

Genotype x Environment Interactions and Resource Allocation in Sugarcane Yield Trials in the Rio Grande Valley Region of Texas

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ABSTRACT

Data from an advanced stage selection trial from the Texas Sugarcane Improvement Program (TSIP) were analyzed to determine the relative magnitude of genotype x environment (GxE) interactions components namely, genotype x location (GxL), genotype x crop-years (GxC), and genotype x location x crop-years (GxLxC) on sugar yield and its components cane yield and sucrose content. The objective was to determine the relative importance of testing across locations and crop-years and to determine the optimum combination of locations, replications and crop-years necessary to provide an adequate level of discrimination among genotypes in the TSIP. The GxL, GxC and GxLxC variance components for all three traits were significant ($P = 0.05$) and associated with changes in the relative ranking of genotypes across environments (locations and crop-years). The GxC variance component was identified as the more important of the two first order GxE components (GxL and GxC) highlighting the importance of testing for ratooning ability and suggesting that substantial gains from selection could be achieved by increasing the number of crop-years over which genotypes are tested. An exploratory analysis to identify a more efficient use of resources revealed that, increasing crop-years from three to four improved heritability, while increasing the number of replications beyond two and the number of locations beyond four did little to improve heritability. However, an objective discrimination between genotypes based on performance means could only be achieved when the means differed by at least 15 to 20 %. The resources required to improve experimental precision and detect smaller difference (10 % or less) would be prohibitively large, especially when using small trial plots. Therefore, to guard against discarding genotypes with commercial potential, genotypes not differing from the commercial check (s) by at least 10% should be retained for further testing in larger strip plot trials.

INTRODUCTION

Genotype x environment (GxE) interactions is a widely recognized phenomenon in sugarcane clonal selection trials (Kang and Miller 1984; Milligan et al. 1990; Mirzawan et al. 1993, 1994; Jackson et al. 1991; Kimbeng et al. 2002). Genotype x environment interactions complicates selection decisions because when present, the definition of an elite genotype becomes conditional on the environment under which the genotype is evaluated (Rathey and Kimbeng 2001). The consequence is that, for quantitatively inherited traits such as sugar yield, genotypic performance and the relative ranking of genotypes change from one environment to the other. These rank changes make it difficult for the breeders to decide the true genetic value of prospective genotypes and to select among them.

The presence of GxE dictates that breeders sample the appropriate environmental conditions likely to be encountered by the target environments under which the prospective genotypes will eventually be grown. As sugarcane is a perennial crop, environments constitute locations and years as well as crop stages (plant-cane or ratoon crops). In most breeding programs, advanced stage trials are planted at several locations and evaluated over several years. Measurements in the first and second ratoon are taken on the same plots as the plant-cane crop in order to assess ratooning ability. Therefore, the effects of years are confounded as each crop stage is grown in a different year. The combined effect of years and crop stages are often referred to as crop-years (Kang et al. 1987).

Knowledge from GxE studies are useful for developing strategies for testing and selection of genotypes most adapted to the target environments under which the genotypes will be grown (Rea and De Sousa-Vieira 2002). In north Queensland (Australia) Jackson et al. (1991) and Jackson and Hogarth (1992) found genotype x location (GxL) interactions to be of greater importance than genotype x crop-years (GxC) and genotype x location x crop-years (GxLxC) interactions. They advocated testing across several locations to maximize gain and suggested that minimal gains will be achieved from testing multiple crops within a location. Similar results were reported by Milligan et al. (1990) in Louisiana. In the Burdekin region of Queensland where sugarcane is grown under irrigation, Rattey and Kimbeng (2001) found GxC to be of significant magnitude to affect response to selection while GxL was negligible. These examples suggest that the results from GxE studies in sugarcane are not universal such that the implications and potential selection strategies that develop from them may differ among sugarcane improvement programs.

Comparable GxE studies have not been conducted for the TSIP. In Texas, sugarcane production is limited to the Rio Grande Valley located in the southern part of the state. The Rio Grande Valley Sugar Growers Incorporation (RGVSG) is a cooperative of 120 growers that operate the only sugar mill in Texas. Texas is the fourth largest producer of sugar from cane in the U.S., with 1.5 million tonnes of cane harvested and 180 thousand tonnes of sugar produced annually on about 17, 000 hectares of land. One hundred percent of the sugarcane is grown under irrigation and the crop is traditionally planted and harvested over five crops (plant-cane and four ratoon crops) on average. Common soil types in the Rio Grande Valley sugarcane producing area include: Matamoros silty clay, Raycombes sandy clay loam, Harlingen clay, Willacy fine sandy loam and Raycombes sandy clay loam (United States Department of Agriculture - Natural Resources Conservation Services Web Soil Survey Online; <http://websoilsurvey.nrcs.usda.gov/app/WebSoilSurvey.aspx>). The TSIP routinely samples locations within these diverse soil types when testing sugarcane genotypes in the advanced stages of the program.

The objective of this study was to determine if GxE interactions are present for sugar yield (tonnes of sugar per hectare (TSH)) and its two main component traits (tonnes of cane per hectare (TCH) and sucrose (%)) in advanced stage selection trials in Texas, and if present, to determine the relative importance of testing across locations and crop-years. A second objective was to determine the optimum combination of locations, replications and crop-years necessary to provide an adequate level of discrimination among genotypes in the TSIP.

