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Characterisation of Sugarcane * Erianthus arundinaceus Hybrids Using PCR and in situ Hybridisation

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E. arundinaceus is a species related to sugarcane with desirable attributes including excellent vigour and ratooning, adaptability to environmental stresses such as moisture deficits and excesses, and resistance to *Pachymetra* root rot. Numerous attempts have been made to cross *E. arundinaceus* with sugarcane to introduce these characters into modern cultivars. However, no conclusive results have been achieved to date. Very few progeny have been produced, despite the number of intergeneric crosses made. In most cases intergeneric hybrids were produced from crosses involving pure *S. officinarum* ($2n=80$) as the female parent and *E. arundinaceus* as the pollen donor (D'Hont et al., 1995; Besse et al., 1997; this study). One of the major obstacles in using *E. arundinaceus* in the past has been the identification of true hybrids using morphological characters, which is time-consuming and unreliable. Molecular diagnostic tools have recently been developed for use in sugarcane to overcome this difficulty (D'Hont et al., 1995). These tools include sequence-tagged PCR to identify true hybrids at the seedling stage, and genomic in situ hybridisation (GISH) to characterise the chromosome complement of these genuine hybrids. An introgression program involving *Erianthus* commenced several years ago at the Bureau of Sugar Experiment Stations (BSES) in Australia. Here we report on the significant progress achieved in this program since these molecular tools were implemented.

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The Origin of " North Indian and Chinese Sugarcanes" Investigated by Genomic in situ Hybridization and RFLP Markers

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Genomic in situ hybridization (GISH), detection of species-specific repeated sequences and RFLP analysis were performed on a sample of North Indian and Chinese sugarcane clones (referred to as *S. barberi* and *S. sinense*) in order to investigate their origin. GISH proved the interspecific hybrid origin of these taxa. Together with the distribution of species-specific repeated sequences and previously reported RFLP data, the results show that these taxa are derived from interspecific hybridization between *S. officinarum* and *S. spontaneum* and that no other genus has been directly involved. RFLP showed that these clones belong to a few groups each one derived from a single interspecific hybrid that has subsequently undergone a few somatic mutations. These groups correspond quite well with the sub-groups already defined based on morphological characters and chromosome numbers. However, the calculated genetic similarities do not support the existence of two taxa. The "North Indian and Chinese sugarcanes" represent a set of horticultural groups rather than established species.

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Performance of Selected Clones from Genetic Base Broadening Programme in Barbados

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The genetic base broadening (BB) programme through the incorporation of wild germplasm, has produced an array of clones with diverse genetic background some of which are very promising parents or commercial varieties. At present over 983 clonal selections representing various levels of incorporation of 72 *Sacharum officinarum*, 49 *S.spontaneum*, 7 *S.robustum* and 9 *Erianthus arundinaceus* clones are being used in many combinations with commercial parents in the West Indies Sugarcane Breeding and Evaluation Network (WISBEN) programme. Two varieties selected from the BB population are grown commercially. The BB clones maintain considerable variability for cane yield and other agronomic characters. The range of variability for quality characters was: Brix 10.6 - 26.2, sucrose % cane 5.1 - 18.0, purity 47.3 - 93.9% and fibre % cane: 12.3 - 26.2.

A yield trial was conducted with 17 selected BB clones and a standard variety in two locations and harvested as plant cane and three ratoon crops. There were significant differences between the standard and BB clones for cane/ha, sugar/ha, sucrose % cane and fibre % cane. The top five BB clones gave between 10 and 34% more cane and the top three clones gave between 15 and 20% more sugar per hectare than the standard variety. BB clones had a slightly lower sugar and higher fibre. BB clones seem to maintain better yield in ratoons.

The performance of the first set of BB clones is quite encouraging. In addition to broadening the genetic base and providing a broad range for useful agronomic characters, these clones provide much needed parents to exploit hybrid vigour for commercial varieties. The potential for higher biomass production, higher fibre and varying levels of purity also make these clones useful to produce cane for other than commercial sugar production.

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Long-term Benefits Accrued from Photoperiod Facilities for the Breeding and Selection Programme at Mt Edgecombe, South Africa

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Most sugarcane parent varieties do not flower freely at Mt Edgecombe (30°S) because of the latitude affecting flower initiation and pollen fertility. A large crossing glasshouse and a photoperiod facility were constructed in 1965 and 1971, respectively, to aid the supply of flowers for producing seed and seedlings for the selection programme.

