Milestone #12 Final Report

SRDC Project CTA028

Evaluation and re-structuring of regional selection programs to maximise efficiency and speed of cultivar release

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Appendices/attachments

Note that these file links are to the .DOC files, but that the files also exist in PDF format.

cta028 Final report Appendix 01 Summary of genetic and genotype by environment variances from published experiments.doc

cta028 Final report Appendix 02 Pattern analysis of climatic effects.doc

cta028 Final report Appendix 03 Experiment protocols trial locations and clone entries.doc

cta028 Final report Appendix 04 Trial results.doc

cta028 Final report Appendix 05 Trial data.doc

cta028 Final report Appendix 05B Trial data PLOTS.pdf (257 pages. NOT PRINTED)

cta028 Final report Appendix 06 Location and environment covariates.doc

cta028 Final report Appendix 07 Project meetings and workshops.doc

cta028 Final report Appendix 08 Press release.doc

cta028 Final report Appendix 09 Extract from milestone 8 report.doc

cta028 Final report Appendix 10 ASSCT paper.doc

cta028 Final report Appendix 11 G and GxE.doc

cta028 Final report Appendix 12 BSES-FATS.DOC

cta028 Final report Appendix 13 BSES-Across Results.doc

cta028 Final report Appendix 14 Important files.doc

Table of Contents

Tables

Figures

Executive summary

Issue

Continual delivery of new cultivars is required to maintain resistance to existing and new pests and diseases, and to provide constant improvement in crop productivity, quality and profitability for an internationally competitive sugar industry. Sugarcane breeding comprises two major activities: genetic variation is created by crossing parents (selected on historical performance of their progeny in the case of proven parents, or performance for heritable traits in trials in the case of new parents), and the best clones for release are selected through a multi-stage selection process that involves progressively more intensive testing of fewer clones over several years in multiple sites.

In Australia, the geographic variation in climate and other conditions in the different regions, the difficulties of moving sugar cane planting material, and differences between regions for some diseases (e.g. the Fiji disease line between the Central and Burdekin regions) had resulted in six cultivar crossing and selection programs, each targeting different regions: North (inc. Atherton Tableland), Herbert, Burdekin, Central, South and northern NSW. The small Ord irrigation area is serviced via testing and selection of elite clones from all of these regional trials. Currently crosses are made in each of four specific regions based on performance of parents (in trials or via progeny performance) in that region. Clones from crosses are initially chosen from small plots in one site per region. In further selection, breeders conduct multi-row plot trials across sites and seasons, with intensive testing within regions, and later exchange of the most promising clones between regions.

At the start of this project, there was no basic information on whether clones generated directly from crosses generally perform consistently relative to each other between regions, or whether many clones exhibit specific adaptation to regional environments. This information, and quantifying the relative sizes of genotype, genotype x region interaction, and genotype x within-region interaction variances, in genetic populations generated in breeding programs, is basic information needed for designing an optimal selection system that collectively targets all regions.

R&D Methodology

The central activity involved the growing of trials on experiment stations and grower properties at 24 sites with 59 harvests (which include plant and ratoon crops) between 2000 and 2004. A common set of between 36 and 48 (avg. 45) ‘unselected’ clones from a range of different crosses were grown, along with four to six commercial cultivars. The multi-row plot trials and managed using conventional commercial practices within each region. Data were collected at harvest on cane yield, CCS, stalk number, height and ratings of morphological traits (lodging, suckering, arrowing etc.) and diseases.

The results were analysed and interpreted using a quantitative genetics framework and multi-variate methods to explain relationships between trials (and regions) and develop recommendations for breeding programs. Environmental characterisation of the trials aimed to identify factors that can be related to observed relationships. Historical and current field

trials were also analysed to determine genetic parameters characteristic of later stages of selection.

Outputs and outcomes

The major outputs of this research are the collated dataset and interpreted results from these, including workshop reports and research papers, plus recommendations for changes in the breeding program. The trial datasets have been organised in spreadsheets/databases and can be utilised by breeders for additional analyses in future.

The *major finding* was that for both cane yield (TCH) and CCS, genotype x region interactions were small relative to genotype main effects and genotype x environment interactions within regions. Associated with this, correlations between any pair of trials within regions on average were similar to correlations between pairs of trials from different regions. Overall, the results indicate that *selection trial data within any particular region is relevant and important to selection programs targeting any of the sugarcane growing regions*.

Based on the above finding, the major recommendation has already been implemented: a greater number of superior clones (identified within any region) are now exchanged between regional programs, and the best of these are now included in final assessment trials (FATs), rather than in earlier stage trials. This will lead directly to:

(i) faster release of broadly adapted clones across multiple regions (3 to 4 years earlier)

(ii) better quality clones in FATs with an associated increase in selection gain and the release of improved clones within each region.

In a new project (BSS267), that was proposed on the basis of early results of CTA028, a data analysis methodology is being developed and implemented that integrates data collected across all regions appropriately, using genetic parameters obtained from this project. Together with data from BSS250, information from this project should be further utilised in additional research to develop optimal selection systems within and across regions.

Apart from selection of clones for commercial deployment, the small size of genotype x region interaction relative to other sources of variance also indicates that a review is justified of the existing regionalised parent population improvement and crossing operations. Other recommendations for the overall structuring of the Australian sugarcane breeding effort at this stage are detailed in the report (see section on Recommendations and future research needs).

The implementation of the above recommendations and other changes requires the industry to have a vision, not of 4 or 5 regional breeding programs, but of the development of one national program that most efficiently integrates effort across all regions. The ultimate objective though, will remain to develop clones (during later-stage testing) that are suited to the different environments within any given region.

Impact

As noted above, the major outcome will be earlier releases of superior varieties and faster genetic gains over time. Protocol alterations (see recommendations) should reduce the time from identification of superior varieties outside their region of origin from >5 years to 2 years. Benefits from this and from the faster rates of genetic gain are economically substantial, although they difficult to predict precisely and quantify. Over the past 20-30 years, many improvements have been made to the technical aspects of crossing and evaluation. With this project and BSS267, the industry is entering a new phase of best-practice breeding analysis that utilises industry-wide databases and powerful computer algorithms to better predict performance and interactions of clones among environments and across traits.

Background

- background to the Research Project including technical information and existing knowledge concerning the problem or research need addressed by the project.

General project context

Australian sugarcane yields vary from 50 to more than 200 tonnes cane per ha (on-farm) as a result of different combinations of soil type, growing environment (temperature, radiation and rainfall) and crop management (including irrigation and trash management) over a large number of diverse production areas. Generally, varieties have been selected for perceived specific adaptation to each of six geographically diverse regions. Prior to this project, we had limited information to evaluate whether this is the best way to address the needs of industry, or whether we could improve the process of selecting both broadly-adapted and specifically-adapted cultivars across the sugar regions as a whole.

While much research has been completed or was in progress to improve the efficiency of these specific aspects of selection, including investigation of GE interactions, little research had been focused on industry-wide GE interactions. Within any production region, the selection of cultivars is complicated by the genotype by environment (location and season) interaction; an understanding of which can sometimes be exploited to advantage. Firstly, if this interaction can be identified as 'repeatable' (e.g. associated with regions or soil type, rather than the annual variations in weather), we may be able to focus on key representative testing sites and increase the number of clones tested to improve the chances of finding superior clones. Secondly, if we understand the incidence of genotype by environment interaction in different production regions, we should be able to determine the relevance of data collected in any particular regions or sites, to other regions and sites. Both of these processes are enhanced by understanding the soil and environmental factors driving the interactions. Because of the substantial climate variability in Australia, we would also like to identify sites that are representative of the overall range of production environments that might be experienced.

Previous experiments by Bull et al (SRDC BS15), Mirzawan et al (1993), BSES and CSR/CSIRO (BS76 and CR11S) have identified in Bundaberg and the Herbert/Burdekin that within-region clone by environment interaction can be exploited to modify selection protocols (see summary of these and other results in Appendix 1). For example the results of Bull (BS15) were used to justify the selection of clones for both South and NSW by growing stage 1 and 2 trials only at Bundaberg. Knowledge of the relative importance of genetic, genotype x environment interaction and error variances, and environmental factors driving GE, can be used to design selection strategies that maximise genetic gains per cost. For example, an analysis may indicate that the number of sites can be decreased, using the conserved resources to increase the number of clones tested, perhaps using managed environments (e.g. low/high N or dryland/irrigated at the same site), or used in other ways which could improve selection gains. At the start of the project, detailed information on clone by environment interactions was not available to compare interactions across regions. While the theory of indirect selection (selection for performance in region A, based on performance in region B) could be applied across regions, it has not generally been utilised, although there may be great potential

in such application. This should also lead to identification of clones for evaluation in new areas such as the Atherton Tableland and the Ord where a large breeding or selection effort is not economically justified.

The major information output of this project is knowledge of size of genotype by region interactions and documentation of the range of environmental challenges experienced by sugar crops in Australia. As part of this project, this information is synthesised to propose opportunities to re-structure the selection process and increase the rate of release of new cultivars within and across regions.

The main SRDC strategy addressed by this project at the time of the proposal was strategy 1.3 - to improve and accelerate the selection and characterisation of new varieties.

Additional historical and technical background

Sugarcane breeders strive to improve cane yield per ha (TCH) and the sucrose content of that cane which, in Australia, is measured by a formula that converts brix, pol and fibre measurements to Commercial Cane Sugar (CCS). In parallel to this major objective, breeders select to some degree for other "maintenance" traits (e.g. disease resistance, harvestability, fibre and quality traits). At the time when the trials reported here were planted, BSES Limited operated six regional breeding programs along a coastal growing region of over 2000 km that are separated by latitude (Hogarth and Mullins, 1989) to service the Australian sugarcane industry. CSR Limited also operated a smaller breeding program in the Herbert and Burdekin regions. Two reasons for the existence of regional programs are quarantine requirements to limit the spread of several diseases, and the logistics and difficulties in transporting large quantities of sugarcane planting material (i.e. stalks) without damage, compared to crops such as cereals where true seed is used and is cheap and easy to transport without adverse effects. However the major underlying reason was a view that the different regions elicit different responses among genotypes and therefore would benefit from dedicated breeding programs.

Each regional program breeds and tests clones that are adapted to the environmental and farm management system challenges that are present within that region in order to identify and commercially release superior cultivars. These programs all have the same basic operational design, but some differences do exist. These are most noticeable in the Northern regional program where the clones are graded based on visual assessment of some traits (Berding and Hurney, 2000) and used to adjust a "net merit grade" selection index derived from measurements of cane yield and CCS (Skinner, 1965). This grading is based on observations of lodging, suckering, arrowing (flowering) plus other important traits thought to be related to crop performance and/or suitability for harvesting and processing. By contrast, in all other regions, selection is based only on measurements of cane yield and CCS in trials, with much more limited, or no, adjustment made for visually based observations, especially in the earlier selection stages.

As sugarcane is a perennial crop with annual harvests, environments can include locations, crop class (plant or ratoon crops) and calendar year. In general, each regional breeding program makes ca 350 crosses between 'proven parents (i.e. as demonstrated by past performance of their respective progeny) or experimental parents (selected on the basis of

performance in trials without yet producing progeny performance data). The resulting 20 000 to 30 000 seedlings are tested in PATs (Progeny Assessment Trials) grown as families in plots comprising plants of individual genotypes (seedlings). In the plant (1st year) crop, TCH and CCS are determined for each family and together with other visual scores, 2000 to 3000 seedlings are selected from the 1st ratoon (2nd year) crop for planting as single-row plots into the next stage of trials: CATs (Clonal Assessment Trials). Following two years of assessment and selection as plant and 1st ratoon crops, about 100 clones are then evaluated in 3 to 6 sites in replicated multi-row plots for 3 years: FATs (Final Assessment Trials). Other traits, particularly disease resistance, are considered before any worthy clones are recommended for release and distribution by regional productivity boards. Thus, in the later stages of selection, crop class and calendar effects are confounded, with the combined effect often referred to as crop-years (Kang et al 1987). Therefore, the Genotype by Environment Interaction (GEI) effects in a sugarcane dataset can include clone*location (C*L), clone*crop-year (C*Y) and clone*location*crop-year (C*L*Y).

From past research, there has developed a reasonable understanding of the performance and genotype by environment interactions for either unselected or advanced selection stage genotypes within particular regions, e.g. Southern (Mirzawan *et al.*, 1993); Central (Kimbeng *et al.*, 2002); Herbert (Jackson and Hogarth, 1992; Jackson *et al.*, 1995); Burdekin (Rattey and Kimbeng, 2001); Northern (Pollock, 1979). The majority of these studies had found substantial GEI variance component effects within regions, often greater than was observed for Genotype (G) main effects. However, the reported magnitudes and relative importance of the GEI components varies across regions. The Herbert (Jackson and Hogarth, 1992) and Southern regions (Mirzawan *et al.*, 1993) reported large C*L effects, with C*Y relative unimportant, whilst CCS was less effected than TCH. Rattey and Kimbeng (2001) found C*Y more important than C*L in the Burdekin, with all traits equally affected, whilst Kimbeng *et al.*, (2002) found the second-order interaction (C*L*Y) greatest. Unfortunately, some of the early studies were undertaken on 1-row plot trials, which likely have resulted in large competition effects and bias in the estimated variances of G and GEI effects. All studies only included a relatively small sample of environments.

To date, little research has explored GxE interactions across different regions. Cox (1995) found little C*L or C*Y across three regions (Northern and Southern Queensland, and NSW) for CCS or TCH, whilst C*L*Y tended to be large (relative to G) for TCH but not CCS. However, as only one trial was planted per region, no insight into GEI between regions versus GEI within regions is available. An additional issue is the use of single row plots which may inflate the importance of G main effects relative to interaction effects due to competition variance. Further, as the majority of the past trials were focussed on the last stage of selection, they are of unknown relevance to early stage populations. The genetic variance of earlier stage germplasm and its interaction with the environment must be known if we wish to determine repeatability and genetic correlations among and within regions and allow the potential for plant breeders to utilise indirect selection between different regions. Additional research in this area should enable plant breeders to utilise indirect selection between different regions if possible, especially in early selection stages and in progeny performance for parent and cross evaluation.

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Objectives

Statement of original objectives

The central objective is to obtain the basic data required to rationalise and improve the overall cost effectiveness of BSES and CSR breeding programs in Australia. Specifically, the project aims to:

1. Assess the importance of clone by region interaction and determine the number of regions required to adequately sample the Australian production environments;

2. Identify opportunities to link selection sites within and between regions by determining whether similar selections are made at different sites;

3. Attempt to maximise the cost effectiveness of servicing new regions by identifying sites in current production regions that adequately predict performance in the Atherton Tableland and in the Ord;

4. Characterise environments to identify factors driving clone by environment interactions and the incidence of specific challenges (e.g. water stress) that might be addressed by direct breeding; and

5. Establish a basis to utilise specifically managed environments to improve the efficiency of core selection.

While these objectives were not changed during the project, a greater effort was made in obtaining and analysing similar datasets from more advanced stages of the breeding process. These analyses were also reported.

Assessment against original objectives

The project has achieved and made recommendations in relation to the above objectives, although progress was less for objectives 4 and 5. Below is a summary of achievements/recommendations against objectives, though these are detailed later in the report and should be referred to for completeness. The optimal arrangements, based on current knowledge, are recommended on page 43.

The project achieved its central objective of obtaining the basic data required to rationalise and improve the cost effectiveness of Australian sugar breeding programs, and to make recommendations from interpretation of these data. The initial plan was to collect data from 50 harvests (plant and 1st ratoon) over 25 locations. Between 2000 and 2004, trials were grown at 24 locations (one in the Ord) and data collected for 59 harvests: 24 plant and 1st ratoon, with 2nd ratoon from 11 sites. Over 140 000 data points were collected on crops for observed and scored traits, together with several thousand points from soil chemical and pathology analyses and describing fertiliser, irrigation and management operations. This type of data where the same clones were grown together had never been collected on an industry-wide basis and so the base levels of clone and clone × environment (location and crop class (plant, ratoon)) effects had never been determined within and across regions simultaneously. The data are additionally valuable in that they arise from random, unselected clones grown in multi-row plots, and enable inferences to be made about potential modifications to early stage selection.

With regard to objectives 1 to 3, we found that genotype by region interaction for TCH and CCS in unselected clones was relatively small compared to other sources of variation (location and crop class), i.e. data from trials within and across regions are equally relevant in the prediction of clonal performance. This finding, which was only confirmed late in the

project when sufficient data were to hand resulted in the specific aspects of the first two objectives to become less relevant. At the earliest selection stage where 'random clones' are being evaluated, relatively few regions are apparently needed to characterise genetic variation. Hence, we shifted out focus in the report on these objectives to be more on how to best use *all* of the information from different regions in making decisions. However, we do not yet know whether (a) this applies equally to small plot trials of early stage trials or (b) how data from the early stage sites (usually one per region) are related to later stage sites within and between regions. Recommendations have been made and adopted with respect to these objectives. These are that:

1. Routine data analysis of all trials (i.e. including prior trials) should be used to predict commercial and breeding value of clones across all regions, not just the data from the region in which the clone is currently evaluated (being implemented in SRDC BSS267);

2. Superior clones in regional trials should be transferred earlier to other regions and be promoted directly into regional FAT (Final Assessment Trials), rather than re-tested in the less precise small-plot early stage trials (already implemented);

3. that the economic values of secondary agronomic traits should be considered for each region to determine whether their use is justified in predicting commercial or breeding value of clones (being implemented in BSS267).

An extension of the above recommendations (and objectives 1 and 2) was to question whether it is necessary to maintain the current regional structure of breeding populations. A recommendation to evaluate this question has been adopted in the form of a set of experiments that have begun this year in the BSES-CSIRO Joint Venture breeding program to evaluate family by region interaction. The intention is to extend those experiments in the future to better understand the family by site interaction and how to best exploit the potentially broad or narrow adaptation of different crosses when tested in their 'home region' or, at later selection stages, in other regions.

With regard to objective 3, indirect selection for TCH in the Ord and Atherton Tableland can be achieved through the transfer of superior clones from other regions, with Central and Burdekin regions providing slightly better genetic correlations of performance. For CCS, the Ord apparently does not correlate well with other regions, and so indirect selection is difficult. Therefore, the adopted recommendation is that data from all regions be used to choose potential clones for these two sites, with trials in the Ord to continue to focus on evaluation of CCS in clones with that already have proven yield and smut resistance.

The difficulties in addressing objectives 4 and 5 arose due to the previously unrecognised complexity of factors that are apparently involved in driving GE interactions. In addressing objective 4, we collated substantial datasets on observed disease and appearance scores, additional traits, weather conditions, soil chemistry and soil pathology. While these covariates were found to vary across the dataset, few were able to explain more than a minor amount of the observed clone by environment interaction, i.e. there were no environment factors (including patterns of water stress) that could be found in addition to the existing disease and

agronomy priorities of the current breeding programs. It appears likely that GxE interactions are driven by a number of different factors giving rise to complex responses, rather than being dominated by a small number of major factors.

In relation to objective 5, and following on from objective 4, the utility of managed environments for any specific stress would initially appear to be small. Two major causes of GxE interaction in early generation selection are competition among small-plots and the effects of micro-nutrient deficiencies, both of which were deliberately avoided in this project. With this variation controlled, there were no apparent environment effects to be managed apart from controlling influences on the level of error variance of trials. Increased error was associated with trial management (especially fertiliser and irrigation) when TCH was raised to a point where substantial lodging occurred and/or mean trial CCS was lowered below a point that discriminates well among clones (see last section of Appendix 4). Hence, the major specific outcome related to trial management is that, for both TCH and CCS, there was a strong association between the mean value of a trait and both repeatability and genetic variance. An interaction of irrigation (amount and timing) and the rankings of clones for both TCH and CCS has been observed in the Burdekin, and demonstrates some possibilities for optimisation. This interaction between management and genotypic variation for TCH and CCS is the topic of a new Burdekin-based project led by Dr. Geoff Inman-Bamber (CSIRO-CSE) in collaboration with the CTA028 investigators and others in CSIRO and BSES.

Methodology

- *methodology, activities and project management to deliver outputs and outcomes. (As indicated above, reference may be made to publications containing this information, which should be included as Appendices to the report.)*

- *Clearly enunciate the project process and its links to the outputs. Include where appropriate details of stakeholder participation, systems integration, implementation/adoption strategies and enhancement of human capacity.*

- *Specify method(s) used to evaluate success in delivery of outputs and outcomes. In particular, clearly enunciate the method(s) of evaluation used within the project to assess:*

    - *the impact of the project,*

    - *the learning experiences/capacity building achieved from the project, and*

    - *the implications of the project in guiding future R&D.*

The project funding began in July 1997. While clones were being propagated for field trials with the first plantings in April-Sept 1999, the first period of the project was used to collate data on past analyses of genotype and genotype by environment interactions and to begin the characterisation of the production environments of sugar-growing regions and the specific environments of testing sites. The latter task was to be used as additional explanatory information to interpret the trial results. As harvest data were returned from the CTA028 trials

(known as the 'MegaGxE' dataset), annual updated analyses were made and reported to SRDC and to the sugarcane breeding team. During 2003 and 2004, additional analyses, using the similar methods to the MegaGxE dataset were undertaken on two other datasets collated from the BSES trial databases to estimate genetic parameters (size of variance components for genotypic and genotype by environment interaction). These were used for comparison with the MegaGxE dataset as the trials comprised 'advanced stage' selected clones that would inform about how the effects of genotype and genotype by environment interaction are changed during selection. Hence, in addition to the initial objectives, two more large datasets were analysed during the project (see below). The three datasets are described as:

1. MegaGxE – trials on unselected clones conducted by the project

2. BSES-FATs – later-stage trials of selected clones collated within each region

3. BSES-Across – data extracted from BSES-FATs for individual clones that had been tested in more than four regions.

In Nov/Dec 2004 the analyses of the complete CTA028 datasets were undertaken and the results compared with the analyses of BSES trial datasets. The MegaGxE data were further interpreted to look for potential environmental drivers of differences in performance between different regions, locations and/or crop classes.

Collation of prior analyses of genotype and genotype by environment interaction

A brief summary of past work in estimating genotype and genotype by environment variance components is given in (Appendix 1). None of the past work encompassed the entire sugarcane growing region, and where more than one region was studied there were rarely more than 2 or 3 locations. At the time they were done, the analytical methods used for most of these analyses were dependent on the data being largely balanced, i.e. specific experiments needed to be done or subsets of genotypes had to be extracted to do the analysis.

New analytical methods based on restricted maximum likelihood (REML) estimation, as used to analyse the trials in this project, would now allow more precise estimates of variance components in these datasets. However, the data are not easily reassembled, and in most cases, the trial designs are limited or irrelevant in some way by the choice of germplasm and/or small plot sizes (high error for TCH and TSH). Therefore, a decision was made later in the project to collate more relevant data from existing BSES trial results (coincident with the time of the MegaGxE trials) for use in additional analyses (see below).

Characterisation of climatic patterns across sugarcane regions

Weather and soil description information from different testing locations were collated and used to run model simulations using long-term climate records (Appendix 2). While physical measurements inform about the 'permanent' attributes of testing sites, the data from simulation models using historical weather data established a guide to the seasonal variation experienced at different sites, e.g. how much the rainfall or temperature might vary from year to year at different parts of the season.

Collection and analysis of MegaGxE dataset

Experiments

The details of the experimental methods used in the trials are given in Appendix 3 and are summarised here. 'Unselected (random) clones' were distributed from a nursery trial in the Herbert in 1998 and 1999 for further propagation within regions during 2000. Trials were planted between 5 May 1999 and 3 Sep 2002 and were harvested between 24 Jul 2000 and 21 Sep 2004. Experiments (2 replicate row-column designs) were planted on grower's properties or on research stations and were managed using standard practices with regard to fertiliser, irrigation and control of weeds, insects and diseases. Data were collated from a total of 59 harvests with 24 sites harvested in plant and 1st ratoon, and 11 of those also harvested in 2nd ratoon. The sites were allocated to existing region names: the North/Tully (4 trials), Herbert (4), Burdekin (4), Central (4), South (3), NSW (2), Atherton Tableland (2: N3 and N6) and Ord (1). The mean and variance of TCH and CCS for each harvest is given inAppendix 3.

The 'random' or 'unselected' clones used in the MegaGxE study had been randomly chosen from random crosses in the BSES Limited and CSR Limited Herbert breeding programs. In most sites, 48 clones were planted per trial, including four to six commercial checks ('Q canes'). Some problems with propagation and correct identification of germplasm required additional DNA fingerprinting work (see Appendix and section below on project management etc).

In all of the trials, diaries of agronomic management were kept; soil samples collected for chemical and pathological analysis and weather data were either logged or retrieved from the nearest Bureau recording sites (Appendix 6).

In each trial, observations were made of TCH (mechanically harvested) and CCS (from 8 stalk sub sample) as well as other traits: visual percentage scores for lodging, suckering, arrowing (flowering), stool-tipping (i.e. stool lodging), stalk breakage, rat damage and existence of gaps in plots; measurement of average length, diameter and single stalk fresh weight of the stalks taken for CCS determination.

Statistical analysis

As results were returned for each year of harvests, data were summarised by region, trial and genotype and genetic parameters (variance components and phenotypic and genetic correlations) were derived and compared between regions. It was this analysis that alerted the propagation problems that were encountered in the Burdekin B1 and B2 trials.

For every trial, environment data were collated for potential use as covariates (see Appendix 6). These environment data covered 4 classes of information:

- location covariates (soil chemical analyses + physical location)
- environment covariates (weather data, irrigation and fertiliser application)
- soil pathology covariates

- trial observations (trial means of all observed variables)

For each trial, all traits were analysed with design effects fitted and clones fitted as either random (BLUPs) or fixed (BLUEs) effects for later use in other analyses. Variance components were estimated for clones and the other random design effects, and an approximate error mean square (i.e. derived from the mixed model) was used to compute the trial mean heritability. Summaries were made of the variance components against trial mean and region and changes in ranking of clones based on the different analyses were also examined.

Variance components and standard errors were estimated for all traits, with focus on TCH, CCS and TSH for the random effects of genotype and random interactions with either trial (E=environment) or with the location (L), crop class (CC i.e. plant or ratoon 1, 2 or 3) and location x crop class effects. These analyses were repeated using region and trial within region as interaction effects to determine the magnitude of region effects. Other breakdowns of the variance components were also examined, particularly in grouping trials together on the basis of mean trial TCH, CCS or TSH. Ratios of GxE/G were calculated and compared across traits and regions and other genetic parameters (repeatability, phenotypic and genotypic correlation) were estimated and averaged over regions or other groupings. Using the variance component estimates for each region, expected repeatabilities were computed for traits and regions.

Multi-variate methods (principal component analyses) were used in

1. interpretation of relationships among locations (or harvests or regions) based on observed performance data; and

2. identification of suitable environment covariates to be used in further analysis of variance components

In the former, plots of loadings were used to compare environments and look for any patterns in region, location and/or crop class effects. In the latter, bi-plots of the covariate matrices were inspected and a small number of combinations (i.e. 2 to 3 soil chemical properties) that best summarised the representation the range of loadings observed was used. The chosen environment or location variables were evaluated as fixed effect covariates using the same statistical models as for genotype by environment interaction analyses. The extent to which any of the random effects relating to genotype by environment interaction (location, region, crop class) was decreased by the use of a covariate was an indicator of whether the covariate was explaining any of the genotype by environment interactions.

Collation and analysis of within-region later stage trials (BSES-FATs) to complement data from MegaGxE trials

In this project, our objective was particularly to examine the characteristics of data collected on unselected clones across the industry. Part of our interest was to compare the analyses of these data against collected data from selected clones, i.e. at later stages of the selection process (Appendix 12). This has implications for how the genetic parameters might be used for further simulation of alternative breeding program scenarios. However, after collation of

prior published and internal analyses, it was apparent that there had been few attempts to conduct this type of analysis in all of the regions. Therefore, when Allan Rattey joined the project in 2001, he collated a large dataset from the BSES final assessment trials (FATs) that were harvested in 2000 and 2001 to coincide with the major seasons of the CTA028 harvests. These are final assessment trials for clones that have been heavily selected as described in the introduction (i.e. about 100 clones from an original set of ca. 25 000 seedlings) for performance within the region. Across regions these trials have in common only a small number of check and test clones. These data provided useful 'within-region' estimates of variance components of selected clones, compared with the 'unselected clones' used in our experiments (see below). These data were subjected to similar analyses (to those for variance components and genetic correlations for the MegaGxE trials project), though the analyses were limited to 'within-region' interpretations. Appendix 12 contains a summary of the methods and the results obtained from this analysis and Appendix 11 contains a draft paper that reports on the comparison of the MegaGxE trials with the analyses on these BSES-FATs.

Collation and analysis of clones tested across regions in BSES-FATs

Methods and detailed results are given in Appendix 13. Genotype mean data from the BSES Limited trial database for trials planted in 1989 to 2002 in 5 regions (North, Herbert, Burdekin, Central, South (inc. NSW)) were filtered to find genotypes that had been grown in trials in at least four regions in advanced stage trials at any stage of the breeding program. The dataset therefore comprised of 7714 observations from 12 plant years for 40 genotypes distributed across 465 location-plant year combinations and harvested in plant and 1st ratoon and sometimes in 2nd ratoon. Almost all of the genotypes analysed were commercial clones and, having passed through the selection process, there is expected to be relatively low genotypic variances in the dataset.

Given the imbalance in this dataset (genotypes over locations and years), the data were not suitable for comparisons of correlations between locations and years etc. Hence, the analysis was utilised only to examine the relative size of variance components associated with genotype and genotype interactions with region, location, crop class and location x crop class.

Communication and reporting

The major methods of reporting results were milestone reports and workshop meetings (Appendix 7). Two important additional communications were a press release, and the milestone 7 report. Part of that report extract is reproduced below, as it had implications for the methodology used in the project when propagation issues were flagged and it was realised that the project needed to be extended.

This experience demonstrated the value of analysing data soon after receiving it and allowed us to correct a major problem in being able to compare the Burdekin with other regions. However, it took us almost 3 years of part-time use of CSIRO molecular marker skills to sample clones from many of the trials and confirm their identities. Several other propagation mistakes were found. This project was unique in planting the same trials in every region, which placed the propagation process under greater scrutiny than normal. Following these incidents, technical staff reviewed the standard propagation process and put in new check

systems to try to reduce this problem in any inter-region propagation. The new procedures were distributed and discussed among technical staff in the project.

Project staffing, management and history

Significant staff changes occurred in the project within BSES. This together with disruptions due to cyclones and some propagation problems did at times create difficulties in meeting milestones and undertaking activities. These were revised as needed to ensure that the project was still able to collect the required basic set of data.

Staffing

The project officially began in July 1997, though preliminary activity had been initiated in 1996, in the selection of clones by Phillip Jackson (CSIRO/CSR) and Jason Bull (BSES). Jason and another BSES breeder, Tony McRae, who were jointly responsible for leading the project within BSES, both left BSES in early 1998, shortly after the start of the project. With these departures, Mike Cox and Collins Kimbeng (a new appointment in Mackay in 1999) took over these respective roles, although they also had commitments in other projects. In late 2001 (see milestone 9 report), when Mike Cox took on the role of Program Leader, Plant Improvement in BSES, Allan Rattey become the major BSES contact and has contributed substantially to the project since then, particularly helping considerably in addressing some ongoing challenges with field trial management. Also, Allan has collated updated data from advanced BSES variety testing trials to allow interpretation of GEI in 'selected' germplasm, cf. the 'unselected' germplasm used in this project.

Management

Under the direction of the investigators, Bill Messer (a CSIRO technician) played a coordinating role between the investigators and field staff. He liaised directly with BSES staff in each region and with CSR staff in Ingham and Ayr to ensure that the planting, observation and harvesting of the trials was undertaken in a consistent fashion in each region. The investigators met in person, or communicated via email/phone to ensure that management instructions and requests for information were the same for each trial. Dr. Chapman wrote the milestone reports following meetings with the other investigators. Milestone reports and workshops were the main form of communication of outputs to the major clients (plant breeders) of this project (see appendices).

Regarding the other aspect of the project – environment data collation – Dr. Chapman employed two casual staff (Joanne Walker and Ky Mathews) for short periods to organise datasets at the beginning (ca. 1999/2000) and later stages (late 2003) of the project.

Project history and milestone changes

One consequence of the staff changes was a modification of the original experimental schedule, as noted in milestone reports. The plan had been to plant all of the sites at the same time, but with the staff changes, it became necessary to split the planting times over years and to extend the life of the project (see milestone 4 report). Two other factors resulted in the project being extended:

1. Cyclone Rhona in Feb 1999 destroyed the propagation plots for the North that were planted in Meringa. This loss was not certain until May 1999 when it become clear that there was insufficient propagation material for planting even a single trial in the northern region. It had been planned to plant 3 trials there in 1999 and 3 in 2000, but all 6 trials had to be delayed by a year.

2. The discovery of propagation errors in the Burdekin, required a substantial effort on the part of Lynne McIntyre's lab (CSIRO) to unravel the identities of the clones that were planted in trials B1 and B2 via DNA analysis. However, while it seems that we were able to identify that at least half of the clones in these trials were correct, it was decided that additional ratoon harvests of the B3 and B4 trials in the Burdekin should be undertaken to be sure to obtain reliable estimates of effects there. We also cross-checked clones in all regions using DNA testing, which led to identification and resolution of some other differences (although small in number) in clones that were supposed to be identical.

A project extension to enable harvests in 2003 was requested in the milestone 9 report. Subsequently, the current extension was requested to allow time for analysis of these data, and inclusion of the 2004 harvest data that were deemed important for the Burdekin and South regions in particular.

An additional problem was the reporting of sugarcane smut as an issue in the Ord. Smut only appeared as a challenge in the Ord after the start of this project. Staff at the Ord raised two concerns about the CTA028 project. One was that funding for the Ord part of this project may be insufficient. Secondly, it was thought that the trials may not be of as great value to the Ord at a time when it is necessary to be concentrating on developing germplasm with resistance to smut. Consequently, the CTA028 clones sent to the Ord were first screened for smut tolerance, before an evaluation trial was planted. Given that half of the clones were eliminated by this process, research trials planned for the Ord were scaled down to be a single site. The issue was raised in the milestone 5 report, discussed at the April 2000 project review and the actions confirmed in the milestone 6 report.