MATERIAL AND METHODS

Seventeen experimental genotypes and 3 commercial cultivars were planted by hand using whole stalk seed-pieces to minimize losses due to diseases such as ratoon stunting disease caused by *Leifsonia xyli* subsp. *Xyli* (Davis and Bailey 2000; International Society for Plant Pathology, http://www.isppweb.org/names_sugarcane_pathogen.asp, Verified 23 February, 2009). All the entries were planted at five locations chosen to represent diverse soil types in the sugarcane producing area of the Rio Grande Valley. The trials were planted in a randomized complete block design with four replications. Plots consisted of four 10-meter rows spaced 1.5 meters apart. Whole plots were harvested mechanically (combine harvester) and cane weight (yield) was measured with a weigh wagon (John Deere Thibodaux, Inc.) and the value was converted to tonnes of cane per hectare (TCH). One random sample of approximately 500 g of cane was taken from each plot using a sampling device present in the weigh wagon for juice quality and fiber analyses. Percent sucrose content was determined as described by Gravois and Milligan (1994). The secondary trait, tonnes of sugar per hectare (TSH), was calculated as the product of TCH and percent sucrose.

Data Analysis

The data were subjected to analyses of variance (ANOVA) using the following model:

$$Y_{ijkl} = \mu + L_l + R(L)_{kl} + G_i + GL_{il} + GR(L)_{ikl} + C_j + LC_{jl} + CR(L)_{jkl} + GC_{ij} + GLC_{ijl} + E_{ijkl}$$

where, Y_{ijkl} = observation for genotype i , in Crop-year j , in rep k nested within location l ; μ = overall mean; L_l = the effect of the l^{th} location; $R(L)_{kl}$ = the effect of the k^{th} rep nested within the l^{th} location (Error 1); G_i = the effect of the i^{th} genotype; GL_{il} = the interaction effect between the i^{th} genotype and l^{th} location; $GR(L)_{ikl}$ = interaction effect between the i^{th} genotype and the k^{th} rep nested within the l^{th} location (Error 2); C_j = effect of the j^{th} crop-year; LC_{jl} = interaction effect between the l^{th} location with the j^{th} crop-year; $CR(L)_{jkl}$ = interaction effect between the j^{th} crop-year and the k^{th} rep nested within the l^{th} location (Error 3); GC_{ij} = interaction effect between the i^{th} genotype and j^{th} crop-year; GLC_{ijl} = interaction effect between the i^{th} genotype, l^{th} location and j^{th} crop-year; and E_{ijkl} = the residual term (Error 4).

A basic assumption of the analysis of variance is the independence of error effects among observations. The data may violate this basic assumption as each ratoon crop is grown from the previous year's stubble crop, all of which originated from the initial plant-cane crop. Therefore, error terms of observations are correlated as the measurements were done on the same experimental unit over time. Furthermore, crop year effects are fixed and cannot be randomised to treatment effects. To minimize the effect of a possible violation of independence of error terms, the covariance structure was modelled using repeated measures analysis in the Proc Mixed procedure (SAS Inc. 1990). The autoregressive model was chosen as the appropriate covariance structure for the analysis as it had the lowest Akaike's information criterion (AIC) value. The AIC value is a parameter used in comparing models and the model with the lower AIC value is preferred. The autoregressive model considers the variance of the current error term (say the second ratoon) to be a function of the variances of the previous crop's error terms (the first ratoon and plant-cane crops) and is adjusted using a correlation coefficient. The fact that correlations were generally higher among crop-years within the same location compared to crop-years across

locations and among adjacent crops compared to non-adjacent crops (data not shown) favors our analytical approach.

All factors were considered to be random in this analysis. The genotypes, although selected, are taken in this study to represent a random sample of several possible advanced stage genotypes in the TSIP. Similarly, although the locations were chosen to represent sugarcane production areas differing in soil characteristics, together with crop-year they represent a random sample of possible sugarcane growing environments being targeted by the TSIP.

Variance components with their approximate standard errors (Anderson and Bancroft, 1952) were estimated from this analysis. The variance components were used to estimate the variance of a genotype mean (V_k) for different combinations of locations, replications and crop-years within a location (Fehr, 1987):

$$V_k = \sigma^2_E/jc + \sigma^2_{GLC}/lc + \sigma^2_{GL}/l + \sigma^2_{GC}/c \quad [1]$$

where, σ^2_E is the variance component for the residual term in the model; σ^2_{GLC} is the variance component for the interaction between genotype, location and crop-year; σ^2_{GL} is the variance component for the interaction between genotype and location and σ^2_{GC} is the variance component for the interaction between genotype and crop-year.

From the above, it was possible to calculate broad-sense heritability or genetic repeatability (h^2) on a plot mean basis as:

$$h^2 = \sigma^2_G/(\sigma^2_G + V_k) \quad [2]$$

where, σ^2_G is the variance component for the main effect of genotype.

These variance components were also used to estimate the number of locations (L) required to detect a specified difference between two genotypes (Addock *et al.*, 1997):

$$L \geq [2*(t_{\alpha/2} + t_b)^2(\sigma^2_E/jc + (\sigma^2_{R/L})/j + \sigma^2_{GLC}/c)]/d^2 \quad [3]$$

where, $(\sigma^2_{R/L})$ is the variance component for the j^{th} replication nested within the l^{th} location; $t_{\alpha/2}$ is the tabular t value ($\alpha = 0.05$); t_b is the t value associated with committing a type 2 error ($\beta = 0.25$) and d is the difference between genotypic means for the trait expressed as a percentage of that trait's trial mean.