The benefits of using such facilities are described. These include the increased number of crosses made; most parent clones flowered and flowering could be induced to be early, mid or late in the season; most stalks of most varieties flowered; and pollen shed and pollen fertility were enhanced. In the crossing glasshouse, the minimum temperatures can be maintained and the humidity can be adjusted to create optimum conditions for seed set.

Three varieties, N24, N25 and N26 were selected from crosses made in these facilities that otherwise would not have been made. These facilities enable the breeders to plan the crosses to be made and with the controlled conditions, the chances are good that the crosses can be made.

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Flowering Control for the Utilisation of Wild and Cultivated Sugarcane Germplasm in Barbados

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Most of the sugarcane germplasm flowers profusely in the elevated central parts of Barbados located at 130 4' N latitude. Commercial varieties flower between late October and early December, peaking in the first three weeks of November. The S.spontaneum clones in our collection flower between early July and late December depending upon their origin between 9 0 0' S and 320 1' N latitude. This wide range of flowering times made it necessary to control flowering in order to incorporate wild germplasm into the commercial breeding parents and to make many wide combinations for the West Indies Sugarcane Breeding and Evaluation Network (WISBEN) which is spread over the large geographical area.

After conducting research into floral induction, initiation, emergence and intensity with many clones, two methods were adapted. The most effective method was to delay flowering, whereby natural induction was prevented by a night light break regime (NLB) for a predetermined duration to be followed by a day length extension in the early morning, imitating natural inductive day lengths. This was achieved by growing plants in cans or in field plots and by giving a one hour NLB at midnight using 40 watt bulbs hanging over the plant for several days followed by appropriate day length extension in the morning using a 100 watt bulb suspended over the plant for several days. Advance of flowering was affected by shortening day lengths for various periods prior and during floral development using dark rooms. Advancing flowering was more difficult with fewer clones responding precisely and with reduced intensity of flowering.

During the last 30 years, a total of 703 clones including species, interspecific hybrids and commercial were treated with different light regimes either to advance or delay flowering. These clones include 78 S.spontaneum, 12 S.officinatum, 12 S.robustum, 389 interspecific hybrids and 212 commercial hybrids. The maximum delay in flowering time achieved was 13 weeks. Some clones responded very well producing flowers throughout the eight weeks of the Crossing Season. Without manipulating flowering time in this many clones it would not have been possible to exploit the potential of the wild germplasm and so broaden the genetic base. The problems associated with failure to respond to floral induction or floral emergence and resulting induced male sterility in the treated clones are discussed.

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Development and Application of Microsatellite Markers in Sugarcane

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We report on the development of microsatellite (simple sequence repeats or SSR) markers and their applications in sugarcane. Several small insert microsatellite enriched libraries have been constructed from the sugarcane variety R570. These include libraries enriched for the dinucleotide repeats GT, GA, and a mixture of the tri and tetra repeats. Two hundred and fifty clones from these libraries were sequenced to confirm the presence of the microsatellite. Primer pairs were designed for one hundred microsatellites and tested on the cultivar R 570 as well as two S. officinarum and two S. spontaneum clones. Products were analyzed by polyacrylamide gels and autoradiographies. The resulting patterns ranged from simple patterns with a few bands to highly complex patterns. Seventy five of the primer pairs tested produced good quality profiles. A few of them were tested on a sample of cultivars and several progenies revealing a high potential for testing cultivar identity and progeny legitimacy and for genetic mapping.

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New Approaches for Introgression Breeding in Australia

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There has been an interest and activity in breeding to utilise basic species in sugarcane breeding in Australia since the 1960's. Introgression breeding programs are generally considered to be long term and risky, and in Australia the commercial success of this work has been small. A major problem is associated with the difficulty of transferring genetic components of commercial value from the exotic genome (which might be small in proportion to the whole genome) into a commercially elite genetic background while at the same time eliminating the non-valuable components. Without a highly effective selection process during several backcrossing cycles there is a high probability of loss of some valuable components but retention of some components of negative value.