Project evaluation methods

This project has the fortunate attribute of being directly involved (day-to-day) with the key stakeholders: plant breeders. Hence, the best measure of success in terms of delivery is the interest that the breeders and BSES take in the progress of the experimental and analytical components of the project, and the changes in the breeding program that will occur as a result of the project. The workshops have been well attended with substantial discussion of the results and suggestions for additional analyses. Learning experiences were largely those of the project staff and are noted in the outputs. While CTA028 does not take credit for decisions to combine the South and NSW programs (that was already happening at the start of the project based on the results of SRDC BS15), the project and subsequent discussions made a contribution to the recent combining of the North and Herbert programs.

Outputs

- including knowledge, skills, processes, practices, products and technology developed

The main outputs from this project are the large data set collated, knowledge generated from those data, and recommendations arising from the findings. The dataset is extensively annotated and prepared for further analysis. The main findings are described in detail in the appendices to this report, and are summarised below. *The recommendation outputs are given in the recommendations section that follows.*

Findings

Major research points are made under these headings. During the course of the analysis of this dataset, there were opportunities to test a variety of hypotheses relevant to statistical design and analysis of sugarcane evaluation trials. These are not detailed here, but can be found in Appendix 4 and relate mainly to observations that rankings of clone performance from large-plot 2 rep row-column design trials were not greatly changed when spatial analysis was used and that relationships existed across trials between the trial mean and the trial variance for both TCH and CCS traits.

Finding 1: Genotype by region effects were only a relatively small proportion of total genotype by environment effects

In the pooled analysis of cane yield across regions (

Table 1 and Appendix 4, Table 4-15), it can be seen that genotype x region interaction, while significant, was only about 10% of the size of genotype main effects, was smaller than the location interaction effects and about the same as the averaged genotype x crop class interaction.

The collective size of the genotype x location or crop class interaction components, indicate that selection in even a highly variable, unselected population of clones as used in this project, would derive benefit from evaluation across multiple environments (see below for further discussion). However, the relatively small size of the genotype x region interaction effect indicates that environmental factors driving GxE interaction were not strongly associated with regional differences, and a large proportion of GxE interactions could be sampled from multiple sites and crop-years within regions.

For CCS, the genotype by region effect was relatively larger (about 9% of the genotype main effect), but still less than half of two of the other genotype interactions. The interaction with crop class was again negligible, and the 3 way interaction averaged across regions was similar to the genotype by location interaction effect.

Table 1 Results from analysis of variance of the random clones across all environments for cane yield and CCS. The error variances given are the means across all trials (see Appendix 4, Table 4-11 for regions), although the genetic variance components were fitted using a heterogeneous error model (i.e. error fitted simultaneously for each trial).

Source of variation	Cane yield (t^2/ha)	CCS
Genotypes (G)	175±32	0.789±0.14
G x Region (R)	22±6	0.071±0.02
G x Location within R	76±7	0.167±0.02
G x Crop class	19±4	0
G x Crop class x Location within R	70±5	0.168±0.02
Error	215±41	1.000±0.18

Finding 2: Genetic correlations among environments were similar within and between regions

The relative similarity of trial results within and between regions (with Q cane checks removed) is further illustrated in Table 2 and Appendix 4. The average of all genetic correlations between different trials within each region was compared with the average of genetic correlations between trials from different regions. Genetic correlations are an informative statistic because gain from indirect selection in one environment for performance in another is directly proportional to this statistic.

In most cases, trials within regions had a slightly higher genetic correlation with each other (the correlations given along the diagonal), compared with their correlation with trials from other regions (correlations away from the diagonal). However, in most cases this difference was not large, and in some cases, especially for CCS, the results suggested that similar gains could be achieved from selection in other regions. For example, for CCS in the Herbert, the genetic correlations with the Central and Southern environments were greater than those for environments within the Herbert itself.

For cane yield, the relative advantage of selecting within a region compared with other regions was greatest for the Herbert and North regions, although indirect selection in either region for the other would be almost as good (0.68 and 0.74 for within-region correlations, versus 0.65 – or >92% relative gain – for between-region correlations). The Ord and the

Atherton Tableland were well correlated with each other for TCH. The Herbert and Burdekin were the best existing breeding regions for prediction of TCH in the Ord and Herbert.

To further interpret the results in terms of regions, locations and crop classes, the matrix of genetic correlations was used as input to a principal component analysis. The results of this, presented as environment loadings in Appendix 4 showed that there was no region, location or crop class basis to the correlations among trials. Overall, the results reinforced the conclusions based on the variance components that variation among locations (regions) was greater for TCH than for CCS and that sampling of more environments is more important for the former.

The Ord clearly had low correlations with environments in all other regions, especially for CCS. However, the limited number of clones in this trial and the fact that only a single location was used, due to resource constraints, limited the level of confidence in any conclusions drawn from this result.

Table 2 The average of genetic correlations (for CCS and cane yield, TCH) between environments in each region versus (i) all independent environments (i.e. different sites) in the same region (along the diagonal) and (ii) all environments in each other region. Figures in bold are correlations of 0.5 or greater while those in italics are less than 0.3 (i.e. non-significant at p< 0.05, n = 40 genotypes). Note that the Ord comparison is of only a plant and ratoon trial in one location. Standard errors are not shown, but are between 0.1 and 0.2 in most cases.

CCS	North-coast	North-Tableland	Herbert	Burdekin	Central	Southern	NSW	Ord[1]
North-coast	**0.74**	**0.62**	**0.65**	0.48	**0.73**	**0.76**	**0.60**	*0.13*
North-tableland	**0.62**	**0.75**	**0.68**	**0.53**	**0.73**	**0.71**	**0.61**	*0.17*
Herbert	**0.65**	**0.68**	**0.68**	0.49	**0.78**	**0.78**	**0.50**	*0.19*
Burdekin	0.48	**0.53**	0.49	0.50	**0.52**	**0.53**	0.45	*-0.11*
Central	**0.73**	**0.73**	**0.78**	**0.52**	**0.82**	**0.87**	**0.59**	*0.22*
Southern	**0.76**	**0.71**	**0.78**	**0.53**	**0.87**	**0.88**	**0.69**	*0.15*
NSW	**0.60**	**0.61**	**0.50**	0.45	**0.59**	**0.69**	**0.67**	*-0.02*
Ord	*0.13*	*0.17*	*0.19*	*-0.11*	*0.22*	*0.15*	*-0.02*	**0.58**

TCH	North-coast	North-Tableland	Herbert	Burdekin	Central	Southern	NSW	Ord[1]
North-coast	**0.74**	0.40	**0.67**	**0.57**	0.45	0.46	**0.51**	0.49
North-tableland	0.40	**0.59**	0.46	0.48	0.43	0.41	0.46	**0.68**
Herbert	**0.67**	0.46	**0.75**	**0.60**	**0.54**	**0.53**	**0.58**	**0.54**
Burdekin	**0.57**	0.48	**0.60**	**0.67**	0.43	**0.55**	**0.52**	**0.59**
Central	0.45	0.43	**0.54**	0.43	**0.63**	0.47	**0.53**	0.40
Southern	0.46	0.41	**0.53**	**0.55**	0.47	**0.53**	**0.64**	0.39
NSW	**0.51**	0.46	**0.58**	**0.52**	**0.53**	**0.64**	**0.80**	*0.29*
Ord	0.49	**0.68**	**0.54**	**0.59**	0.40	0.39	*0.29*	**0.74**

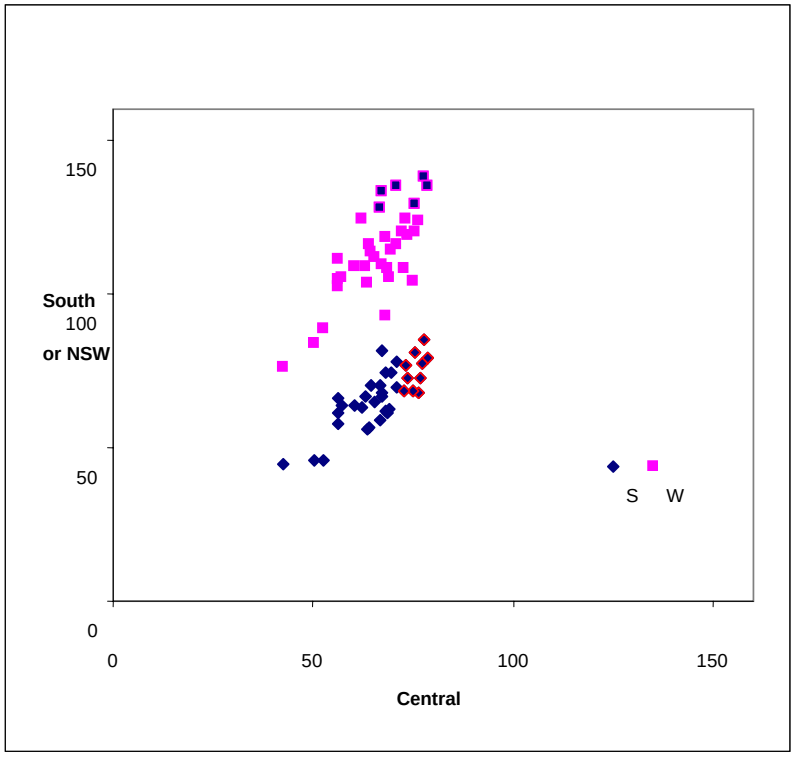


Figure 1 Relationship between cane yields (t ha^{-1}) of the random clones averaged over Cental environments and averaged over either South or NSW environments. The best 1/3 of clones in Central that are also in the top 1/3 in either the South or NSW are indicated by bordered symbols.

The effect of these genetic correlations can be illustrated by an example of indirect selection in Central environments whereby some broadly adapted clones are identified selection of the top 1/3 of clones predicts their performance in South or NSW environments (Figure 1).

Finding 3: Prior analyses of variance components were not consistent or conclusive with respect to the importance of interaction with environments and/or regions

The results of 7 prior studies (including SRDC CSR11S and UQ7S) to estimate variance components for genotype and genotype by environment interactions were reviewed and summarised (Appendix 1). Perhaps because of the relatively small numbers of environments in these studies and therefore limited sampling of GE effects within each, a large range was observed for the size of effects of genotype and GxE interaction (location, region and/or crop class) for TCH, CCS and TSH. Generally, it can be concluded that interactions were greater relative to the genotype (clone) main effect for TCH and TSH when compared to CCS. Where effects were partitioned into those interactions due to crop class, location and location x crop class, the latter two interactions were generally larger than that for crop class (i.e. genotype interaction between plant and ratoon crops).

Finding 4: In this study, the ratio of Genotype to Genotype by environment interaction variance was 1.8 for CCS and 1.3 TCH

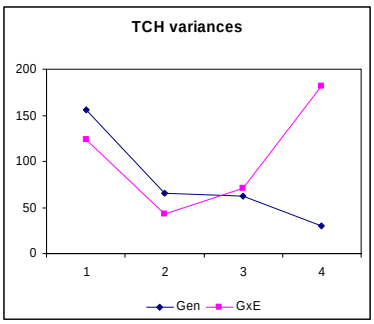
Given that Genotype by Region interaction was a relatively small component of genotype by environment interaction, it was helpful to examine the size of GxE interaction at the different stages of the selection program. Such information can be used to determine how many trials need to be conducted at each stage to achieve specified levels of confidence in identifying the best clones.

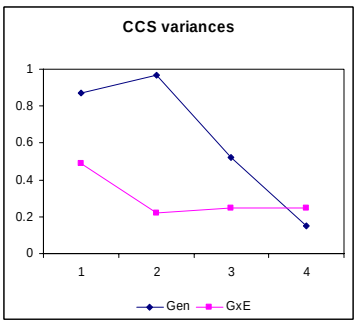
When examined over all trials in the current study (excluding the Ord), the variance components for genotype and genotype by environment interaction were 156 and 124 $(t/ha)^2$, respectively for TCH and 0.87 and 0.49 $units^2$ for CCS. This implied that CCS was less influenced by GxE and can be measured with the same reliability using fewer environments than can TCH (Appendix 4) consistent with previous studies.

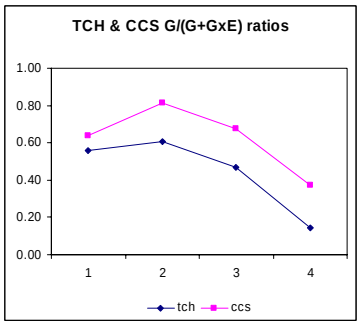
Compared to several other datasets (parental clones from BS5S, advanced clones from BSES-FATs, and commercial clones tested across regions), the observed genotypic variances for TCH and CCS were high, as were the genotype by environment variances, except for TCH in the last dataset (see Table below).

Table 3 Reproduced from Appendix 13, Table 13-4. Summary of genotype and genotype by environment variance components in four sets of experiments: 1. MegaGxE, 2. BS5S (re-analysis of Cox 1995: 1 location in each of 3 regions), 3. BSES-FAT (variances analysed within region, averaged across regions) and 4. BSES-Across (variances from FAT trials across regions using 12 years of data).

Source	1. MegaGxE		2. BS5S report		3. BSES-FAT		4. BSES-Across (model 1)	
	Tch	ccs	tch	ccs	Tch	ccs	tch	ccs
Gen	156	0.87	66	0.97	62	0.52	30	0.15
GxE	124	0.49	43	0.22	71	0.25	182	0.25
G/GxE	1.26	1.76	1.54	4.45	0.87	2.1	0.18	0.55
G/(G+GxE)	0.56	0.64	0.61	0.82	0.47	0.68	0.14	0.38







Finding 5: Genotypic variance was significant for TCH and CCS in almost all environments with trial precision maximised at moderate levels of TCH and moderate to high CCS

The presence of significant genetic variance in unselected clones in multi-row, replicated trials across a wide range of environments was confirmed and the magnitudes of these variances were documented. While this result was not surprising, as past genetic progress

would not have been realised without this variation, these trials confirmed that variation for a small set of unselected clones can be expressed in all regions and through a large range of yield and CCS (Appendix 4).

In some regions, plant breeders have partially restricted irrigation (compared to farm practice); to keep crops smaller to allow early season sampling and to reduce damage from crop lodging. In terms of trial precision, the comparison of the large number of trials here allowed us to confirm that trials with a mean TCH of ca. 70 to 110 t/ha and CCS > 12 or 13 units were more reliable (had a higher repeatability) than did trials outside these ranges. The greater relative error in high TCH trials was apparently associated with the greater incidence of lodging typical in such trials (see Appendix 4).

Finding 6: Mean trial TCH and CCS were negatively correlated across the dataset, but within trials, locations or regions there was no genetic correlation between TCH and CCS for unselected clones

While high trial mean TCH and CCS can be simultaneously realised through judicious management of irrigation, they are often negatively correlated when examined over a large number of trials (r = -0.51 in the case of the MegaGxE dataset). This is an additional reason for being careful in trial management, as observed in Finding 5. Note that the genetic correlation between TCH and CCS within any single environment is usually close to 0.

Although some of the higher CCS clones had a low TCH, there existed at the trial, location and region levels a range of clone types with all combinations of low/high TCH and CCS, i.e. identification of high TCH/high CCS clones across multiple environments should be possible.

Finding 7: Compared to commercial clones, unselected clones yielded 80 to 85% of the TCH and 90% of the CCS with the best unselected clones matching the commercial clones

Unselected clones had never been tested against commercial clones in large plots. The size of this difference gives a kind of benchmark for the expected selection differential when the best clones have been found in a set of random clones. The differences were relatively consistent, amounting to a mean TCH advantage in Q canes of ca. 21 t/ha TCH, 1.1 CCS units and 4 t/ha of sugar yield (Appendix 4). However, as mentioned elsewhere the TCH advantage was apparently greater in the South and NSW. Since most of the Q canes used as checks originated from regions further north, we have no clear explanation for this. It may be that the lower temperatures created greater genotypic variance that was observed only in the NSW trials particularly for TCH (Appendix 4). In any case, this observation does not compromise the findings about genetic correlations being relatively consistent across environments within and between regions, for this set of random clones.

Compared to commercial clones, the best 10% of unselected clones for each of TCH, CCS or TSH had a small advantage (about 5 t/ha, 0.5 units CCS and 2.5 t/ha on average), respectively, over the commercial checks (Appendix 4).

Finding 8: Early season CCS of unselected clones was correlated with harvest CCS

For a substantial set of unselected clones, this result confirmed those of past studies which have found a correlation between these two observations. These studies have formed the basis for the expectation that selection for early season CCS in early stage populations should also improve later season CCS (and vice versa), and is supported here.

Finding 9: Averaged over trials, most secondary agronomic trait scores were unrelated to clonal rankings for TCH or CCS

While clones that are susceptible to major diseases are culled through the selection process, there is variation among the regions in the use of secondary morphological/agronomic traits during selection. Where measured, significant genotypic variation for secondary traits existed in most trials (Appendix 4). However, for the trait scores of arrowing, lodging and suckering scores there was no relationship between a clone's score and either TCH or CCS when averaged over trials where the secondary trait was substantially expressed.

Small positive relationships were observed between TCH and the secondary traits of stalk length, stalk diameter (at chest height) and single stalk fresh weight.

Finding 10: Several sets of environmental variables were found that could capture a significant amount of the variation for environmental variables among trials

Appendix 6 summarises the results of this work. In terms of weather, maximum temperature and rainfall during the period November 15 to March 15 allowed for reasonable discrimination among the trials.

For soil chemical makeup, there was a contrast between the variables pH, calcium and Cation Exchange Capacity against zinc, manganese, iron and copper.

Soil nematode infestations were significant in the sites N1, H1, H2 and H3 (*Pratylenchus spp.*), N6 (*Helicothlenchus spp.*) and marginal in B2 and B3 (*Tylenchorhynchus spp.*) while *Pachymetra was* significant in C3, C4, N1, N4, N5.

Finding 11: No combinations of soil, location, weather or pathology variables yet tested had a significant impact on genotype by environment interaction variances

The environment variables listed in section 5.10 were tested in mixed models as fixed covariates to see if they can explain part of the observed genotype by environment interactions (Appendix 6). However, thus far they do not. For example, in the North, clonal rankings were not substantially affected when compared between the nematode infested sites (described above) and non-infested sites from trials. Further work is on-going in the new project BS267 to investigate other combinations of these factors.

Finding 12: Across the whole dataset, Genotype by location effects for TCH and CCS were greater than interactions associated with crop class

When conducting evaluation trials, it is useful to know whether environmental effects are greater between locations or years, or both. Table 4 and Appendix 4 shows that the genotype

by crop class (i.e. plant, ratoon etc) effects was 0 for CCS and relatively about ¼ of the genotype by location effect for TCH. For TCH, the 3-way interaction of these effects was similar to the genotype by crop class effect, while for CCS it was similar to the genotype by location effect. The table demonstrates that it was more important to sample environments as locations for TCH, compared with CCS where locations and crop classes are equally important.

Table 4 Variance components and standard errors for TCH and CCS for entire dataset with environments fixed and genotypes and interaction effects with location and crop class as random.

source	TCH	TCHse	CCS	CCSse
Gen	161.5	27.9	0.82	0.13
Gen:Loc	73.8	5.3	0.22	0.02
Gen:Cclass	15.0	2.8	0.00	NA
Gen:Loc:Cclass	12.4	3.1	0.17	0.02

Finding 13: No opportunity to select indirectly for CCS in the Ord

The results indicate that apart from the Ord, indirect selection for CCS in some other regions could often be just as effective as selection within the target region itself (Table 1). CCS in the Ord was poorly correlated with all other regions. However, it is emphasised that because of a reduced number of clones evaluated in the Ord (because clones highly susceptible to smut could not be evaluated properly and were not included in the Ord trial) and the fact that only one site was sampled, that this result should be interpreted with caution, and further investigation of this issue is needed to draw a confident conclusion.

Finding 14: Overlaps exist in historical climatic patterns of testing locations across regions and for low temperature coincide with magnitude of differences in TCH between unselected clones and commercial checks

This analysis aimed to identify high frequencies over time of stresses due to low temperature, solar radiation and water supply (Appendix 2). This aspect of the work would only have become particularly relevant to the field activities, if it could be shown that there were location or year specific differences in the performance of clones. However, it was found that climate was not a strong driver of genotype differences, or the differences in climate were not sufficient to cause large differences.

Cooler periods during establishment (April to October) in the South and to a lesser extent, Central region, limit potential CGR of lower LAI crops (say 0.2 to 1.5). Without irrigation, there are substantial ‘overlaps in season type’ among northern and southern locations, i.e. there were frequently years when the CGR pattern in a northern location was similar to that in a southern location in the same or different years.

Comparisons of the TCH of the unselected clones against the Q canes (commercial checks) showed that the commercial checks had a greater mean advantage in the South and NSW regions. Hence, it seems that adaptation to lower temperatures may be important in the broad adaptation of successful commercial germplasm. Other comments about climate variability from the report in Appendix 2 remain pertinent to the design of selection and evaluation processes. Perhaps the most important of these is that in years when rainfall is sufficiently

well distributed to result in high yields and increase lodging, there is likely to be an increase in the experimental error for TCH and therefore a reduced efficiency of selection.

Communications

Workshop discussions are reported in Appendix 7. These were an important component of the technology transfer in this project. Given the small audience and direct participation, formal surveys were not conducted on the workshop process. Useful discussion and feedback into the design and analysis of the trials, and the instigation of a new collective research project were taken to be positive indicators of this project.

June 2000 - Press release to industry (see milestone 6 report)

Following the project review in April 2000, Dr. Phillip Jackson (CSIRO) and Dr. Mike Cox (BSES) prepared a draft press release regarding the CTA028 project (see Appendix 8). The press release was designed to explain the objectives of the research and also to allay concerns of both industry players and researchers who may not be connected to the research. The concerns have been largely reactions to the growing of "poor" clones in the trials, which is contrary to the familiar practice of evaluating "elite" genotypes in variety trials. It was essential in the project to grow this range of germplasm to properly evaluate the potential value of understanding genotype by region interactions and obtain estimates of variances unbiased due to effects of selection.

Papers – to be inserted in Appendix

See list of publications below

Project training and learning experiences

The skill development in the project comprised the staff directly, and other plant breeding staff, to the extent that understanding about various analysis methods was transferred. This occurred through the joint writing and/or review of analysed results from the experimental trials and through workshops. Below are given descriptions of direct skill developments in project staff.

Technical training in sugarcane breeding and data collection/collation

- Bill Messer was newly redeployed from pasture research principally to look after technical activities in this project and another on lodging (CTA030). From both BSES and CSR technical staff (particularly in Ayr), Bill quickly learnt about the many practical aspects of sugarcane breeding and the type of data to be collected.

- Several other staff were employed on a part-time or casual basis in the project. One of these, Franco Zaini, worked on trials in the Ingham area. Franco developed into an excellent field technician and, following his experience in CTA028 and CTA030, became a cane productivity officer in the region.

May 1998. International Sugarcane Breeding and Germplasm Workshop, Mauritius. Partially funded by the project (see reports on milestones 2 and 3).

- Dr. Chapman presented an outline of the new project and experiments that had only just been planted. The meeting was a useful introduction to the world of sugarcane breeding and the complexity of commercial and public breeding interacting with the politics of germplasm development and maintenance. Dr. Scott Milligan, then at Louisiana State University was a useful contact from the meeting, being one of the few researchers outside Australia to work on genotype by environment interaction in sugarcane. At that time and in several email exchanges, Dr. Milligan offered some helpful insights into dealing with GxE and its possible basis in sugarcane.

November 2003. Contact with Prof. Fred van Eeuwijk, Department of Plant Breeding, Wageningen University Research.

- This visit helped to consolidate upon an earlier encounter with Fred (for other work) and email exchanges about interpreting GxE effects and accounting for the effects of fixed covariates in such analyses. Over the 7 days that Dr. Chapman visited with Fred, he was able to develop code to conduct these analyses in GenStat, and to replicate these analyses in S-Plus (the statistical program being utilised for the work here). The results of that experience were communicated to the other breeders in the June 2004 workshop (see Appendix 7).

- Dr. van Eeuwijk was also able to visit Australia in September 2004 (4th International Crop Science Congress) and present his research methodologies in a forum which was also attended by Phil Jackson and Mike Cox.

Intellectual property

The results of this work have been/are being published in various public fora. However, the basic datasets are not being distributed directly as they comprise a useful resource for the Australian breeding program.

The set of probe random clones used in this project (with the associated data set collected) are potentially valuable for further studies and should be conserved. These clones could be potentially useful in international collaboration. A subset of clones is already being used in an ACIAR funded CSIRO-BSES project with China to compare selection in China versus Australia with a view to understanding whether results obtained in China are relevant to Australia. This is of basic importance in any international collaborative research on sugarcane improvement and in rationalising exchange of varieties between countries.

Environmental and social impacts

- including any expected or actual adverse or beneficial environmental and social impacts of conducting the project and/or implementing its findings.

The project is expected to contribute to economic benefits to the Australian sugar industry and associated social benefits from this, through more profitable sugarcane varieties in the future. Exact size of these benefits is not possible to predict, but are commented on in the section below.

During the project, these trial results had impacts on decisions about follow-up research and on some of the rationalisations that were being considered by BSES Limited in the face of changes in funding scenarios. The finding that data from trials in different regions were quite relevant to each other (finding 2 above) provided strong impetus to the development of in-house database systems and tools in BSES to better utilise data collected on clones in prior as well as current evaluation experiments. The same finding was an important part of the decision to submit the request to undertake the new SRDC research project BS267 ("Maximising whole-of-industry benefits from the Australian sugarcane improvement program through an optimal genetic evaluation system"). At the start of CTA028, BSES had the opportunity to amalgamate the South and NSW regions into one program, and the trial data helped to confirm that locations in these regions were reasonably well correlated. In 2004, with trial data from CTA028 as a contributor, BSES Limited further decided to combine the North and Herbert programs. These amalgamations of operation make it possible to change the way that breeding resources are utilised to attempt to improve the return on investment for these.

Expected outcomes

- including assessment of the likely impact for the sugar industry in Australia and elsewhere and where possible the cost and potential benefit to the Australian sugar industry and/or the community. Qualitative and/or quantitative baseline data collected in the early stages of the project and compared with data collected towards the end of the project should be analysed and presented to demonstrate impact, learnings and additional outcomes of the project.

Several recommendations from the project have already been adopted (see recommendations section below). These are related to an increase in both the exchange of superior clones between identified within regions, and in the use of prior performance data of superior clones (and their relatives) when they are grown in further evaluation trials within a region of origin, or elsewhere.

The major longer-term outcome will be earlier releases of superior varieties and greater genetic gains in the Australian sugarcane breeding program. New varieties are currently worth 0.19 tonnes of sugar per hectare per year, or $20 million dollars at a sugar price of $260/tonne of sugar (Cox et al, 2005) to the industry. While it is difficult to determine the eventual impact of this project to the program, we expect an increase in the value of new varieties, and in the rate of identification of new varieties. In addition, protocol alterations (see recommendation point 2) should reduce the time from identification of superior varieties outside their region of origin from 5 to 2 years.

The expected outcomes from this improved use of information and the results of new projects are a continual refinement and increased efficiency of sugarcane selection process. Outputs of CTA028 have already been adopted by the BSES breeding program during consideration of

major restructuring and will continue to be used for at least the next 5 years. It is a major task of the new project BSES267 led by the BSES-CSIRO-PI Joint Venture to determine the best structure to use the information provided by CTA028.

Most of the results will be of direct value to plant breeders and their managers. The direct involvement of breeders from the joint venture will ensure that the results are communicated within Australia's sugar breeding programs and will promote collaboration amongst all of these staff.

Cox, M.C., Stringer, J.K., Cervellin, R.J. (2005) Productivity increases from new varieties in the Queensland sugar industry. ASSCT, Bundaberg, May 2005 (accepted).

Recommendations and future research needs

- recommendations on activities or other steps to further develop, disseminate or exploit the Project Outputs, and/or to achieve benefits

Background and general comments

In the past, distinct regional sugarcane breeding (crossing and selection) programs have been conducted in Australia. The implicit assumption has been that data collected from trials at a particular site had much greater value for predicting relative clone, cross, or parent performance within the region the trial was situated, compared with its predictability to other regions. This is illustrated by some procedures used for exchange of clones among the regional programs. For example, in the past, approximately 50 clones performing the best in final stage trials in each region were sent to other regions for assessment. However, despite their 'proven performance' in the source region, these clones were put into earlier stage trials for assessment in the new region. These earlier stage trials have higher error variation and bias due to competition effects, and the data from the early stage trials would be used to select clones for advancement within the region, ignoring the prior knowledge on the clones from other regions.

Similarly, segregation of breeding programs to regions may have caused locally sourced data and germplasm to be given greater weighting in choosing parents and crosses relative to data and germplasm available from other regions, so that region specific parent populations have been developed.

A key finding from this project was that genotype x region interaction variance, while significant, was small relative to genotype main effects and other larger genotype x environment interactions not associated with regional differences. From this, it follows that data obtained from trials in other regions is valuable for predicting performance in any given region, and sometimes just as valuable as trials within the region, as illustrated by the tables of genetic correlations (Table 2). This has implications for how an optimal multi-regional program should be conducted, and specific proposals are suggested below.

It is important to emphasise that, although data on relative clone performance in one region is of value in making selections for other regions, the statistical parameters and

recommendations arising from their interpretation relate directly to earlier stage selection, and not to final stage selection or cultivar recommendations. The presence of some genotype x region interaction variance in the data set in CTA028, genotype x region interaction for highly selected genotypes (Appendix 13), coupled with past industry experience with cultivars being region specific, infers that there is still potential for region specific environmental factors affecting some comparisons between standard cultivars and individual experimental clones considered for release. For this reason, the current practice of evaluating clones within a region prior to release in that region (as opposed to relying completely on data from other regions for this purpose) is not questioned by this project.

As can be seen from the recommendations below, the results suggest that improvements can be made in the current breeding program (points 1. and 2.). However, there are also further questions to address before making other significant changes, and suggestions are made on how to proceed in addressing these (points 3 to 7). Finally, some suggestions are made for optimal structuring of the Australian breeding program, considering both what is known at present, and the important questions that still remain (point 8.).

Step-wise improvements rather than radical restructuring are recommended, with a cautious approach to making larger changes. Past sugarcane breeding has delivered substantial productivity improvement to the Australian sugar industry (Cox *et al., 2005*) and it is important not to eliminate favourable aspects of the program that may not have been revealed in this project.

Specific recommendations and adoption:

Recommendation 1: Given the low genotype by region effect (objective 1), that routine data analysis of all trials should be used to predict commercial and breeding value of clones across all regions, not just the region in which the clone is evaluated

This recommendation to use results derived from CTA028 is being developed in project BSS267. Implementation is facilitated by a breeding program database that combines data from all selection stages and regions, which is currently being developed by BSES.

Rationale and caveats: Breeding effort and selection within any particular region should be regarded as being of high relevance not only to that region but to all other regions. From that, it follows that for all trials, data should be examined so that the value of clones or parents is predicted for all regions, not just the region in which the trial is conducted. This is particularly important for selecting the best set of clones, from the combined effort in all regions, to enter final assessment trials (FATs) within any individual region, as discussed in point 2, below, and in selection of parents and crosses, as discussed in point 3 below. The analysis methodology for integrating data across regions will take account of the error variance in different trials, and genetic correlations between environments among and within regions (estimates of the latter can be initially provided from this project).

Recommendation 2: Selection sites can be better linked (objective 2) by choosing superior clones in final assessment trials in any region to be entered directly into final assessment trials in all other regions, without having to go through earlier stage trials again

This recommendation has been adopted based on this project, with the following system currently in operation:

- The top 25 clones within a region, based on plant crop final assessment trials (FATs) ,are immediately propagated in other regions
- The top 5-10 clones from a region, based on plant and first ratoon FATs, are propagated for FATs in other regions; with the remainder of the 25 planted into earlier stage single-row replicated trials
- The top 2-8 clones from each program, based on plant, first and second ratoon FATs, are planted into FATs in other regions

Rationale and caveats: Following recommendation 1, and given that genetic correlations found between trials from different regions were frequently almost as high as with other trials within the same region, a greater priority had to be given to rapid transfer and testing of clones performing well in any region to/in all other regions (while taking due account of differences in some disease resistance requirements between some regions – see recommendation 4 below). This new system differs from that used up to recently, in which clones transferred were put back into relatively unreliable single row plot trials for evaluation.

In coming years (i.e. within next 2-5 years), a significant proportion of clones entering FAT trials in each region will likely comprise material selected from FAT trials in other regions compared with local earlier stage trials. Details of an optimal system including proportions should be determined by stochastic modelling of options, and from actual comparisons of clones sourced from each regional program in the other regions in the future.

Regardless of final details, implementation of the above recommendation will lead to at least two benefits: (i) faster release of suitable cultivars across multiple regions, (ii) better quality populations being evaluated in FAT trials and therefore improvements in selection gains and cultivars within each region.

In relation to point (i), growers have been critical in the past for the lag phase in the release of cultivars in different regions. Under the system being implemented, most cultivars should have plant crop data in FATs in all regions at the time of first release in any region. That data, combined with ratooning characterisation and disease resistance data obtained in the original region should be sufficient to make a decision on whether to begin to bulk up for subsequent release in the new region. Under this system most varieties could be released in the new region within 2 years of the original release (presuming suitable FAT performance in the new region), which would be 3-4 years (or more) quicker than past practices.

Recommendation 3: To conduct future research to examine the value of retaining separate regionally based parent populations and crossing operations, and the relative value of

breeding for specific regional adaptation versus broad adaptation (extension of objectives 1 & 2)

We recommend two lines of related investigation. First, the breeding value of the *current* five regional parent populations should be compared in each region. This would (i) test for evidence for region specific adaptation being developed in the past in each of the current parent populations and, (ii) benchmark against each other the relative breeding values of the current parent populations developed in the each regional program. Second, in looking forward, relative gains from selecting on breeding value within specific regions, versus selecting on breeding value across all regions should be predicted based on parameters from suitable data sets. Both these objectives could be done as part of routine core breeding programs within 3-4 years, but requires coordination in design of crosses for the regional selection programs.

A research strategy to test the breeding value of existing parent populations above is planned to commence on a limited scale within the routine breeding program selection trials in the BSES-CSIRO JV program in 2005, by evaluation of a common set of families across all regional programs. However, this should be repeated across years because of likely random and specific combining ability (SCA) variation and year effects. Further discussion and funding is required for this exercise because it is essential that testing of families occurs in more than one site per region, so that parent x environment-within-region interaction effects are partitioned from parent x region effects. Some testing away from the regional experiment stations must be done in case there is specific adaptation for the experiment station sites (where much parent selection has been made in the past) in some populations, which may not be representative of adaptation to the region as a whole.

