multi-normal distribution functions using the mean, the additive genetic variance of each character, and the additive genetic correlation between characters. Mixed model analysis (MMA) can also provide multivariate predictions when the variance-covariance matrices of genetic and error terms are provided. These matrices are used to adjust the family estimate for genetic and environmental correlations among traits. Multiple trait predictions from MMA can be used as selection indices when the economic weights of each character are given (Hendersen 1984).

---

* Approved for publication by the Director of the LAES as manuscript no. 91-09-5344. Received July 22, 1991
Correspondence to: S. B. Milligan

A clonally propagated crop such as sugarcane is not affected by genetic segregation after the initial sexual cross. Thus, predictions over generations are for clonal progeny rather than for sexual generations. Brown and Caligari (1988) suggested that for a clonally propagated crop the cross prediction could be compared with the frequencies of progeny advanced to later stages of selection from each cross. While sucrose content and cane yield are the primary yield components of sugarcane (Kang et al. 1983; Milligan et al. 1990), other traits such as pith, tube, vigor, disease, and insect resistance must also be considered by the breeder. At the early selection stages, Brix (juice % soluble solids) measured by a hand refractometer is used to screen for sufficient sucrose content. Stalk diameter and stalk length are used to assess stalk weight, and these two traits are further combined with stalk number to evaluate cane yield.

The objective of the study presented here was to identify the best statistic for simultaneously evaluating family potentials for two traits. Bivariate predictions of Brix combined with the cane yield components of stalk number, stalk diameter, stalk length, stalk weight, and stool weight were examined. The statistics studied were the multivariate normal probability, the best linear unbiased predictor, and the sum of the mean performance ranks.

Materials and methods

The study was initiated in 1989 by evaluating 1,800 seedlings from 15 crosses among 23 adapted sugarcane parents. Three test stages were studied: plant cane seedlings (PC), first ratoon seedlings (FR), and first clonal plots (FC). Seedlings were planted in April, 1989 at two intrarow plant spacings (41 cm and 82 cm; 1.8-m wide rows) in three blocks in a randomized complete block (RCB) design. Two intrarow spacings were used to test their effect on family variability. Clonal plots (single row 1.8 m long, 1.8 m wide) were planted in November, 1989 in three blocks in an RCB design. All tests were conducted at the St. Gabriel Research Station, St. Gabriel, La. More detailed descriptions of the tests and data collected have been given by Chang and Milligan (1992).

Family appraisal was based on a simultaneous evaluation of Brix combined with the cane yield components: stool weight, stalk number, stalk weight, stalk diameter, and stalk length. The statistics estimated were: the sum of ranks (RANK) based on mean performances for different traits (e.g., for a given family, traits were ranked among the 15 families according to their mean values. RANK = rank for trait 1 + rank for trait 2), the multivariate normal probability (PROB) that exceeded acceptable target values, and the best linear unbiased predictor (BLUP) for multiple traits. The thresholds used for PROB were Brix = 20%, stalk diameter = 2.7 cm, stalk number = 10 stalks stool^{-1} (for PC and FR), 25 stalks plot^{-1} (for FC), stalk length = 2.0 m (for PC and FR), 2.3 m (for FC); stalk weight = 0.85 kg (for PC), 1.0 kg (for FR), 1.3 kg (for FC); stool weight = 7.5 kg (for PC), 8.5 kg (for FR); plot weight = 30 kg (for FC).

Henderson's mixed model equations were used to calculate BLUPs of each cross for multiple traits (Henderson 1973, 1984). The following model was used:

$$y_{ij} = \mu + B_i + C_j + e_{ij}$$

where y_{ij} was observation for block i (B_i, i = 1, 2, 3) and cross j (C_j, j = 1, 2, ..., 15) with the overall mean, μ. Block effects were assumed to be fixed, while cross and error effects were assumed to be random (Chang and Milligan 1992). Spacing and cross by spacing effects were pooled with the residual, e_{ij}. This pooling did not affect the univariate prediction (Chang and Milligan 1992) and was assumed not to effect the bivariate prediction. Economic weights were considered to be uniform for all traits. The solution to the mixed model equations for a bivariate prediction was given by Henderson (1984) as:

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

where **X**, **Z** were design matrices of fixed and random effects, respectively. **G** was the genetic variance-covariance matrix of traits 1 and 2 and weighted by the additive genetic numerator relationship matrix among crosses. **R** was the error variance-covariance matrix of traits 1 and 2; M combined with **X**, **Z**, and **y** was used to indicate multivariate BLUPs. SAS IML (1985b) uses the BLOCK (**X**, **X**) or BLOCK (**Z**, **Z**) statement to combine the matrices (**X**, **X** or **Z**, **Z**) diagonally to form a new matrix for bivariate predictions. For example

$$M\mathbf{X} = \text{BLOCK}(\mathbf{X}, \mathbf{X}) = \begin{bmatrix} \mathbf{X} & \mathbf{O} \\ \mathbf{O} & \mathbf{X} \end{bmatrix}$$

$$M\mathbf{Z} = \text{BLOCK}(\mathbf{Z}, \mathbf{Z}) = \begin{bmatrix} \mathbf{Z} & \mathbf{O} \\ \mathbf{O} & \mathbf{Z} \end{bmatrix}$$

$$M\mathbf{y} = [y_{11}\, y_{12} \cdots y_{1n}\, y_{21}\, y_{22} \cdots y_{2n}]'$$

where $y_{11} \cdots y_{1n}$ $y_{21} \cdots y_{2n}$ were individual observations for traits 1 and 2, respectively. Variance and covariance components for multiple traits were obtained using REML variance component estimation methods (Proc Varcomp, SAS 1985a).

BLUP estimates that use additive genetic relationship matrices in their calculations use additive genetic variances and covariances estimates. The crosses studied were full-sib families. The genetic variance estimates were from the full-sib family covariances:

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

where σ^2_{a} was additive variance, σ^2_{d} was dominance variance, and σ^2_{aa}, σ^2_{ad}, σ^2_{dd} were types of epistatic variance (Becker 1984). The genetic variance and covariance estimates contained dominance and types of epistatic variances and, thus, may not accurately represent the additive variance-covariance relationships in this population. Since the study was aimed at prediction of future family performance, not individual progeny, the genetic variance estimates were not twice the full-sib family covariances. They were, however, adjusted for additive genetic relationships among families in the BLUP estimates.

Multivariate normal probability predictions (PROB) were estimated following the methods described by Pooni and Jinks (1978), wherein a computer program written by Schervish (1984) was used for all calculations. The PROB used the family mean and phenotypic standard deviation for each trait and the genetic correlations (from full-sib family analysis) between traits in its estimate.

Genetic correlations (r_{ij}) between traits were calculated following the formula:

$$r_{ij} = \sigma_{ij}/(\sigma_i\, \sigma_j)$$

where σ_{ij} was the genetic covariance between traits i and j, and σ_i and σ_j were the genetic standard deviations of traits i and j, respectively.

Phenotypic correlations between traits for PC and FR were estimated by the SAS GLM MANOVA procedure (1985a) using the model:

$$y_{ij} = \mu + \beta_i + S_j + e_{ij}$$

where y_{ij} was an individual with the overall mean, μ, in block i (β_i) and spacing j (S_j, $j = 1, 2$). The residual, e_{ij}, contained all genetic effects (cross, cross × spacing) and error effects. The clonal test did not contain spacing effects in its model.

Correlations between bivariate predictions of stool weight and Brix were made to the selection rates of the crosses. The selection rates were the percentage of initial progeny that had progressed to the third clonal stage in the Louisiana Sugarcane Variety Development Program (LSVDP). These genotypes had undergone three major selection stages, each involving two to three substages of selection that typically reduces an initial population of some 75,000 genotypes to less than 300 genotypes. Selection rate at this stage is considered the best selection time versus accuracy compromise by which to appraise crosses since they have been screened through larger plots (single row: 4.3 m) for cane yield than used in the initial two stages.