RESULTS AND DISCUSSION

Variance Components

The GxL, GxC and GxLxC variance components were significant ($P = 0.05$) for all three traits (Table 1). These GxE effects were too important to be ignored especially since in some instances the GxE interactions seemed to be associated with changes in the relative ranking of genotypes across environments (Figure 1). Therefore, testing in multiple environments

(locations and crop-years) would be necessary to identify and select the most productive and stable genotypes in the TSIP.

Table 1: Variance Components (\pm standard errors), their relative rankings and broad sense heritability for sugar related traits in sugarcane

Trait	G	GxL	GxC	GxLxC	Error	H
TCH	124.94 \pm 6.83	42.23 \pm 4.60	54.44 \pm 4.08	77.29 \pm 7.05	174.03 \pm 10.31	78.3
Sucrose, %	0.42 \pm 0.02	0.05 \pm 0.01	0.20 \pm 0.01	0.13 \pm 0.02	0.62 \pm 0.04	81.5
TSH	2.05 \pm 0.12	0.75 \pm 0.08	1.14 \pm 0.08	1.67 \pm 0.14	3.00 \pm 0.18	74.8

TSH = tonnes of sugar per hectare; TCH = tonnes of cane per hectare; G= genotype; GxL = genotype x location interaction; GxC = genotype x crop-year interaction; GxLxC = genotype x location x crop-year interaction; H = broad sense heritability.

The proportion of the combined GxE variance to the variance of the G main effect (Table 2) showed that GxE was proportionately higher for TCH and the secondary trait TSH than for percent sucrose and this was reflected in the relative values of the broad sense heritability (repeatability) for these traits (Table 2). Ranking of the GxE variance components showed that for TCH and TSH, GxLxC accounted for the largest source of the GxE variance and was double that of the GxL which was the least. For percent sucrose, GxC was found to be the largest (53%) source of variance while GxL was again the least, accounting for only 13% of the total GxE variance. These results highlight the importance of testing for ratooning ability and suggest that substantial gains from selection could be achieved by increasing the number of crop-years over which genotypes are tested. The results differ from those reported by Jackson and Hogarth (1992), Mirzawan et al. (1993) and Bull et al. (1994) in Australia who found location to be the most important source of variation. Similar results were reported in the Burdekin region of Queensland in Australia by Rattey and Kimbeng (2001) and in Zimbabwe by Zhou (2004). A common feature among the Burdekin, Zimbabwe and Texas studies not shared by the other Australian studies is that the crops were grown under irrigation such that drought stress was probably not a limiting factor across locations and crop-years.

Table 2: Variance Components as a proportion of the genotype main effect for sugar related traits in sugarcane. Values are expressed as a ratio (or percent), i.e., interaction variance component/variance component for genotype main effect

Trait	GxE	GxE:G	GxL: G	GxC: G	GxLxC: G	GxE ranking
TCH	173.96	1.39 (100)	0.34 (24)	0.44 (31)	0.62 (44)	GxLxC>GxC>GxL
Sucrose (%)	0.38	0.89 (100)	0.12 (13)	0.47 (53)	0.31 (35)	GxC>GxLxC>GxL
TSH	3.56	1.74 (100)	0.37 (21)	0.56 (32)	0.81 (46)	GxLxC>GxC>GxL

TSH = tonnes of sugar per hectare; TCH = tonnes of cane per hectare; G= genotype main effect; GxE = total of the three interaction components namely, GxL = genotype x location interaction, GxC = genotype x crop-year interaction and GxLxC = genotype x location x crop-year interaction.