Rationale and caveats: Given the small size of genotype x region interactions relative to other sources of variation, the benefits in maintaining and developing separate populations of parents that are based on (perceived) differences in region-specific breeding value, as done up to now, is at least questionable and should be evaluated. At the same time, we emphasise that given the presence of at least some genotype x region interactions, it is important not to "rush" into a re-structuring of the current region specific breeding programs without such evaluation. Such a move, without good characterisation of relative breeding value of current parental populations in each region, could result in the throwing away of possible region specific gains in parent breeding value made from many decades of past effort by BSES.

It is recognised that some diseases are important in some regions and not in others – eg. Fiji disease resistance is a critical selection criterion in the South and Central regions but much less in the others; resistance to *Pachymetra* is not important in the Burdekin but is important in all other regions. Variation in relative economic importance of some other traits between regions, such as flowering, is debatable, and should be examined as per recommendation 1.

The existence of any real region specific factors will always be an important in selection of parents and crosses for different regions. However, providing that such factors do not dominate selection, such differences can still be accommodated within any programs targeting multiple regions.

Recommendation 4: To conduct further research to determine the optimal number of sites across the state in which to evaluate families (extension of objectives 1 & 2)

The results of CTA028 indicate that there is a substantial genetic correlation between regions, apart from the Ord (for CCS), i.e. in theory, only one region needs to be sampled to represent Australian production environments. Due to experimental error, it is always necessary to sample multiple sites, but the data suggest that, for random clones, these may as well be distributed across regions. However, the project has not tested whether this will also be the case for early-stage testing of families in small plots. The relative importance of family, family x region interaction, and family x environment within region interaction, should be examined in future as part of the routine breeding program effort in order to optimise future selection gains from family selection in the earliest stages. This objective could be conducted using the experiments recommended above in point 3.

Rationale and caveats: In sugarcane selection systems, families may be tested across sites in the earliest stages. An optimal configuration (i.e. plot size, replicate number, number of environments etc.) for evaluating families cannot be derived from data in this project, since family and plot size related variance components cannot be partitioned given the experimental design. Several prior projects have investigated this issue, at least in part, within individual regions in the past. However, results were usually affected by use of single row plots (which can potentially cause upward bias in main effects due to competition) and small sample sizes of environments conducted within individual regions. As indicated previously, a vital inclusion in such an investigation is multiple sites within regions to allow partitioning of family x region interactions from other family x environment effects.

Because CTA028 has shown that genotype x region interactions in early stage (unselected) populations are small, the number of regions in which early stage selection is conducted is not critical to maximising gain from selection. Therefore, the effort at early stages could be either concentrated within a couple of regions (one would be risky in the face of disease or weather disasters) or spread across all regions, with only a small advantage with increased numbers of regions, i.e. assuming the same *total* resources allocated to the combined program in terms of total seedling or plot number etc. *However*, given the importance of genotype x site and genotype x site x crop-year interactions, selection gains will always be increased by testing genotypes across multiple environments in the early stages of selection. Because genotype x region interactions are significant (albeit small), there would be always be a small advantage in spreading sites between regions rather than within regions.

Recommendation 5: That results from CTA028 and emerging data from BSS250 (Optimising selection systems) be combined to recommend details of optimal selection systems targeting multiple regions (extension of objectives 1, 2 & 3)

Genotype x environment statistical parameters obtained in this project should be used in association with data being obtained in project BSS250, and other sources of data, to recommend details of optimal selection systems targeting multiple regions, including such details as number of selection stages, plot size (row number) in each stage, replicate number in each trial at each stage, number of sites at each stage and use of new trial designs across multi-site trials (eg super-replication), selection criteria in each stage, and selection intensity in each stage.

Rationale and caveats: none.

Recommendation 6: Introductions to the Ord should continue to be based on selection for smut resistance and good performance in any east coast region, but possible unique genetic responses to CCS in the Ord justifies further verification (objective 3)

A set of clones contrasting for CCS in the east coast regions should be examined under Ord environments to verify the responses observed in this project. Meanwhile, the selection of advanced stage clones with good cane yield and smut resistance is an appropriate strategy to serve the small industry in the Ord. The level of GE interaction within the Ord (associated with time of sampling, location, crop management etc) is an important issue which could not be addressed in this project and should be given a priority in the future.

Rationale and caveats: The data obtained in this project suggested unique genetic responses observed in the Ord region for CCS. However, the data set was limited due to culling of the original population due to smut susceptibility. Confirmation of no relationship for CSS between east coast regions and the Ord may suggest a two-phase selection system is appropriate where introduced clones are first tested for CCS in small plots in the Ord, with high CCS clones subsequently evaluated in multi-row plots.

Recommendation 7: Incorporate the estimated value of selecting for secondary traits to predicting economic value for selection, and determine whether different weightings between regions are justified (extension of objectives 2 and 4)

Differences in economic value of secondary traits between all regions, but most notably between the far North and other regions, for arrowing propensity should be investigated and quantified further because currently perceived differences will have a dominant role in predicting different estimates of commercial and breeding value of clones in selection trials between the North and other regions.

Rationale and caveats: While not directly related to the original project objectives, the data collected allowed the examination of correlations between a range of secondary crop traits (arrowing propensity, lodging propensity, yield components etc.) and economic value across a wide range of environments. The use of such traits could add value to selection programs as terms in selection indices, both within and between regions. For example, strong positive genetic correlations were observed for the early CCS vs CCS and stalk length vs TCH in almost all harvests (Appendix 4). Small positive correlations were also observed in many trials for tch predicted by stalk diameter and stalk number per unit area.

Recommendation 8: Undertake further analysis of the CTA028 and further experiments to determine environmental factors causing GE interactions (objectives 4 & 5)

One major lead on understanding the causes of GxE was the relationship between trial mean values and trial genetic variance (or trial error variance) for both TCH and CCS, i.e. better estimates of genotype differences were achieved when trials were managed such that TCH was in the range of ca. 70 to 110 t ha-1 and CCS was in a range of ca. 13-17 units. This issue was raised in industry forums in 2004 and the interaction between trial management and genotypic variation for TCH or CCS is a major aim of a new SRDC project being led by Dr.

Geoff Inman-Bamber of CSIRO-CSE in collaboration with investigators from the CTA028 project.

Not knowing what the environmental drivers for GE interaction, while not uncommon in many breeding programs in all crops, is a serious deficiency in our knowledge. This lack of knowledge means trials cannot be deliberately sited or managed in a way which is known to give rise to larger selection gains compared with what would be expected by randomly sampling the same number of sites and years. One limitation in identifying key causal environmental factors was the time limitation between obtaining the final data in this project (in the 2004 season) and undertaking the detailed analyses for this report. Further analysis and novel methods of data analysis could progress this goal. Given the potential value of such knowledge in improving genetic gains, the investment made in the last 7 years in obtaining such a high quality, extensive data set, some further effort in analysis of these data in the near future does seem justified.

Rationale and caveats: At this stage, no recommendations can be made on how to best sample environments for early stage testing in terms of their biophysical characteristics (eg. soil type, biotic factors, climate, etc). This is because we have not identified key causal environmental factors driving GE across the production area. Many obvious candidates for important environmental factors, such as water availability, were examined but were not apparently associated with patterns of genetic response. These results suggest that GE interactions may be a result of a range of environmental factors interacting, giving rise to complex patterns that are difficult to reveal, as opposed to dominating factors impacting independently. Because the mean values of TCH and CCS do have some regional basis, we do not know if these relationships are linked to regional factors (it seems unlikely, given the above), but the indication is there to study this relationship in other trials to see if it does apply within regions.

Recommendation 9: The optimal arrangements for Australian sugarcane breeding program at this stage

At this stage, based on the results from this project, and considering the key questions arising from these results not yet addressed (points 3 to 6 above), and logistics of transport of cane seed, appropriate arrangements for the Australian sugarcane breeding effort (targeting all regions) are suggested below:

(i) Retain 4 selection programs, with each responsible for conducting early stage selection trials within its region. The objectives of each program are to provide an elite set of clones for inclusion into local FAT trials and promotion into other regional FAT trials.

(ii) Initially continue to develop parental populations and crossing strategies regionally, toward the above objective, based on current knowledge and experience. However, based on results from this project, breeders should accommodate the relevant data and germplasm derived from other regions in developing their own program. Implementation of the “Genetic Evaluation System” data system as part of BSS267 within 2 years will facilitate this, but the process should be commenced immediately.

(iii) A program-wide and objective process should be used for selecting clones derived from all regions for propagation and entry into the regional FATs in all regions. An optimal allocation of local early stage selections and elite clones from FATs in other regions will be determined. This process has already commenced but will be further refined during BSS267 and beyond. Direct annual benchmarking of performance of clones from the different regional programs will be possible.

Publications

A paper presented at the ASSCT meetings in 2004 is included in Appendix 10

Another paper in internal review is listed in Appendix 11.

The paper in Appendix 2 is being considered for incorporation into another paper.

Three more papers are in various states of presentation, and we propose to submit a final paper on the project to ASSCT in 2006.

Acknowledgements

Apart from the project investigators and those mentioned in section on project management, this project has benefited from an immense effort by a large number of technical staff, scientists and of course growers who agreed to plant and maintain these trials. The technical staff who are thanked for trial supervision in the different regions include Felicity Atkin (BSES, South), Anthony Cattle (BSES, NSW), John Foreman, Graeme Holzberger and Adam Royle (CSIRO and BSES, Herbert), Mark Hetherington (BSES, Central), Catherine Kettle (BSES Burdekin), Terry Morgan (CSR Burdekin), Michael Porta (BSES North), and Tim Treglone (WA Dept. Agr. Ord).

Apart from the current (Nils Berding, Mike Cox, Xianming Wei) and past (Mac Hogarth, Collins Kimbeng), BSES plant breeding staff, other scientific staff who have assisted at various times with the trials and the analysis and interpretation of results have included Rob Magarey (BSES Tully), Ky Mathews (UQ), John Panitz (BSES South) and Andrew Wood (CSR Ingham), Joanne Walker (CSIRO casual).

Mike Cox has also contributed substantially in the preparation of the final report. We also appreciate the contributions of Tony McRae, Jason Bull and Ray Shorter who were part of the team who helped initiate this project,

We also thank the numerous growers who tolerated the cultivation of a diverse set of unselected clones on trials on their farms. Some of the clones were truly poor performers, and we and the technical staff were frequently called upon to diplomatically explain the importance of knowing the yield of poor as well as good clones in the field.

During the project, the investigators developed analytical skills through informal collaborations with biometricians working in BSES (Jo Stringer), NSW Department of Primary Industries (Brian Cullis and Arthur Gilmour) and Wageningen University Research (Prof. Fred van Eeuwijk).

Australian Government
Sugar Research and Development Corporation

Appendix 1. Summary of genetic and genotype by environment variances from published experiments and unpublished theses and reports

(compiled by Mac Hogarth, April 1999 and Allan Rattey, Jan 2005)

Table of Contents

1.1. Pollock, J S (1978). Variety-environment interaction and selection of sugarcane. M.Sc.Agr. thesis. University of Queensland. 161 pages.

Plots of 17 varieties were harvested from 13 trials planted on commercial farms located in the costal areas of the Northern region. Trials were planted in 1970 (six), 1971 (five) and 1972 (two) and harvested across plant, first and second ratoon crops, giving 39 harvests (environments). The analysis of these 39 environments produced the following C and CxE components of variance. For both TCH and CCS, the ratios of CxE to C were 77% and 46% respectively.

Table 1-1 Variance components for several traits for 17 clones in 13 locations (planted in 1970-72) over 39 harvests. Pollock (1978). M. Agr. Sci. thesis, The University of Queensland.

Source	Cane t/ha	ccs	Sugar t/ha	Stalk No.	Weight per stalk	NMG
σ^2_C	60.7	0.94	1.79	1702	25.3	1.03
σ^2_{CxE}	47.3	0.43	1.35	661	7.3	0.92
σ^2_E	82.1	0.41	2.01	560	9.2	1.11
$\sigma^2_{CxE}/\sigma^2_C$	0.77	0.46	0.75	0.39	0.29	0.89

1.2. Cox, M C (1995). Seasonal distribution of growth and sugar accumulation in sugarcane. Final report SRDC project BS5S.

Fifty clones, representative of the BSES breeding collection, were assessed for growth and sugar accumulation at Meringa, Bundaberg, and Harwood in plant and first ratoon crops. Plots were 4-rows wide by 10m long and were sampled five times during the season for CCS and TCH, but the TCH was only mechanically harvested at time 5. The yield traits (TCH and TSH) were more affected than CCS, with the second-order interaction effect (CxLxY) always 2 to 3 times greater than either of the first-order (CxL and CxY) interaction effects. Overall, CxL (effectively Clone by Region) interaction effects were small, even in the time 5 harvest when the TCH sample was taken as a large mechanically harvested whole plot sample.

Table 1-2 Variance components for 3 traits estimated at 5 sampling times for 50 clones grown at Meringa (North), Bundaberg (South) and Harwood (NSW) locations in plant and 1st ratoon crops. Cox (1995) SRDC Final Report BS5S. Note that CxL is effectively CxRegion.

Time	Effect	Cane t/ha	ccs	Sugar t/ha
1	C	34.80	1.62	0.87
	CxL	0.00	0.29	0.30
	CxY	7.70	0.00	0.00
	CxLxY	58.70	0.44	0.79
	CxE/C	1.91	0.45	1.25
2	C	70.30	1.45	1.46
	CxL	0.00	0.26	0.42
	CxY	0.00	0.00	0.00
	CxLxY	58.60	0.36	0.86
	CxE/C	0.83	0.43	0.88
3	C	59.60	1.04	1.49
	CxL	0.00	0.11	0.27
	CxY	0.00	0.00	0.00
	CxLxY	46.30	0.17	0.62
	CxE/C	0.78	0.27	0.60
4	C	54.30	0.86	2.13
	CxL	0.00	0.29	0.16
	CxY	6.50	0.00	0.15
	CxLxY	37.80	0.04	0.52
	CxE/C	0.82	0.38	0.39
5	C	46.00	0.96	2.85
	CxL	0.00	0.17	0.00
	CxY	26.00	0.00	0.45
	CxLxY	47.20	0.12	1.18
	CxE/C	1.59	0.30	0.57

1.3. Bull, J K (1997). Genotype x environment interaction for clones and crosses planted in southern Queensland and northern New South Wales. Final report SRDC project BS15S.

In 1988, 97 clones, in trial series of 54 and 43 clones, were planted and evaluated for sugar yield at seven locations (four in Queensland, three in New South Wales) in plant and first ratoon. In 1989, 69 clones were planted and evaluated for sugar yield at eight locations, five in Queensland and three in New South Wales, in plant and first ratoon crops. Plots in all trials were single row by 12 to 15m long.

Actual variance components are not readily available, as the report discusses relative values of CxE variance components compared to the C variance component. Over all trials, and within South Qld and NSW the ratios of CxE to C for sugar t/ha were:

Table 1-3 Variance component ratios (CxE/C) for sugar yield from > 40 clones planted in Southern Qld and NSW in 1988 and 1989 and harvested in plant and 1st ratoon. Bull, J.K. (1997). SRDC BS15S Final Report.

Series	All trials	South Qld	NSW
1a	0.89	0.60	0.41
1b	1.25	0.71	0.97
2	1.32	0.91	0.91

The CxLxY interaction component was similar in magnitude to the CxL component.

1.4. Hogarth, D M (1988). Variety x location interactions. Internal BSES report.

Variety x location experiments were conducted in north Queensland, central Queensland and southern Queensland.

1.4.1. North Queensland and Herbert

Fifty-two clones, including 26 random and 26 selected clones, were planted in trials on Meringa and Tully Experiment Stations and two sites at Ingham. Trials were harvested in plant and first ratoon crops. Data are available for cane t/ha, ccs, sugar t/ha, and net merit grade, but only sugar t/ha is reported here. Results were:

Table 1-4 Variance components for sugar yield of 52 clones (half random, half selected) grown in North and Herbert at two sites each and harvested in plant and 1st ratoon crops. Hogarth (1988). Internal BSES report.

Source	North (Meringa/Tully)	Herbert 2 sites near Ingham	All Trials
σ^2_C	2.92	-0.06	0.94
σ^2_{CL}	-0.88	4.57	1.91
σ^2_{CY}	-0.63	-0.45	-0.03
σ^2_{CLY}	2.51	3.18	2.41
CxE/C	0.86	NA	4.60

The results of the Ingham trials were particularly disturbing, with substantial negative variance components. These results might well be different if the data were to be reanalysed with new methods.

1.4.2. Central Queensland

Fifty clones, including 25 selected and 25 random clones, were planted in three trials, and harvested in plant and ratoon crops. Plots in all trials were three rows wide by 10m long.

Table 1-5 Variance components for sugar yield of 50 clones (half random, half selected) grown in 3 trials in Central region and harvested in plant and 1st ratoon crops. Hogarth (1988). Internal BSES report.

Source	*Sugar yield*
σ^2_C	1.52
σ^2_{CL}	-0.04
σ^2_{CY}	1.71
σ^2_{CLY}	0.94
CxE/C	1.74

1.4.3. South Queensland

Sixty clones, including 30 random and 30 selected clones, were planted in three trials. Plant and ratoon crops were harvested. Plots in all trials were three rows wide by 10m long.

Table 1-6 Variance components for sugar yield of 60 clones (half random, half selected) grown in 3 trials in South region and harvested in plant and 1st ratoon crops. Hogarth (1988). Internal BSES report.

Source	*Sugar yield*
σ^2_C	2.85
σ^2_{CL}	1.92
σ^2_{CY}	0.25
σ^2_{CLY}	0.59
CxE/C	0.97

1.5. Jackson, P A and Hogarth, D M (1992). Genotype x environment interactions in sugarcane. I. Patterns of response across sites and crop-years in north Queensland. Aust. J. Agric. Res., 43, 1447-59.

Two series of experiments were analysed from Nothern Queensland. In series 1, 65 clones were planted to four sites in the Herbert River district, with plots in all trials being one row wide by 15m long. Data were collected for plant + two ratoon crops for three sites; at the fourth site, which was unreplicated, only plant and first ratoon crops were harvested. In series 2, 52 clones were planted to two sites in the North (Meringa and Tully) plus two in the Herbert. Plots in all trials were three rows wide by 9.2m long and harvested in plant and first ratoon crops.

Table 1-7 Variance components for 3 traits in two series of 65 random clones grown in 4 sites in the Herbert region and harvested in plant, 1st ratoon (all) and 2nd ratoon (3 sites). 1.5. Jackson and Hogarth (1992) Aust. J. Agric. Res., 43, 1447-59.

Series	Source	Cane yield	ccs	Sugar yield
1	σ^2_C	124	0.15	3.23
1	σ^2_{CL}	92.2	0.13	2.54
1	σ^2_{CY}	20.9	0.03	0.61
1	σ^2_{CLY}	13.2	0.11	0.47
	CxE/C	1.02	1.80	1.12
2	σ^2_C	74.5	0.64	1.7
2	σ^2_{CL}	116.5	0.42	3.11
2	σ^2_{CY}	22.8	0.15	1.17
2	σ^2_{CLY}	98.5	0.27	2.45
	CxE/C	3.19	1.31	3.96

1.6. Mirzawan, P D N, Cooper, M and Hogarth, D M (1993). The impact of genotype x environment interactions for sugar yield on the use of indirect selection in southern Queensland. Aust. J. Exp. Agric., 33, 629-638.

This analysis used sugar yield data from BSES regional selection experiments, in particular the substation yield trials planted in south Queensland in 1987. There were 80 clones at 4 sites, each with 3 crops (plant, first ratoon, second ratoon). Plots in all trials were one row wide by approximately 10m long.

Table 1-8 Variance components for sugar yield for 80 advanced stage clones grown in 4 sites in the South region and harvested in plant, 1st and 2nd ratoons. Mirzawan et al. (1993). Aust. J. Exp. Agric., 33, 629-638.

Source	*Sugar yield*
σ^2_C	2.59
σ^2_{CL}	1.78
σ^2_{CY}	0.56
σ^2_{CLY}	1.04
CxE/C	1.31

1.7. Berding, N. Specific v. general adaptation. Unpublished analysis of project data.

This project had 78 clones planted at three locations in far north Queensland. Plots in all trials were four rows wide by 10m long. Only the analysis of plant crop data is available.

Table 1-9 Variance components for sugar yield for 78 clones grown in 3 sites in the Norht region and harvested in plant crop. Berding, N. Unpublished analysis.

Variance Component	Cane t/ha	ccs	Sugar t/ha	NMG	Conductivity	Fibre
σ^2_C	89.1	0.52	1.20	1.14	125,134	1.22
σ^2_{CL}	74.9	0.19	1.45	1.26	53,680	0.20
CxL/C	0.84	0.37	1.21	1.11	0.43	0.16

Appendix 2. Prepared paper on pattern analysis of climatic effects

"Pattern analysis of climatic effects on sugarcane growth in Australia"

S.C. Chapman, K. Mathews and P.A. Jackson

Abstract

This analysis used historical weather data records to estimate monthly crop growth rates as limited by radiation, low temperature and water supply for simulated crop canopies with a leaf area index of 0.2, 1.5 or 6 growing in soils that differed in soil water capacity and starting soil water.

Cooler periods during establishment (April to October) in the South and to a lesser extent, Central region, limit potential CGR of lower LAI crops (say 0.2 to 1.5). The highest CGR for crops with larger canopies (LAI or 1.5 to 6) is in November to January in southern locations, but in October to December in northern locations. This is related to the onset of the wet season (and lower radiation) from about January in the northern locations. Analyses of the frequencies with which different patterns of CGR occur reveal that some locations consistently experience seasons of the same type, while other locations overlap each other greatly in terms of the season types being sampled. In irrigated trials, where CGRlowt is an appropriate measure, there is a clear distinction in the annual CGR pattern between Kununurra, northern and southern locations. Bundaberg (South) and Mackay (Central) have a proportion of years that overlap in terms of the CGR for a full canopy, i.e. in certain years, one might expect that genotype performance in irrigated trials would have some similarities between these two sites.

Without irrigation, the overlaps among northern and southern locations are greatly increased, i.e. there are frequently years when the CGR pattern in a northern location is similar to that in a southern location in the same or different years. If these patterns are expressed in the cane and sugar yield of the trials, then they may result in confounding effects on genotype performance over years.

Introduction

Sugarcane in Australia is grown along some 2500 km of the eastern coast from Grafton NSW (29.7°S 152.9°E) to Mossman, QLD (16.5°S 145.5°E), and in the late 1990s has expanded to the Ord river region in Western Australia (16.7°S 128.9°E). The industry is concentrated around sugar mills in river valleys that are generally within 50 km of the access to shipping. The mill "regions" provide a convenient grouping that is often used in the planning of research and extension programmes, including those to improve the crop through plant breeding (Table 1). Sugarcane breeding in Australia has been undertaken by both a state authority (Bureau of Sugar Experiment Stations – BSES) and, until a recent announcement to terminate, the Colonial Sugar Refining company (CSR). Breeding programmes are run within several broad regions and clones that have been proven within a region are exchanged and tested in other regions.

While sugarcane is grown as a rainfed crop over the majority of the area, a relatively larger proportion of the total tonnage is grown under full irrigation in the Burdekin, Ord and Atherton Tableland regions. Supplementary irrigation is applied in much of the central Queensland region and in the northern part of the southern region. Sugar is usually grown as a plant crop, followed by 3-4 ratoons with growing seasons of 10 to 18 months, although in the far south, some 2 year crops are grown. Across the regions, sugarcane experiences a range of

temperature, radiation and rainfall regimes. These different environments generate substantial main effects on the yield of clones such that sugar yield across the regions varies from 6-7 t/ha in the wet tropics to >25 t/ha in irrigated dry tropical areas. The identification of superior clones becomes difficult when genotype by environment interactions (GxE) overcome the main effects of genotype and environment. Even excluding the differential occurrence and intensity of diseases, these combinations of growing conditions together with soil type can generate substantial GxE interactions. The GxE effects have been demonstrated within both the southern region (Bull et al. 1992) and the Herbert river environments within regions. However, they have not been measured across the sugar growing region.

Genotype by environment interaction can arise from both site/location effects and from effects due to year/climate effects. In many dryland crops in Australia (see Basford and Cooper 1998 for some examples), genotype by location and genotype by year effects are less important than genotype by location by year effects, i.e. there is a complex interaction between locations and annual weather patterns. For sugarcane, the genotype by location effects have been relatively greater than in dryland crops (e.g. Bull et al. 1992; Jackson and Hogarth 1992, Mirzawan et al. 1994), although this may also be due to the expense and difficulty in sampling a large number of seasons, and the partial confounding of ratoon crop effects with season effects. The degree to which genotype by location effects contribute to clone adaptation is important, as clones can be targeted to particular locations, but not to particular seasons, i.e. location effects like soil type etc. are fixed, but we cannot generally predict the coming seasons, and nor can growers economically replace clones once they have been planted.

As a part of research in progress (not reported here), we are conducting trials across all of the mill regions, using the same clones in each trial. These trials can be considered to be a sample of the target population of environments (TPE, Comstock 1977) for the Australian sugarcane breeding programs. To make inferences about the effects of environment on genotype performance, we need to obtain independent information from the trials and place them in the TPE. This requires the development of suitable environmental measures and methods to group these and determine how representative the trials are of the total TPE.

The effects of different locations and years on crop growth and genotype performance can be summarized either by direct interpretation of the climatic and soil variables, e.g. McLaren 1996 used climatic variables to explain GxE in rice trials, while van Eeuwijk and associates have used combinations of weather and soil measures to explain GxE, e.g. Voltas et al. (1999). An alternative to using these large numbers of variables is to integrate the effects of the weather and soil conditions on crop growth. Simulation models can be adapted for this purpose. While many crop simulation models have the objective of estimating final yield, they can also be used to determine the ‘environment limited yield’ (e.g. Nix 1981), or can be used to output integrating variables, like stress indices, e.g. Muchow et al. (1996) and Chapman et al. (2000).

In climate research, scientists commonly use pattern analysis methods (cluster and pattern analysis) to group together weather indicators collected from different seasons and locations to describe climate patterns. Similarly, weather data averaged over years has been grouped across GIS surfaces to describe climate adaptation for crops like maize, e.g. Pollak and Corbett (1993). This approach though did not account for the variability of the weather when we know that genotype by season effects are often substantial. Whether the environment variables are used directly or are filtered by a simulation model, pattern analysis methods can be used to place a season/location combination within the TPE. When comparing locations, we can then examine the frequency with which locations experience similar environments, and the likelihood that different genotypes will perform similarly at these locations over the longer term.

The objective of this first paper is to use direct and indirect measures of the climatic environment to describe the average environments at different locations across the region and to summarise the frequencies with locations experience similar environments over years. These interpretations can then be used as part of the analysis of genotype by environment interactions from clonal trials that are currently in progress.

Materials and Methods

Climate data

Climate data was obtained for years from 1956 to the 1999 for 16 locations along the coast (Table 1). While rainfall data are available prior to 1956, temperature data are generally not in electronic form. The datasets used are updated versions of those referred to by Muchow et al. (1997).

Simulation model

A complete cropping systems simulation model (e.g. APSIM McCown et al. 1995) could be used to integrate the climatic variables as used by Chapman et al. (2000) for sorghum. However, to do this for all of the sugar-growing regions simultaneously would require substantial assumptions to be made about the management of crops (inc. fertiliser amounts and irrigation) and the timing of operations such as planting, ratooning and harvesting. A further complication is that at almost any time of the year, sugarcane crops at different stages of development can be present within the same or different regions.

We have adopted a simpler approach here to examine climatic effects alone using a growth index model (e.g. similar to that of Nix 1981) that requires fewer assumptions about crop management and allows us to develop an understanding of the target population of environments. A crop growth rate model was developed to determine growth rate over one month as limited by:

- light (incident and intercepted radiation)
- low temperature (low temperature decreases radiation use efficiency)
- water supply (given starting water of 100mm in profile with a capacity of 200mm)
- actual - minimum of the above 3 effects

The major assumptions behind this model are as defined in APSIM-Sugar (Keating et al. 1999):

- c_RUE = 1.8 (radiation use efficiency)
- c_extinction_coef = 0.38 (canopy ability to intercept radiation)
- c_svp_fract = 0.75 (proportion factor to model vapour pressure deficit)
- c_transp_eff_cf = 0.008 (transpiration efficiency)
- kl = 0.07 (ability of roots to extract water)

A further assumption was eff_rain = 0.8 (effective rain , assimilates runoff, evap effects). The analyses were repeated for a factorial of scenarios for leaf area index and soil depth/water holding capacity. The results presented here assume an LAI of 6.0 and a soil water holding capacity of 100mm, equivalent to a sandy or alluvial soil of 1 to 1.5m depth.

The simulation was applied to the 1956-1999 weather record for each site, initially assuming that no irrigation was applied. At the start of each month in the record, the model was initialised as described above, and then run for the remainder of the month accumulating biomass but not changing leaf area. At the end of each month, we calculated the amounts of biomass potentially accumulated given the limitations of radiation, low temperature or water. Details of the main steps in the code for this biomass model are given in the appendix.

These biomass estimates and 'actual' biomass (the minimum growth on any day) were converted to crop growth rate by dividing by the number of days in a month to give 4 variables as limited by the effects described above: CGR_{light}, CGR_{lowt}, CGR_{water} and CGR_{actual}.

Pattern analysis

For each CGR variable, the CGR value from the 640 simulations were written into a table of columns (ordered from June to July) and rows (seasons and locations) and were then independently processed by cluster analysis to combine similar seasons into different 'environment types'. This type of analysis is similar to that for a stress index that was described by Muchow et al. (1996) and Chapman et al. (2000). The initial analyses here are all presented for non-irrigated conditions.

After clustering, the groups were described by averaging within each month across seasons and locations for the members of the group. These average data and their frequencies of occurrence at different locations are presented and discussed.

Results

Climatic variables

As most of the locations are close to the coast and near sea-level, it is not surprising that the seasonal temperature patterns are largely reflected in differences in latitude, from the coolest (19.4°C average) and southern location (Grafton) to the contrasting (28.3°C) Kununnra location (Table 1, Fig. 1). The latitude gradation is most clear in moving up the Southern region from Grafton to Bundaberg. In the Central region (ca. 800km north of Bundaberg), Mackay and Prosperine are slightly warmer than Bundaberg with Ayr and Ingham being warmer again. The two southern-most locations in the "wet tropics" Northern region (Tully and Innisfail) have temperature regimes that are more similar to the Central region (Mackay and Prosperpine) than to the closer regions of the Herbert (Ingham) and Burdekin (Ayr) (Table 1 and Fig. 1). Similarly, the elevated inland Tableland site of Mareeba (405 masl) is more similar to Tully or Mackay than to the warmer adjacent coastal locations of the Northern region (Cairns and Mossman). The patterns over years are relatively consistent, with months across years differing by less than 2 or 4 degrees (Fig. 1).

While there is a general increase in average rainfall moving from south to north, there are parts of the coast that experience lower or higher rainfall due to topographic features and general weather patterns associated with the Pacific Ocean (Table 1, Fig. 2). Most of the irrigation in the industry is practiced in the locations where annual rainfall is < 1100 mm. In the Burdekin, Ord and Tableland regions where rainfall is <1000mm, all crops receive irrigation. While the wet tropic locations (Table 1) are clearly distinguished in Fig. 2, in all locations the rainfall patterns are substantially more variable from year to year.

Simulated crop growth rates

These have been analysed for 3 stages that are associated with early season (leaf area index = 0.2), mid-season (LAI = 1.5) and full canopy (LAI = 6.0) growth. Generally, the expectation is that for all locations, the amount of incident radiation sets the climatic upper limit of average CGR for all months, and water supply (rainfall) sets the lower climatic limit, while in some locations, lower temperatures in winter will limit crop growth rates.

For an establishing crop with LAI of 0.2, Kununurra is the only location where water is limiting average CGR over years (Fig. 3a). This occurs in August through November as indicated by the coincidence of the "water-limited" and "actual" CGR lines at that time. In Mareeba and Central region locations, average "actual" CGR is reduced by less than than 30-40% by low temperatures in June to August. From Bundaberg south, the limiting months for

low temperature extend from May to October, and may reduce average CGR by more than 50%.

For a crop entering an exponential period of growth (LAI of 1.5), the low temperature limitations on growth remain, particularly in the southern region (Bundaberg and below) (Fig. 3b). In virtually all locations, average CGR from September to December is limited by water supply. The relative effects are least in Nambour and Murwillumbah followed by the other southern locations, the wet tropic locations and then the remaining locations. In the Ord (Kununurra) and Burdekin (Ayr) regions, water is limiting for virtually the entire year. This obvious effect is also partially due to these locations having the highest "radiation-limited" CGR in most cases.

Patterns of CGR and the limitations of low temperature are essentially the same when considering a fully established crop with an LAI of 6 (Fig. 3c). In this case, the major difference is an extension of the number of months for which water is a limiting factor, on average. In the wet tropics, water becomes limiting from August to January while in southern locations September to April is water limiting and the remaining months are temperature limiting. In all areas, the months with the fastest average CGR are Jan to Mar, but water is limiting in all months in the 3 irrigation areas (Burdekin, Tableland and Ord).

Fig. 4 shows the coefficient of variation for the CGR variables for a crop with LAI of 6. In most locations, the CV for CGRlight was less than 10%, although it tended to be higher in the months of December to April. This effect is likely to be inversely related to rainfall – higher radiation tends to be received in years when the monsoon rainfall is lower than normal. The high CV of CGR_{water} simply demonstrates that water is the dominating factor in season to season variation in CGR and that this variation is generally lower over the year in the southern locations than in other locations. The months of June and July show less variation, but rainfall is normally small at these times in any case. Apart from Proserpine, Ayr, Mareeba and Kununurra, variation in the months of February to May in locations north of Mackay is less than in the southern locations. However, for virtually all locations from Mackay north, the variation in spring and early summer (September to December) is greater than in the south. The only exception is Kununurra in August/September where the season appears to be consistently low in rainfall.

Analysis of the annual pattern of CGR across years and locations

Pattern analysis has been used to summarise the patterns of growth for the different measures of CGR (Fig. 5). Location/year combinations with a similar pattern of CGR across the year were grouped together during this process. Inspection of the amount of variance explained and the differences in the mean responses (Fig. 6), suggested the use of the 4, 3, 3 and 3 group levels for CGR_{actual}, CGR_{water}, CGR_{actual} and CGR_{light}, respectively. For each of the 4 CGR measures, Fig. 6 shows the mean responses of the respective number of groups derived from the pattern analysis.