In Australia, a research program was commenced in 1999 to seek new genes of value from basic S. officinarum clones which may contribute to higher sucrose content in commercial varieties. Molecular markers are being used to determine if QTL's of value for sucrose derived from the S. officinarum sources can be identified and then backcrossed into an elite genetic background using marker assisted selection. Four case study populations are being used to explore the value of using marker assisted selection during introgression. At the same time a larger number of S. officinarum clones (180) are being characterised for sucrose accumulation and components. If marker assisted selection shows promise, then an ongoing program to identify and incorporate QTL's of value from apparently elite S. officinarum clones will probably be commenced. It is considered that marker assisted

selection to identify and select for QTL's of value from exotic sources could also be applied to introgression programs targeting other species. This paper discusses the approach being used in Australia and factors which may affect the success of using molecular markers in introgression breeding programs.

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The Basic Theory for Selecting Single-dose Molecular Markers as a Marker-assisted Selection Tool for QTL Selection in Sugarcane

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In the past ten years, the theory of single-dose molecular markers for mapping genomes of highly polyploid species such as sugarcane has been developed. A single-dose molecular marker can divide a mapping population into two sub-populations or two marker classes: marker-present class vs. marker-absent class. The most reliable linkage of single-dose molecular markers with a mapping population size of 75 to 100 individuals is the linkage of markers (marker-present) in coupling phase, especially for autopolyploids. Single-dose molecular markers linked in repulsion phase and double-dose molecular markers are necessary for the identification of homologous chromosomes in polyploids, but they are useless for marker-assisted selection in a breeding program. Breeders need a straightforward and simple method for the identification of useful single-dose molecular markers. Intuitively, single-dose molecular markers linked in coupling phase flanking alleles of QTLs are the most useful markers for marker assisted selection. The basic theory for the identification of useful single-dose molecular markers linked to alleles of QTLs is presented in this report. The steps toward marker identification start with the identification of single-dose molecular markers that have significant association with a quantitative trait value by using one of the three statistical tests: t-test, F-test, and regression test. Insignificant markers are eliminated from further analysis. The selected markers are then separated into positive effect and negative effect markers, based on the difference between the mean trait value in marker-present class and marker-absent class for each marker. If the value is greater than zero, the marker (present) has a positive effect; otherwise the marker (present) has a negative effect. Positive and negative effect markers are then analyzed separately for coupling linkages, so that each cosegregation group contains markers having the same effect and all are linked in coupling phases. The relative location of allele of QTL within a marker cosegregation group can then be determined by partial regression analysis of trait values on every two markers.

Coupling phase linkage of markers in each cosegregation group could assure that allele of QTL and markers are linked on the same chromosome. And finally, from each marker cosegregation group, markers closely linked to an allele of a QTL can be identified as the useful markers for marker assisted selection. Numeric examples are presented to illustrate the procedures. The theory for selecting useful markers is indeed simple and straightforward, but marker-assisted selection has not yet been proven in a sugarcane breeding program. The real challenge is not so much the biotechnology but how to install large field experiments and collect reliable measurements on economically important, especially low heritability, traits.

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Building Parental Populations with Very High Sucrose Content Through Recurrent Selection

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The frequency of potential parental clones with very high sucrose content in the West Indies breeding programme is relatively low. To increase the number of clones that could be used as donor parents for high sucrose content a recurrent breeding and selection programme was carried out. Starting from a base population of thirty-seven clones, three closed cycles of crossing and selection were made. Each step was of two phases; crossing among the selected clones to produce seedlings, followed by selection of those seedlings with the most extreme brix levels to become the parental clones for the next cycle of crossing. Selection was made on in field brix alone, ignoring all other characteristics. Each year an indicator standard variety, B 77602, was used to decide when to carry out the selection, this being done when it had reached maturity. This was an attempt to reduce the year to year seasonal differences in the cane-ripening pattern in Barbados. The 147 selections made in cycle three had a brix range of 115-129 % of B 77602. The highest in field brix recorded was 30.1 compared to the standard variety, B 77602, with a brix of 23.4. Complete cane analysis showed a similar range of values for sucrose percent of cane the maximum being 126% of B 77602. The results of crossing the high quality clones with commercial varieties and the implications for the general breeding programme are discussed.