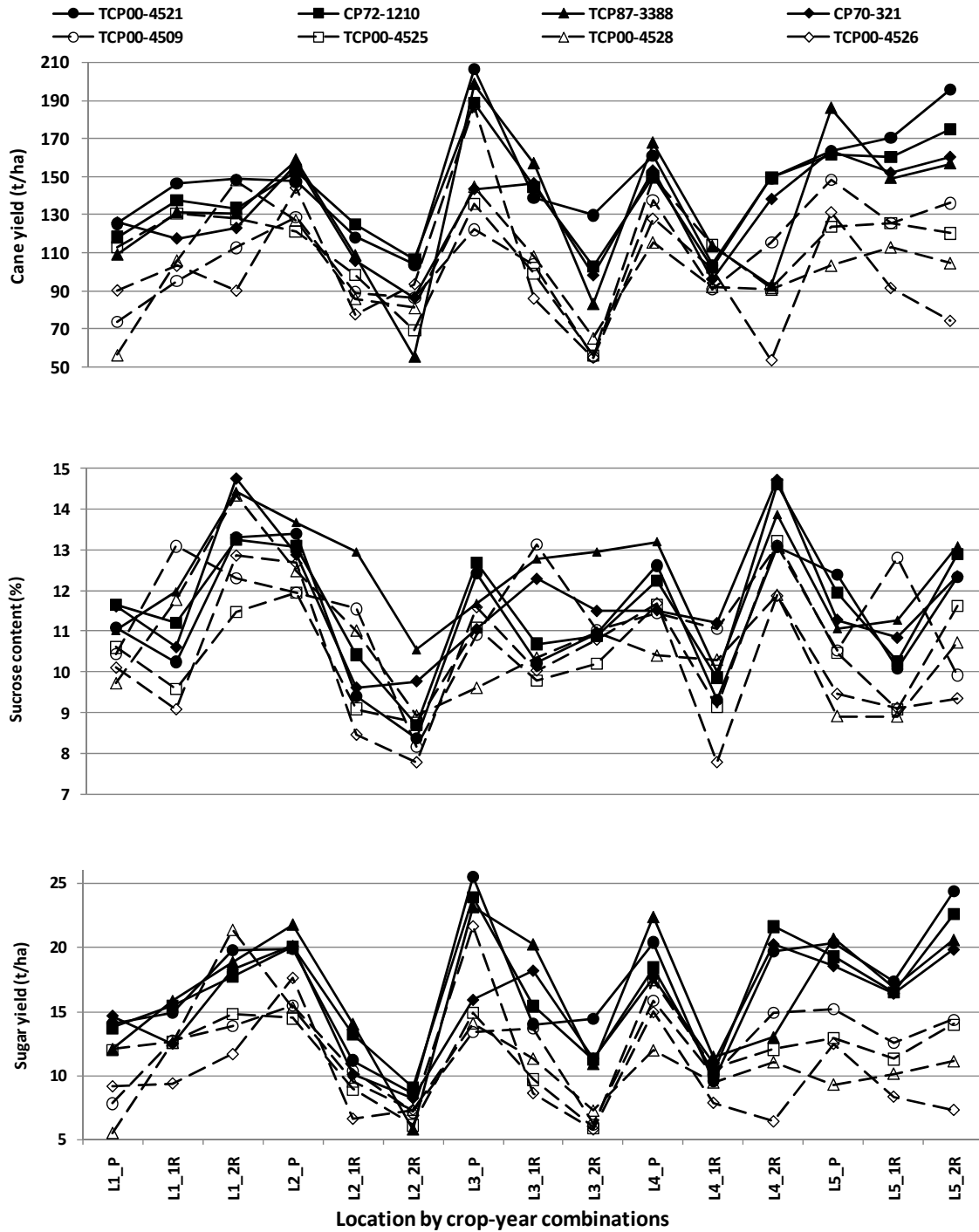


Figure 1. Performance of the top (TCP00-4521, CP72-1210, TCP87-3388 and CP70-321) and bottom four (TCP00-4509, TCP00-4525, TCP00-4528 and TCP00-4526) sugarcane genotypes across environments (locations and crop-years). The genotypes were ranked across all environments based on sugar yield (t/ha) to select the top and bottom performers.

Although the GxLxC variance was significant ($P = 0.05$) for the two primary traits, TCH and percent sucrose (Table 1), the GxLxC:G ratio was disproportionately larger for TCH than for percent sucrose. Second order interactions are by nature difficult to interpret and model and this

may present added challenges if one attempts to select genotypes, for use as parents, based on their performance for a primary trait (e.g., cane yield or percent sucrose). For example, while the ratio of the GxC:G was similar for TCH and percent sucrose, judging from the GxL:G ratio and its proportion to the total GE:G ratio, it appears that testing across locations is of greater importance to detect genotypic difference for TCH than for percent sucrose. Therefore, compared to percent sucrose, more resources (replication, location and crop-years) would be required to adequately detect differences among genotypes for TCH.

Resource allocation: the variance of a genotype mean and broad sense heritability

The selection process requires that genotypes deemed as inferior are identified and eliminated from further consideration. To declare one genotype as superior to another, one must be able to adequately discriminate between their means. The ability to accurately detect significant differences between means depends on the variance associated with these means. The variance of a genotype mean (V_k), as estimated using testing resources (e.g. locations, crop-years and replications within locations) can vary depending on the relative importance of the σ^2_G , σ^2_E , and σ^2_{GE} (σ^2_{GL} , σ^2_{GC} , σ^2_{GLC}) (Equation 1). The discriminating ability is enhanced as the variance decreases and the broad sense heritability increases. We assessed the relative importance of various combinations of the three testing resources (locations, crop-years and replications) in estimating a genotype mean using broad sense heritability. Heritability in this case measures repeatability or the consistency with which we can distinguish between the genotypic means, based on the proportion of the variation among genotype means that is due to the variation in genotype effects (Equation 2). By altering the number of replications, locations and crop-years (Equation 1) we can determine what resources would be required to detect repeatable differences among the genotypes.

When broad sense heritability values for TSH were plotted for replications within locations (Figure 2), the plots showed that increasing the number of replications beyond two did little to increase the heritability values even as the number of locations increased. This was consistent in the plant-cane, first and second ratoons crop-years. Therefore, resources at this stage of the TSIP could be better spent by reducing the number of replications planted per location from four to two or possibly three (in case a replication is destroyed). Similar studies of the Louisiana Sugarcane Variety Development Program by Milligan (1994) showed marginal gains in broad sense heritability beyond two replications while Brown and Glaz (2001) were able to reduce replications from eight to four in Florida. Rattey and Kimberg (2001) found two replications to be optimum for the Burdekin region in Queensland, Australia.

Increasing the number of locations beyond four resulted in very minimal increments in the heritability values (Figure 3). This trend was consistent over the three crop-years and even as the number of replications increased. Therefore, four locations will be appropriate to test differences among genotypes at this stage of the program. Figure 4 shows the heritability values for crop-years with different combinations of locations and replications. There were marginal increases in broad sense heritability beyond the fourth crop-year (third ratoon). Therefore, four crop-years would be adequate to test differences among genotypes at this stage of the program. Brown and Glaz (2001), in Florida, found that three crops were appropriate for testing ratooning ability but noted that this view was driven by the fact that fewer than 10 % of growers in Florida grow crops