Results and discussion

High correlations between the observed and the predicted proportions of elite progeny confirmed the normality of distribution for each trait investigated (Chang and Milligan 1992). Since individual trait distributions were normal, we assumed that the data for joint predictions were generated from a multivariate normal distribution. While data are never exactly multivariate normal, the normal density is a useful approximation to the "true" population distribution (Johnson and Wichern 1988). The bivariate normal probability and observed elite proportion were generally significantly correlated within each test with only a few exceptions (Table 1). These correlations indicated that bivariate normality was a reasonable assumption in this study.

Table 1. Correlations between the bivariate normal probability and the observed proportion that exceeded the same target values for pair of traits

Bivariate trait	PC	FR	FC
Brix and stool weight	0.28	0.92**	0.82**
Brix and stalk number	0.33	0.93**	0.62*
Brix and stalk weight	0.87**	0.92**	0.85**
Brix and stalk diameter	0.61*	0.64**	0.85**
Brix and stalk length	0.86**	0.40	0.37

*,** Significant at 5% and 1% probability level

The correlation coefficients between RANK and other statistics tended to be negative since the lower the sum of rank, the higher the potential of the cross to produce elite genotypes. To facilitate explanations discussion of all negative correlation coefficients between RANK and the other two statistics simply considered their absolute values.

The three statistics (RANK, PROB, BLUP) within tests were moderately to strongly correlated in their joint prediction of Brix and stalk diameter ($0.60 \leq r \leq 0.87$) (Table 2). Between tests, the statistics were slightly to moderately correlated ($0.38 \leq r \leq 0.79$). The correlation coefficients of BLUP among the tests (PC, FR, FC) were significant ($0.63 \leq r \leq 0.76$) and generally higher than those of RANK ($0.45 \leq r \leq 0.79$) and PROB ($0.38 \leq r \leq 0.53$). The strong correlations between tests for BLUP suggested that the joint prediction of Brix and stalk diameter can be best made in the PC using BLUPs. Correlations between tests for RANK showed that FR versus FC displayed a better association ($r = 0.79$) than PC versus FR ($r = 0.45$) or PC versus FC ($r = 0.58$). These correlations also indicated that RANK could be a joint indicator of these two traits for crosses. PROB had positive but smaller correlation coefficients between tests ($0.38 \leq r \leq 0.49$) than the other statistics.

Joint prediction BLUPs of Brix and stalk length were significantly correlated between tests ($0.58 \leq r \leq 0.66$)

Table 2. Correlation of the sum of ranks, the predicted elite proportion, and the BLUP among plant cane and first ratoon seedlings and first clonal plots for Brix and stalk diameter

	PC		FR			FC		
	PROB	BLUP	RANK	PROB	BLUP	RANK	PROB	BLUP
PC[a] RANK[b]	−0.87**	−0.67**	0.45§	−0.57**	−0.52*	0.58*	−0.51§	−0.42
PC PROB		0.84**	−0.49§	0.53*	0.48§	−0.45*	0.38	0.46§
PC BLUP			−0.59*	0.49§	0.63*	−0.62*	0.46§	0.70**
FR RANK				−0.72**	−0.65**	0.79**	−0.61*	−0.65**
FR PROB					0.60*	−0.52*	0.49§	0.39
FR BLUP						−0.63*	0.53*	0.76**
FC RANK							−0.73**	−0.76**
FC PROB								0.81**

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

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

[b] RANK, Sum of ranks; PROB, predicted elite proportion: BLUP, best linear unbiased predictor

Table 3. Correlation of the sum of ranks, the predicted elite proportion, and the BLUP among plant cane and first ratoon seedlings and first clonal plots for Brix and stalk length

	PC		FR			FC		
	PROB	BLUP	RANK	PROB	BLUP	RANK	PROB	BLUP
PC[a] RANK[b]	−0.88**	−0.87**	0.44§	−0.48§	−0.53§	0.71**	−0.53*	−0.51§
PC PROB		0.84**	−0.29	0.24	0.33	−0.60*	0.56*	0.47§
PC BLUP			−0.34	0.36	0.58*	−0.70**	0.56*	0.61*
FR RANK				−0.80**	−0.86**	0.52*	−0.47§	−0.53*
FR PROB					0.74**	−0.35	0.43	0.41
FR BLUP						−0.59*	0.53*	0.66**
FC RANK							−0.75**	−0.83**
FC PROB								0.92**