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Assessing the Impact of Selection for High Sucrose on Molecular Diversity in Sugarcane

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A population with very high sucrose content has been created at WICSCBS by three cycles of recurrent selection, as illustrated by mean brix increasing from 21.0 to 28.5 % in the selected populations. We are using molecular

markers to analyse the diversity of this enriched population and compare it to the population of parents initially used. Markers whose frequency has been affected may have evolved through genetic drift but also through linkage drag associated with selection for sucrose; this may help identify genome regions implicated in the genetic control of sucrose content. Four AFLP primer combinations were used on the 37 parents and the 145 clones selected after the three recurrent cycles ; this allowed the generation of 228 polymorphic AFLP bands. Calculation of a similarity index (Dice Index) indicates that there has been a slight reduction of the global diversity in the progeny compared to the parents. However, the mean number of bands and the distribution of the number of bands indicate that the progeny is more heterozygous than the parents. Two of the markers for which the frequency has been highly modified in the progeny revealed significantly associated to Brix. These markers represent good candidate markers for sugar content. Additional AFLP primers will be used to identify more candidate markers. Their relation with sugar content will have to be confirmed on other segregating populations of cane the maximum being 126% of B 77602. The results of crossing the high quality clones with commercial varieties and the implications for the general breeding programme are discussed.

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Gene Analysis of Sucrose Accumulation Related Enzyme

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A physiological pathway through sucrose phosphate is considered to be a main route to sucrose accumulation in sugarcane storage tissue. Sucrose phosphate synthase (SPS) is thought to be an important enzyme in this pathway. The activity and genetic diversity of SPS and the related enzyme, sucrose phosphate phosphatase (SPP), were investigated in relation to sucrose content. Higher SPS and SPP activity were observed in high sucrose content commercial clones, whereas lower activities were observed in wild clones. The SPS activity increased under ripening conditions such as low temperatures. These results imply that the activity of these enzymes play an important role in sugar accumulation in sugarcane storage tissue. Seven signals of SPS gene, as a maximum number, were observed in commercial clones by RFLP analysis, whereas only two signals were observed in some of the wild clones. There was a positive correlation between sucrose concentration of the juice and the numbers of SPS gene signals among genetic resources. In total thirteen different SPS signals were observed in genetic resources. Some of the SPS gene signals were not found in the commercial clones. The introduction of these unused SPS genes, which are found in *Saccharum spontaneum* or *S. sinense*, to commercial clone, is available through crossing. The results of this study suggest that SPS gene accumulation increases sucrose content in sugarcane. However, SPS is expressing in both photosynthetic tissues in leaves and sucrose storage tissues in stem. Further investigation on tissue specific gene analysis will be required.

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Potential Versus Realized CCS: Lessons for Crop Improvement

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The dramatic decline in commercial cane sugar (CCS) levels in the tropical Queensland industry in the past six years has prompted an examination of crop composition and quality components, changes in these from field to mill, and implications for crop improvement. The objective of research reported here was to quantify crop composition and quality in-field and post-harvest, and relate these and mill-realized CCS. During the 1999 harvest, 17 diverse crop sites were sampled, predominantly in the Mulgrave Mill area, south of Cairns. About 10 sub-samples were taken in-field and post-harvest at each. A separate rake was generated from each for determination of mill-realized CCS. In-field fractions of sound stalks, unsound stalks, sucker culms, and extraneous matter and post-harvest fractions of sound billets, unsound billets, cabbage, and leaf were weighed. Routine laboratory analyses were performed for Brix, fibre, moisture, and pol. reading, and CCS calculated for all available crop fractions within sub-samples. Mean values for in-field, post-harvest, and mill-realized CCS were 110.6, 117.6, and 117.4 g kg⁻¹, respectively. Potential in-field (sound + unsound stalks) and post-harvest (sound + unsound billets) CCS of 154.6 and 141.7 g kg⁻¹ were well above the mill-realized value. In-field sucker culm and extraneous matter fractions constituted 29.7% of the crop, on average, this being reduced to 18.9% by harvesting. Sound and unsound stalks constituted 53 and 17% of the in-field crop, translating to 72 and 9%, respectively, as sound and unsound billets, post harvest. These data question the basis of the CCS determination that best serves crop improvement. They reinforce the necessity for ideotype selection for sound stalk content and suckering propensity. They quantify a transition that is confounded with a crop loss of some 10%. They seriously question the efficacy of current harvesting philosophy and technology. Currently, the latter completely overshadow consideration of plant traits to facilitate harvesting.