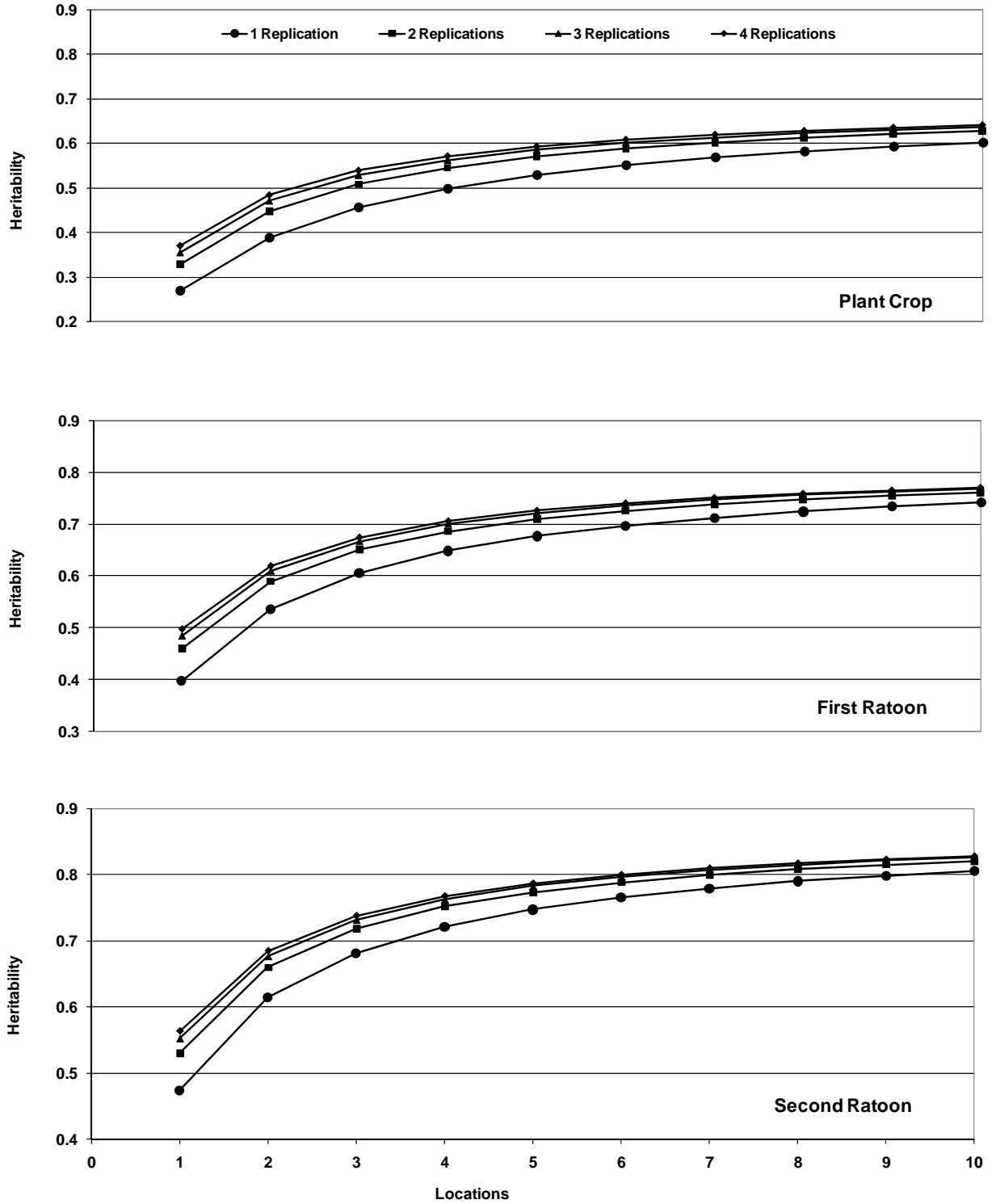


Figure 2. Replication effect on the broad sense heritability values for tonnes of sugar per hectare.