At the 3 group level for CGR_{light}, mean CGR of one group (641) was higher than in the other groups for the months of April to September, and lower than that of the other groups in December to February. This group occurred only at Kununurra (Fig. 7). Group 665 was also distinct in having the lowest CGR_{light} during winter months and the highest values in December to February, and occurred in more than 80% of years in the southern locations, but occurred in less than 10% of years in other locations (Fig. 7). The distribution of years at locations was reversed for the remaining intermediate group, which occurred more than 80% of the time in the locations from Mackay, north (excepting Kununurra). In summary, when low temperature and water are not limiting, the seasonal patterns of growth on the east coast in the southern locations are different from those further north in >80% of years. Kununurra is different again in the pattern of CGR_{light}.

The differences among groups are more pronounced when the effect of low temperature on CGR is taken into account (Fig. 6, 8). However, the separation of the locations remains essentially the same. The CGR pattern for Kununura (group 644) is the same as for CGR_{light} and no other years from other location overlap with it. The sites south of Bundaberg are all in the same group (668) with lower CGR_{lowt} during the winter and the sites north of Mackay are in another group (669) where CGR_{lowt} is intermediate between Kununurra and the southern sites. Bundaberg and Mackay have a "complementary" overlap of years where they are either intermediate or low in terms of CGR_{lowt} during the winter months (Fig. 8).

In terms of CGR_{water}, Kununurra (group 653) is still distinctly different in seasonal pattern to any other location/year combinations (Figs. 6, 9). CGR_{water} for this group is less than 5 g/m2/d between April and November, rising to almost 10 during February. The other 2 groups occurred in all of the locations, but at different frequencies. With a value ca. 5 g/m2/d higher than the Kununurra group was group 665. The majority of years were in this group in Murwillimbah and Nambour, while in the 3 "wet tropics" locations (Tully, Innisfail, Babinda), about half of the years were in this group (Fig. 9). Ayr, Ingham and Mareeba had relatively few years in this group and a majority of years in a group (669) where the CGR_{water} was intermediate between the other 2 groups.

The results for CGR_{actual} were best summarised at a 4 group level (Fig. 5). At this level, Kununurra was again all within one group (649) with the lowest CGR all year (Figs. 6, 10), largely driven by the water-limitation at this location. The highest overall CGR_{actual} (group 666) was experienced at the "wet tropics" locations in >60% of years, and at a lesser frequency in the other east coast locations from Bundaberg north. The remaining years at the northern locations were in a group (668) that was similar to 666, but with a reduced growth during July to December, but particularly between September and December. These first 3 groups 649, 666 and 668 largely arise from the effect of CGR_{water}. The last group (667), which occurs mostly in locations south of Bundaberg shows CGR_{actual} to be depressed during June to August, mainly as a result of CGR_{lowt} (see Fig. 6), although summer growth is still depressed by lack of water.

Discussion

While there is variation across the sugar-growing region, the crop is planted in the dry season between April and October, and so is often establishing during the cooler periods of the year (Fig. 2). In the Southern and to a smaller extent, Central region, these cool temperatures limit potential CGR, as indicated by the effects on a crop with LAI of 0.2 (Fig. 3a). By October in the south and even earlier in the north, crops will have developed beyond this level. The highest CGR for these types of crops is in November to January in southern locations, but in October to December in northern locations. This is related to the onset of the wet season (and lower radiation) from about January in the northern locations.

The general pattern of CGR_{light} across the season is, not surprisingly, similar across the different stages of the crop (LAI of 0.2, 1.5 and 6.0, Fig 3abc). The magnitude of the effect of low temperature is also similar across the different LAI scenarios, although in a more complete simulation model it would be more substantial, as leaf growth would be affected as well as the radiation use efficiency (assumed in our model here).

Analyses of the frequencies with which these different patterns of CGR occur reveal that some locations consistently experience seasons of the same type, while other locations overlap each other greatly in terms of the season types being sampled. In irrigated trials, where CGR_{lowt} is an appropriate measure, there is a clear distinction in the annual CGR pattern between Kununurra, northern and southern locations (Fig. 8). Bundaberg and Mackay have a proportion of years that overlap in terms of the CGR for a full canopy, i.e. in certain

years, one might expect that genotype performance in irrigated trials would have some similarities between these two sites.

Without irrigation (i.e. CGR_{water}, Fig. 9), the overlaps among northern and southern locations are greatly increased, i.e. there are frequently years when the CGR pattern in a northern location is similar to that in a southern location in the same or different years. If these patterns are expressed in the cane and sugar yield of the trials, then they may result in confounding effects on genotype performance over years. While some of the conclusions reached from this analysis may seem quite obvious, it is the classification of environments in terms of years and locations that will help to determine whether the related field trials are appropriate samples of the TPE. This is still under investigation.

Obviously, CGR is not the only measure that determines sugar yield. However, these analyses begin to give us a picture of how the different environments vary across locations and seasons. This information on the frequencies of environments will be become part of the dataset used to explain variation in GxE in the clone trials, being conducted over the next 3 years.

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Appendix – pseudo-code

The following pseudo-code describes how monthly crop growth rate, limited by radiation, temperature and water was computed in the growth index model. Values of the constants (names defined with "c_" at the start) are given in the materials and methods.

```
!Radiation limited growth
g_frac_radn_int = 1 - exp(-c_extinction_coef * LAI)
bio_light = g_frac_radn_int * c_RUE * radn

!temperature limited growth
tavg = (maxt+mint)/2.0
tfac = linear_interp_real (tavg,x_ave_temp,y_stress_photo,5)
bio_temp = bio_light * tfac

!Waterlimited growth
g_vpd = c_svp_fract* (svp (maxt) - svp (mint))
g_transp_eff = divide (c_transp_eff_cf, g_vpd, 0.0) /g2mm

sw_avail = min(AvailSW + eff_rain * rain - yesterday_tran, sw_avail_pot)
if(sw_avail .lt. 0.0)sw_avail = 0.0

ftsw = divide(sw_avail, sw_avail_pot, 0.0)
sw_supply = max(sw_avail * kl * root_exploration, 0.0)
bio_water = sw_supply * g_transp_eff
sw_demand = divide(bio_temp, g_transp_eff, 0.0)
sw_supply_demand_ratio = divide(sw_supply, sw_demand, 0.0)

yesterday_tran = min(sw_supply, sw_demand)
print*,yesterday_tran,sw_supply, sw_demand
AvailSW = sw_avail

!      Actual bio

bio_actual = min(bio_temp, bio_water)
```

Table 1 Climate station locations and mill region allocations, together with mean and range of radiation, temperature and rainfall from 1956 to 1999.

Location (lat., long.)	Mill Region	Radiation (MJm-2d-1)	Temperature (°C)	Rainfall (mm)
(locations are in Queensland, except where otherwise stated)		Annual mean (mean for lowest and highest months)	Annual mean (mean for coolest and warmest months)	(range in annual total)
1. Grafton, New South Wales	Southern	17.4	19.4	1036
29.70S, 152.93E		(10.7-22.9)	(13.2-24.4)	(503-1948)
2. Murwillumbah, New South Wales	Southern	17.8	19.8	1663
28.34S, 153.38E		(11.3-23.1)	(14.4-24.3)	(853-3189)
3. Nambour	Southern	18.1	20.5	1754
26.62S, 152.97E		(12.1-23.2)	(15-24.8)	(984-3958)
4. Maryborough	Southern	18.4	21	1098
25.55S, 152.68E		(12.6-23)	(15.1-25.6)	(533-1913)
5. Bundaberg	Southern	18.7	21.7	1068
24.93S, 152.20E		(13-23.3)	(16.3-25.8)	(483-1754)
6. Mackay	Central	19.3	22.5	1695
21.17S, 149.12E		(14.2-24.4)	(16.9-26.6)	(739-3381)
7. Proserpine	Central	19.4	23.4	1495
20.50S, 148.53E		(14.5-24.3)	(17.9-27.3)	(699-2906)
8. Ayr	Burdekin	19.5	24.1	996
19.57S, 147.4E		(14.5-24.3)	(19.2-27.7)	(264-2354)
9. Ingham	Herbert	19	24.1	2040
18.65S, 146.17E		(14.5-23.7)	(19.3-27.7)	(998-3860)
10. Tully	Northern	18.5	23	3897
17.94S, 145.93E	(wet tropics)	(14-23.3)	(18.5-26.3)	(2160-6342)
11. Innisfail	Northern	18.4	23.6	3558
17.52S, 146.03E	(wet tropics)	(13.8-23.3)	(19.6-26.8)	(1800-5798)
12. Babinda	Northern	18.6	24.1	4338
17.34S, 145.92E	(wet tropics)	(14.1-23.4)	(20.1-27.1)	(2082-6708)
13. Mareeba	Northern	19	22.9	919
17.00S, 145.42E	(Tableland)	(14.8-23.8)	(18.7-26.1)	(375-1948)

14. Cairns	Northern	18.9	24.9	2024
16.88S, 145.75E		(14.7-23.6)	(21.3-27.6)	(986-3423)
15. Mossman	Northern	19.2	25.6	2379
16.46S, 145.38E		(15.3-23.8)	(21.9-28.2)	(1111-4677)
16. Kununurra, Western Australia	Ord	20.4	28.3	801
15.66S, 128.71E		(18.3-24.2)	(23-32.1)	(431-1532)

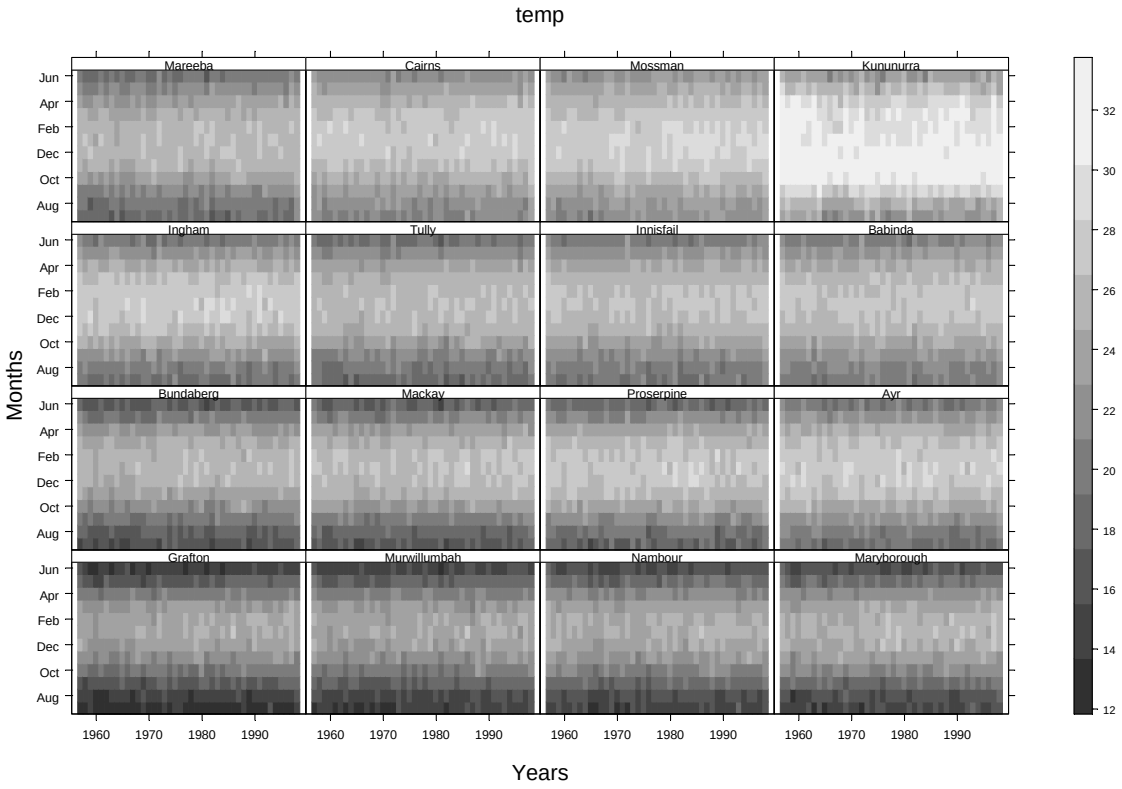


Figure 1 Variation in mean monthly temperature (°C) over years (1956 to 1999) for 16 locations across the sugar-growing regions of Australia. Locations are ordered left to right and bottom to top from Grafton (29.7°S 152.9°E) up to Mossman (16.5°S 145.5°E) along the eastern coast, and Kununura in Western Australia (16.7°S 128.9°E). Note that the months are ordered from June to July so that the time of maximum growth rates during the summer wet season is in the middle of each levelplot.

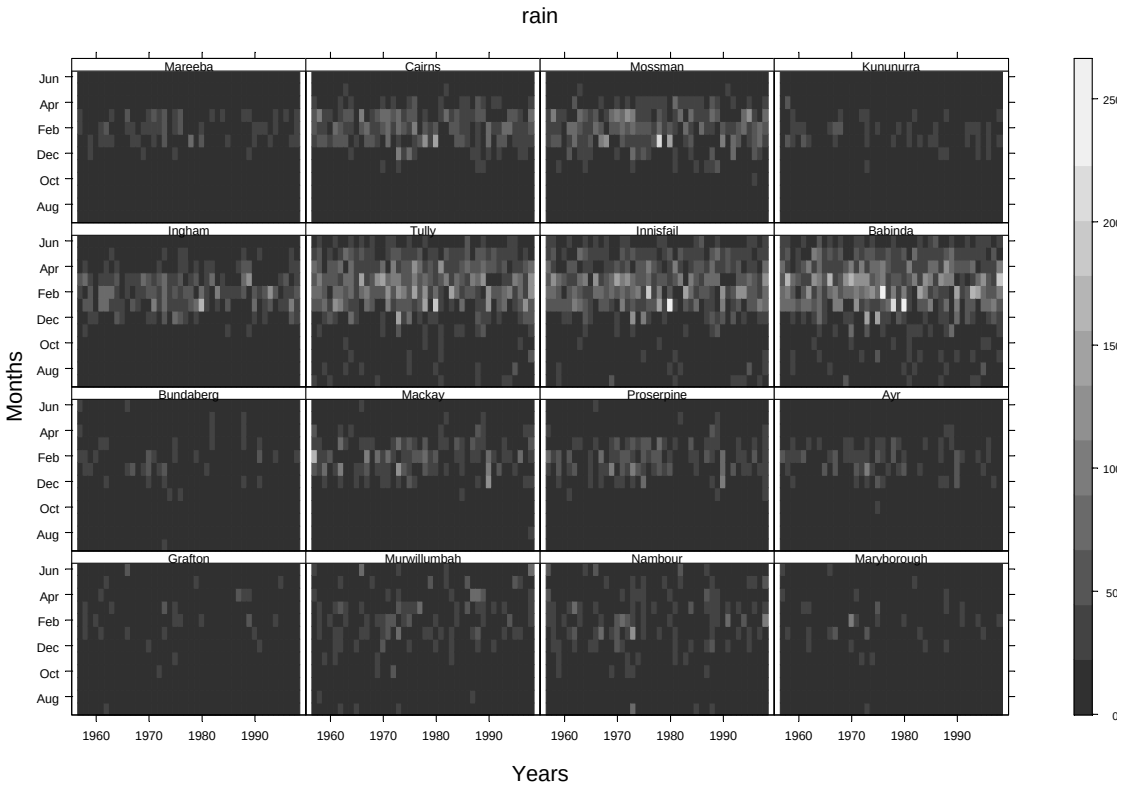


Figure 2 Variation in total monthly rainfall over years (1956 to 1999) for 16 locations across the sugar-growing regions of Australia. Locations and layout are given in Fig. 1.

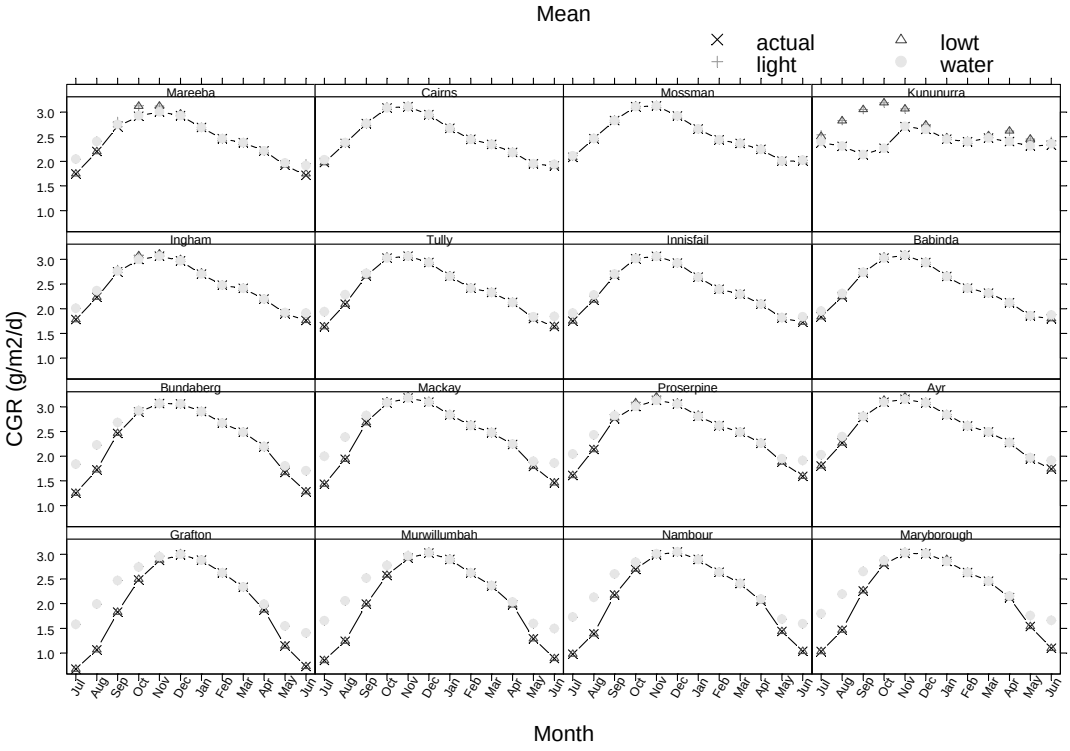


Figure 3a Mean monthly crop growth rate for 1956-1999 in 16 locations as affected by radiation (light), low temperature (lowt) or water supply and actual crop growth rate for a crop with a leaf area index of 0.2.

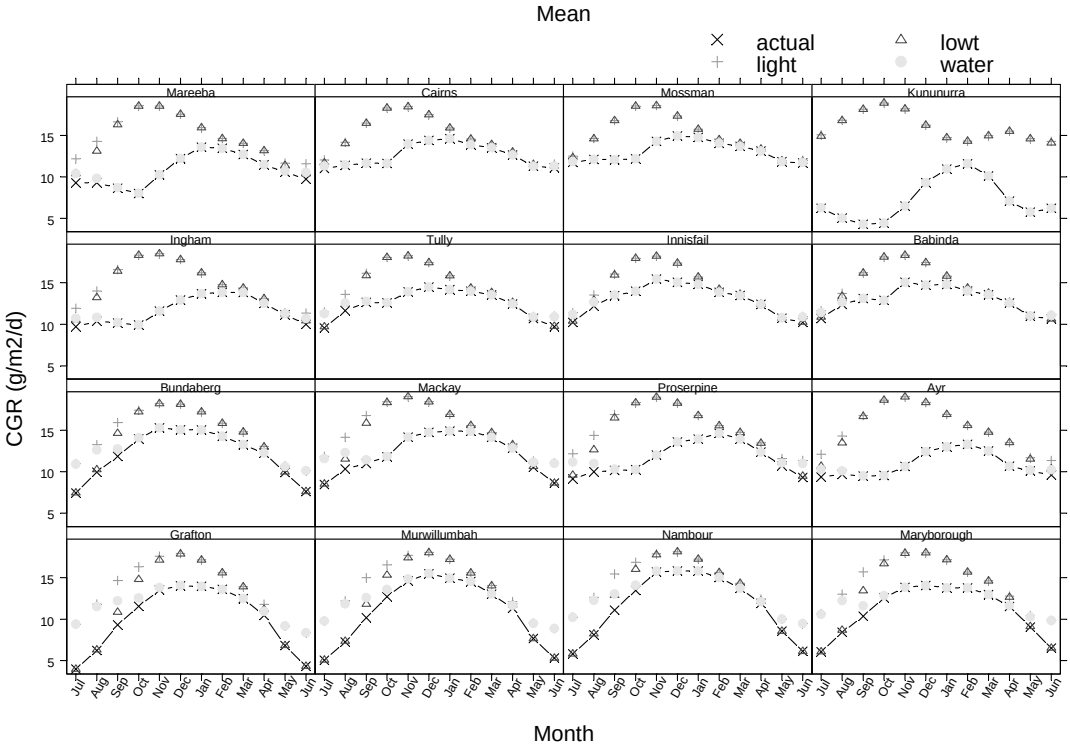


Figure 3b Mean monthly crop growth rate for 1956-1999 in 16 locations as affected by radiation (light), low temperature (lowt) or water supply and actual crop growth rate for a crop with a leaf area index of 1.5.

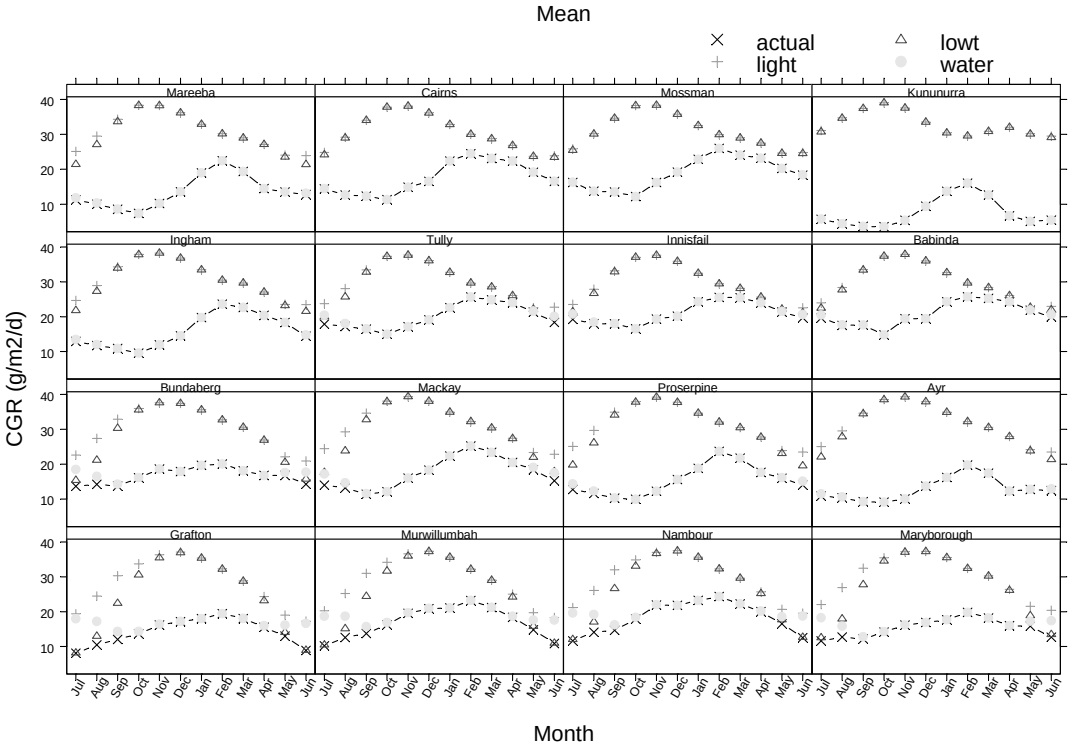


Figure 3c Mean monthly crop growth rate for 1956-1999 in 16 locations as affected by radiation (light), low temperature (lowt) or water supply and actual crop growth rate for a crop with a leaf area index of 6.0.

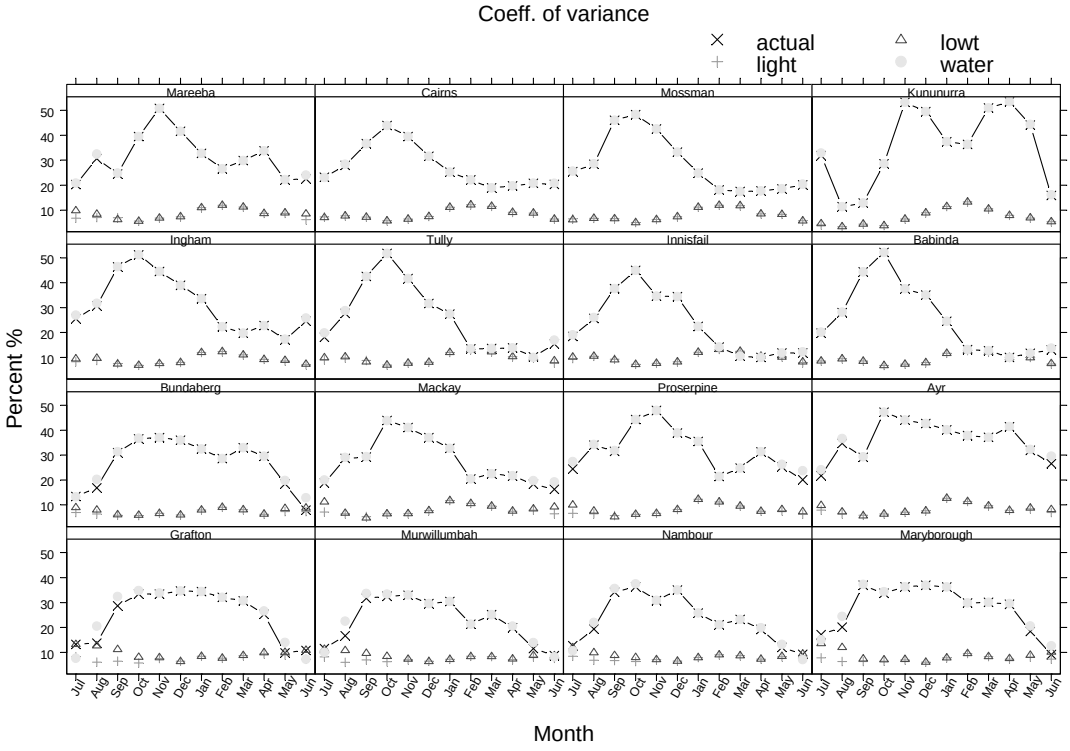


Figure 4 Coefficient of variation for monthly crop growth rate for 1956-1999 in 16 locations as affected by light, low temperature (lowt), water supply and actual crop growth rate for a crop with a leaf area index of 6.0.

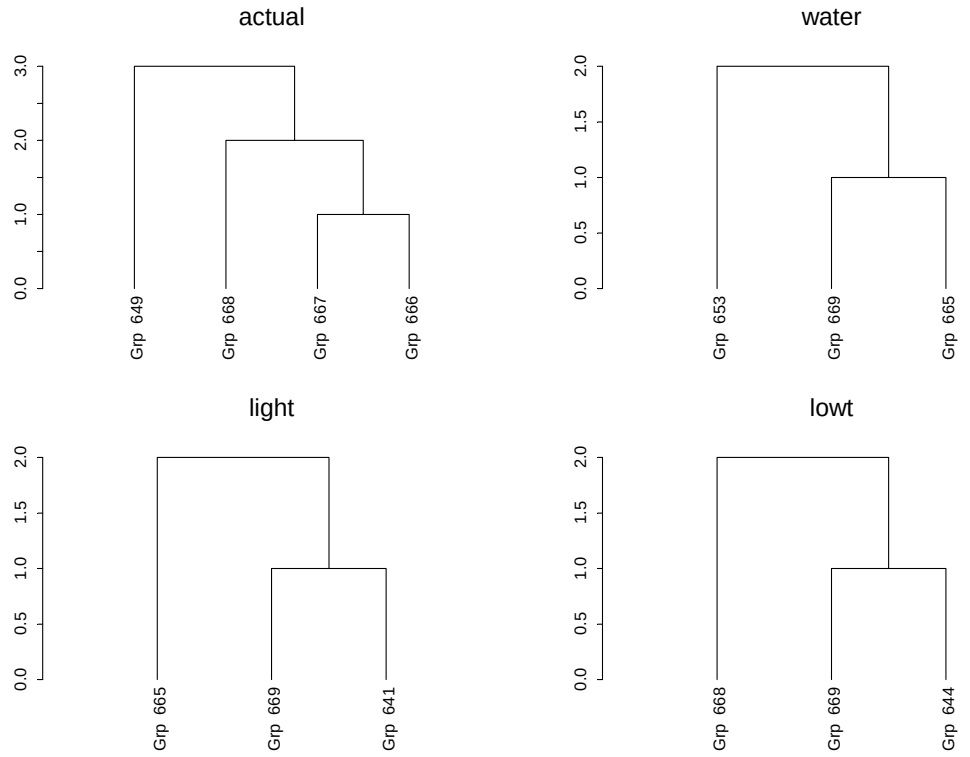


Figure 5 Dendrograms for the 4 different CGR measures based on the pattern of CGR across months. Each group consists of location/years that were most similar in the annual pattern of the monthly CGR.

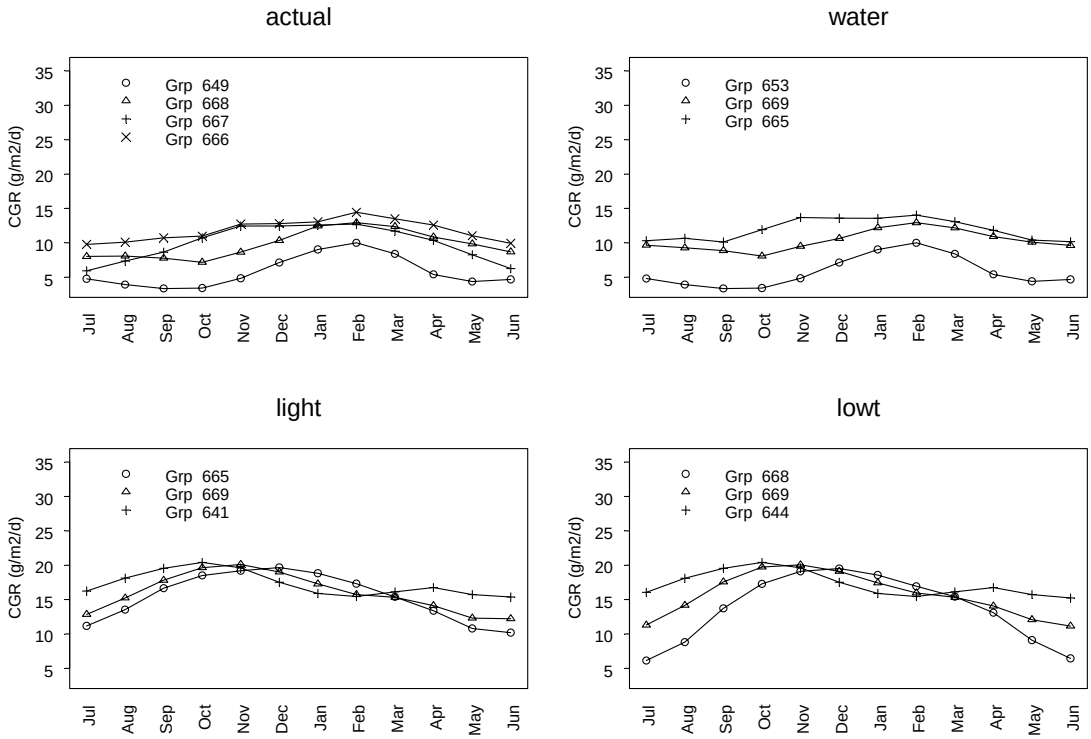


Figure 6 Values of monthly CGR averaged over the members of the each group indicated in the figures. The 4 measures of CGR are discussed in the text and in Fig. 3c and are for an LAI of 6.0.

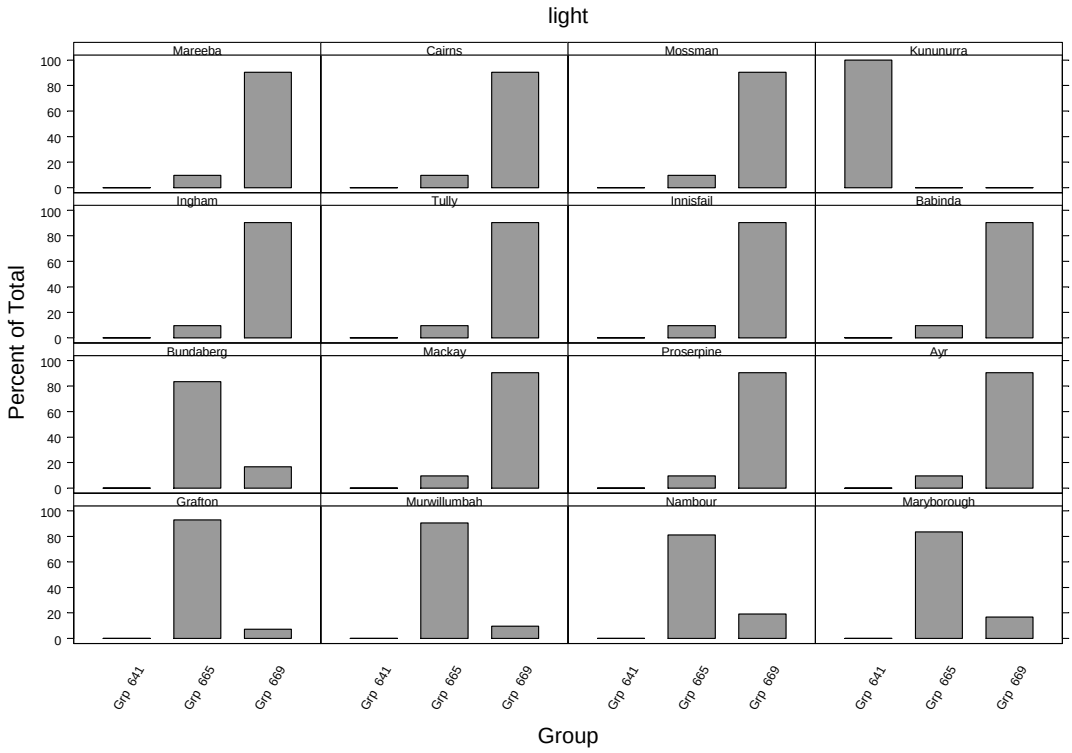


Figure 7 Frequency distribution (years within locations) of the different annual patterns of CGRlight for a crop with LAI = 6. Groupings are given in Fig. 5 and the responses are in Fig. 6.