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Research in Genetic Marker for Screening Sugarcane Rust Resistance

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RAPD analysis was carried out on sugarcane varieties to search useful genetic marker for rapid screening of rust resistant strains. Cultivars were grouped into two groups, F160, NiF3, and NiF8 for the rust-resistant, or KF75-

398, NiF5, and NCo310 for the rust-susceptible. DNA extraction was carried out on those groups to construct 'rust-resistant' and 'rust-susceptible' bulk DNA. The two bulks were applied to PCR as template DNA, using 267 different 10bp arbitrary oligomers (Operon) as primers. Seven out of 267 primers revealed polymorphism to distinguish the bulks. In order to screen the exact polymorphism due to rust resistance itself, the seven primers were applied to PCR analysis using rust-susceptible cultivar Ni1 or its rust-resistant mutants NiM1 and NiM2 for sources of template DNA. The primer "OPG-06" was the only primer to produce rust-resistance-dependent polymorphism in the analysis, suggesting that the fragments specially amplified in resistant mutants have good possibility to be useful genetic marker for sugarcane rust resistance.

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Inheritance of Rust Resistance and Breeding Strategies at the Mauritius Sugar Industry Research Institute

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Common rust (*Puccinia melanocephala* H & P Syd.) is considered as a major disease of sugar cane in the humid and very humid environments of Mauritius, covering about 45 % of the acreage under cane cultivation. The disease became prevalent in several commercial varieties in 1978 and in the 1980's and cane yield losses of 8-11% were recorded on varieties M 555/60, M 2370/62 and M 1030/71 in trials. The systematic screening of promising varieties for their reaction to rust was established in final phase trials as from 1991. In an attempt to increase productivity particularly in the very humid areas and where cane cultivation has recently been extended to the former tea lands, the programme of directed crosses and site specific selection was intensified. It became necessary to incorporate rust resistance to segregating populations that would be evaluated in these areas. The inheritance of rust resistance was studied in sugar cane seedling populations using a factorial mating design over one summer and two winter seasons to guide breeding strategies. Frequency distributions for rust infection showed that resistant (R) x resistant parents produced the majority of progenies in the resistant classes whereas susceptible parents produced a high percentage of susceptible ones. Distributions of infection within the selfed resistant parent 'R 570' and in the majority of the crosses tended to support a major gene hypothesis with a dominant effect for resistance. The segregation pattern also suggested the effect of minor genes acting in a quantitative way. Female (F) and male (M) parents differed significantly for their reaction to rust and F x M interactions also indicated the existence of non-additive effects. F x season (S), M x S, and F x M x S interaction mean squares were generally low. Broad-sense heritability for individual season rating and combined rating (0.75-0.90) were high suggesting the trait to be highly repeatable. Susceptible families and/or susceptible clones can be effectively eliminated from segregating populations in rust-prone areas early in the selection programme. Narrow-sense heritability was moderate (0.40-0.52) with additive genetic effects accounting for 44-68 % of total genetic variation. Computer-aided crossing lays emphasis on resistant and slightly susceptible parents but the limited availability of these categories of parents may necessitate the use of crosses between resistant and susceptible parents. The first clonal stage is now being screened for rust susceptibility prior to the selection of clones for rust prone areas. Concurrently, at this stage, crosses are screened from databases, on the basis of their parent reaction before channelling to the humid areas. This philosophy corroborates with various stations which screen for rust as from the early selection stages.

Keywords: Biotic stresses, Heritability, Major gene, *Puccinia melanocephala*, Rust, Sugar cane.

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Feasibility of Inoculating Seedlings with Smut at First Stage of Selection

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Smut resistance is one of the most important criteria of selection for the sugarcane breeding program in Guadeloupe. At the early stages of selection, clones are usually discarded because of smut susceptibility under natural disease pressure. The first smut inoculated trial is conducted at stage 4 of the breeding program. At this stage, 10 to 20% of the clones are still susceptible to smut. Testing sugarcane for resistance to smut at the first stage of a breeding program, i.e. at seedling stage, should increase the efficiency of selection.

Two inoculation methods were tested with seedlings from 20 families. The first method consisted of applying smut spores with a brush on sugarcane wounded roots, and the second of soaking the seedlings in a smut spore suspension containing approximately 5×10^6 spores/ml. The two inoculation methods were performed before planting the seedlings in the field and compared in a replicated family selection trial to a set of non inoculated seedlings. Smut whips were counted 3.5 and 5.5 months after planting.