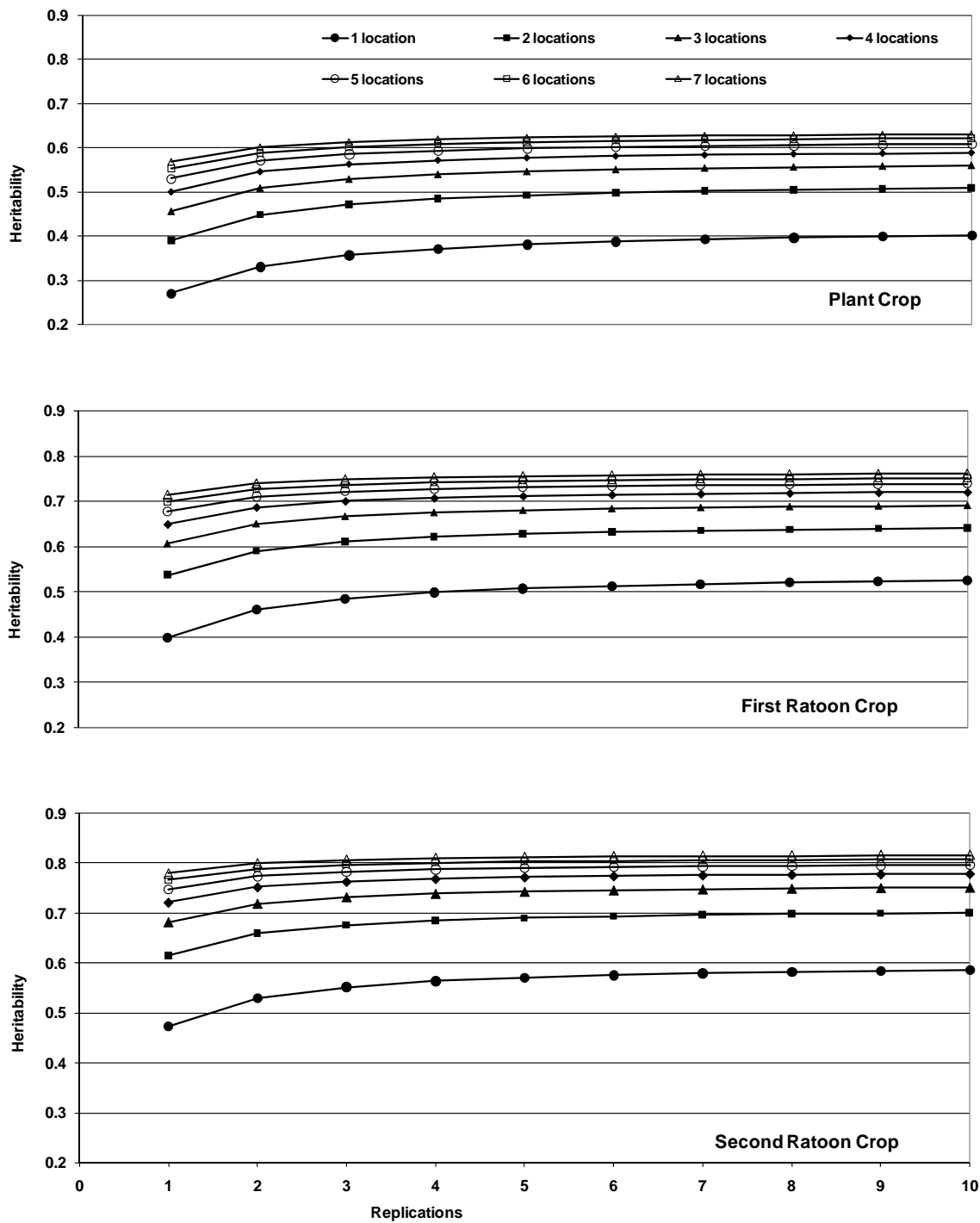


Figure 3. Location effect on the broad sense heritability values for tonnes of sugar per hectare.

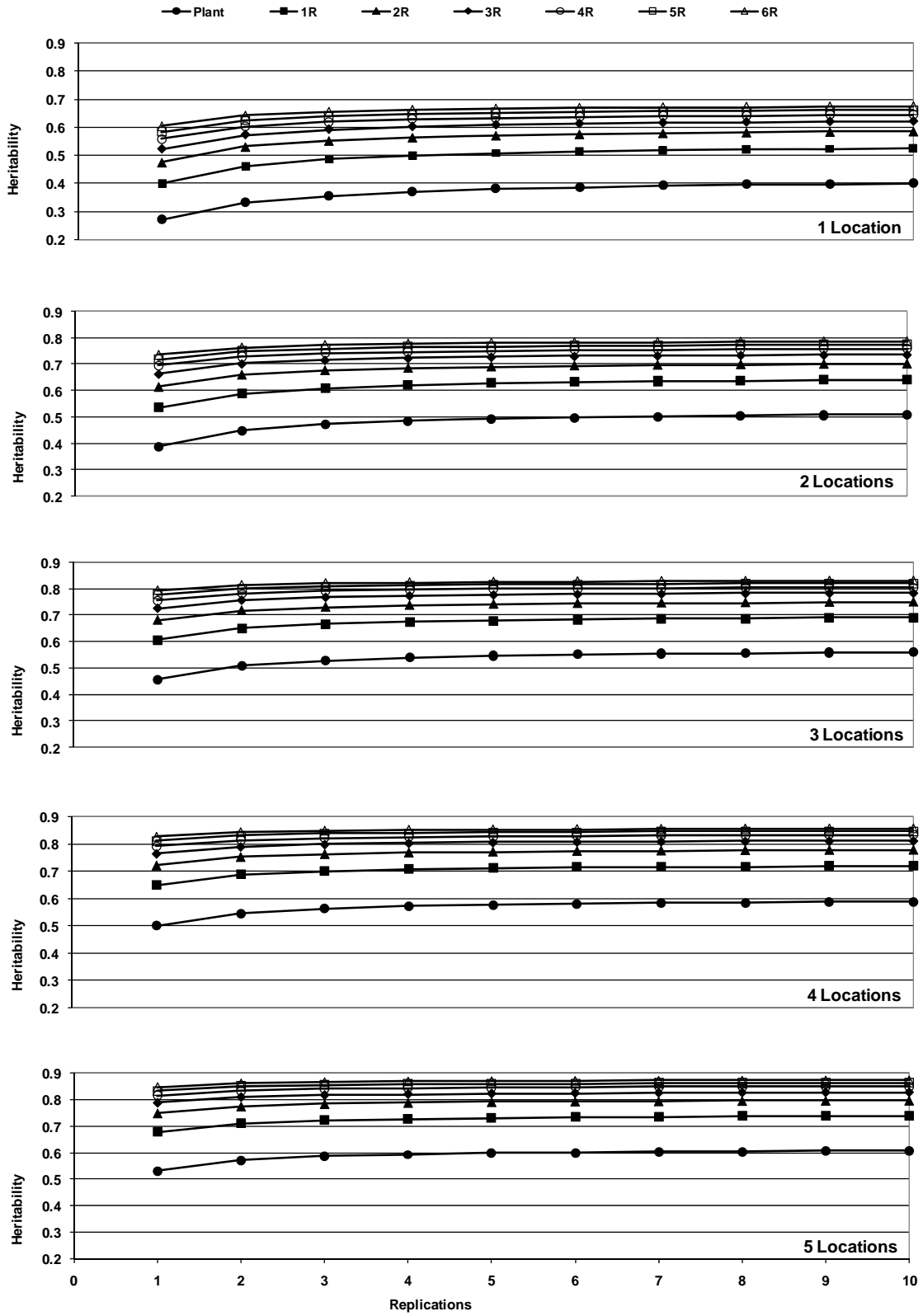


Figure 4. Crop-year effect on the broad sense heritability values for tonnes of sugar per hectare.