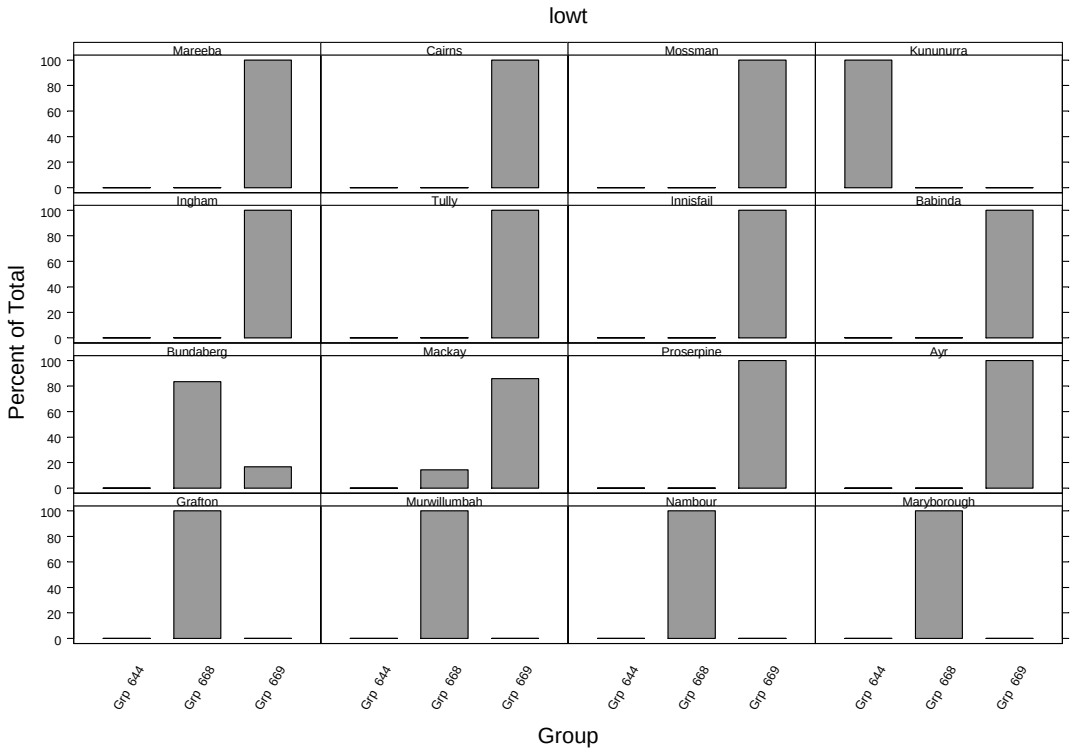


Figure 8 Frequency distribution (years within locations) of the different annual patterns of CGRlowt for a crop with LAI = 6. Groupings are given in Fig. 5 and the responses are in Fig. 6.

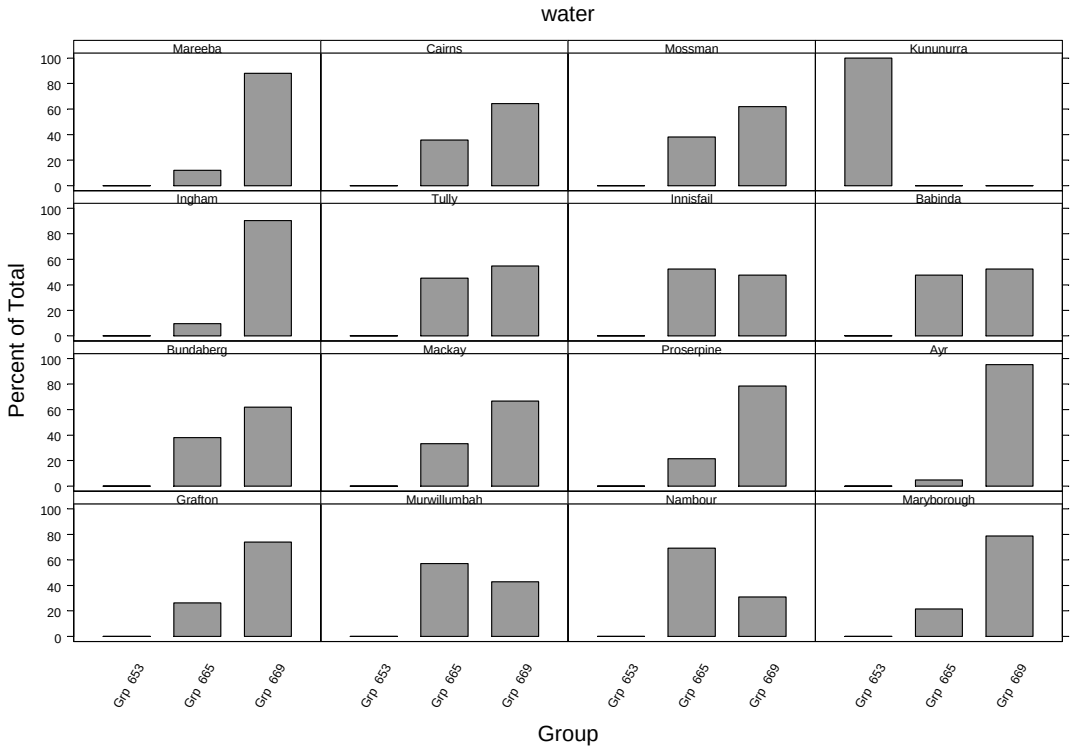


Figure 9 Frequency distribution (years within locations) of the different annual patterns of CGRwater for a crop with LAI = 6. Groupings are given in Fig. 5 and the responses are in Fig. 6.

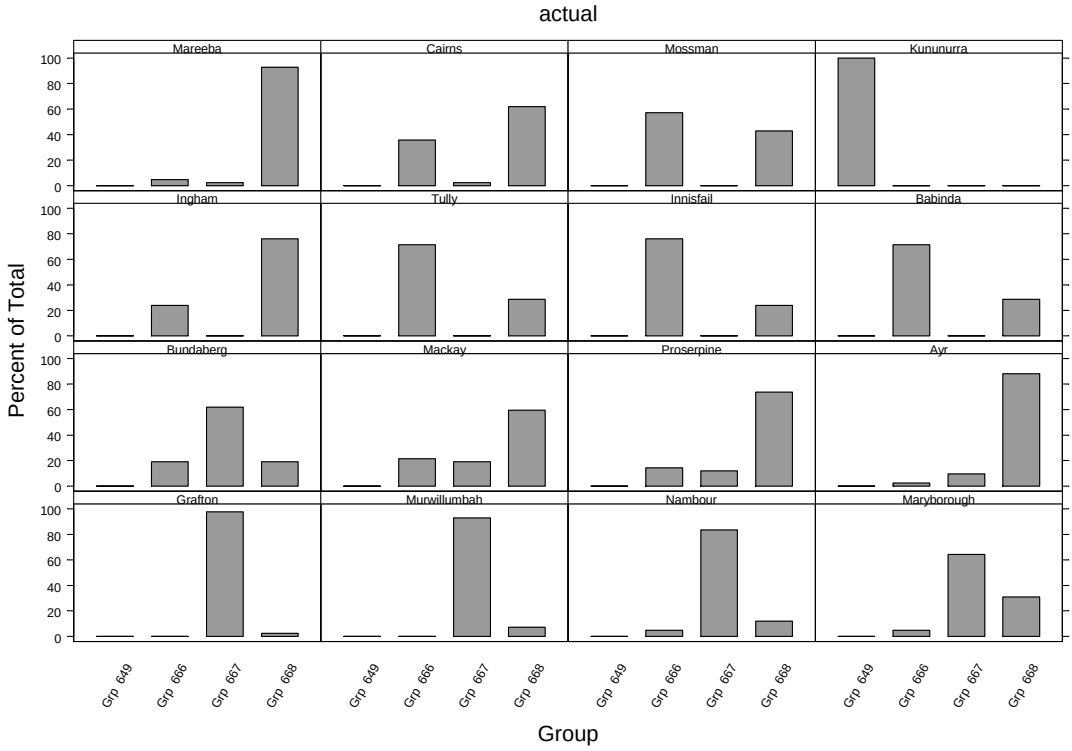


Figure 10 Frequency distribution (years within locations) of the different annual patterns of CGRactual for a crop with LAI = 6. Groupings are given in Fig. 5 and the responses are in Fig. 6.

Appendix 3. Summary of trials, clone entries and experiment methods, protocols and statistical analysis procedures

Table of contents

This appendix details the experimental methods to undertake and measure the trials (3.1), a description on work needed to apply DNA fingerprints to confirm germplasm identities (3.3) and a copy of the experimental management and measurement protocol that was followed by co-operators to ensure that trials were conducted uniformly (3.4).

3.1. Experimental methods for MegaGxE trials

3.1.1 Propagation and harvest times

All seed material was ensured to be free of ratoon stunting disease and was distributed from Macknade near Ingham. The seed material was sourced from a BSES 4-sett (family) trial, and from trial being run in SRDC project CSR11S. Stalks derived from the seedlings were initially transferred to other regions in 1997, and where required, again in 1998 and 1999. Following 1-2 years of propagation within regions to provide sufficient planting material, trials were planted between 5 May 1999 and 3 Sep 2002 and were harvested between 24 Jul 2000 and 21 Sep 2004 (Table 3-1). Stalks of commercial checks were sourced from stocks within each region. The original plan was to have done all of the experiments between 1999 and 2002. However, problems with propagation resulted in an essential extension of the experimental program (see below section on Project staffing, history and management).

3.1.2 Locations and germplasm

Twenty-four sites were harvested in plant and 1st ratoon, with 11 sites harvested in 2nd ratoon. The sites were allocated to existing region names: the North/Tully (4 trials), Herbert (4), Burdekin (4), Central (4), South (3), NSW (2), Atherton Tableland (2: N3 and N6) and Ord (1). The mean and variance of TCH and CCS for each harvest is given in Table 3-2. In a random effects analysis, all the genotypic effects for TCH were significant except for trials B3-0-2 and B3-2-4; for CCS, all were significant except B4-0-3.

Table 3-3 also shows the pedigrees and abbreviated names of the 'random' clones used in the MegaGxE study. Each random clone had been randomly chosen from a random cross in either of the existing Herbert breeding programs, run by CSR Limited and BSES. In most sites, 48 clones were planted, including four to six Q canes. Three additional random clones were planted in several Herbert trials, and, in fewer than five trials, up to six additional Q canes were planted. Propagation errors resulted in up to 5 clones being planted in a small number of trials within a region. These are not listed. The number of entries varied slightly from this in several trials and was lower in the Ord (35) due to smut-screening and S3 (36), due to propagation problems. These issues are also detailed in the section below on Project staffing, management and history.

3.1.3 Management and monitoring

Experiments were planted on grower's properties or on research land owned by either BSES Limited or CSR Limited. The trials were managed using standard within-region grower practices with regard to fertiliser, irrigation and control of weeds, insects and diseases. Cane setts were treated with fungicide to prevent sett rotting caused by *Ceratocystis* paradoxa. In Burdekin experiments, a controlled release formulation of chlorpyrifos (suSCon Blue) was incorporated to control the white larvae of *Lepidiota* and *Dermolepida* genera (cane grub). Trials in the Burdekin and Ord regions were fully irrigated (up to 7 ML ha^{-1} per season), while most trials in the Central and Southern regions received supplementary irrigation in early to mid-summer (usually <0.5 ML ha^{-1}). Diseases that did affect the trials to varying degrees, due to their endemic nature in mono-cropped cane lands include *Pachymetra chaunorhiza* (root rot), root nematodes, common and/or orange rust and yellow-spot virus. These effects were monitored by soil sampling for *Pachymetra* and nematodes and by visual scoring for foliar disease at harvest or earlier.

In all of the trials, diaries of agronomic management were kept, soil samples collected for chemical and pathological analysis and weather data were either logged or retrieved from the

nearest Bureau recording sites. Soil samples for chemical analysis were taken from 0-30cm and 30-60 cm cores (at least 6 per field, diagonally sampled), usually 4-8 weeks before planting or ratooning, but in some cases at that time. For pathology analysis, soil samples were taken between February and April in the year after planting or ratooning. Appendix 6 contains a summary of the soil chemical analysis results and a presentation on the multi-variate interpretation of these results and for environment and soil pathology variables (see below, and Outputs section).

3.1.4 Design

All experiments were row-column (latinized in the column direction) designs with two blocks in usually in the column direction (three in the Ord). Plots were 4 rows by 10m long, with observations taken only on the two central rows.

3.1.5 Measurements

In each trial, other observations were made to be later used as explanatory variables: visual percentage scores for lodging, suckering, arrowing (flowering), stool-tipping (i.e. stool lodging), stalk breakage, rat damage and existence of gaps in plots; measurement of average length, diameter and single stalk fresh weight of the stalks taken for CCS determination. Just prior to the harvest of each plot area, a sub-sample of 8 sound stalks was hand-harvested from the observation rows. The remaining stalks were machine-harvested and their fresh mass determined by a weigh-bin to estimate TCH (tonnes of fresh cane per ha). The sub-sample was processed in a BSES or CSR laboratory to estimate sucrose concentration by fresh weight (CCS = commercial cane sugar) from observations of brix, pol and fibre, according to standard protocols.

Table 3-1 For MegaGxE: locations, planting and harvest dates for plant crop (P0) and ratoons 1 and 2.

SiteCode	Region	SiteName	Latitude	Longitude	Plantdate	Plant harv	1st R harv	2nd R harv
N1	Northern	Silkwood	-17.75	146.02	01/08/2001	07/10/2002	20/10/2003	
N2	Northern	Tully BSES	-17.93	145.92	18/06/2000	20/09/2001	18/11/2002	30/10/2003
N3	Northern	Arriga (Tableland north)	-17.13	145.34	04/05/2000	14/06/2001	27/06/2002	
N4	Northern	Mulgrave	-17.09	145.79	21/05/2001	17/07/2002	23/08/2003	
N5	Northern	Babinda	-17.34	145.92	09/07/2001	06/09/2002	15/09/2003	
N6	Northern	Atherton (Tableland south)	-17.27	145.48	25/05/2000	29/08/2001	07/10/2002	
H1	Herbert	Ingham BSES	-18.65	146.16	29/06/1999	31/08/2000	06/09/2001	
H2	Herbert	Abergowrie CSR	-18.44	145.92	24/06/1999	07/08/2000	17/09/2001	12/11/2002
H3	Herbert	Mutarnee BSES	-18.95	146.29	01/06/2000	14/06/2001	22/08/2002	18/08/2003
H4	Herbert	Macknade CSR	-18.54	146.25	06/07/2000	17/09/2001	04/11/2002	29/09/2003
B1	Burdekin	Ayrville	-19.55	147.35	05/05/1999	26/07/2000	19/07/2001	08/08/2002
B2	Burdekin	Kalamia CSR	-19.52	147.42	07/05/1999	24/07/2000	17/07/2001	
B3	Burdekin	Brandon BSES	-19.55	147.35	18/05/2001	17/06/2002	12/06/2003	7/06/2004
B4	Burdekin	Clare	-19.78	147.23	04/04/2002	08/09/2003	21/09/2004	
C1	Central	Racecourse (Baker's Creek)	-21.21	149.16	09/06/1999	19/09/2000	26/09/2001	01/10/2002
C2	Central	Proserpine	-20.4	148.58	25/08/1999	14/09/2000	29/08/2001	
C3	Central	Marian	-21.15	148.94	11/08/2000	04/09/2001	10/10/2002	24/10/2003
C4	Central	Plane Creek	-21.42	149.17	24/08/2000	10/10/2001	01/10/2002	15/10/2003
S1	Southern	Bundaberg	-24.87	152.35	08/09/1999	07/09/2000	13/09/2001	08/09/2002
S3	Southern	Maryborough	-25.54	152.7	30/08/2000	01/11/2001	31/10/2002	27/11/2003
S4	Southern	Isis	-25.18	152.45	03/09/2002	23/07/2003	3/08/2004	
W1	NSW	Condong	-28.32	153.43	16/09/1999	03/08/2000	15/10/2001	
W2	NSW	Harwood	-29.42	153.24	22/10/1999	17/08/2001	13/10/2002	
O1	Ord	Ord1	-15.77	128.74	31/05/2001	10/07/2002	15/09/2003	

Table 3-2 MegaGxE: Summary of trial TCH and CCS values for 59 environments (harvest/site combinations) using a total of 105 clones. Trial Code: 1st two letters = sitecode (appendix 3); 3rd symbol = crop (0=plant, 1= 1st ratoon, 2= 2nd ratoon); 4th indicates year of harvest (0=2000, 1=2001, etc). In a random effects analysis, all the genotypic effects for TCH were significant except for trials B3-0-2 and B3-2-4; for CCS, all were significant except B4-0-3.

Harvests	nrow	Ncol	nclones	TCH	nmissing	CCS	nmissing	TCHvar	CCSvar
B1-0-0	16	6	47	130.38	0	12.46	0	433.02	2.65
B1-1-1	16	6	47	140.78	0	14.64	0	463.45	0.98
B1-2-2	16	6	47	114.77	0	13.65	0	262.24	1.82
B2-0-0	18	6	53	163.87	0	11.97	0	442.58	1.46
B2-1-1	18	6	53	117.14	0	13.69	0	221.82	0.88
B3-0-2	12	8	47	123.08	0	11.26	0	331.06	1.83
B3-1-3	12	8	47	111.77	0	10.02	0	279.53	3.76
B3-2-4	12	8	47	119.8	1	11.23	1	384.94	2.78
B4-0-3	10	9	44	156.86	0	14.17	0	472.99	1.40
B4-1-4	10	9	44	104.58	0	16.76	0	161.81	0.37
C1-0-0	16	6	48	89.23	0	16.17	0	244.22	1.49
C1-1-1	16	6	48	68.36	0	16.03	0	125.33	0.88
C1-2-2	16	6	48	73.26	0	15.67	0	114.50	0.94
C2-0-0	16	6	48	64.48	0	16.66	0	271.95	0.87
C2-1-1	16	6	48	54.77	0	16.33	0	209.07	0.55
C3-0-1	16	6	48	59.79	0	14.61	0	204.58	1.03
C3-1-2	16	6	48	93.75	0	15.2	1	227.45	0.91
C3-2-3	16	6	48	83.29	0	14.13	0	147.75	1.50
C4-0-1	16	6	48	68.43	1	16.89	1	129.67	0.55
C4-1-2	16	6	48	33.98	0	15.97	0	48.50	0.96
C4-2-3	16	6	48	58.73	0	16.12	1	78.53	0.77
H1-0-0	16	7	56	58.14	0	15.13	0	187.67	0.69
H1-1-1	16	7	56	47.65	0	15.76	0	183.64	0.76
H2-0-0	16	7	55	75.16	0	12.8	0	178.01	1.02
H2-1-1	16	7	55	93.45	0	13.64	0	287.08	1.27
H2-2-2	16	7	55	83.75	0	16.14	0	240.53	1.13
H3-0-1	28	4	56	101.66	2	15.14	2	218.28	1.22
H3-1-2	28	4	57	59.09	0	14.93	0	115.44	1.66
H3-2-3	28	4	57	23.3	0	14.84	3	24.62	0.81
H4-0-1	12	8	48	70.68	2	16.7	0	165.02	0.52
H4-1-2	12	8	48	89.81	2	16.38	2	194.96	0.61
H4-2-3	12	8	48	73.8	0	14.27	0	170.37	0.88
N1-0-2	24	4	48	82.45	0	15.88	0	286.61	1.01
N1-1-3	24	4	48	80.76	0	13.92	1	241.14	2.09
N2-0-1	16	6	48	65.05	0	16.26	1	235.14	0.87
N2-1-2	16	6	48	114.57	0	15.47	2	489.99	1.45
N2-2-3	16	6	48	74.4	0	15.67	0	279.15	1.11
N3-0-1	24	4	48	118.8	0	12.72	0	328.00	0.95
N3-1-2	24	4	48	125.78	0	13.32	0	404.06	1.56
N4-0-2	24	4	48	76.07	0	14.53	0	131.72	1.95
N4-1-3	24	4	48	72.67	0	14.65	0	200.33	1.41
N5-0-2	16	6	48	99.32	0	14.69	0	211.92	1.17
N5-1-3	16	6	48	112.24	0	13.79	1	359.41	1.25
N6-0-1	16	6	48	65.81	0	15.05	0	139.73	1.32
N6-1-2	16	6	48	72.43	0	15.63	0	230.93	0.81
O1-0-2	15	7	33	147.68	0	10.34	1	339.53	2.95

Harvests	nrow	Ncol	nclones	TCH	nmissing	CCS	nmissing	TCHvar	CCSvar
O1-1-3	15	7	33	109.82	0	12.07	5	340.16	1.77
S1-0-0	16	6	48	85.6	0	14.08	0	190.70	1.05
S1-1-1	16	6	48	99.52	0	15	0	263.58	0.81
S1-2-2	16	6	48	68.37	0	14.23	0	211.28	0.83
S3-0-1	18	4	36	81.74	0	14.85	0	134.63	0.69
S3-1-2	18	4	36	66.93	0	15.96	0	145.30	0.67
S3-2-3	18	4	36	64.09	1	15.23	2	157.20	0.68
S4-0-3	14	6	42	51.96	0	10.47	0	432.72	1.04
S4-1-4	14	6	42	46.58	0	14.43	0	163.72	0.75
W1-0-0	12	8	48	82.69	0	8.3	0	234.01	1.49
W1-1-1	12	8	48	112.17	0	13.47	0	247.09	0.74
W2-0-1	16	6	48	121.98	1	13.61	0	1041.78	0.59
W2-1-2	16	6	48	154.82	2	11.16	0	804.13	0.87

Table 3-3 MegaGxE: Pedigree of random clones and commercial checks used in the MegaGxE dataset and number of times harvested. 'Q' canes are commercially released while the other clones were randomly selected from random crosses (one clone per cross) in either the CSR Limited or BSES Limited (95H) breeding programs.

Clone	Female parent	Male parent	ntrialsnharvests
84-608-3	MQ67-494		57
84-608-6	MQ67-494		44
86-1151-3	H56-752	66C760	52
87-105-10	MQ55-2160	POLYCROSS	38
88-271-6	MQ73-584	H49-3666	54
89-393-3	MQ80-968	POLYCROSS	53
89-503-10	PELORUS	MQ79-1123	51
89-680-6	CENTAUR	MQ77-281	57
90-110-1	TS68-830	MQ79-141	38
90-110-9	TS68-830	MQ79-141	48
90-77-2	CP70-1547	TS64-375	55
90-83-5	MQ68-203	MQ79-212	39
95H4001	78A383	90N6006	60
95H4003	88B71	83N947	55
95H4004	ARRIS	85N511	60
95H4005	73C214	87S7427	43
95H4006	75C87	75C553	45
95H4007	83C623	86A3050	57
95H4008	83C627	79N96	52
95H4010	F177	Q135	68
95H4012	H52-663	Q161	51
95H4018	Q179[A]	CP74-2005	57
95H4020	80N1042	77N405	57
95H4021	80N4350	MQ75-1000	41
95H4022	80N4422	74C82	55
95H4023	81N289	77N676	53
95H4024	82N300	73C214	50
95H4027	84N4500	78F1025	57
95H4028	85N774	88B78	49
95H4029	85N799	84C275	41
95H4030	85N2169	79N587	55
95H4032	86N1833	83N976	49

95H4033	88N5000	79N1283	31
95H4035	Q96	85N2522	41
95H4037	Q115	82N238	49
95H4038	Q117	MEX59-1828	54
95H4039	Q120	VMC67-315	47
95H4040	Q125	Q165 [A]	57
95H4044	Q138	F168	55
95H4046	Q160	71C413	57
95H4047	R573	85N1647	47
95H4048	81S1049	Q170 [A]	60
Q117	Q77	58N829	60
Q124	NCO310	54N7096	60
Q135	NCO310	54N7096	60
Q138	58N829	66N2008	60
Q141	NCO310	54N7096	46
Q165	Q117	CP33-372	46

3.2. Statistical Analysis methodology

The historical climatic analysis is reported separately in Appendix 2 and here is presented a description of the data processing, checking and analysis that was done on the CTA028 trials. As results were returned for each year of harvests, data were checked and genetic parameters (variance components and phenotypic and genetic correlations) were derived and compared between regions. It was this analysis that alerted the propagation problems that were encountered in the Burdekin B1 and B2 trials.

3.2.1 Data checking and calculation of covariates

Genotype names were updated, particularly for B1 and B2 on the basis of the molecular marker analysis. Trials were coded to allow comparison of trials at different levels (region, location, crop class) and clones to allow separation of random clones and checks. For each trial and trait, the trials have been processed individually to identify outliers and replace these with missing values as appropriate. Summaries by trial, genotype etc were produced.

For every trial, environment data were collated for potential use as covariates (see Appendix 6). These environment data covered 4 classes of information:

- location covariates (comprising a matrix of soil chemical analyses taken in the plant crop plus latitude, longitude, elevation of the location)
- environment covariates (comprising for each trial, plant, harvest dates (and months), and summaries of observed weather data, irrigation and fertiliser application)
- soil pathology covariates (comprising the results of soil tests for *Pachymetra spp.* and soil nematodes)
- trial observations (trial means of all observed variables)

For the location covariates, soil chemical analyses were averaged over the 0-30 and 30-60cm samples. Data were also averaged over plant and ratoon crops. Results for elements that are substantial components of applied fertilisers were not utilised.

The ‘environment’ weather data were averaged for the period plant/ratoon to harvest, and also over 3 periods between those times:

1. plant/ratoon to Nov 15 (establishment)
2. Nov 15 to Mar 15 (major growth period)

3. Mar 15 to harvest (‘maturation’ period)

Soil pathology results (counts of infecting species per unit mass of soil) were expressed either for each location and crop class or averaged over locations. Because they were count data, some of the trial observations (scores of disease or plants subject to stool tipping etc) were log transformed to normalise them.

3.2.2 Analyses of individual trials

For each trial, tch, ccs and tsh were analysed using both the design model and a spatial model. i.e. in the design model, random effects were fitted according to the Row/Column trial design (Rep + Column:Rep + Row:Rep) and in the spatial model, only Rep was fitted as a random effect, while Row and Column were both fitted as autoregressive residual effects. The genotypes were fitted as either random (BLUPs) or fixed (BLUEs) effects for later use in other analyses. Genotypes were fitted first as fixed? effects and the parameters for the other random effects and the residual effects were set to not change while the genotypes were re-fitted as random. More details are given in the results (Appendix 4). For other traits, the trial design model with Genotypes random or fixed was used.

Variance components were estimated for genotypes and the other random design effects, and an approximate error mean square (i.e. derived from the mixed model) was used to compute the trial mean heritability. The variance components for genotype and residual are then able to be used to estimate response to selection on an individual trial basis.

Summaries were made of the variance components against trial mean and region to determine if there were any consistent patterns in the size of single trial genotypic or residual variance.

Changes in ranking of clones based on the different analyses were also examined.

3.2.3 Estimation of interaction variance components

Variance components and standard errors were estimated for all traits, with focus on TCH, CCS and TSH for the random effects of genotype and interactions with either trial (E=environment) or with the location (L), crop class (Cc i.e. plant or ratoon 1, 2) and location x crop class effects. These analyses were repeated using region and trial within region as interaction effects to determine the magnitude of region effects. i.e. the 4 GxE models can be described as fitting the following random treatment effects

Model 1: G + GxE

Model 2: G + GxCc + GxL + GxLxCc

Model 3: G + GxR + Rx(GxE)

Model 4: G + GxR + Rx(GxL) + Rx(GxCc) + Rx(GxLxCc)

In models 3 and 4, the interaction effects from models 1 and 2 are averaged over regions and a separate genotype by region effect is fitted to determine how large this effect is relative to the effect of genotype by environment (location and/or crop class) within region.

Given that the analysis of individual trials did not show a great difference between the design model or the spatial AR1 model, the GxE models above were fitted with (Rep + Column:Rep + Row:Rep and residual effects) at each trial, i.e. a heterogenous model was used to fit trials. This avoids the assumption that errors are homogeneous across trials, which they clearly are not when compared across such a large dataset (see results from individual trial analyses).

In each GxE model, environments were regarded as fixed effects, as were regions, locations or crop years, when fitted. Check genotypes and ones that had been identified as errors by the DNA analysis (see Appendix 3), were also fitted as fixed effects for the final estimates of variance components.

Other breakdowns of the variance components were also examined, e.g. irrigated vs non-irrigated, high vs low yielding etc. and are discussed in the results. These took the form of Model 3 with the Region effect being replaced by an alternative classification. In the individual trial analyses, strong relationships had been found between mean trial TCH, CCS or TSH and their respective genotypic or residual variance components (see results). Therefore, the trials were split into several groups based on the level of TCH, CCS or TSH and the between and within group variance components were estimated.

These analyses produced variance components for genotype and genotype by environment interactions, given several types of classifications of environments (regions, trial mean etc) and were summarised in tables. Ratios of GxE/G were calculated and compared across traits and regions.

3.2.4 Estimation of other genetic parameters

Phenotypic (r_p) and genotypic (r_g) correlations were calculated for all combinations of trials, and between regions. Genotypic correlations are phenotypic correlations that have been weighted by the precision of the two trials (or regions) being compared, and provide a better picture of the future expected relationship between them. The phenotypic correlations between each pair of environments were calculated using all of the genotypes that were grown in each pair. The genotypic correlations for each pair of environments were estimated by dividing the phenotypic correlation by the product of the square roots of the repeatabilities of the environments, i.e. for a single pair of environments (1 and 2):

$r_{g1,2} = r_{p1,2}/(H_1.H_2)$

where H = sqrt(Vg/(Vg + Vems/nr)); Vg = estimate of genotypic variance; Vems = estimate of trial residual variance; nr = number of replicates (= 2).

The matrices for r_p and r_g were then averaged over regions, to determine whether the average relationships among trials were the same between and within regions.

The correlation matrices were also determined directly from BLUPs that had been computed for a matrix of genotype by region effects using models 3 or 4.

Using the variance component estimates for each region, and the average residual trial errors for each region, repeatability was computed for both traits and each region. This gives an indication of the number of locations and years required to have a certain degree of confidence in estimates of clone performance. Graphs of various combinations of locations, years and replicates were used to summarise expected repeatability (H^2) within regions given:

$H^2 = Vg/(Vg + Vge/ne + Vems/(ne*nr))$ or

$H^2 = Vg/(Vg + Vgl/nl + Vgc/nc + Vglc/(nl*nc) + Vems/(nl*nc*nr))$

where Vge = variance component for genotype x environment interaction ; ne = number of environments; l = location ; c = crop class etc. and nl = number of locations, nc = number of crop classes.

Other methodological details are given in other appendices on trial results (Appendices 4 and 11) or analyses of other sets of trial data (Appendices 12 and 13).

3.2.5 Multi-variate analyses

Multi-variate methods are useful to reduce the dimensionality in such large datasets to try to reveal underlying patterns. These were applied in two ways in this project:

1. interpretation of relationships among locations (or harvests or regions) based on observed performance data.

2. identification of suitable environment covariates to be used in further analysis of variance components

Relationships in trial performance data

Principal component analyses (PCA), and biplots derived from it, are a useful way to summarise relationships among environments (and genotypes) in terms of their effects on relative adaptation of a set of genotypes. However, PCA requires balanced data, and the data from our experiments were somewhat imbalanced by the propagation problems and some constraints on the number of entries used at several sites (Ord and S1 in particular). Hence, standard PCA could only be applied using a subset of the entries grown. The matrix of genotype by environment BLUPs was standardised within columns (environments) prior to applying PCA. This ensures that the angles between vectors on the bi-plot therefore represent the degree of correlation between each vector.

To enable more complete comparison of environments, PCA was also conducted using the correlation (r_p) matrix instead of the raw data. This results in a plot of loadings that can be used to compare environments, although the genotypes do not appear as scores on the plot as they would in a traditional bi-plot. These analyses were filtered and presented to look for any patterns in region, location and/or crop class effects.

Relationships in Environment data

Principal components analysis and biplots were also used to visualise the relationships among environments or locations (rows) for potential covariates (columns) using the matrices described above in section 3.2.1. Further details and results are given in Appendix 6. Because many potential environmental covariates are likely to be correlated with each other, the biplots can be used to choose covariates that appear to explain much of the environmental differences among trials. For each matrix, the observations were first standardised within columns. The biplots drawn from these PCAs were used to choose a small number of variable combinations (i.e. 2 to 3 soil chemical properties) that best summarised the representation of all of the locations or harvests, i.e. variables were chosen such that they represented the range of loadings observed across the matrix.

3.2.6 Fixed factor analyses

The environment or location variables that were chosen in the biplot analyses described above were then were evaluated as fixed effect covariates using the same statistical models for genotype by environment interaction analyses. The covariates were entered into the model as a fixed effect of Genotype x Covariate. A Wald test was used to determine of this was a significant effect. The extent to which any of the random effects relating to genotype by environment interaction (location, region, crop class) was decreased by the use of a covariate was an indicator of whether the covariate was explaining any of the genotype by environment interactions.

3.3. MegaGxE: Notes on propagation issues and germplasm fingerprinting

In such a large sugarcane experiment over this many locations, with distribution of large quantities of seed material (stalks), there is the possibility of error during propagation and planting of trials. During an early stage of analysis, we noticed poor correlations between the first Burdekin trials and the other locations. With the assistance of Lynne McIntyre (CSIRO), two microsatellite DNA probes (mSSCIR19 and SMS21SA) from the International Sugarcane Microsatellite Consortium (Cordeiro et al 2000) were used to screen DNA extracted from leaf material of all clones at sites B1 and B2, and from clones grown in the first trial within each region. As sugarcane is a polyploid, each microsatellite marker generates a large number of allelic bands that can be used to fingerprint clones. The markers indicated that errors apparently occurred during propagation in the Burdekin,

such that 20 clones in the B1 and B2 locations could not be correctly identified as being part of the core set. Any errors found in other regions (there were 7 in Central and Southern trials) were checked further by screening the same clones from other trials in the region. In most cases, the errors had occurred during propagation and so the errors were also ‘propagated’ through the region. Any genotypes that were found to be incorrect were assigned a new name to distinguish them from all others in the dataset. These ‘unknown’ clones are not listed in

Table 3-3. In the two worst cases (B1 and B2), the number of random clones was as low as 24, while in almost all other trials, there were at least 40 random clones from the original set, plus the additional checks. When computing correlations and relationships among the B1 and B2 trials, the ‘unknown’ clones are kept in the dataset, as they are still effectively to be random selections from the nursery block, but they are dropped from cross-regional analyses as they were not grown elsewhere.

Reference

Cordeiro, G.M., Taylor, G.O. and Henry, R.J. 2000. Characerisation of microsatellite markers from sugarcane (Saccharum sp.), a highly polyploid species. Plant Science. 155: 161-168.