The results obtained for wounded root inoculated seedlings were not significantly different from those observed for the non inoculated seedlings (respectively 3.6 and 4.8 % of smut showing stools). In contrast, the percentage of diseased stools was higher for the seedlings inoculated by soaking (8.7 % of smut showing stools) than for the non inoculated seedlings. In addition, a family effect was observed for the number of diseased stools after 5.5 months of growth in the field of the seedlings inoculated by soaking. Screening for smut resistance at the first

stage of selection appears, therefore, possible. Evaluation of the resistance level of the two selected populations (inoculated and non inoculated) is in progress to confirm the usefulness of this method.

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Sugarcane and Sugarcane Weevil Borer: Probing Facets of Resistance with NIS

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Cultivar resistance is the only economical solution available for sugarcane weevil borer, *Rhabdoscelus obscurus* Boisduval (Coleoptera: Curculionidae). This pest again has assumed importance in the tropical Queensland sugarcane industry with the move away from pre-harvest burning in the past 15 years. Research on host-plant resistance reported here focuses on the use of near infra-red spectroscopy (NIS) to probe and understand facets of host-plant resistance, and possibly develop an insect-free selection screen for crop improvement. Replicated trials of parental clones and advanced clones in the selection program were established in two weevil borer "hot spots" in the Mourilyan mill area, approximately 100 km south of Cairns. Leaf samples were taken early (February) and late (July) in the plant and first ratoon crops, dried, milled, and scanned using NIS. Calibrations were developed for nitrogen and silica. Physical traits (rind hardness, trash habit, stalk height, and leaf colour) were measured in the plant crop, with selected repetition in the first-ratoon crop. Late in each crop, stalks in each plot were sliced to yield three measures of resistance - percent bored stalks, and number of bored internodes per stalk and per bored stalk. Following this, the outer 2.5 mm (rind) was removed from the basal portion of random stalks, prepared, and scanned. The parenchyma remaining after removal of nodal tissue from the "naked" stalks resulting from this treatment was treated similarly. Relationships between the three measures of resistance and physical traits, canopy components, and rind and parenchyma spectral data were analyzed. There were moderate relationships between rind spectral data and resistance measures, but none of these was better than the best relationship between the physical traits measured and resistance - rind hardness. While additional analyses remain, the prospects of developing an insect-free screen using a chemical signature(s) indicating host-plant resistance, and detected with NIS, appear slight.

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The Effect of Intra-row Plant Spacing on the Effectiveness of Family Selection in Sugarcane Repeatability Analysis

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Cross appraisal is performed in the Louisiana Sugarcane Variety Development Program (LSVDP) since 1992. It comprises the evaluation of progeny from the hybridization of two parents to measure its potential to produce elite individuals. Studies on the cross appraisal methodology have showed that intra-row plant spacing influences the variance and reliability of a trait. Thus, affecting the efficacy of progeny testing and family selection. Those studies indicated that selection using widely spaced plants (82 cm) would be more accurate than selection using narrowly spaced plants (41 cm). Selection efficiency is enhanced if a trait is repeatable across test environments. In order to evaluate the effectiveness of family selection at an early stage of selection under Louisiana environmental conditions, family repeatability of plant weight and the major components of plant weight were examined. This study shows the effect of two intra-row plant spacings in the estimation of family repeatability for a given trait between all possible pairs of three environments. Repeatability values at both intra-row plant spacings were reasonably high compared to other studies. Nevertheless, repeatability values were higher for wide intra-row plant spacing than for narrow spaced plants. Number of stalks per plant was the least repeatable trait. Repeatability values between all possible environment combination were high showing a low effect of the environment on the traits studied. Genetic associations calculated with data taken from wide spaced plants were generally higher than those associations determined with data taken from narrow spaced plants. This difference clearly shows, as it did at the phenotypic level, the effect of the spacing factor on the genetics of a trait.

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Genotype X environment interactions across regions in Australia - The Mega GxE Project.