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

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

[b] RANK, Sum of ranks; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

Table 4. Correlation of the sum of ranks, the predicted elite proportion, and the BLUP among plant cane and first ratoon seedlings and first clonal plots for Brix and stalk number

	PC		FR			FC		
	PROB	BLUP	RANK	PROB	BLUP	RANK	PROB	BLUP
PC[a] RANK[b]	−0.84**	−0.87**	0.57*	−0.78**	−0.51§	−0.29	−0.03	−0.29
PCPROB		0.88**	−0.74**	0.87**	0.73**	−0.48§	0.18	0.47§
PC BLUP			−0.67**	0.77**	0.64**	−0.45§	0.09	0.38
FR RANK				−0.73**	−0.96**	−0.52§	−0.13	−0.47§
FR PROB					0.69**	−0.43	0.15	0.35
FR BLUP						−0.52*	0.21	0.53*
FC RANK							−0.70**	−0.83**
FC PROB								0.69**

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

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

[b] RANK, Sum of ranks; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

(Table 3). Correlations between tests for RANK ($0.44 \le r \le 0.71$) were better than those for PROB ($0.24 \le r \le 0.56$). A predictor with higher correlations between tests should indicate the future performance of the family more reliably. BLUPs seemed to be the best predictors. The statistics within tests were highly correlated ($0.75 \le r \le 0.92$), implying that they had similar predictive abilities within tests for Brix and stalk length. In general, statistics between tests were moderately correlated. Correlations between tests showed that PC versus FC ($0.47 \le r \le 0.71$) was more strongly related than PC versus FR ($0.29 \le r \le 0.48$) and FR versus FC ($0.41 \le r \le 0.66$). The joint predictions of family Brix and stalk length can be improved by means of BLUP or RANK as compared with PROB with the family data collected in the PC if these two traits are used as selection criteria.

The statistics for the joint prediction of Brix and stalk number showed strong correlations within tests ($0.69 \le r \le 0.96$) (Table 4). The correlations between tests were highly variable ($0.03 \le r \le 0.87$). Joint prediction for these two traits between tests were more repeatable for PC versus FR ($0.51 \le r \le 0.87$) than for other combinations of tests ($0.03 \le r \le 0.53$). The stalk number in FC represented stalk number per plot, but in PC and FR it represented stalk number per stool. This trait is the major component of cane yield (James 1971; Milligan et al. 1990). Brix and stalk number are two important factors for sugar yield. BLUP and RANK were significantly correlated between the PC versus FR tests ($r = 0.64$, 0.57, respectively) and between FR versus FC tests ($r = 0.53$, 0.52, respectively), which suggested that reasonable predictions for Brix and stalk number could be achieved by use of BLUP or RANK statistics. The multivariate prediction of these traits could use BLUPs or RANKs to first select among the best families in the PC and then select within elite families in the FR.

Correlations of statistics within tests for the joint prediction of Brix and stalk weight were strong ($0.73 \le r \le$

Table 5. Correlation of the sum of ranks, the predicted elite proportion, and the BLUP among plant cane and first ratoon seedlings and first clonal plots for Brix and stalk weight

	PC		FR			FC		
	PROB	BLUP	RANK	PROB	BLUP	RANK	PROB	BLUP
PC[a] RANK[b]	−0.89**	−0.81**	0.61*	−0.60*	−0.57*	0.55*	−0.53*	−0.48§
PC PROB		0.87**	−0.43	0.50§	0.41	−0.37	0.45§	0.39
PC BLUP			−0.46§	0.55*	0.62*	−0.49§	0.47§	0.61*
FR RANK				−0.87**	−0.81**	0.65**	−0.64**	−0.59*
FR PROB					0.78**	−0.55*	0.65**	0.54*
FR BLUP						−0.57*	0.52*	0.68**
FC RANK							−0.73**	−0.74**
FC PROB								0.84**