beyond the second ratoon crop. In Texas, sugarcane is traditionally harvested through a plant-cane and four ratoon crops (five crop-years). Irrigated sugarcane farming is capital intensive and ratooning the crop for longer could ensure greater profitability (Clowes 1998). This can only happen if genotypes are selected for suitable levels of ratooning ability. Milligan et al. (1990) found that selection to improve a particular crop's yield component value is most effective when performed within that crop and that genetic advance was greatest among the older crops. Moreover, harvesting ratoon trials is generally more efficient on resources than planting more locations and could eventually lead to the selection of genotypes with increased levels of ratooning ability and productivity beyond five crop-years.

Resource allocation: optimal number of locations, replications and crop-years

We used a second metric to assess the best allocation of resources based on the precision to which the resources would detect differences among genotypes in the TSIP (Equation 3). Components of the GxE interactions were used to calculate the number of locations required at a given Type I ($\alpha = 0.05$) and Type II ($\beta = 0.25$) error probability to detect a specified mean difference between two genotypes for varying number of replications and crop-years (Table 3). The results show that, except for percent sucrose, with the current set up of five locations, four replications and three crop-years, genotypic difference could reliably be detected only for means which differ by above 15 to 20 %, while mean differences less than 15 % would go undetected (Table 3). Percent sucrose is generally known to be more stable and can be measured with greater precision compared to TCH (Kimberg et al., 2001; Jackson and McRae 2001) and, therefore, requires comparatively fewer resources to adequately detect differences among genotypes. For example, with four replications and five locations, only the plant-cane crop data would be needed to detect differences among genotypes for percent sucrose at the 10% level (Table 3). Cane yield (TCH) would require comparatively more locations, crop-years and replications to detect smaller (10%) differences. The relatively large magnitude of the GxLxC for TCH is directly responsible for this.

For TSH, the best combination of replications (2), crop-years (4) and locations (4) identified through heritability (Figures 1, 2 and 3) would reliably detect differences among genotypes if the means differ by at least 20 % (Table 3). Planting an additional replication within a location is likely to improve the precision with which genotypic differences can be detected by at least 5 %. The logistics and resources (seed-cane and man-hours) required favour planting an additional replication or harvesting an extra crop rather than planting a new trial location. However, the resources required to detect smaller difference (10 % or less) would be prohibitively large to accomplish, especially using small trial plots. Therefore, to guard against discarding genotypes with commercial potential, genotypes not differing from the commercial check (s) by at least 5 to 10 % should be retained for further testing in larger plots. Because of the limited resources available to most breeding programs, such large plot tests are best carried out by extension personnel, agronomists or sometimes mill managers. In Australia for example, extension personnel routinely plant large plots known as strip trials at multiple farm locations to compare new releases. To obtain sufficient amount of seed-cane, the TSIP program could start propagating the top 25% of genotypes after accumulating two crop-years of data. This is because a 25% difference can be reliably detected using four locations and two replications after two crop years (Table 3). The top 10 % of genotypes, based on cumulative data from four crop-years, could subsequently be planted to strip trials at multiple locations. Such trials enhance the

opportunity to obtain added and useful information relating to location specific management practices on these genotypes. Moreover, location specific management practices have been speculated (Milligan 1994) and implicated (Jackson and Galvez 1996) as having a role in affecting GxE interactions in sugarcane.

Table 3. Number of locations required to detect a specified percentage difference (d) between genotypes for tonnes of cane per hectare, tonnes of sugar per hectare (TSH) and percent sucrose (% S)

No. reps within a trial	d value	Crop-years at a trial											
		Plant-cane crop			First ratoon			Second ratoon			Third ratoon		
		TCH	TSH	%S	TCH	TSH	%S	TCH	TSH	%S	TCH	TSH	%S
1	10%	54	76	16	32	42	8	24	31	6	21	26	4
2	10%	34	50	10	19	27	5	14	20	3	12	16	2
3	10%	27	41	7	15	22	4	11	16	2	9	13	2
4	10%	24	37	6	13	20	3	9	14	2	8	11	2
5	10%	22	34	6	12	18	3	8	13	2	7	10	1
1	15%	24	34	7	14	19	4	11	14	2	9	11	2
2	15%	15	22	4	9	12	2	6	9	1	5	7	1
3	15%	12	18	3	7	10	2	5	7	1	4	6	1
4	15%	11	16	3	6	9	1	4	6	1	3	5	1
5	15%	10	15	2	5	8	1	4	6	1	3	4	1
1	20%	13	19	2	8	11	1	6	8	1	5	6	1
2	20%	8	12	2	5	7	1	4	5	1	3	4	1
3	20%	7	10	2	4	6	1	3	4	1	2	3	1
4	20%	6	9	2	3	5	1	2	3	1	2	3	1
5	20%	5	9	1	3	5	1	2	3	1	2	2	1
1	25%	9	12	3	5	7	1	4	5	1	3	4	1
2	25%	5	8	2	3	4	1	2	3	1	2	3	1
3	25%	4	7	1	2	4	1	2	3	1	1	2	1
4	25%	4	6	1	2	3	1	2	2	1	1	2	1
5	25%	3	5	1	2	3	1	1	2	1	1	2	1