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In Australia separate selection programs are conducted within each of seven regions. Varieties that exhibit adaptation within each region are selected and released. At an advanced stage in the selection process within each region selected varieties are transferred to other regions for evaluation. Genotype x environment interaction has been studied within regions but not across different regions. Knowledge of the magnitude and nature of interactions between and within regions may affect how selection programs are structured, the relationship of selection systems across regions, and perhaps in decisions on variety release.

A project is being conducted to investigate G x E interactions across regions in Australia. An unselected population of clones from a diverse range of parents has been evaluated in trials in different regions. Six

commercial varieties were also included. This paper will report on initial analyses of the results - showing magnitude of interactions across and within sites, relationships of interactions with environmental factors, and potential implications for structuring efficient selection systems across Australia.

It is suggested that a probe set of genotypes chosen on the basis of this work - ie. a subset of clones representing different patterns of response across environments - could be used for further work relating to international variety exchange involving Australia. Given the high expense (especially quarantine costs) and time needed for safe international exchange of varieties, clones for exchange should be chosen in source countries and tested in destination countries in a way that maximises the chances of success. It is proposed that a probe set of genotypes could be tested within selection trials in other countries to assess the relevance (or not) of selection results between environments from different countries, and to provide guidelines on selection (eg. which countries, which environments within countries to target the most).

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Developing selection strategies for high fertility soils.

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Ideotype selection in the tropical Queensland sugarcane improvement program is receiving increased emphasis. The aim, particularly on more fertile soils, is to select clones to maintain an erect habit, and a closed canopy, well into the crop. This will minimize sucker culm development, and so improve commercial cane sugar (CCS) levels directly and indirectly. The research reported here aimed to determine plant traits that facilitate clonal selection for erect habit on more fertile soils. Tentative selections based on a plant-crop assessment in Stage 2 at BSES Meringa were screened for early-season CCS in the first-ratoon crop. Clones with a high early-season CCS showed wide variation for yield in the plant crop. Each year, selected clones were established on a high-fertility site in multi-row plots in an un-replicated format. Seven simple ideotype traits were measured early (February) in the plant and first-ratoon crops. Quality components and habit were assessed early (July) and mid (September) harvest-season, as was yield at the latter. The predictive value of early-season traits for habit early and late in the crop was examined. There was ample genetic variation for the ideotype traits, and the sub-sampling strategy used was acceptable for most traits. Correlations among ideotype traits were weak and variable, with some attaining significance. Over populations (sites), the ideotype traits lacked consistency as predictors of erectness for early and mid harvest. Clones with high CCS and acceptable habit were present in the populations. Selections from two populations were planted to replicated trials for further assessment, as well as being used for further selection trait development. As simplistic ideotype traits had little predictive value for habit at harvest, either early or late, two new traits will be assessed. These traits are the force required to displace stalks 20° from the vertical and the force to shear basal stalks internodes.

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Progress in Sucrose Yield Improvement for the irrigated area of South Africa.

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The main goal of plant breeders is the development of new improved varieties. Monitoring the progress of the development of varieties can be done at different levels and can be expressed in different ways. To make progress is to advance, to develop or improve continuously. From the growers' point of view, progress is probably related to increased profitability of farming operations from new commercially released varieties. From a breeder's perspective, selection in one form or another is the means whereby progress is made. The change produced by selection that mainly interests plant breeders is the change in the population mean. This is commonly referred to as the response to selection. The efficiency of selection from stage to stage within a selection program could also be a measure of progress. The measurement of progress, particularly the response, introduces several problems such as; the variability of generation means, deciding on the generation interval to use and identifying controls for benchmarking over years. The measurement of progress also allows for the opportunity to compare predicted and actual values. This has further complications such as; distinguishing between the expected and the effective selection differential, and estimating the heritability of the base population. The progress made in sucrose yield improvement for the irrigated northern area of South Africa was reviewed from a number of standpoints. Issues relating to the estimation of progress and possible implications for the selection and breeding strategy are discussed.