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

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

[b] RANK, Sum of ranks; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

Table 6. Correlation of the sum of ranks, the predicted elite proportion, and the BLUP among plant cane and first ratoon seedlings and first clonal plots for Brix and stool weight

	PC		FR			FC		
	PROB	BLUP	RANK	PROB	BLUP	RANK	PROB	BLUP
PC[a] RANK[b]	−.46**	−0.89**	0.68**	−0.81**	−0.64**	0.59*	−0.21	−0.47§
PC PROB		0.48§	−0.47§	0.26	0.62*	−0.19	0.01	0.43
PC BLUP			−0.64**	0.77**	0.59*	−0.64**	0.09	0.30
FR RANK				−0.74**	−0.93**	0.61*	−0.02	−0.50§
FR PROB					0.66**	−0.48§	0.08	0.27
FR BLUP						−0.47§	0.14	0.53*
FC RANK							−0.55*	−0.64**
FC PROB								0.73**

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

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

[b] RANK, Sum of ranks; PROB, predicted elite proportion; BLUP, best linear unbiased predictor

0.87) (Table 5). In general, correlations between tests were of moderate strength ($0.37 \leq r \leq 0.68$), however, BLUP and RANK correlations were more stable between tests than the PROB correlations. Joint prediction of these traits in the PC by BLUP or RANK could provide the information for family selection.

Brix and stool weight are two major yield components. Joint prediction of these two traits is close to the prediction of sugar yield. In this prediction, RANK was strongly to moderately correlated with BLUP within tests ($0.64 \leq r \leq 0.93$) and between tests ($0.47 \leq r \leq 0.64$), respectively (Table 6). PROB was moderately correlated with BLUP within tests ($0.48 \leq r \leq 0.73$). Correlation between tests for RANK were more stable ($0.59 \leq r \leq 0.68$) than for other statistics. PROB predictions were poorly correlated between tests ($0.01 \leq r \leq 0.26$). The correlations of BLUP for PC versus FR ($r = 0.59$) and FR versus FC ($r = 0.53$) suggested that the joint predictions of these two traits could be as reliably made in the PC as in the FR, and that they could be used as selection criteria for high sugar yielding families.

The results demonstrated that the joint prediction of two traits could, in many cases, be made dependably at the PC seedling stage. Tests of significance among correlations were not made in this study. It is likely, given the range and overlap of the correlations in many of the comparisons, that many were not significantly different. Thus, our stated results were observed trends of unknown value. But in general, BLUP and RANK showed higher repeatability between tests than the PROB method for bivariate predictions of sugarcane yield components. BLUP has been used as a selection index in animal breeding for many years (Henderson 1984) and has been adjusted for environmental and genetic relationships among crosses. For multivariate cross prediction, BLUP is equivalent to the selection index for family potential. In potato, it was found the sum of ranks (RANK) provided a reasonable estimation of cross potential for multiple

Table 7. Proportion of clones advanced to third clonal year for seven crosses where more than 1,000 progeny for each cross had been evaluated in the LSVDP and grouped according to ranking on the basis of bivariate cross predictions of Brix and stool weight in the PC, FR, and FC

Predicted family rank[a]	RANK[b]			PROB			BLUP		
	PC	FR	FC	PC	FR	FC	PC	FR	FC
	% progeny advanced[c]								
1	0.5_1	0.5_1	2.2_2	0.5_1	1.3_3	2.2_2	0.5_1	0.5_1	2.2_2
2	2.2_2	1.3_3	1.3_3	2.2_2	0.5_1	1.3_3	1.3_3	2.2_2	1.3_3
3	1.3_3	2.2_2	0.5_1	0.9_4	0.6_5	0.3_6	2.2_2	1.3_3	0.3_6
Subtotal	4.0	4.0	4.0	3.6	2.4	3.8	4.0	4.0	3.8
4	0.9_4	0.6_5	0.3_6	0.3_6	0.9_4	0.5_1	0.6_5	0.3_6	0.5_1
5	0.6_5	0.3_7	0.6_5	0.6_5	2.2_2	0.3_7	0.9_4	0.6_5	0.9_4
6	0.3_6	0.3_6	0.9_4	0.3_7	0.3_6	0.9_4	0.3_6	0.3_7	0.6_5
7	0.3_7	0.9_4	0.3_7	1.3_3	0.3_7	0.6_5	0.3_7	0.9_4	0.3_7
Subtotal	2.1	2.1	2.1	2.5	3.7	2.3	2.1	2.1	2.3