CONCLUSIONS

In summary, appreciable amounts of GxE interactions were revealed in this study. The GxE was associated with considerable changes in the relative ranking of genotypes across environments, even among the top performing genotypes. The implication of these results is that advanced stage trials in TSIP would have to be designed in such a way as to accommodate, manage and exploit these GxE interactions. It appears increasing the number of crop-years over which genotypes are tested offered the best option to maximize selection gain in the TSIP. Two replications, four locations and four crop-years appear to be an efficient use of resources to provide an adequate level of discrimination between genotypes in the TSIP without

compromising the level of experimental precision being attained under the current regime of four replications, five locations and three crop-years. Currently, reliable differences among genotypic means can only be detected if the means differ by at least 15%. The amount of resources in terms of land and labor required to reliably and consistently detect smaller differences among genotypic means, using small trial plots, are not readily available to the TSIP. Therefore, the top 10% of genotypes in advanced stage selection trials should be selected for further consideration perhaps in larger strip plot trials. Such trials would also be useful in gathering more information about location specific management practices on these genotypes.

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REFERENCES CITED

- Adcock, R.A., N.S. Hill, H.R. Boerma, and G.O. Ware. 1997. Sample variation and resource allocation for ergot alkaloid characterization in endophyte-infected tall fescue. *Crop Science* 35: 31-35.
- Bull, J.K., M. Cooper, and K.E. Basford. 1994. A procedure for investigating the number of genotypes required to provide a stable classification of environments. *Field Crops Res.* 38: 47-56.
- Clowes, M.St.J. and W.L. Breakwell. 1998. *Zimbabwe Sugarcane Production Manual*. Zimbabwe Sugar Association Experiment Station, Chiredzi, Zimbabwe.
- Davis, M.J. and R.A. Bailey. 2000. Ratoon Stunting, pp. 49-54. *In* Rott, P., R.A. Bailey, J.C. Comstock, B.J. Croft, and A.S. Sauntally (eds). *A guide to sugarcane diseases*, Centre de Cooperation Internationale en Recherche Agronomique pour le Development (CIRAD) and International Society of Sugar Cane Technologists (ISSCT) Montpellier, France.
- Fehr, W.R. 1987. *Principles of cultivar development: Theory and technique*. Macmillan Publishing, New York. pp. 97, 256.
- International Society for Plant Pathology. Committee on Common Names of Plant Diseases, Sugarcane diseases. http://www.isppweb.org/names_sugarcane_pathogen.asp (Verified 23 February 2009).
- Jackson, P. and T.A. McRae. 2001. Selection of sugarcane clones in small plots. Effects of plot size and selection criteria. *Crop Science* 41: 315-322.
- Jackson, P.A. and D.M. Hogarth. 1992. Genotype x environment interactions in sugarcane. I. Patterns of response across sites and crop-years in North Queensland. *Australian J. Agric. Res.* 43: 1447-1459.

- Kang, M.S., J.D. Miller, P.Y.P. Tai, J.L. Dean, and B. Glaz. 1987. Implications of confounding of genotype x year and genotype x crop effects in sugarcane. *Field Crops Res.* 15: 349-355.
- Kang, M.S. and J.D. Miller. 1984. Genotype x environment interactions for cane and sugar yield and their implications in sugarcane breeding. *Crop Science* 24: 435-440.
- Kimbeng C.A., A.R. Rattey, and M. Hetherington. 2002. Interpretation and implications of genotype by environment interactions in advanced stage sugarcane selection trials in central Queensland. *Australian J. Agric. Res.* 53: 1035-1045.
- Kimbeng, C.A., D. Froyland, D. Appo, A. Corcoran, and M. Hetherington. 2001. An appraisal of early generation selection in the central Queensland sugarcane improvement program. *Proc. Australian Soc. Sugarcane Technol.* 23: 129-135.
- Milligan, S.B., K.A. Gravois, K.P. Bischoff, and F.A. Martin. 1990. Crop effects on broad sense repeatabilities and genetic variances of sugarcane yield components. *Crop Science* 30: 344-349.
- Milligan, S.B. 1994. Test site allocation within and among stages of a sugarcane breeding program. *Crop Science* 34: 1184-1190.
- Mirzawan, P.D.N., M. Cooper, and D.M. Hogarth. 1993. The impact of genotype x environment interactions for sugar yield on the use of indirect selection in southern Queensland. *Australian J. Exper. Agric.* 33: 629-638.
- Rattey, A.R. and C.A. Kimbeng. 2001. Genotype by Environment interactions and resource allocation in final stage selection trials in the Burdekin district. *Proc. Australian Soc. Sugarcane Technol.* **23**: 136-141.
- Rea, R. and O. De Sousa-Vieira. 2002. Genotype x environment interactions in sugarcane yield trials in the Central Western region of Venezuela. *Interciencia* 27: 620-624.
- SAS Institute. 2003. SAS for windows, Version 9.1.3 Service Pack 4, Cary NC, USA.
- United States Department of Agriculture - Natural Resources Conservation Services Web Soil Survey [Online]. Available at <http://websoilsurvey.nrcs.usda.gov/app/WebSoilSurvey.aspx> (Verified 10 June, 2008).
- Zhou, M. 2004. Strategies for variety selection in the breeding program at the Zimbabwe Sugar Association Experiment Station. *Proc. of SASTA* 78: 137-147.