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NIS analyses for Sugarcane Quality Components: Targets and Successes

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Crop improvement activities require analytical methods that are precise, cost effective, and pose minimal risk to personnel and the environment. An increasing demand to address more quality traits means the number of selection criteria and analytical requirements increase. Such operations are subject to increasingly stringent demands for cost effectiveness. Research reported here demonstrates the evolution of near infra-red

spectroscopic (NIS) analyses for crop improvement applications. An at-line sample presentation module was developed which passes a sample of disintegrated tissue contained in a bottomless cassette over a remote reflectance probe connected by fibre optics to a scanning spectrophotometer. Analysis of disintegrated tissue, rather than juice, was a more difficult objective, but is more relevant. NIS analysis is an inferential technique, using sophisticated regression methods to relate routine laboratory analyses to spectral data. Global equations for five quality components of disintegrated clean cane were developed in 1995. These incorporated genetic, spatial and temporal variation, and have been enhanced with additional data collected from 1995 to 2000. The majority of clonal samples from crop improvement trials conducted in the tropical Queensland program in this period have been analyzed using NIS. Recently, research has focussed on the impact of sucker-culm content on crop quality. Calibrations for samples of clean cane and sucker culms have been successfully developed and applied. Further application development occurred in research examining potential in-field and harvested crop quality components. Calibrations for all crop fractions in these situations - sound and unsound cane, sucker culms, and extraneous matter and sound and unsound billets, cabbage, and leaf, were developed. Such calibrations have been extensively used in the current season. Calibrations have proven remarkably robust. Although NIS analyses are less precise than conventional analyses, they are amply adequate for crop improvement. The advantages of NIS ensure increased cost effectiveness for quality component analyses in sugarcane improvement.

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World Sugarcane Variety Census revisited

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A worldwide sugarcane variety census was conducted by the author in 1985-1986. Information from the census was summarized and presented in the chapter entitled "New varieties" in the monograph "Sugarcane Improvement through Breeding," edited by Dr. Don Heinz, published by Elsevier Science Publishers. Some 15 years later, another snapshot showing how the variety picture has changed seemed appropriate. Data from the current census is presented alongside data from the mid-1980's census. Where provided, the upward, static, or downward trend for each major variety is displayed, and its parentage is shown. Information was sought from some 80 sugarcane-growing areas of the world; 47 areas responded. Data for an additional 11 areas was obtained from Sugarcane Variety Notes, 7th Revision, with the permission of Guilherme Rossi Machado., Editor. There have been substantial variety shifts in virtually all areas where sugarcane is grown. Of the 58 countries from which current information is displayed, most do not depend on the same leading variety as 15 years ago. Several areas that were using foreign commercial varieties extensively 15 years ago have shifted to locally bred varieties, including Australia, Colombia, Dominican Republic, Japan, Malaysia, and Thailand. Similar to POJ 2878 and NCo 310 in previous years, a handful of more recent commercial varieties, including CP 72-2086 (USDA-ARS, Florida) and R 570 (CERF, Reunion) are competing successfully in a wide range of environments. Based on the success of POJ 2878 and NCo 310 as parents, breeders (especially those with fledgling programs) should consider importing and breeding with newer varieties which are shown to be an immediate parent of at least nine different commercially important varieties bred and selected in at least six different countries.

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A Sugarcane Genetic Database

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We started to build a database in order to rationalize storage and improve accessibility to breeding and genetic data on sugarcane germplasm. It is gathering pedigree information, agronomical information and also a start on genomic. It is using the ACeDB software (AceDB for Microsoft windows R. Durbin, J.Thierry Mieg, R. Bruskiwich) designed for genomic data management. This could become an interesting tool for Sugarcane breeders and geneticists as we supply it with more and more information about sugarcane genome organization (genetic and physical mapping of interesting traits, syntenic relationships.).

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Photoperiod Management Experiences in Colombia

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Sugarcane flowering in the Cauca Valley in Colombia has received special attention from Cenicaña's Varietal Programme. Since 1980 the Programme has looked for places where environmental conditions favour natural flowering. Caribia on the Caribbean Coast was the place where most varieties flowered, but high temperatures did not provide good conditions for producing viable seed. Thus the efforts are strongly aimed at improving the flowering process in photoperiod chambers at Cenicaña's Research Centre as well as under natural conditions in the Valley. Several photoperiod experiments have been established, and they have given very useful results with respect to synchronising flowering, the way to plant the stalks, how much artificial light the stalks have to receive and when, how many leaves the stalks should have in order to receive the treatment successfully, what is the best age to receive the treatments, and how GIS, GPS and the automated meteorological network can help us to

improve our knowledge of the flowering process. Genetic diversity analysis using similarity index of Dice by NTSYS will be a tool for programming new crosses.