[a] Within each column the crosses were ranked by the predictive statistic

[b] RANK, Sum of ranks based on means; PROB, probable elite proportion; BLUP, best linear unbiased predictor

[c] Subscript on the % advanced value is the cross number

traits (Brown and Caligari 1988). Since the RANK statistic was just as accurate as BLUP and easier to compute, RANK seemed to be the most efficacious statistic to use for joint prediction.

Bond (1977) and Wu and Tew (1989) reported that the mean yield of sugar obtained from replicated plots of full-sib families could be used as a guide to the potential of sugarcane crosses. Walker (1962) suggested that the selection percentages from the first three stages of selection were useful as a measure of family performance and worth. However, Arceneaux (1968) proposed that selection rates in later stages, those approaching the commercial level, were of great significance in the assessment of cross worth. In this study, the bivariate Brix-stool weight or Brix-plot weight estimate was used to predict the sugar yield of the family and then compared with progeny selection rates of the crosses. There was no correlation between the selection rate and any of the bivariate Brix-stool weight prediction for crosses in which 200–500 progeny per cross had been evaluated (8 crosses). For the 7 crosses where more than 1,000 progeny had been evaluated, the statistics were generally able to identify the better crosses (Table 7). In addition to sugar yield, selection among genotypes in a breeding program includes evaluation for lodging, pith, hollow stalk (tube), growth cracks, general vigor, disease, and borer resistance. These latter traits were not evaluated in this study. Thus, a perfect correlation was not expected between selection rates and the predictive statistics. The process of initial selection among progeny stools is subjectively based. In Natal, the subjective evaluation of crosses at the single stool stage was reported to be unreliable (Bond 1977). In the LSVDP, about 5% of the progeny are advanced from the initial seedlings to the first clonal stage. Approximately one-third are advanced from the first clonal stage to the second clonal stage, and a similar proportion is advanced to the third clonal stage from the second clonal stage. The clonal stages are more heavily scrutinized and objectively evaluated. James and Miller (1975) demonstrated that advancing approximately 10% of the seedlings to the first clonal stage would discard approximately 80% of the desirable genotypes for stalk number. Most sugarcane breeders will agree that considerable improvement is made in stalk and juice quality by single stool selection, but stalk number is also an important consideration in selection. On the assumption that selection for stalk number in the single stools is random, then family appraisal for stalk number based upon selection rate should be based upon the initial clonal number of progeny. A 5% selection rate would advance only 10 individuals from a 200 progeny family. Selection rates based on such a small population are likely inaccurate and probably partially account for the lack of correlation between the predictive statistics and the selection rates of families with less than 500 initial progeny. The assumption that single stool selection for stalk number and hence cane yield may be futile is not completely valid, but correlations are not strong between single stool stalk number and clonal stalk number on a single plant basis (Miller and James 1974). Selection among families for stalk number before selection within families would at least favor the process to advance desirable genotypes (Chang and Milligan 1992a). It would additionally allow relaxation of the single stool selection intensity.

Sugarcane cross prediction would enable breeders to concentrate on elite families, thereby increasing the efficiency of the breeding and selection process. Although family selection in sugarcane breeding had been proposed (Hogarth 1971; Skinner et al. 1987; Milligan 1988) and shown to produce greater gains from selection (Hogarth 1977, Chang and Milligan 1992a), it has not been carried out in any sugarcane breeding program. Our study suggests that effective family selection could be made based on a cross prediction method that is 2 years faster than the currently employed method.