3.4. Experiment protocol distributed to cooperators

Note that these protocols were prepared in 1999 and updated several times during the project. They encompass the 'best practice' expectations of our cooperators. Not all of the data were able to be collected on all of the trials. The results and output sections describe where we succeeded or otherwise in obtaining various data.

3.4.1 Summary notes

1. **Mike Cox** (mcox@bses.org.au, 07-4159-3228) is main contact regarding the selection of clones and implementation of appropriate experimental design and trial management. **Bill Messer/Scott Chapman** (@tag.csiro.au, 0419-741 398, 07-3214-2254) are main contacts for protocols regarding soil sampling, datalogging and extra measurements to be taken in these trials.
2. This document is not complete. Still need some discussions about observations etc.
3. The primary concern in these trials is to plant as many clones as possible in each trial and to adopt **uniform** methods of experimental design and characterising sites, soils, weather and crop growth. This is crucial if the aims of the project are to be met. Trials should be It is important that we make as many common observations on the clones as practical, to improve the value of the dataset.
4. Important dates during season:
    - 4-6 weeks before planting. Take soil samples to **60cm** according to the protocol here, which is slightly modified from the standard 'fertility test'. The sampling of both surface (0-30cm) and sub-surface (30-60) is crucial based on previous results in the Herbert.
    - Planting. Ensure that appropriate **design** is used and that the soil N and water **cores** are taken. Install temperature **loggers**, rain gauges and crop log books.
    - **Early in next calendar year**. Download temperature loggers, stalk counts and visual evaluation of clones for canopy health, general value etc. Stalk counts should not be done until canopy has fully developed and most small tillers etc. have died off and crop has ca. 1m of millable stalk.
    - **February each year** – take pathogen samples and biomass harvest of Q124 according to protocol.
    - In **one trial** per region, take **early CCS** samples
    - At harvest, score for canopy health, value etc. Take **random** 8 stalk sample and weigh it so that stalk weight and count (from bin weight) can be estimated.
    - After harvest, take another set of soil **cores** and **replace** dataloggers.

3.4.2 Staffing and field responsibilities

Mike Cox (MC) will provide advice on generating experimental designs using CYCGEN program, where needed. Scott Chapman (SCC) and BM will design a master spreadsheet with all trial details, and a template spreadsheet to collate all of the data collected from each trial. These will be used as the basis for the entering of environment and soil data into the SugarBag database so that it can be used to generate input files for the APSIM-Sugar simulation model. Yield and other field data need not necessarily be entered into SugarBag, but will be collated in a form suitable for variance and pattern analysis.

Bill Messer (BM) will be the coordinator of data collection for all trials. BM will be maintaining files of all information relating to the environment and soil descriptions and eventually the yield results of the trials. Field technical staff refers to BSES/CSR staff with day-to-day responsibility for managing trials and collecting standard harvest data.

Collation/collection of soil data

1. Fertility/Pathology tests – field technical staff (BSES/CSR) who will be responsible for the planting and harvesting of trials. These tests have to be the same across all trials. To do this, we'll need to supply all subsamples to BM in Townsville (see below). They will be processed either by Incitec or another lab to comply with minimum data set specifications.
2. Soil cores. Start/end status for water/N – requires approx. 0.5d/trial/year with 1 casual + travelling time. Nominated staff (Bill Messer in Townsville for Central/Northern/Herbert/Burdekin trials; BSES technician based in Bundaberg for Southern trials). All samples to be delivered to BM in Townsville. In southern sites, samples to be dried and ground before delivery to BM. Processing site for N is yet to be determined, but will probably be CSIRO Land and Water lab at Townsville.

Collection of meteorological Data (inc. loggers)/crop logbooks

1. Weather stations and logbooks to be 'assembled' in CSIRO Brisbane/Townsville and distributed by BM in north and BSES technician in Bundaberg for installation in the field. Install these at the same time as the soil cores or at planting, whichever is earlier. Requires 2d/trial/year to install/check loggers and logbooks for rainfall.
2. Dataloggers to be swapped every 6-10 months (not known yet if 6 months is long enough) and to be coordinated by BM. Approx. 1-2 weeks/year managing data by coordinator.

Collation of trial plant data – Bill Messer

1. To be collected by field technical staff responsible for the planting and harvesting of trials. When data has been collected and checked, it should be supplied to BM. Pathologists/breeders expected to be consulted where input required regarding pest incidence/scores. Input required is during time of harvesting (2d/trial/year) and for a stalk count/pest scoring in Jan/Mar of each year (2d/trial/year).
2. To be collated by BM into separate spreadsheets for each trial.

3.4.3 Overall design

The data recording practices for these trials will based on those applied by the CRC in determining the minimum dataset for collection of crop performance (see reference below). While we will not be conducting hand sampling (as prescribed by the CRC), it is extremely important that we collect as much environment, soil and experiment information as possible to explain GxE interactions. There are two objectives in collecting the additional environmental information: 1. To be used as

explanatory data, per se, in explaining GxE and 2. To run the APSIM-sugar simulation model and generation additional explanatory variables to interpret GxE. In keeping with the CRC database model, the environmental data for each trial will be stored in the SugarBag database (but in Excel files first). However, the experiment results will be stored in a separate dedicated database for the project.

Reference

D.K. Mazzucchelli, M.F. Spillman and R.C. Muchow, March 1997, "Minimum Dataset Manual for the collection of Crop, soil and Climate data in Sugarcane", CRC for Sustainable Sugar Production.

Table 3-4 Approximate time schedule for activities in each trial

Step	Time	Activity	Responsibility	time input
1	2-3 months prior to planting	site selection	field tech staff (FTS)	?
2	4-6 wks prior to planting	fertility/pathology tests	field tech staff. Samples delivered to BM	0.5d FTS, 0.5d BM
3	4-6 wks prior to planting	met station and crop log book preparation	BM to initialise temperature logger and prepare for installation	0.2d BM
4	1-4 wks prior to planting	field trial design and layout generated	Mike Cox to use same method of design for each trial and distribute design to field staff and copy to BM	0.1d BM
4	1-2 wks prior to planting (or up to 2 weeks after)	soil residue samples and soil cores to 1.8m	BM/field tech staff	0.5 to 1d BM and FTS
5	At time of coring or planting (whichever is earlier)	install met station and crop log book	BM/field tech staff	0.1d BM
6	planting	cut propagation material and plant trial	field staff	1d FTS
7	planting to end of year	- check trial at least twice - score plant establishment - check and copy log books/rainfall records	field staff	1d FTS
8	Jan to April when millable stalks are at	- replace/exchange dataloggers	field staff/BM	1d FTS, 1d BM

Step	Time	Activity	Responsibility	time input
	least 1m, and canopy development relatively complete	- take soil pathology samples (FEB) - check and copy log books/rainfall records - stalk count (5m x 2 rows) - scores for disease, pest incidence and visual appearance for cane yield - 10 stalk sample from outer row of 4 plots (2 reps of Q124)		
9	April/early May	4 stalk sample for early CCS in one trial per region	field staff	1d FTS?
10	Plant crop harvest	harvest trial for cane yield and CCS. Ratings as per protocol	field staff	2d FTS, 1d BM
For ratoon crop…				
11	After harvest/prior to fertiliser application on ratoon	- replace/exchange dataloggers and crop log books - fertility test and soil cores for N/water - Sample diag. across trial	BM/field staff	1d
12	Ratooning to end of year	- check trial at least twice - score plant establishment - check and copy log books/rainfall records	field staff	1d FTS
13	Jan to April when millable stalks are at least 1m, and canopy development relatively complete	- replace/exchange dataloggers - take soil pathology samples (FEB) - check and copy	field staff/BM	1d FTS, 1d BM

Step	Time	Activity	Responsibility	time input
		log books/rainfall records - stalk count (5m x 2 rows) - scores for disease, pest incidence and visual appearance for cane yield - 10 stalk sample from outer row of 4 plots (2 reps of Q124)		
14	April/early May	4 stalk sample for early CCS in one trial per region	field staff	1d FTS?
15	Ratoon crop harvest	harvest trial for cane yield and CCS. Ratings as per protocol	field staff	2d FTS, 1d BM
16	After harvest/prior to fertiliser application	- replace/exchange dataloggers - fertility test and soil cores for N/water - Sample diag.	BM/field staff	1d

3.4.4 Trial locations/seasons/activities

NOTE: THE BELOW TABLE WAS MODIFIED DURING THE PROJECT AND IS INCLUDED ONLY FOR COMPLETENESS OF INSTRUCTION SHEET

This table summarises the planting, harvesting and ratooning activities for the entire project. This will enable us to determine if a datalogger is required or if a weather station is sufficiently close by. Trials are conducted by BSES, except as indicated to be conducted by CSR/CSIRO. More detail is given in the master spreadsheet that Bill Messer will be looking after.

Region	*Trial code*	*Location*	*Nearest met. station (name/km)*	*1999*	*2000*	*2001*	*2002*
NSW	W1	Condong		1yr plant crop	harvest/ratoon	harvest	-
	W2	Harwood		2 yr plant crop, sample harvest at 1 year	sample plant crop	harvest plant crop and ratoon	harvest
Southern	S1	Bundaberg		plant	harvest/ratoon	harvest	-
	S2	Moreton		delayed	plant	harvest/ratoon	harvest
	S3	Isis		-	plant	harvest/ratoon	harvest
	S4	Maryborough		-	plant	harvest/ratoon	harvest
Central	C1	Mackay 1		plant	harvest/ratoon	harvest	-
	C2	Prosperpine		plant	harvest/ratoon	harvest	-
	C3	Mackay 2		-	plant	harvest/ratoon	harvest
	C4	Plane Creek		-	plant	harvest/ratoon	harvest
Burdekin	B1	Bkin 1 (BSES)		plant	harvest/ratoon	harvest	-
	B2	Bkin 2 (CSR)		plant	harvest/ratoon	harvest	-
	B3	Bkin 3 (BSES)		-	plant	harvest/ratoon	harvest
Herbert	H1	Herbert 1 (BSES)		plant	harvest/ratoon	harvest	-
	H2	Herbert 2 (CSR)		plant	harvest/ratoon	harvest	-
	H3	Herbert 3 (BSES)		-	plant	harvest/ratoon	harvest
	H4	Herbert 4 (CSR)		-	plant	harvest/ratoon	harvest
Northern	N1	Coast 1		delayed	plant	harvest/ratoon	harvest
	N2	Coast 2		delayed	plant	harvest/ratoon	harvest
	N3	Tableland 1		delayed	plant	harvest/ratoon	harvest
	N4	Coast 3		-	plant	harvest/ratoon	harvest
	N5	Coast 4		-	plant	harvest/ratoon	harvest
	N6	Tableland 2		-	plant	harvest/ratoon	harvest
Ord	O1	Ord 1		-	plant	harvest/ratoon	harvest
	O2	Ord 2		-	plant	harvest/ratoon	harvest

Region	*Trial code*	*Location*	*Nearest met. station (name/km)*	*1999*	*2000*	*2001*	*2002*
Activities				plant 9 trials	harvest 9 plant 16	harvest 25 ratoon 16	harvest 16

3.4.5 Crop Management

Crop management is to be farmer best-practice, usually using BSES recommendations. Each cooperator (i.e. grower) will be provided with a crop log book (from the CRC) to record rainfall and operations on the crop and major events (see attached). The record books are designed to minimise demands on the grower's time. They are simply a record of the management of the crop that can be reviewed later when interpreting the experiment results and used during the process of simulation modelling later. Each cooperator should be assured that the data from the crop log books is important in the success of the project, and that the information will be confidential and not distributed to other growers or researchers.

3.4.6 Expected planting times

Burdekin	April
North	July/August (from May in Atherton)
Central	"
Southern	"
Herbert	"
NSW	September

3.4.7 Soil sampling – three types

THREE types of site characterisation need to be undertaken. The approximate experimental area will be 140m by 60m long. For the fertility tests, attempt to take samples in two diagonals across the block. For the deep cores, take 12 cores - 4 samples each in about 3 rows across the width of the site. For the pathology tests, take samples from 2 reps of the same 3 varieties in each trial (more detail below).

1. Fertility (0-30, 30-60cm)

It is essential that this test be standardised across all of the trials and the samples analysed in the same laboratory. These tests should be taken as part of the standard BSES fertility testing to establish whether there are any chemical 'limitations' in the soil. We need data from the surface and sub-surface to analyse these separately for their effects on GxE. Where practical, amelioration of deficiencies will be done by the grower and recorded on the crop log sheet later.

Timing: 4-6 weeks prior to planting

Procedure:

1. Take between 12 and 18 cores over the experimental site, according to normal BSES procedure, but keeping the two depths in two plastic-handled buckets (one for 0-30cm and one for 30-60cm).
2. Record approximate soil type descriptions as per minimum data set manual

3. Mark 4 plastic bags as “0-30cm A”, “0-30cm B”, “30-60cm A”, “30-60cm B”. After bulking the cores, mix the soil thoroughly and remove samples for any standard BSES tests. Take 2 samples of about 2kg of soil from each depth and place into the marked bag.
4. Contact BM and send the 4 plastic bags to Townsville according to the easiest method. In the north, we can usually send them internally with whoever is travelling. Charge the transport costs to Bill Messer on delivery to CSIRO Davies Laboratory, Aitkenvale.
5. BM will air-dry the samples, and sieve them (2mm) and have them analysed for the following:

- soil colour, texture, pH (1:5) water, buffer pH
- organic carbon %C
- electric condut. Ds/m
- Ca, Mg, Na, K (Amm. Ac. meq/100g)
- N (nitrate), S, P (BSES), P (Colwell), Cl, Cu, Zn, Mn, Fe, Bo (mg/kg)

2. Soil surface residue and soil cores (0-15, 15-30, 30-60, 60-90, 90-120cm, 120-180cm).

These samples are required to initialise the simulations and document starting soil water and N profiles. Ideally, these should be taken 1 or 2 weeks prior to planting. If this is not possible, they should be taken within 2 to 3 weeks after planting each trial. If taken after planting, the samples should be taken in the centre of the interrow, to avoid the fertiliser band. NOTE: if surface residue is NIL, then please also inform BM of this. Obviously, the following procedure is then not required.

Timing: 1-2 weeks prior to planting **and** 1-2 weeks after plant crop harvest

Procedure:

1. Residue (required to establish C:N ratio).

- Across the trial area, take 4 x 2m^2 samples of crop residue (p.33 of crop manual).
- Record the approximate location of the crop residue samples on a map of the trial.
- Rake up all residue in each quadrant and place into a single plastic bag marked with the location and date.
- In the lab, weigh this material fresh and then weigh out a small subsample (about 1 to 2 litres) and record fresh weight.
- Oven dry the sample and send to BM
- BM to oven-dry sample and record weight, grind to 2mm and obtain C and N levels by analysis lab.

2. Soil N/water content

- Mark each of 6 buckets with the soil depth increments given above. Mark 6 plastic bags with the soil depth increments above, and the date and location of sampling.
- Take 12 core samples to 1.8m, recording the approximate position of each core on a map of the trial.
- After each core is taken, lay it out against a 1.8m ruler and cut the core into the above depth increments.
- For each depth increment, record a description of the soil texture, colour and degree of mottling.
- Place the soil from each depth increment into the appropriate bucket.
- On completion of sampling, mix the soil in each bucket and put about 1kg of from each bucket into a plastic bag and seal the bag closed. Keep the samples in the shade or a cooler until delivered to BM.

3. For all sites except southern, deliver bags to Bill Messer at CSIRO Davies Laboratory as soon as possible. At southern sites, deliver the samples to Scott Chapman at CSIRO Cunningham Laboratory. The following steps will then be undertaken:

- for each bag, empty the soil and mix thoroughly.
- Take a subsample (A) of 300 to 500g and place into a tared tin or paper bag and weigh fresh.
- Weigh the remaining sample (B) in the plastic bag.
- Oven –dry subsample A at 105°C for 3-4 days, weigh again and then discard sample.
- Air-dry subsample B for 7 days in a dehydrator with the fans only switched on and weigh again.
- Grind subsample B through a 2mm sieve for determination of mineral (nitrate) N

Normally, we would hope to characterise the soil water holding capacity completely. However, this is not practical for these trials, and so we will attempt to use soil characterisation data for a similar soil type, as gathered by researchers in CRC Program 3.

3. Soil samples for diseases

Routine soil pathogen tests are to be made at the start/end of experimentation. Provision had been made for $400 per trial to pay for these. Phil Jackson spoke to Rob Magarey regarding protocols for sampling for soil pathogens and they thought the following procedures would be appropriate (8 July 99, modified Jan 00):

1. Only do Pachymetra and nematodes.
2. Take samples for both in all trials in February - this timing is important for nematodes but not for Pachymetra but it would be convenient to take samples for both at the same time.
3. Take samples from plots of the same 3 standard varieties (Q117, Q124, Q138) in each trial.
4. For Pachymetra just soil needed (not roots). Take 8 cores per plot to depth of 30cm. Mix up and take 150g minimum subsample but more can be sent. Cores should be put down in middle of stool or immediately adjacent.
5. For nematodes, take spade of root + soil approx 10cm from stool. Spadeful should be 10cm x 10cm wide x 20cm deep. Take 8 spadefuls per plot, mix up and subsample 500 g of soil and roots.
6. Place each sample in a sealed plastic bag (marked with variety, rep, date and sample type (pachy or nemotodes). Store in an Eskie to keep the temperature below 30 °C (room temperature is ok). Do not store in a refrigerator.
7. As soon as possible, forward the samples in a small Eskie or polystyrene container to Dr. Rob Magarey at BSES, PO Box 556, Tully, Q. 4584.
8. Cost of each assay is $25 - for both nematodes and pachymetra. If we do 3 varieties per trial x 2 reps that equals 3 var x 2 reps x 2 assays x $25 = $300 which should keep within budget.
9. Again, please ensure that exactly the same procedure is used in all trials.

3.4.8 Climate

These data are to be recorded as explanatory data for use in the GxE analysis. They will also be used to run the simulation model to provide an index of the environment experienced by the crops. Normally, the minimum requirement would be to record daily radiation and rainfall and maximum and minimum temperatures are each site. This is not possible for such a large number of trials (>$120 000 of automatic weather stations would be needed!). Our compromise will be to use a combination of manual and automatic recording. For some sites in the north, we'll try to provide radiation sensors where there are none nearby.

Location

All met stations are to be located near the grower's house, as long as it is within about 1km of the experimental site. Use a GPS to record the exact location of the met station, the trial site and the GPO in the nearest town.

The station should be positioned so that it is not shaded by trees or buildings during the day, with at least 10m of clear fetch in all directions. The screen should be installed at 1m above ground and the rainfall gauge at ground level (and kept free of weeds/grass). If the house is >1km from the site, then the met station should be located near the field and within a couple of meters of some large object like a sign, electrical post or culvert (so that the station doesn't get run over).

Rainfall

Rainfall needs to be recorded into the crop log book by cooperators. At the least, we'll require weekly rainfall, but daily would be better, if possible. Rain gauges will be supplied by the project and are to be left with the cooperator at the completion of the trial.

Temperature and RH%

At each site, mini dataloggers will be installed in housings on 1m star pickets to measure temperature and relative humidity. These will have to be downloaded at the end of the calendar year and at harvest, using a laptop computer. The loggers will need to be calibrated against a check station at least once per year, and the batteries replaced at this time.

Solar radiation

This is expensive to log. We'll try to install at least one sensor in each of the major regions, especially in the north. Otherwise, we'll use the nearest weather station. The locations of trials will need to be reviewed to ensure that we have adequate coverage of this parameter at all sites.

3.4.9 Experiments

Design and plot management

- All of the experiments will be 2 replicate alpha-lattice designs (using CYCGEN to account for balance of rows and columns) with a core of 48 clones (12 CSR, 30 BSES, 6 commercial) that must be planted in all trials. There are 6 extra clones (3 CSR, 3 BSES) that should be planted if at all possible (probably in a 49, 50 or 54 entry design).
- Plot size will be 4 rows by 10m long.
- Individual plot lengths will be measured following rotary hoeing or spraying out gaps in trials and will require measuring plots and gaps.
- An accurate map with approximate dimensions should be made of each experiment showing the relative layout and orientation of the plots (relative to North)

- Use a GPS to record the exact location of the corner of the first plot (row 1 range 1)
- A mud map is required showing the location of the farm, block and trial.
- Other information about trials is given in the master spreadsheet.

Please forward field design, maps and GPS information to Bill Messer (CSIRO Davies Lab).

Crop observations

All scores should be on the basis that 1=good, 9=poor

1. **During the crop** – periodic observation of the crop for general or genotype differences. These are to be taken on an opportunistic basis. i.e. if any are seen then record notes about them.

- strike rate and gappiness of establishment (3-4 months after planting)
- date of first substantial lodging in experiment (and if possible, the genotypes affected)
- significant pest damage (record genotype variation)
- waterlogging.(record date and approx. depth of free water in the field standing for more than one day)

2. **Between Jan and May of the harvest year**, when millable stalks are at least 1m high, but prior to any substantial lodging, take the following observations at the same time. In each plot, record:

- stalk counts on 5m of the both of the central 2 rows. Walk several metres into the plot, mark a stalk in each row with flagging tape, and using a 5m piece of conduit count all stalks in each row. Stalks should be counted if there is sound stalk up to ca. 1-1.5m (chest high). the objective is to count sound stalks that would still be likely to be present at harvest. Do not count small tillers/stalks or suckers.
- a visual score for canopy health (1=good, 9 = poor);
- a visual score for appearance (cane yield rating estimate)
- Harvest a biomass sample (from the 2 plots of Q124 ONLY) to check simulation model:
  - remove 10 randomly chosen complete stalks from the outer rows of the plot
  - Weigh these stalks fresh in the field to the nearest 0.1 kg, and also weigh a subsample of 4 stalks
  - Keep the 4 stalk subsample and take to laboratory to separate the stalks into green leaves, dead leaves, millable stalk and cabbage. Bulk parts together from all 4 stalks.
  - Measure and record the length and width (at broadest point when flattened out) of each green leaf that is greater than about 20cm long
  - Cut the stalk into small pieces (< 10cm long)
  - Place plant parts into separate paper bags on which is recorded the name of the plant part, location and date of sampling
  - Oven dry all of the bags at 80C for 2d and record the dry weights of the parts

3. **Early CCS sampling**

For one site in each region, take a sampling for early CCS to determine approximate GxE effects for this. This sample should be taken in late May. From each plot in the trial:

- remove 4 representative stalks from the outer row of each plot
- process these to determine CCS

4. **Final harvest**

For each of the two central rows, follow BSES protocols to make visual scores (1=good, 9=poor) for:

- suckering
- arrowing
- sideshooting
- canopy health
- general appearance

In addition, make scores for

- stool tipping (amount and severity)
- rat damage (amount and severity)
- lodging (proportion of cane still standing)

From the central 2 rows, take 8 representative sound stalks, ensuring that the sample is truly random. Tie into a bundle and weigh and record these fresh. Transport to the processing site and record:

- average stalk diameter at 1m height (using calipers) and average millable stalk length of the bundle
- CCS using Carver Press or bag method? (after grinding 6 stalks)
- juice conductivity on same juice sample
- fibre (using 2 stalks)

Record cane bin weights from each of the centre 2 rows.

Appendix 4. Trial Results

Table of Contents

4.1. Overview of trial results

This dataset has a substantial utility for many interpretations and analyses that have not been undertaken as part of this project and form part of potential future work. Even so, for the objectives set here, there are a substantial number of supporting analyses to address each question. Following the overview section below, to present an adequate report of the supporting evidence for the objectives and outputs, we have tried in this section to present the results in small pieces that are essentially a series of small hypothesis tests that have been converted into statements. e.g. in the first case in section 4.2 below, the hypothesis is "Do spatial analysis models improve estimates of trial error variance?"

The conditions regarding soil chemistry and nematodes and the weather experienced during the trial are given in detail in Appendix 6. On average, the Ord and Burdekin trials were planted in April/May, the Herbert and North in June, Central in July, and the South and NSW in August to October. Planting in the North though ranged from May (Tableland sites) to August. Excluding the W2 plant crop (22 months), the mean length of the plant crop was 13.7 months, the 1st ratoon 12.6 and the 2nd ratoon 12.2 months. All locations in the Burdekin and Ord were irrigated, and none in the Herbert or NSW regions. Two Central trials (C1 and C3, ca. 375mm per crop), a Tableland trial (N3, ca. 1800mm per crop) and two of the South trials (ca. 200mm per crop) received supplementary irrigation.

4.1.1. Mean trial cane yield and sugar content varied with region

Across the 59 harvests, mean TCH per trial varied from 33 to 163 t/ha (Appendix 3 and Table 4-1), CCS from 8.3 to 16.9 and TSH from 5.5 to 22.2 t/ha. Trial yields were greatest in the Burdekin and Ord trials (all irrigated, ca. 130 t/ha), followed by NSW (including a 2 year plant crop, ca. 120 t/ha), the North (including Tableland, ca. 90 t/ha) and then the Herbert, Central and South which were quite similar at ca. 70 t/ha (Table 4-2). The region with the highest CCS was Central (ca. 16), followed by Herbert and North (ca. 15), South (ca. 14), the Burdekin (13) and NSW and the Ord (< 12). TSH consequently was most determined by TCH and similar rankings ensued.

There was a general negative relationship between trial mean TCH and CCS (r = -0.51, Figure 4-1). There may be exceptions to this. For example, in the Burdekin where high TCH trials can be established, withdrawal of irrigation can result in a trial that also has a high CCS. This apparently did not occur in our experiments B1 to B3 which were harvested in June or July(Appendix 3), although in B4 (harvested in September) a high TCH/high CCS result was realised in the plant crop.

The negative relationship between TCH and CCS did not hold when comparing genotypes when considered at the trial level (data not shown) or averaged over regions (see section 0), i.e. there exist all combinations of genotypes for TCH and CCS, e.g. high TCH/low CCS, high TCH/high CCS etc.

4.1.2. Regional variation in traits other than CCS and TCH

These traits were not recorded in all trials, so comparisons between regions may have some bias, although most traits were recorded in more than 75% of trials (the full list of traits can be determined from Table 4-12. Apart from an early season juice sample for sugar traits, all traits were recorded at or near to final harvest date. Genotypic variance for each trait was significant in the majority of trials where it was recorded. However, genotypic variance for visual scores for traits such as side-shooting (ssh), stool tipping (stp), stool suckering (sts) and sucker weight (suw) were not significant about half of the trials in most regions, except the North and South (Table 4-12).

Lodging occurred in almost 50% of plants in the Burdekin (not scored in the Ord) where the stalks were longest, and it averaged 15 to 25% in other regions (Table 4-2), i.e. higher lodging scores were generally associated with higher TCH (Figure 4-2). Stool tipping and sucker fresh weight (as a proportion of cane yield) were scored as relatively small. Stool suckering (as %

of stools showing suckers) was greatest in the North, Herbert and NSW while side-shooting was greatest in Central. Arrowing was greatest in trials in the Herbert, North and South region. The lowest stalk densities and single stalk fresh weights occurred in the Central, Herbert and South regions, where cane yields were lowest (particularly in several drought affected trials in Central and Herbert).

Fibre was similar in most regions, except that it was substantially higher in the Ord, where the CCS, brix, pol and purity were all the lowest. The early season sugar measurements, taken in two locations per region usually in March, were similar in most regions, but were noticeably lowest in the Burdekin, where the samples were taken quite early (February) to allow access to the crop.

4.1.3. Comparison of unselected clones and Q canes (commercial checks)

More details of clone/check comparisons are given in section 0, with an overview given here. Of the Q cane checks, Q138 was the highest or equal yielding in all regions in which it has been recommended, while its CCS was moderate (Table 4-3). Q117 had the highest CCS, especially in its recommended regions, but had the lowest overall TCH. Q135 had the highest TCH in the Burdekin, but with a lower CCS than Q117. Q124 and Q141 were similar for TCH, though Q124 generally had a higher CCS. Q165 was moderate in TCH and CCS.

While the average CCS, TCH and TSH of the unselected clones was, respectively, 1.1 CCS units, 21 t/ha and 4 t/ha less than that of the Q canes (Table 4-1), the values for these traits of the best clones was comparable to the Q canes, i.e. the unselected clones included some that were at least as good as Q canes and a degree of genotypic variance below that, as would be expected. For CCS, the (unselected) clones were 91 to 93% of the Q canes in each region, but there was greater variation across regions for TCH, with the performance of the clones in regions B, C, H, N, O, S and W, being 90%, 81%, 85%, 84%, 78% and 75%, respectively (Table 4-4). The greatest disparities was noted in the NSW trials, the average of the unselected clones was 0.9, 38 t/ha and 6 t/ha lower for CCS, TCH and TSH (Table 4-1). The mean disadvantage for TCH in the W2 (2 year plant crop) and W1 locations was 51 t/ha and 25 t/ha, respectively. Similarly, the TCH advantage of the Q canes was almost 20 t/ha in the South trials.

Hence, for TCH, there appeared to be a greater regional effect on the clones compared to the checks when comparing the southern locations (South and NSW) and the Ord (24 t/ha advantage for Q canes). This could arise if the clones were either more poorly adapted to these regions (cf. northern regions), or because the Q cane checks were better adapted to these regions than to regions from Central to the North. The latter seems relatively unlikely given that all of the Q canes were first developed in regions from the Central to North, mainly from northern parents. However, three Q canes (Q124, Q135, Q141) do have NCO310 as a parent, which is known to do well in the South.

Table 4-4 shows that, compared with the Q canes, the unselected clones also exhibited other characteristics associated with lower TCH (lower single stalk fresh weight and stalk diameter, especially in South and NSW) and lower CCS (lower brix, pol, purity and higher conductivity and fibre). Stalk diameter and length was lowest in the S and W regions (relative to the Q canes). Here there was also more stool suckering and less stool tipping, perhaps associated with the sparser, canopies where stalk density was more similar to that of the Q canes, rather than higher as was the case in most other regions (Table 4-2). While average sucker weight estimated across all trials was only about 2.5% of the total stalk weight (Table 4-2), it was estimated to be greater in the clones than in the Q canes in the Central, Ord and NSW regions, and less in the Burdekin (Table 4-4).

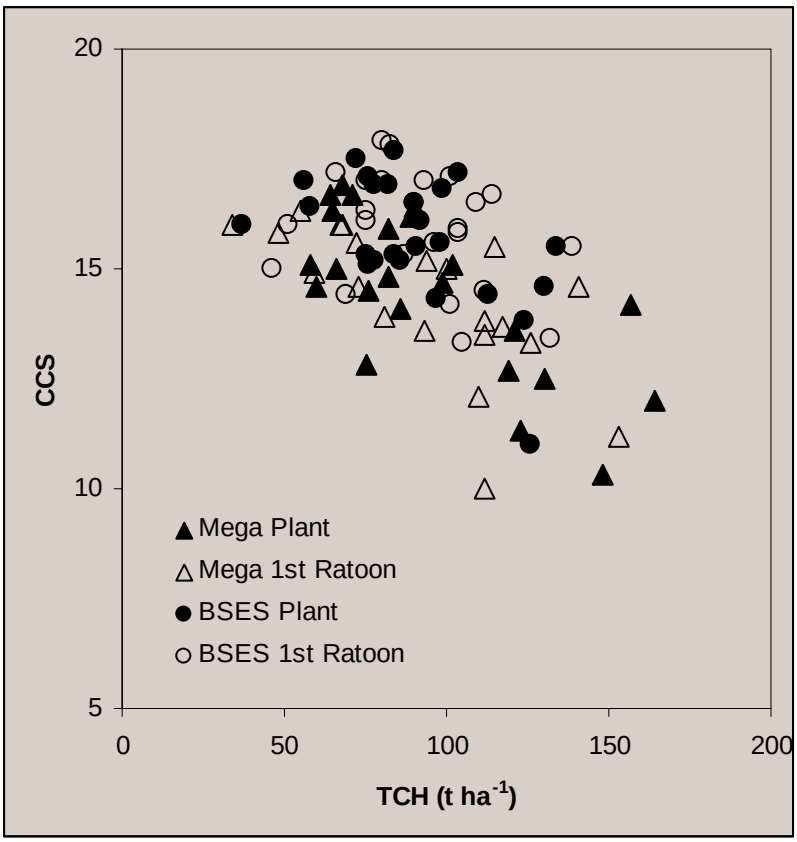


Figure 4-1 Trial mean TCH vs CCS for all of the MegaGxE trials and the BSES-FAT trials (Appendix 12)

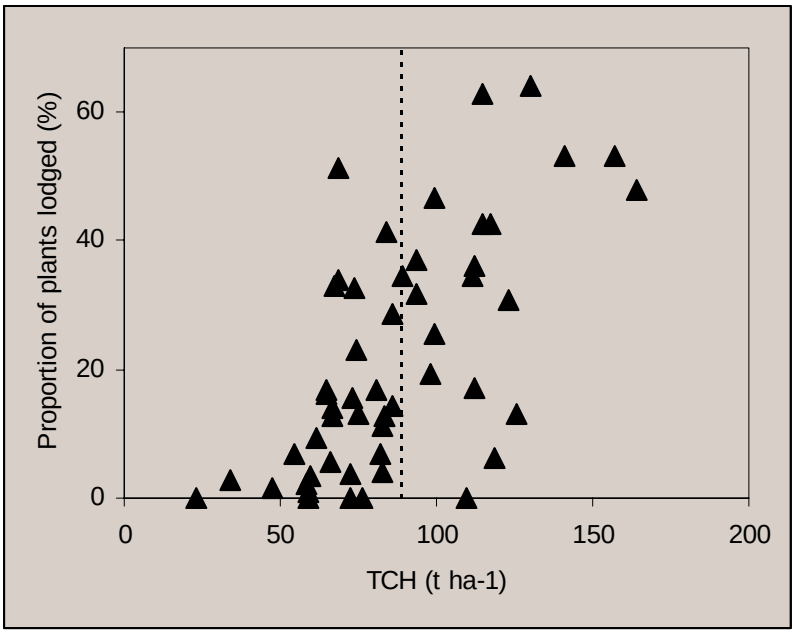


Figure 4-2 Relationship between trial means for proportion of lodged plants and cane yield for all trials

Table 4-1 For CCS, TCH and TSH in the MegaGxE trials, the average and maximum value for unselected clones (C) and checks (Q) in each trial and averaged over locations and regions. Regions are Burdekin (B), Central (C), Herbert (H), North (N), Ord (O) and NSW (W), while the Atherton Tableland trials were locations N3 and N6. Trial Code: 1st two letters = sitecode (appendix 3); 3rd symbol = crop (0=plant, 1= 1st ratoon, 2= 2nd ratoon); 4th indicates year of harvest (0=2000, 1=2001, etc).

			Average of value						Max of value					
			ccs		tch		tsh		ccs		tch		tsh	
Reg	Loc	Env	C	Q	C	Q	C	Q	C	Q	C	Q	C	Q
B	B1	B1-0-0	12.3	14.9	128.7	145.4	15.8	21.6	15.7	16.4	178.4	171.4	20.4	25.1
		B1-1-1	14.3	15.4	144.4	157.5	20.7	24.0	16.4	17.1	186.1	177.2	28.2	27.0
		B1-2-2	13.6	14.9	117.2	124.2	15.9	18.5	15.8	16.8	142.8	129.7	20.0	22.0
	B1 Total		13.4	15.1	130.1	142.3	17.5	21.4	16.4	17.1	186.1	177.2	28.2	27.0
	B2	B2-0-0	12.1	13.0	167.1	175.3	20.3	22.9	14.5	14.8	205.3	214.7	26.7	26.5
		B2-1-1	13.6	14.6	122.0	120.4	16.5	17.6	16.2	15.7	150.9	146.5	20.0	21.8
	B2 Total		12.8	13.8	144.5	147.9	18.4	20.2	16.2	15.7	205.3	214.7	26.7	26.5
	B3	B3-0-2	11.0	12.5	119.2	140.0	13.1	17.3	13.3	14.0	153.9	166.0	17.4	22.2
		B3-1-3	9.9	10.3	107.9	126.8	10.7	13.3	13.8	13.8	142.9	137.6	18.2	18.3
		B3-2-4	11.1	11.6	116.9	136.1	13.0	15.9	14.6	14.8	151.4	179.1	20.3	23.1
	B3 Total		10.7	11.5	114.7	134.3	12.3	15.5	14.6	14.8	153.9	179.1	20.3	23.1
	B4	B4-0-3	14.0	14.9	154.0	169.1	21.4	25.5	16.5	16.1	216.0	193.9	30.9	30.5
		B4-1-4	16.6	17.3	105.1	103.3	17.4	17.9	18.2	18.1	139.1	128.6	22.8	23.0
	B4 Total		15.3	16.1	129.5	136.2	19.4	21.7	18.2	18.1	216.0	193.9	30.9	30.5
B Total			12.7	14.0	126.1	139.7	16.1	19.5	18.2	18.1	216.0	214.7	30.9	30.5
C	C1	C1-0-0	16.1	16.9	85.7	111.6	13.8	18.8	18.3	19.0	140.9	140.1	24.6	22.2
		C1-1-1	15.9	16.9	66.7	71.5	10.7	11.9	18.4	17.8	88.6	88.2	15.4	14.9
		C1-2-2	15.5	17.4	70.8	85.9	10.9	15.1	17.8	18.0	100.3	97.2	15.7	16.7
	C1 Total		15.8	17.0	74.4	89.7	11.8	15.3	18.4	19.0	140.9	140.1	24.6	22.2
	C2	C2-0-0	16.5	18.2	60.8	80.5	10.1	14.5	18.5	19.0	94.9	114.0	16.9	20.5
		C2-1-1	16.2	17.3	51.0	71.9	8.3	12.5	18.0	17.9	89.4	94.9	14.3	16.4
	C2 Total		16.4	17.8	55.9	76.2	9.2	13.5	18.5	19.0	94.9	114.0	16.9	20.5
	C3	C3-0-1	14.5	15.8	58.8	77.4	8.4	12.1	16.1	16.1	99.6	93.6	13.0	14.9
		C3-1-2	15.1	16.3	91.5	99.7	13.7	16.2	17.0	17.8	127.0	105.4	18.2	17.7
		C3-2-3	13.9	16.0	79.8	95.9	11.1	15.3	16.8	16.4	100.2	120.9	14.6	18.2
	C3 Total		14.5	16.0	76.7	91.0	11.1	14.5	17.0	17.8	127.0	120.9	18.2	18.2
	C4	C4-0-1	16.8	18.1	66.6	85.6	11.1	15.5	18.4	18.7	95.6	92.1	14.7	16.2
		C4-1-2	15.8	17.3	32.5	40.2	5.1	7.0	17.7	17.7	48.9	46.1	7.9	7.7
		C4-2-3	15.9	17.5	57.2	69.3	9.1	12.1	18.1	18.0	72.6	82.3	11.7	13.7
	C4 Total		16.2	17.6	52.1	65.0	8.4	11.5	18.4	18.7	95.6	92.1	14.7	16.2
C Total			15.6	17.1	65.6	80.9	10.2	13.7	18.5	19.0	140.9	140.1	24.6	22.2
H	H1	H1-0-0	15.0	16.4	56.4	73.0	8.4	12.1	16.6	17.3	91.3	82.7	13.4	14.0
		H1-1-1	15.7	16.6	45.8	62.8	7.1	10.4	17.3	17.6	80.1	71.6	11.8	11.6
	H1 Total		15.3	16.5	51.1	67.9	7.8	11.3	17.3	17.6	91.3	82.7	13.4	14.0
	H2	H2-0-0	12.7	13.8	72.7	85.8	9.2	11.8	15.2	14.4	110.1	98.2	13.1	12.7
		H2-1-1	13.5	14.6	89.7	110.1	12.1	16.0	16.1	15.5	130.4	138.6	19.4	18.4
		H2-2-2	15.9	17.5	80.6	102.3	12.8	18.0	17.8	18.4	117.9	122.4	18.4	22.4
	H2 Total		14.0	15.3	81.0	99.4	11.4	15.3	17.8	18.4	130.4	138.6	19.4	22.4
	H3	H3-0-1	14.9	16.4	99.1	120.9	14.8	19.8	17.4	17.0	129.5	129.1	20.6	21.8
		H3-1-2	14.8	15.8	57.3	69.9	8.4	11.1	18.3	17.8	87.3	81.0	12.4	13.4
		H3-2-3	14.8	15.2	22.2	29.3	3.3	4.4	17.6	16.9	34.0	40.4	5.1	5.5
	H3 Total		14.8	15.8	59.6	71.3	8.8	11.4	18.3	17.8	129.5	129.1	20.6	21.8
	H4	H4-0-1	16.5	17.9	68.6	84.8	11.3	15.2	18.4	18.8	101.3	95.8	17.1	16.9
		H4-1-2	16.2	17.6	87.9	103.0	14.2	18.1	18.0	18.3	115.5	118.9	18.7	20.6
		H4-2-3	14.0	15.7	70.5	90.5	9.9	14.1	15.8	16.3	128.6	100.1	16.5	16.0
	H4 Total		15.6	17.1	75.7	92.8	11.8	15.8	18.4	18.8	128.6	118.9	18.7	20.6
H Total			14.9	16.1	67.6	83.9	10.0	13.6	18.4	18.8	130.4	138.6	20.6	22.4
N	N1	N1-0-2	15.6	17.4	77.6	105.2	12.1	18.3	18.0	18.3	122.6	117.9	21.2	21.2

			Average of value						Max of value					
			ccs		tch		tsh		ccs		tch		tsh	
Reg	Loc	Env	C	Q	C	Q	C	Q	C	Q	C	Q	C	Q
		N1-1-3	13.9	14.5	77.5	94.4	10.7	13.6	17.4	17.6	134.1	104.7	14.9	18.8
	N1 Total		14.8	16.0	77.6	99.8	11.4	16.0	18.0	18.3	134.1	117.9	21.2	21.2
	N2	N2-0-1	16.0	17.8	63.5	71.9	10.1	12.8	17.9	18.6	109.0	81.9	16.8	14.8
		N2-1-2	15.4	16.9	112.5	130.6	17.3	22.2	17.8	17.4	185.5	152.3	26.8	24.7
		N2-2-3	15.5	17.0	72.4	87.1	11.2	14.8	18.5	18.2	118.5	115.8	19.2	18.5
	N2 Total		15.6	17.3	83.0	95.2	12.9	16.4	18.5	18.6	185.5	152.3	26.8	24.7
	N3	N3-0-1	12.6	13.7	116.4	136.1	14.6	18.7	15.1	14.4	161.9	150.9	21.1	20.6
		N3-1-2	13.3	14.0	124.0	146.7	16.5	20.6	15.3	15.4	169.4	169.5	23.9	23.7
	N3 Total		12.9	13.8	120.2	141.4	15.6	19.6	15.3	15.4	169.4	169.5	23.9	23.7
	N4	N4-0-2	14.5	15.6	74.5	85.6	10.8	13.3	17.0	17.1	102.6	107.3	16.6	16.8
		N4-1-3	14.5	16.2	71.0	82.7	10.3	13.4	17.4	17.7	122.8	106.0	17.4	17.4
	N4 Total		14.5	15.9	72.8	84.2	10.5	13.4	17.4	17.7	122.8	107.3	17.4	17.4
	N5	N5-0-2	14.4	16.6	96.5	115.7	13.9	19.2	17.0	17.0	147.5	139.3	23.8	22.5
		N5-1-3	13.7	14.9	110.0	121.3	15.1	18.0	17.0	16.3	167.0	157.2	24.7	22.7
	N5 Total		14.1	15.7	103.3	118.5	14.5	18.6	17.0	17.0	167.0	157.2	24.7	22.7
	N6	N6-0-1	14.9	16.4	64.2	73.3	9.5	11.9	17.7	16.9	98.3	97.6	15.8	15.6
		N6-1-2	15.5	16.6	68.7	89.8	10.7	14.8	17.5	17.2	101.4	117.9	16.3	19.4
	N6 Total		15.2	16.5	66.5	81.6	10.1	13.3	17.7	17.2	101.4	117.9	16.3	19.4
N Total			14.6	16.0	87.0	102.6	12.5	16.2	18.5	18.6	185.5	169.5	26.8	24.7
O	O1	O1-0-2	10.1	10.7	143.3	163.5	14.4	17.6	14.1	12.9	204.1	170.2	23.6	21.8
		O1-1-3	11.8	13.2	104.3	132.6	12.4	17.6	13.5	14.2	148.9	159.1	17.5	22.5
	O1 Total		10.9	12.0	123.8	148.1	13.4	17.6	14.1	14.2	204.1	170.2	23.6	22.5
O Total			10.9	12.0	123.8	148.1	13.4	17.6	14.1	14.2	204.1	170.2	23.6	22.5
S	S1	S1-0-0	13.9	15.6	82.5	107.1	11.4	16.7	16.3	16.1	108.1	112.0	15.7	17.9
		S1-1-1	14.7	16.4	97.4	109.0	14.4	17.8	16.8	17.0	145.6	122.1	22.1	19.6
		S1-2-2	14.1	15.2	67.2	85.7	9.5	13.0	16.0	15.7	92.6	105.7	14.1	14.8
	S1 Total		14.3	15.7	82.4	100.6	11.8	15.8	16.8	17.0	145.6	122.1	22.1	19.6
	S3	S3-0-1	14.7	15.4	78.5	96.5	11.5	14.8	16.7	16.9	102.4	109.1	15.5	16.7
		S3-1-2	15.8	17.0	62.9	82.4	9.9	14.0	17.7	17.7	81.6	93.0	13.2	16.3
		S3-2-3	15.1	16.0	59.2	79.8	9.3	12.7	16.8	16.8	86.8	104.7	12.8	16.1
	S3 Total		15.2	16.1	66.9	86.3	10.3	13.8	17.7	17.7	102.4	109.1	15.5	16.7
	S4	S4-0-3	10.4	11.3	48.1	78.4	5.0	8.9	13.6	11.9	92.5	107.5	9.3	12.4
		S4-1-4	14.3	15.3	43.7	62.8	6.2	9.6	16.3	16.2	71.3	75.9	9.4	11.9
	S4 Total		12.3	13.3	45.9	70.6	5.6	9.3	16.3	16.2	92.5	107.5	9.4	12.4
S Total			14.1	15.3	68.4	87.7	9.8	13.4	17.7	17.7	145.6	122.1	22.1	19.6
W	W1	W1-0-0	8.2	9.0	79.2	106.8	6.5	9.6	11.9	10.4	117.2	121.8	11.3	11.0
		W1-1-1	13.3	14.4	109.4	131.4	14.6	18.9	15.8	15.2	151.0	153.3	19.1	21.8
	W1 Total		10.8	11.7	94.3	119.1	10.5	14.2	15.8	15.2	151.0	153.3	19.1	21.8
	W2	W2-0-1	13.5	14.4	114.4	174.3	15.3	25.0	15.5	14.9	203.6	201.8	26.3	30.0
		W2-1-2	11.0	11.9	149.8	191.4	16.6	22.8	14.7	12.6	216.3	214.2	24.1	27.0
	W2 Total		12.3	13.1	132.1	182.9	15.9	23.9	15.5	14.9	216.3	214.2	26.3	30.0
W Total			11.5	12.4	113.2	151.0	13.2	19.1	15.8	15.2	216.3	214.2	26.3	30.0
Grand Total			**14.2**	**15.3**	**84.6**	**105.1**	**11.8**	**15.8**	**18.5**	**19.0**	**216.3**	**214.7**	**30.9**	**30.5**

Table 4-2 For all observed traits the mean trial value, averaged within regions. Note that while ccs, tch and tsh were measured in all trials, the other traits were not, so the means are somewhat unbalanced.

Trait	Abbrev.	B	C	H	N	O	S	W	Mean
Arrowing (% plants)	arr	9.7	10.4	24.3	26.3	NA	25.5	0.1	18.9
Brix	brx	21.5	24.0	23.2	20.9	20.5	21.8	18.8	22.0
Brix (early season)	brxe	12.1	18.3	19.0	17.7	NA	18.3	16.0	17.7
Commercial cane sugar	ccs	12.9	15.8	15.0	14.7	11.1	14.2	11.6	14.3
CCS (early)	ccse	2.5	10.2	9.1	11.1	NA	11.3	8.2	9.4
Conductivity (mS)	con	279.9	266.2	298.2	209.9	497.5	426.8	NA	283.1
Stalk diameter (mm)	dia	25.4	18.2	23.6	24.1	25.3	23.9	25.7	23.8
Fibre (%)	fib	13.2	13.1	12.7	12.4	17.0	12.5	13.4	12.8
Stalk length (m)	len	3.0	2.1	2.4	2.3	3.1	2.0	2.0	2.4
Lodging score (% plants)	lod	48.6	18.7	22.9	20.1	NA	16.9	23.9	24.9
Pol	pol	79.7	91.7	89.8	80.5	74.3	84.1	70.9	84.1
Pol (early)	pole	31.3	62.9	62.8	66.0	NA	67.7	54.8	61.0
Purity	pur	87.2	90.5	91.8	89.2	86.3	92.2	90.8	90.4
Purity (early)	pure	NA	82.8	77.8	89.3	NA	89.3	83.3	83.3
Single stalk fresh weight (kg)	sfw	1.5	1.0	1.1	1.1	1.7	1.0	1.4	1.2
Side-shooting (% plants)	ssh	1.0	20.6	10.5	13.4	5.0	3.0	0.1	7.3
Stalk density (per m^2)	stc	9.8	6.9	6.5	8.3	9.3	8.1	9.5	7.9
Stool tipping (% plants)	stp	5.4	0.6	2.1	NA	NA	0.2	10.1	3.6
Stool suckering (% plants)	sts	27.3	25.3	33.3	51.7	NA	12.1	35.1	32.4
Sucker weight (%)	suw	3.6	2.3	3.2	1.8	4.1	0.6	0.6	2.3
Cane yield (t/ha)	Tch	128.3	68.0	70.1	89.3	127.5	71.2	117.9	88.6
Sugar yield (t/ha)	Tsh	16.6	10.7	10.5	13.0	14.1	10.3	14.0	12.4

Table 4-3 By region, TCH and CCS for commercial checks (Q canes) used in the MegaGxE trials. The recommended release areas for the Q canes were: Q117 (N, B), Q124 (H, C), Q135 (H, C, S), Q138 (N, H, C, S, W), Q141 (S) and Q165 (B).

Trait	Gen	B	C	H	N	O	S	W	Grand Total
tch	Q117	136.9	71.3	82.4	98.9	NA	83.9	141.8	98.0
	Q124	133.8	79.7	85.1	101.6	158.5	84.5	151.8	102.9
	Q135	159.6	78.6	86.4	105.5	156.6	92.8	151.4	109.2
	Q138	145.0	93.8	85.4	119.1	132.0	101.6	162.4	113.5
	Q141	135.9	NA	83.1	94.6	NA	84.4	151.7	104.0
	Q165	127.4	NA	79.8	100.6	NA	79.1	146.8	101.7
ccs	Q117	15.7	17.7	16.8	16.5	NA	15.8	12.8	16.3
	Q124	12.3	16.6	16.3	15.9	12.3	15.0	12.8	15.0
	Q135	14.4	17.4	16.5	16.0	12.4	15.4	12.1	15.6
	Q138	13.7	16.5	15.8	15.6	8.9	14.7	12.0	14.9
	Q141	12.7	NA	15.9	15.7	NA	15.2	12.2	14.7
	Q165	14.8	NA	16.1	16.1	NA	15.5	12.7	15.4

Table 4-4 For all observed traits the ratio of the mean value of the unselected clones to the Q canes, averaged within regions. Light shading indicates where unselected clones < 0.9 of Q canes and dark shading for > 1.10. Note that while ccs, tch and tsh were measured in all trials, the other traits were not always measured.

Trait	B	C	H	N	O	S	W
Arrowing (% plants)	0.92	2.84	3.11	1.74	NA	1.02	NA
Brix	0.97	0.96	0.97	0.96	0.96	0.97	0.97
Brix (early)	0.97	1.00	0.98	0.99	NA	0.98	0.97
Commercial cane sugar	0.91	0.92	0.93	0.91	0.91	0.92	0.93
CCS (early)	0.76	0.96	0.96	0.95	NA	0.94	0.92
Conductivity (mS)	1.28	1.36	1.25	1.32	1.16	1.28	NA
Stalk diameter (mm)	0.93	0.94	0.92	0.92	0.96	0.90	0.88
Fibre (%)	1.16	1.12	1.13	1.10	1.04	1.12	1.11
Stalk length (m)	0.97	0.89	0.95	0.94	0.90	0.91	0.91
Lodging score (% plants)	0.99	0.88	0.79	0.74	NA	0.95	0.96
Pol	0.94	0.95	0.95	0.93	0.94	0.95	0.95
Pol (early)	0.91	0.98	0.97	0.97	NA	0.96	0.94
Purity	0.96	0.99	0.99	0.99	0.98	0.98	0.98
Purity (early)	NA	0.98	1.00	0.98	NA	0.98	0.97
Single stalk fresh weight (kg)	0.85	0.76	0.80	0.79	0.84	0.73	0.74
Side-shooting (% plants)	70.56	0.91	3.98	9.79	2.37	30.43	NA
Stalk density (per m^2)	1.11	1.14	1.03	1.11	1.09	1.09	1.06
Stool tipping (% plants)	1.84	NA	1.41	NA	NA	0.72	0.49
Stool suckering (% plants)	1.01	1.00	1.16	1.00	NA	1.78	1.15
Sucker weight (%)	0.82	1.45	0.98	1.03	1.36	1.04	1.50
Cane yield (t/ha)	0.90	0.81	0.81	0.85	0.84	0.78	0.75
Sugar yield (t/ha)	0.82	0.74	0.74	0.77	0.76	0.73	0.69

4.2. Comparison of design models and trial level variances

In the first parts of this section, the statements relate to how the trials varied across locations and years and what type of precision was realised by different analysis methods. It complements the short overview in Appendix 3 as a summary of the basic data analysis at the trial level.

4.2.1. Compared to Row-Column models, trial error variances were reduced by spatial analysis models, particularly for TCH and TSH

Method

Fifty-nine harvests (also termed 'trials' or 'environments') are considered here (Table 1). All of the trials were designed as row-column designs to attempt to control spatial variability that occurs in larger trials. Given a plot size of 60 m^2 (4 row x 10m x 1.5m), the average trial of 100 plots covered ca 0.6 ha. In each trial, two design models were fitted to control error ('design models') and for each of these, genotype values were estimated as either fixed or random effects. All statistical models were fitted with either ASREML (Gilmour et al 2002) under Windows or an implementation of this algorithm (samm) with S-Plus. The code for these analyses is on the CD-ROM.

The first design model was based on the row-column design, such that random effects were fitted for rep, columns within reps and rows within reps. The second design model took replicate as a random effect and fitted an autoregressive (AR1) model for both row and column positions to account for field variability.

Models were fitted separately to estimate genotype values for tch, ccs and tsh as either

- fixed effects (Best Linear Unbiased Estimators –BLUEs, similar to genotype means) for use in 2nd stage analyses of genotype by environment interaction or

- random effects (Best Linear Unbiased Predictors –BLUPs) for comparing trial variances, trial correlations and weighting the genotype values for trial repeatability (error).

For the fitting of the AR1 models, each trial was first fitted with genotypes fixed, and then the AR1 parameters were fixed for the second run of the model when genotypes were set to random.

The models used were named as follows, and these names are used in naming conventions for results etc on the CD.

Table 4-5 Models fitted at individual trial level

	Genotype effects	
Design model	Fixed (BLUEs)	Random (BLUPs)
Random Rep, Row, Column	AOVF	AOVR
Random Rep and AR1 for Row, Column	AOVFAR1	AOVRAR1

The design models with genotype effects random were compared using statistics output from the analysis:

- genotypic variance
- repeatability (also know as broad sense heritability) which approximates the ratio of genotypic to phenotypic variance
- effective error mean square (EMS)

Result

Only the data for EMS are shown here. Other data are on the CD-ROM. Table 4-6 shows that the models did not differ much in precision for ccs. However, the AOVRAR1 model generated a lower EMS (i.e. was more precise) for tch and tsh in most trials conducted in the North and South regions and some in the Burdekin. On average, trials in the Central, Herbert and NSW regions had similar effective EMS for tch using either design model, i.e. spatial analysis was less necessary on average as the row and column design effects were sufficient to control spatial variation.

There was no clear relationship between the EMS ratio (AOVAR1/AOVR) and trial mean, i.e. the spatial model could potentially across all levels of ccs and tch (data not shown). At trials where tch was > 80 t/ha, the spatial model frequently had a lower EMS (Figure 4-3), and therefore seems of more importance in high yielding trials, perhaps due to confounding effects of lodging etc.

In most regions, the estimate of genotypic variance for any trait was not greatly affected by the choice of design model (Table 4-7). The lower value in Central was largely due to one trial (C3-0-1), where the ratio was 0.23, i.e. without the spatial model, genotypic variance was overestimated (data not shown).

Analyses were done of the data using Rep information only, i..e. without the Row and Column effects (data not shown). Row and Column information (whether as random effects or as spatial models) adds greatly to the precision of the trials, but we are assuming that anyone using a Row-Column design will use the effects in any case. Additionally, we fitted the models with Rep, Row and Column fitted as random effects, and Row and Column as AR1 spatial effects. However, this did not generally improve the precision over either the AOVR or AOVRAR1 models.

Overall, the AR1 models improved most of the statistics associated with the precision of the trials and measurements of genotypic and error variance. At the minimum (and as is almost always done now), these types of trials should be laid out in row-column designs with this information used in analysis.

Table 4-6 Ratio of effective error mean square for AOVAR1/AOVR. Light shading indicates AOVR had lower EMS by > 5%, dark shading indicates AOVAR1 was lower by >5%.

Env	ccs	tch	tsh	Env	ccs	tch	tsh
B1-0-0	0.92	0.89	0.99	N1-0-2	0.86	0.78	0.71
B1-1-1	1.20	0.73	0.85	N1-1-3	1.00	0.74	0.87
B1-2-2	0.97	0.95	0.98	N2-0-1	1.03	0.61	0.57
B2-0-0	0.98	1.00	0.98	N2-1-2	1.02	0.92	1.01
B2-1-1	0.97	0.98	0.97	N2-2-3	0.99	0.84	0.90
B3-0-2	0.95	0.99	1.02	N3-0-1	1.16	0.75	0.83
B3-1-3	1.00	0.96	0.83	N3-1-2	1.01	0.87	0.94
B3-2-4	1.00	0.91	0.97	N4-0-2	0.94	0.75	0.90
B4-0-3	1.01	0.78	0.94	N4-1-3	0.88	0.86	0.84
B4-1-4	0.93	0.83	0.84	N5-0-2	1.04	0.93	1.03
B	0.99	0.89	0.94	N5-1-3	0.99	0.95	0.99
C1-0-0	1.00	1.00	1.06	N6-0-1	1.08	1.01	1.03
C1-1-1	0.80	1.03	1.04	N6-1-2	0.98	1.00	0.99
C1-2-2	1.01	1.34	1.14	N	1.00	0.85	0.89
C2-0-0	0.85	0.85	0.83	O1-0-2	1.03	0.95	0.97
C2-1-1	0.91	1.01	0.97	O1-1-3	0.99	1.01	0.90
C3-0-1	0.93	1.22	0.98	O	1.02	0.98	0.95
C3-1-2	1.09	0.76	0.83	S1-0-0	0.99	0.84	0.91
C3-2-3	0.99	0.95	0.91	S1-1-1	1.00	1.01	1.00
C4-0-1	0.98	1.12	1.08	S1-2-2	1.01	0.80	0.85
C4-1-2	1.09	1.01	1.08	S3-0-1	1.03	0.79	0.73
C4-2-3	0.98	0.84	0.96	S3-1-2	0.96	0.81	0.90
C	0.97	1.00	0.97	S3-2-3	1.05	1.13	1.08
H1-0-0	1.07	0.99	1.07	S4-0-3	0.90	0.61	0.51
H1-1-1	1.03	0.87	0.90	S4-1-4	0.91	0.64	0.59
H2-0-0	0.93	1.01	1.07	S	0.98	0.81	0.85
H2-1-1	0.98	0.92	0.88	W1-0-0	0.95	1.05	1.13
H2-2-2	0.94	1.01	0.98	W1-1-1	1.13	0.96	1.20
H3-0-1	1.05	0.95	0.93	W2-0-1	1.07	1.00	1.03
H3-1-2	1.03	1.05	0.92	W2-1-2	0.98	1.03	1.00
H3-2-3	0.99	0.97	0.94	W	1.01	1.01	1.04
H4-0-1	1.08	0.77	0.76	all	0.99	0.91	0.94
H4-1-2	0.75	0.78	0.77				
H4-2-3	0.95	1.40	1.20				
H	0.98	0.95	0.93				

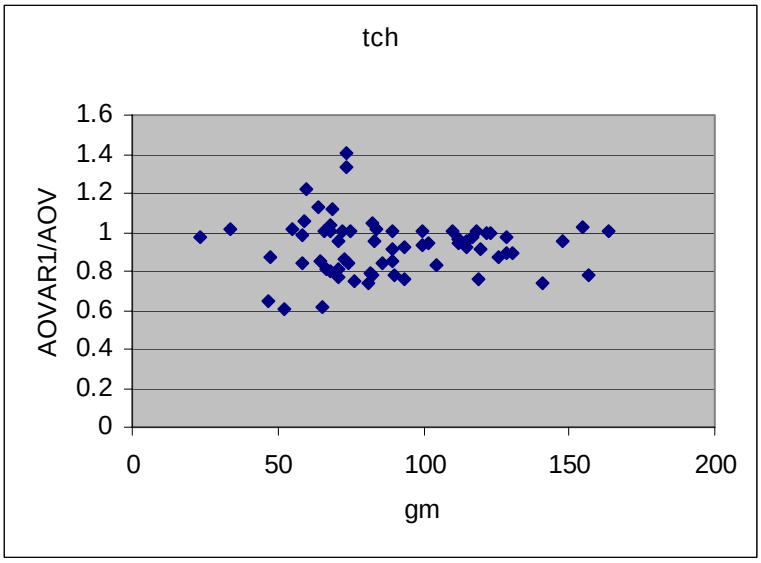


Figure 4-3 The relationship between mean trial TCH and the ratio of the effective error mean square fitted for either AR1 spatial row-column models (AOVAR1) or random row-column effect models (AOV).

Table 4-7 Ratios of genotypic variance estimated for either AR1 spatial row-column models (AOVAR1) or random row-column effect models (AOV), averaged across regions

Env	ccs	tch	tsh
B	0.97	1.02	0.98
C	1.00	0.94	0.96
H	1.02	0.98	1.01
N	0.98	1.05	1.05
O	0.96	0.98	0.95
S	0.99	1.03	1.04
W	0.97	1.00	0.97
all	0.99	1.01	1.00

4.2.2. On a per-trial basis, rankings of unselected clones were not affected by use of spatial analyses compared with standard row-column analysis

Method

While it is generally desirable to improve the control of error and therefore raise the precision of a trial, this becomes more critical in a plant breeding context if the change of statistical model results in substantial changes in ranking of genotypes. In unreplicated trials of early generation lines where replicated checks have been used, spatial analyses have been show to change these rankings.

The BLUEs from the two models (AOVF and AOVFAR1) described above were compared, after dropping the commercial checks from the comparison.

Result

Figure 4-4 shows that the rankings for tch changed little between the two models, with most correlations being > 0.95 or so. In several locations (B1, N3 and W2) there was some re-ranking in the middle range, but in almost all cases, the same top 10 or bottom 10 clones would have been identified in either analysis (data not shown). For tsh, the story was the same, while for ccs there are virtually no measurable differences between the methods (data not shown).

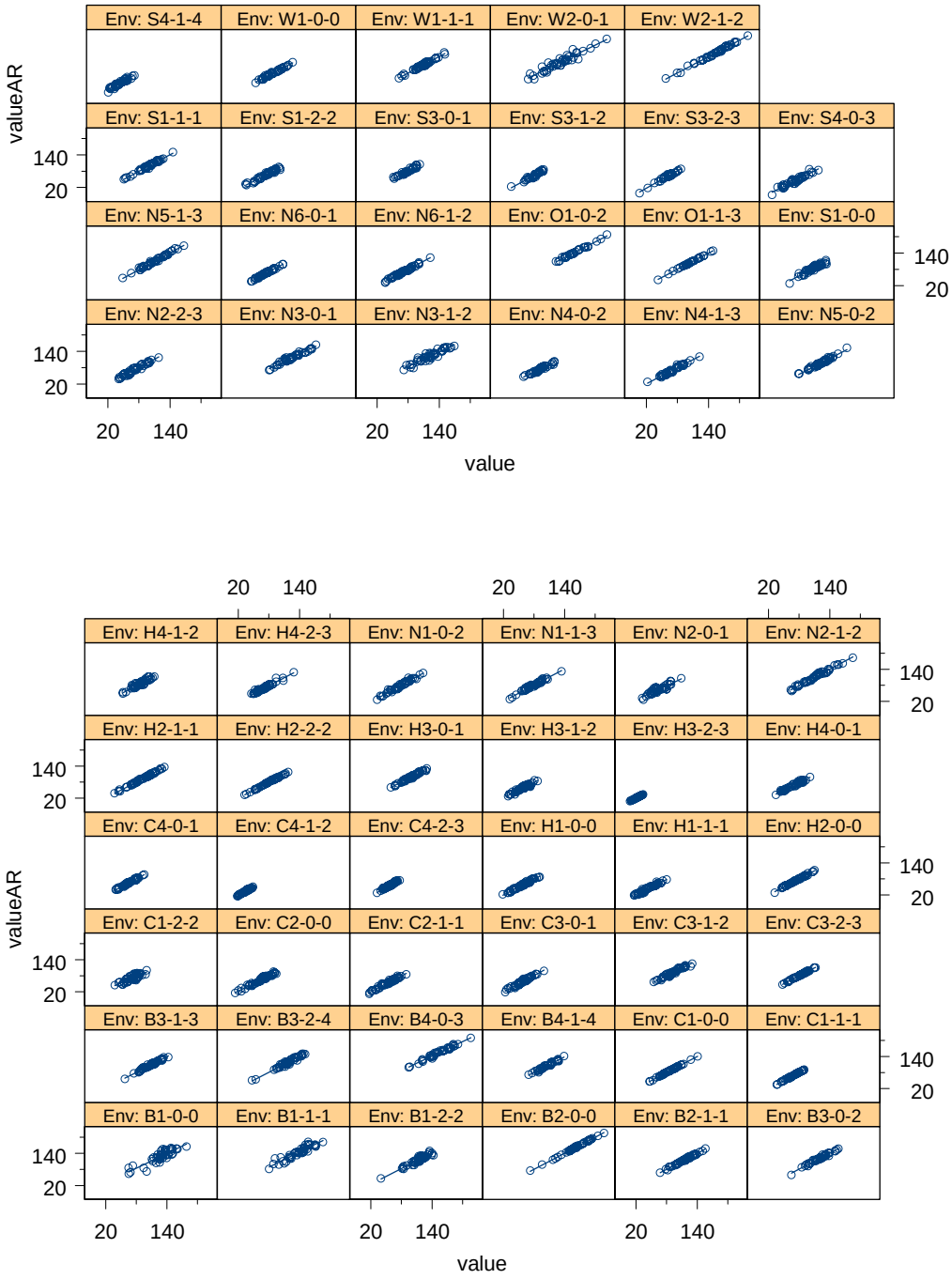


Figure 4-4 Plot of genotype BLUEs for tch of unselected clones calculated for each trial using AOVF model (value) or AOVFAR1 model (valueAR). In AOVF model, rep, row and column were fitted as random, while in AOVFAR1 model, rep was fitted as random, and row and column as spatial AR1 residual effects.

4.2.3. Error and genotypic variance components across trials increased with trial mean for tch and tsh and decrease for ccs

Method

Analyses from the AOVAR1 model are used here.

Table 4-8, Table 4-9 and Table 4-10 summarise these attributes of each trial. The data are presented for a model where Genotypes and Replicates are assumed to be random, and Row and Column effects are fitted using an auto-regressive (AR1) model to take account of spatial variation in the field. The figures following each table are a plot of log(trial mean) vs log(effective Error Mean Square), and also for the trial mean vs the genotypic variance component. The former of these is often observed for biomass or yield data in many types of plant breeding datasets. The final set of figures are a bar plot of means and genotypic variances in a bar plot.

Repeatability (H^2) was calculated for each trial as:

$H^2 = V_g/(V_g + V_{err}/n_r)$

Where V_g = estimated genotypic variance, V_{er} = effective error mean square, n_r = number of trial replicates (2 in all cases, except Ord where it was 3).

Result

In fitting random effects models, a test for 'significance' of the variance components is whether the z ratio (variance component divided by its standard error) exceeds 2. By this criteria, the genotypic variances for the 3 traits were significant in all cases except for TCH in B3-0-2 and B3-2-4, CCS in B4-0-3 and TSH in B4-0-3 and C3-0-1. The z ratios for these traits (and the other traits from Table 4-2) are given in Table 4-12, i.e. from the genotypic variance components in the following tables can be divided by the z.ratios in Table 4-12 to back-calculate the variance component standard errors.