The proposed utility of the statistics is a concurrent replicated cross evaluation test using about 60 progeny per cross in addition to the typical 250 genotypes planted in the routine selection program. Test results could be used to select among the crosses in the routine program and to identify crosses to remake or replant. The proposed method would require substantial resources. Although improved genetic gain by use of this method is indicated, its cost effectiveness on a full-scale breeding program level remains to be demonstrated.

References

Arceneaux G (1968) Breeding sugarcane varieties for the northern Caribbean. Proc Int Soc Sugar Cane Technol 13:1034–1046

Becker WA (1984) Manual of quantitative genetics, 4th edn. Academic Enterprises, Pullman, Wash.

Bonds RS (1977) The mean yield of seedlings as a guide to the selection potential of sugarcane crosses. Proc Int Soc Sugar Cane Technol 16:101–110

Brown J, Caligari PDS (1988) The use of multivariate cross prediction methods in the breeding of a clonally reproduced crop (*Solanum tuberosum*). Heredity 60:147–153

Chang YS, Milligan SB (1992) Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. Theor Appl Genet 84:662–671

Henderson CR (1973) Sire evaluation and genetic trends. In: Proc Anim Breed Genet Symp in honor of Dr. JL Lush. Animal Science Association of America. Champaign, Ill., pp 10–41

Henderson CR (1984) Applications of linear models in animal breeding, University of Guelph, Ontario, Canada

Hogarth DM (1971) Quantitative inheritance studies in sugarcane. II. Correlations and predicted responses to selection. Aust J Agric Res 22:103–109

Hogarth DM (1977) Quantitative inheritance studies in sugarcane. III. The effect of competition and violation of genetic assumptions on estimation of genetic variance components. Aust J Agric Res 28:257–268

James NI (1971) Yield components in random and selected sugarcane populations. Crop Sci 11:906–908

James NI, Miller JD (1975) Selection in six crops of sugarcane. II. Efficiency and optimum selection intensities. Crop Sci 15:37–40

Johnson RA, Wichern DW (1988) Applied multivariate statistical analysis, 2nd edn. Prentice Hall, Englewood Cliffs, N.J.

Kang MS, Miller JD, Tai PYP (1983) Genetic and phenotypic path analyses and heritability in sugarcane. Crop Sci 23:643–647

Miller JD, James NI (1974) Selection in six crops of sugarcane. I. Repeatability of three characters. Crop Sci 15:23–25

Milligan SB (1988) The genetic variance-covariance structure of the Louisiana sugarcane breeding population. PhD thesis, Louisiana State University, Baton Rouge, La. (Diss Abstr 88-19963)

Milligan SB, Gravois KA, Bischoff KP, Martin FA (1990) Crop effects on genetic relationships among sugarcane traits. Crop Sci 30:927–931

Pooni HS, Jinks JL (1978) Predicting the properties of recombinant inbred lines derived by single seed descent for two or more characters simultaneously. Heredity 40:349–361

Powell W, Caligari PDS, McNicol JW, Jinks JL (1985) The use of doubled haploids in barley breeding. 3. An assessment of multivariate cross prediction methods. Heredity 55:249–254

SAS Institute Inc (1985a) SAS user's guide: statistics, version 5 edn. SAS Institute Inc, Cary N.C.

SAS Institute Inc (1985b) SAS user's guide: IML, version 5 edn. SAS Institute Inc, Cary N.C.

Schervish MJ (1984) Multivariate normal probabilities with error bound. Appl Stat 33:81–87

Skinner JC, Hogarth DM, Wu KK (1987) Selection methods, criteria, and indices. In: Heinz DJ (ed) Sugarcane improvement through breeding. Elsevier Science Publ New York, pp 409–453

Thomas WTB, Tapsell C, Powell W (1986) The application of cross prediction in spring barley breeding. In: Kearsey MJ, Werner CP (eds) Proc VI Meet Eucarpia Sec Biometrics. Birmingham, pp 80–89

Walker DIT (1962) Family performance at early selection stages as a guide to the breeding program. Proc Int Soc Sugar Cane Technol 11:469–483

Wu KK, Tew TL (1989) Evaluation of sugarcane crosses by family yields. Proc Int Soc Sugar Cane Technol 20:925–930