Repeatability for ccs (Table 4-9) was generally greater than for tch (Table 4-8) and tsh (Table 4-10). Excluding one trial of particularly low genotypic variance (C3P), the repeatabilities for tch were between 0.79 and 0.83, except for the Burdekin (0.59), NSW (0.75) and Ord (0.90). Note that the Ord had 3 replicates which improved trial precision there.

For ccs, repeatabilities were greatest in Central and South (0.88), followed by the Herbert, North and NSW (0.81) and then the Burdekin (0.70). The values for tsh were mostly around 0.80, but lower in the Burdekin and NSW (associated with W2 – 2 year plant crop which had large genotypic and error variance – see figs).

For tch and tsh, there was a strong relationship between log(trial mean) and log(V_{err}). A weaker relationship also increases when considering trial mean vs genotypic variance (fit is similar for log and non-log data). However, the slope is less than for the comparison with EMS, and this results in the lower repeatabilities observed at higher tch in regions like the Burdekin in particular. At high TCH, both high (NSW) and low (Burdekin) V_g was observed, with a moderate level of V_g in the tonnage range of about 70 to 110 t/ha or so. However, in all cases, high tch resulted in relatively higher error and decreased precision.

The situation is reversed for ccs, with increasing error and genotypic variance occurring at lower trial mean values. The spread of variances at any mean value was greater than for the other traits, with the error increasing substantially at ccs below ca 12%.

The results for trial error variance still applied when averaged at the level of region (Table 4-11). The mean error variance for TCH in each region was related to the trial mean in the region, i.e. trials in the regions with the highest TCH had the greatest error variance. Similarly, greater error variance for CCS was associated with lower values of CCS.

Table 4-8 Trial means and variance components for TCH (from metEachAOVAR1.xls). * = removed. [ns]indicates that ratio of genotypic variance to its standard error did not exceed 2.

Trait						Grand mean	Effective Error MS	Phenotypic variance	Genotypic variance	Repeatability
Reg	Env	Loc	Cclass	HYear	Expid	gm	effems	Vp	Vg	H^2
B	B1-0-0	B1	0	2000	6	130.38	484.01	616.04	379.07	0.62
	B1-1-1	B1	1	2001	30	140.78	381.29	495.05	308.38	0.62
	B1-2-2	B1	2	2002	53	114.77	306.38	339.80	189.80	0.56
	B2-0-0	B2	0	2000	7	163.87	384.04	693.83	505.36	0.73
	B2-1-1	B2	1	2001	31	117.14	163.15	357.92	277.86	0.78
	B3-0-2	B3	0	2002	18	123.08	516.05	396.32	143.67[ns]	0.36
	B3-1-3	B3	1	2003	42	111.77	331.67	327.04	164.66	0.50
	B3-2-4	B3	2	2004	58	119.80	525.45	453.78	193.82 [ns]	0.43
	B4-0-3	B4	0	2003	24	156.86	473.09	509.26	277.97	0.55
	B4-1-4	B4	1	2004	57	104.58	135.38	229.04	162.85	0.71
B Total						128.30	370.05	441.81	260.35	0.59
C	C1-0-0	C1	0	2000	4	89.23	135.66	411.43	343.60	0.84
	C1-1-1	C1	1	2001	28	68.36	101.89	195.38	144.44	0.74
	C1-2-2	C1	2	2002	54	73.26	92.91	166.83	120.37	0.72
	C2-0-0	C2	0	2000	5	64.48	121.67	413.98	353.15	0.85
	C2-1-1	C2	1	2001	29	54.77	86.00	344.05	301.05	0.88
	C3-0-1	C3	0	2001	11	59.79	273.41	171.03	34.33	0.20*
	C3-1-2	C3	1	2002	35	93.75	176.77	272.14	183.76	0.68
	C3-2-3	C3	2	2003	48	83.29	87.24	237.70	194.08	0.82
	C4-0-1	C4	0	2001	12	68.43	92.66	207.40	160.58	0.77
	C4-1-2	C4	1	2002	36	33.98	36.34	71.74	53.57	0.75
	C4-2-3	C4	2	2003	49	58.73	25.18	130.71	118.12	0.90
C Total						68.01	111.79	238.40	182.46	0.74 (*0.79)
H	H1-0-0	H1	0	2000	8	58.14	80.17	289.81	249.72	0.86
	H1-1-1	H1	1	2001	32	47.65	118.88	251.41	191.97	0.76
	H2-0-0	H2	0	2000	9	75.16	122.52	283.21	223.04	0.79
	H2-1-1	H2	1	2001	33	93.45	77.65	547.20	509.06	0.93
	H2-2-2	H2	2	2002	47	83.75	122.11	412.47	352.51	0.85
	H3-0-1	H3	0	2001	13	101.66	168.84	295.74	209.78	0.71
	H3-1-2	H3	1	2002	37	59.09	73.91	187.21	149.59	0.80
	H3-2-3	H3	2	2003	50	23.30	16.51	41.73	33.33	0.80
	H4-0-1	H4	0	2001	14	70.68	81.25	264.91	223.42	0.84
	H4-1-2	H4	1	2002	38	89.81	131.59	280.00	212.80	0.76
	H4-2-3	H4	2	2003	51	73.80	127.64	228.50	164.68	0.72
H Total						70.59	101.92	280.20	229.08	0.80
N	N1-0-2	N1	0	2002	19	82.45	128.82	524.78	460.37	0.88
	N1-1-3	N1	1	2003	43	80.76	42.89	388.53	367.09	0.94
	N2-0-1	N2	0	2001	15	65.05	106.55	253.57	200.29	0.79
	N2-1-2	N2	1	2002	39	114.57	222.31	799.85	688.70	0.86
	N2-2-3	N2	2	2003	52	74.40	127.05	421.90	358.37	0.85
	N3-0-1	N3	0	2001	16	118.80	179.43	398.58	308.87	0.77
	N3-1-2	N3	1	2002	40	125.78	303.44	547.31	395.59	0.72
	N4-0-2	N4	0	2002	20	76.07	64.84	176.13	143.71	0.82

Trait						Grand mean	Effective Error MS	Phenotypic variance	Genotypic variance	Repeatability
Reg	Env	Loc	Cclass	HYear	Expid	gm	effems	Vp	Vg	H^2
	N4-1-3	N4	1	2003	44	72.67	76.82	322.97	284.56	0.88
	N5-0-2	N5	0	2002	21	99.32	143.34	356.33	284.66	0.80
	N5-1-3	N5	1	2003	45	112.24	181.47	644.38	553.64	0.86
	N6-0-1	N6	0	2001	17	65.81	91.10	217.44	171.89	0.79
	N6-1-2	N6	1	2002	41	72.43	104.13	407.12	355.06	0.87
N Total						89.26	136.32	419.91	351.75	0.83
O	O1-0-2	O1	0	2002	22	147.68	200.67	533.83	470.76	0.88
	O1-1-3	O1	1	2003	55	109.82	161.36	595.31	544.60	0.91
O Total						128.75	181.01	564.57	507.68	0.90
S	S1-0-0	S1	0	2000	3	85.60	130.61	268.31	203.00	0.76
	S1-1-1	S1	1	2001	27	99.52	224.40	371.07	258.87	0.70
	S1-2-2	S1	2	2002	46	68.37	112.25	295.83	239.71	0.81
	S3-0-1	S3	0	2001	10	81.74	50.30	194.81	169.67	0.87
	S3-1-2	S3	1	2002	34	66.93	58.22	237.29	208.18	0.88
	S3-2-3	S3	2	2003	56	64.09	79.63	288.39	248.02	0.86
	S4-0-3	S4	0	2003	23	51.96	162.74	565.07	483.70	0.86
	S4-1-4	S4	1	2004	59	46.58	50.83	229.18	203.76	0.89
S Total						70.60	108.62	306.24	251.86	0.83
W	W1-0-0	W1	0	2000	1	82.69	219.25	339.55	229.92	0.68
	W1-1-1	W1	1	2001	25	112.17	125.47	409.28	346.55	0.85
	W2-0-1	W2	0	2001	2	121.98	748.97	1482.36	1103.93	0.74
	W2-1-2	W2	1	2002	26	154.82	559.89	1135.17	849.27	0.75
W Total						117.91	413.39	841.59	632.42	0.75
Grand Total						89.18	181.49	381.81	292.60	0.76

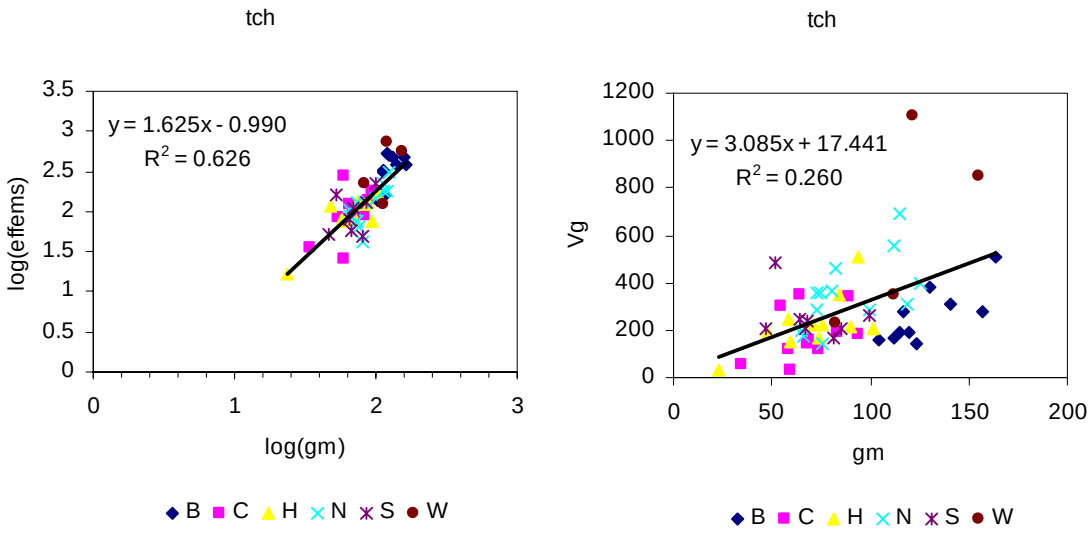


Figure 4-5 For TCH in all trials, coded by region, the relationship between (a) log(trial mean) and log(effective error mean square) and (b) trial mean and genotypic variance.

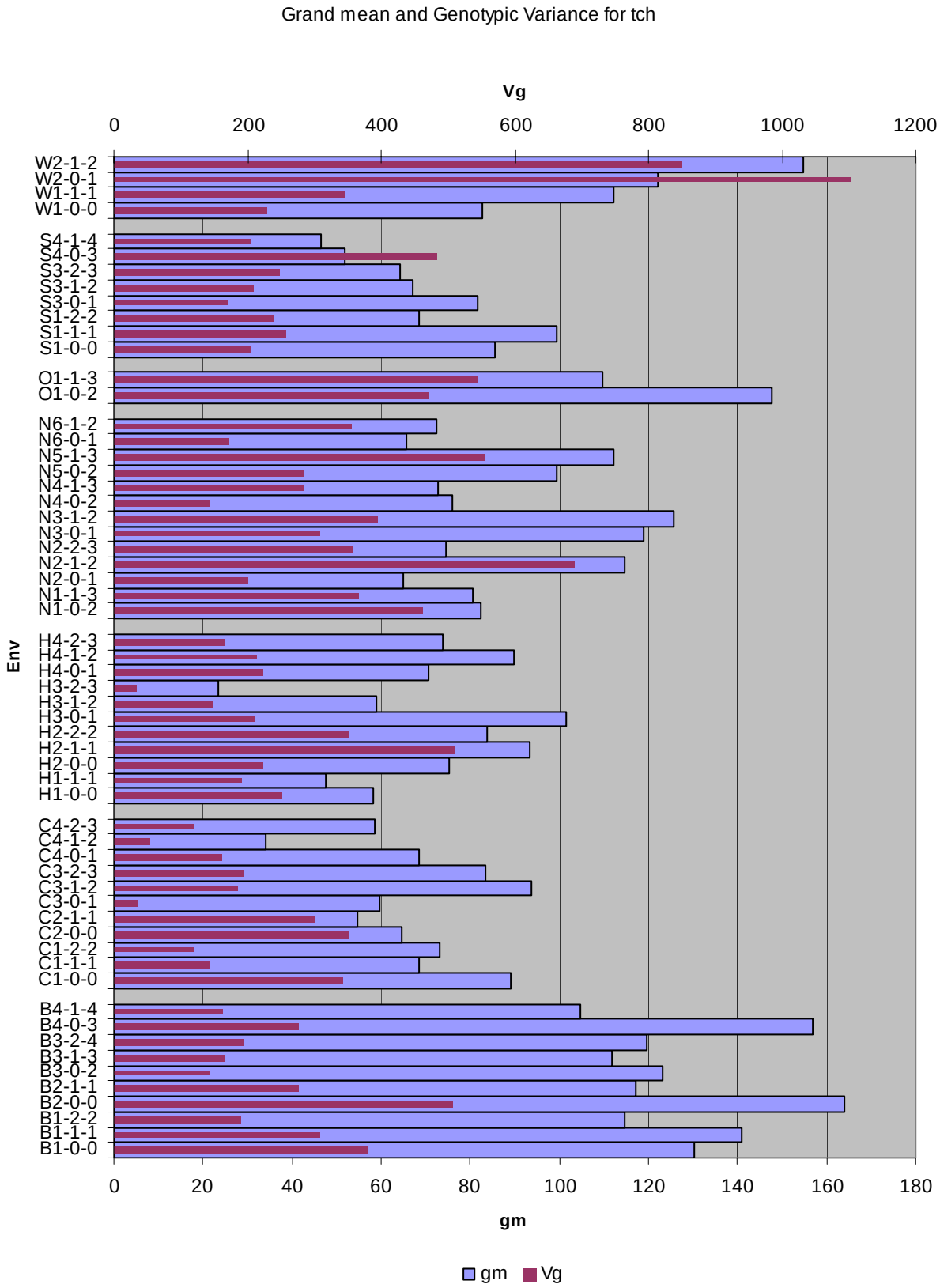


Figure 4-6 Grand mean (gm) and genotypic variance (V_g) for TCH in each trial.

Table 4-9 Trial means and variance components for CCS (from metEachAOVAR1.xls). * = removed. [ns]indicates that ratio of genotypic variance to its standard error did not exceed 2.

Reg	Env	Loc	Cclass	HYear	Expid	gm	effems	Vp	Vg	H2
B	B1-0-0	B1	0	2000	6	12.46	2.08	4.08	3.06	0.75
	B1-1-1	B1	1	2001	30	14.64	0.94	1.12	0.66	0.59
	B1-2-2	B1	2	2002	53	13.65	1.50	2.88	2.15	0.75
	B2-0-0	B2	0	2000	7	11.98	0.88	2.53	2.10	0.83
	B2-1-1	B2	1	2001	31	13.69	0.88	1.26	0.83	0.66
	B3-0-2	B3	0	2002	18	11.26	1.14	2.66	2.10	0.79
	B3-1-3	B3	1	2003	42	10.02	2.99	5.74	4.28	0.74
	B3-2-4	B3	2	2004	58	11.23	2.56	4.20	2.93	0.70
	B4-0-3	B4	0	2003	24	14.17	1.91	1.36	0.43 [ns]	0.32
	B4-1-4	B4	1	2004	57	16.76	0.19	0.63	0.53	0.85
B Total						12.99	1.51	2.65	1.91	0.70
C	C1-0-0	C1	0	2000	4	16.17	0.51	2.75	2.49	0.91
	C1-1-1	C1	1	2001	28	16.03	0.24	0.89	0.78	0.87
	C1-2-2	C1	2	2002	54	15.67	0.30	1.74	1.60	0.91
	C2-0-0	C2	0	2000	5	16.66	0.46	1.41	1.18	0.84
	C2-1-1	C2	1	2001	29	16.33	0.16	0.94	0.86	0.92
	C3-0-1	C3	0	2001	11	14.61	0.33	1.34	1.18	0.88
	C3-1-2	C3	1	2002	35	15.20	0.41	1.62	1.41	0.87
	C3-2-3	C3	2	2003	48	14.13	0.73	2.50	2.13	0.85
	C4-0-1	C4	0	2001	12	16.89	0.49	0.85	0.60	0.71
	C4-1-2	C4	1	2002	36	15.97	0.19	1.84	1.74	0.95
	C4-2-3	C4	2	2003	49	16.12	0.24	1.47	1.35	0.92
C Total						15.80	0.37	1.58	1.39	0.88
H	H1-0-0	H1	0	2000	8	15.13	0.42	1.17	0.95	0.82
	H1-1-1	H1	1	2001	32	15.76	0.41	1.31	1.11	0.84
	H2-0-0	H2	0	2000	9	12.80	0.40	1.92	1.73	0.90
	H2-1-1	H2	1	2001	33	13.64	0.69	2.19	1.85	0.85
	H2-2-2	H2	2	2002	47	16.14	1.08	1.67	1.14	0.68
	H3-0-1	H3	0	2001	13	15.14	0.42	2.17	1.95	0.90
	H3-1-2	H3	1	2002	37	14.93	1.22	2.56	1.94	0.76
	H3-2-3	H3	2	2003	50	14.84	0.76	1.24	0.85	0.68
	H4-0-1	H4	0	2001	14	16.70	0.30	0.86	0.71	0.82
	H4-1-2	H4	1	2002	38	16.38	0.28	1.10	0.96	0.87
	H4-2-3	H4	2	2003	51	14.27	0.70	1.41	1.06	0.75
H Total						15.07	0.61	1.60	1.30	0.81
N	N1-0-2	N1	0	2002	19	15.88	0.45	1.73	1.50	0.87
	N1-1-3	N1	1	2003	43	13.92	0.98	3.70	3.21	0.87
	N2-0-1	N2	0	2001	15	16.26	0.61	1.46	1.15	0.79
	N2-1-2	N2	1	2002	39	15.47	1.89	1.84	0.87	0.47
	N2-2-3	N2	2	2003	52	15.67	0.78	1.73	1.34	0.77
	N3-0-1	N3	0	2001	16	12.72	0.73	1.49	1.13	0.76
	N3-1-2	N3	1	2002	40	13.32	1.34	2.31	1.64	0.71
	N4-0-2	N4	0	2002	20	14.53	1.26	3.34	2.71	0.81
	N4-1-3	N4	1	2003	44	14.65	0.49	2.30	2.05	0.89

Reg	Env	Loc	Cclass	HYear	Expid	gm	effems	Vp	Vg	H2
	N5-0-2	N5	0	2002	21	14.69	0.94	1.87	1.40	0.75
	N5-1-3	N5	1	2003	45	13.79	0.60	2.23	1.93	0.86
	N6-0-1	N6	0	2001	17	15.05	0.86	1.87	1.44	0.77
	N6-1-2	N6	1	2002	41	15.63	0.53	1.40	1.13	0.81
N Total						14.74	0.88	2.10	1.65	0.78
O	O1-0-2	O1	0	2002	22	10.34	4.18	2.74	1.41	0.52
	O1-1-3	O1	1	2003	55	12.07	1.97	2.20	1.55	0.70
O Total						11.20	3.08	2.47	1.48	0.61
S	S1-0-0	S1	0	2000	3	14.08	0.36	1.90	1.72	0.90
	S1-1-1	S1	1	2001	27	15.00	0.38	1.38	1.19	0.86
	S1-2-2	S1	2	2002	46	14.23	0.66	1.26	0.93	0.74
	S3-0-1	S3	0	2001	10	14.85	0.21	1.22	1.12	0.92
	S3-1-2	S3	1	2002	34	15.96	0.14	1.25	1.18	0.94
	S3-2-3	S3	2	2003	56	15.23	0.23	1.28	1.16	0.91
	S4-0-3	S4	0	2003	23	10.47	0.40	1.81	1.61	0.89
	S4-1-4	S4	1	2004	59	14.43	0.37	1.31	1.12	0.86
S Total						14.28	0.34	1.43	1.25	0.88
W	W1-0-0	W1	0	2000	1	8.30	0.59	2.72	2.43	0.89
	W1-1-1	W1	1	2001	25	13.47	0.36	1.03	0.84	0.82
	W2-0-1	W2	0	2001	2	13.61	0.39	0.85	0.66	0.77
	W2-1-2	W2	1	2002	26	11.16	0.58	1.25	0.96	0.77
W Total						11.63	0.48	1.46	1.22	0.81
Grand Total						14.31	0.81	1.88	1.49	0.80

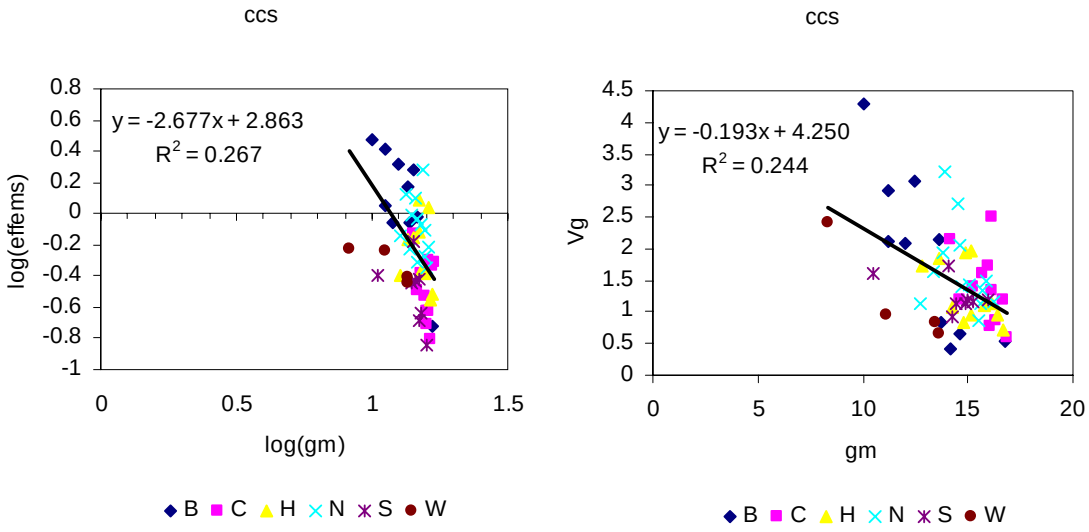


Figure 4-7 For CCS in all trials, coded by region, the relationship between (a) log(trial mean) and log(effective error mean square) and (b) trial mean and genotypic variance

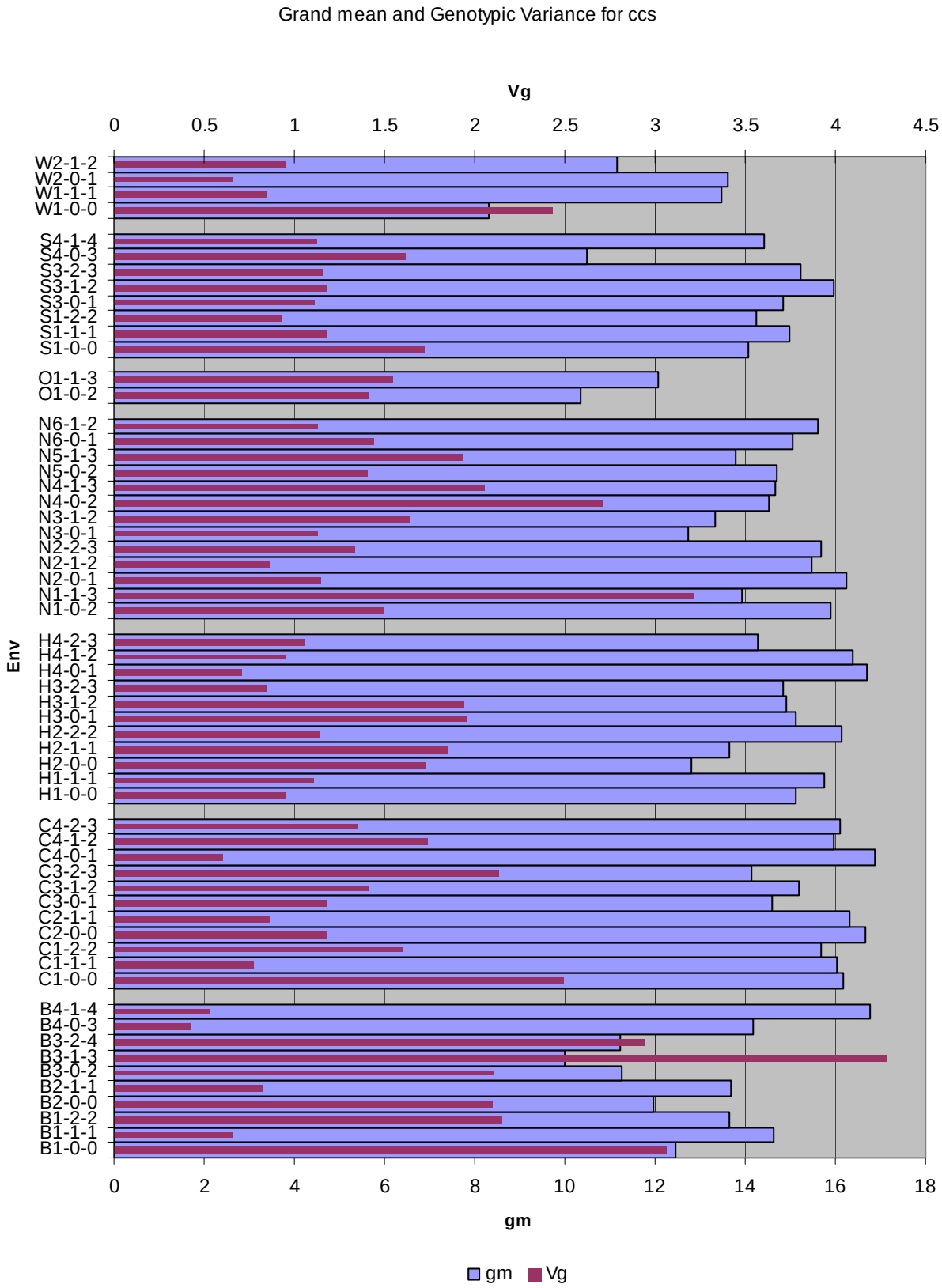


Figure 4-8 Grand mean (gm) and genotypic variance (Vg) for CCS in each trial.

Table 4-10 Trial means and variance components for TSH (from metEachAOVAR1.xls). [ns]indicates that ratio of genotypic variance to its standard error did not exceed 2.

Reg	Env	Loc	Cclass	HYear	Expid	gm	effems	Vp	Vg	H2
B	B1-0-0	B1	0	2000	6	16.30	10.01	18.02	13.12	0.73
	B1-1-1	B1	1	2001	30	20.55	8.89	13.07	8.72	0.67
	B1-2-2	B1	2	2002	53	15.70	7.49	10.27	6.60	0.64
	B2-0-0	B2	0	2000	7	19.71	8.17	17.79	13.78	0.77
	B2-1-1	B2	1	2001	31	16.06	4.34	8.59	6.46	0.75
	B3-0-2	B3	0	2002	18	13.87	10.48	9.87	4.74	0.48
	B3-1-3	B3	1	2003	42	11.28	5.96	12.09	9.17	0.76
	B3-2-4	B3	2	2004	58	13.45	8.53	11.77	7.54	0.64
	B4-0-3	B4	0	2003	24	22.22	17.70	16.21	7.55 [ns]	0.47
	B4-1-4	B4	1	2004	57	17.50	3.66	6.69	4.90	0.73
B Total						16.66	8.52	12.44	8.26	0.66
C	C1-0-0	C1	0	2000	4	14.46	4.39	13.34	11.14	0.84
	C1-1-1	C1	1	2001	28	11.00	2.87	6.28	4.85	0.77
	C1-2-2	C1	2	2002	54	11.49	2.68	5.30	3.96	0.75
	C2-0-0	C2	0	2000	5	10.79	3.88	13.02	11.08	0.85
	C2-1-1	C2	1	2001	29	9.01	2.53	10.37	9.11	0.88
	C3-0-1	C3	0	2001	11	8.67	5.42	3.09	0.38 [ns]	0.12
	C3-1-2	C3	1	2002	35	14.21	4.01	7.66	5.63	0.74
	C3-2-3	C3	2	2003	48	11.75	2.30	6.31	5.16	0.82
	C4-0-1	C4	0	2001	12	11.55	2.75	6.06	4.67	0.77
	C4-1-2	C4	1	2002	36	5.43	1.12	2.10	1.54	0.73
	C4-2-3	C4	2	2003	49	9.45	0.84	3.65	3.23	0.88
C Total						10.71	2.98	7.02	5.52	0.74
H	H1-0-0	H1	0	2000	8	8.81	2.23	7.42	6.31	0.85
	H1-1-1	H1	1	2001	32	7.49	3.30	6.31	4.66	0.74
	H2-0-0	H2	0	2000	9	9.62	2.10	5.69	4.66	0.82
	H2-1-1	H2	1	2001	33	12.79	1.79	12.46	11.58	0.93
	H2-2-2	H2	2	2002	47	13.58	3.36	13.62	11.97	0.88
	H3-0-1	H3	0	2001	13	15.38	4.48	9.79	7.51	0.77
	H3-1-2	H3	1	2002	37	8.78	1.98	4.80	3.80	0.79
	H3-2-3	H3	2	2003	50	3.47	0.46	0.89	0.65	0.73
	H4-0-1	H4	0	2001	14	11.83	2.46	8.62	7.36	0.85
	H4-1-2	H4	1	2002	38	14.73	3.48	9.86	8.08	0.82
	H4-2-3	H4	2	2003	51	10.57	3.42	6.05	4.34	0.72
H Total						10.64	2.64	7.77	6.45	0.81
N	N1-0-2	N1	0	2002	19	13.17	3.63	17.88	16.07	0.90
	N1-1-3	N1	1	2003	43	11.14	2.55	8.36	7.06	0.85
	N2-0-1	N2	0	2001	15	10.59	2.97	7.20	5.70	0.79
	N2-1-2	N2	1	2002	39	17.86	8.32	21.67	17.42	0.80
	N2-2-3	N2	2	2003	52	11.65	3.40	11.87	10.17	0.86
	N3-0-1	N3	0	2001	16	15.15	3.95	8.80	6.83	0.78
	N3-1-2	N3	1	2002	40	16.82	7.21	13.53	9.92	0.73
	N4-0-2	N4	0	2002	20	11.05	2.14	6.23	5.16	0.83
	N4-1-3	N4	1	2003	44	10.67	1.86	9.31	8.38	0.90
	N5-0-2	N5	0	2002	21	14.61	4.92	10.09	7.63	0.76

Reg	Env	Loc	Cclass	HYear	Expid	gm	effems	Vp	Vg	H2
	N5-1-3	N5	1	2003	45	15.48	5.79	15.18	12.25	0.81
	N6-0-1	N6	0	2001	17	9.89	2.32	5.49	4.33	0.79
	N6-1-2	N6	1	2002	41	11.33	3.29	10.68	9.03	0.85
N Total						13.03	4.03	11.25	9.23	0.82
O	O1-0-2	O1	0	2002	22	15.28	11.64	11.85	8.16	0.69
	O1-1-3	O1	1	2003	55	13.46	3.96	14.22	12.91	0.91
O Total						14.37	7.80	13.04	10.54	0.80
S	S1-0-0	S1	0	2000	3	12.10	3.12	7.90	6.34	0.80
	S1-1-1	S1	1	2001	27	14.96	5.21	11.11	8.51	0.77
	S1-2-2	S1	2	2002	46	9.77	2.70	7.51	6.16	0.82
	S3-0-1	S3	0	2001	10	12.14	1.13	5.65	5.08	0.90
	S3-1-2	S3	1	2002	34	10.72	1.77	7.28	6.40	0.88
	S3-2-3	S3	2	2003	56	9.92	2.13	6.60	5.50	0.83
	S4-0-3	S4	0	2003	23	5.49	1.38	7.62	6.93	0.91
	S4-1-4	S4	1	2004	59	6.72	0.95	5.18	4.70	0.91
S Total						10.23	2.30	7.35	6.20	0.85
W	W1-0-0	W1	0	2000	1	6.88	1.59	4.67	3.88	0.83
	W1-1-1	W1	1	2001	25	15.11	4.19	8.66	6.56	0.76
	W2-0-1	W2	0	2001	2	16.49	15.27	28.54	20.82	0.73
	W2-1-2	W2	1	2002	26	17.30	10.73	17.68	12.25	0.69
W Total						13.95	7.94	14.88	10.88	0.75
Grand Total						12.50	4.49	9.79	7.60	0.78

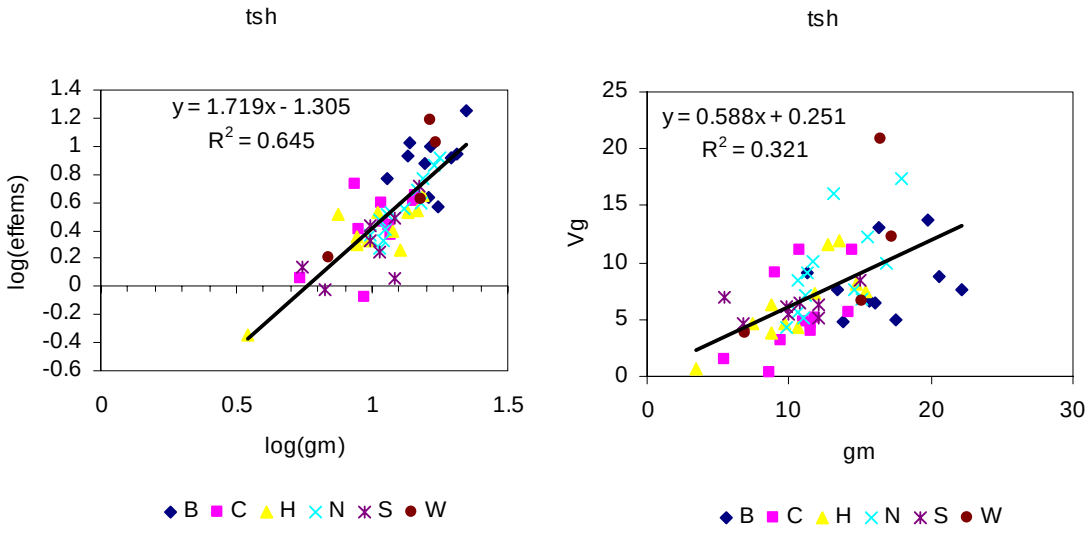


Figure 4-9 For TSH in all trials, coded by region, the relationship between (a) log(trial mean) and log(effective error mean square) and (b) trial mean and genotypic variance

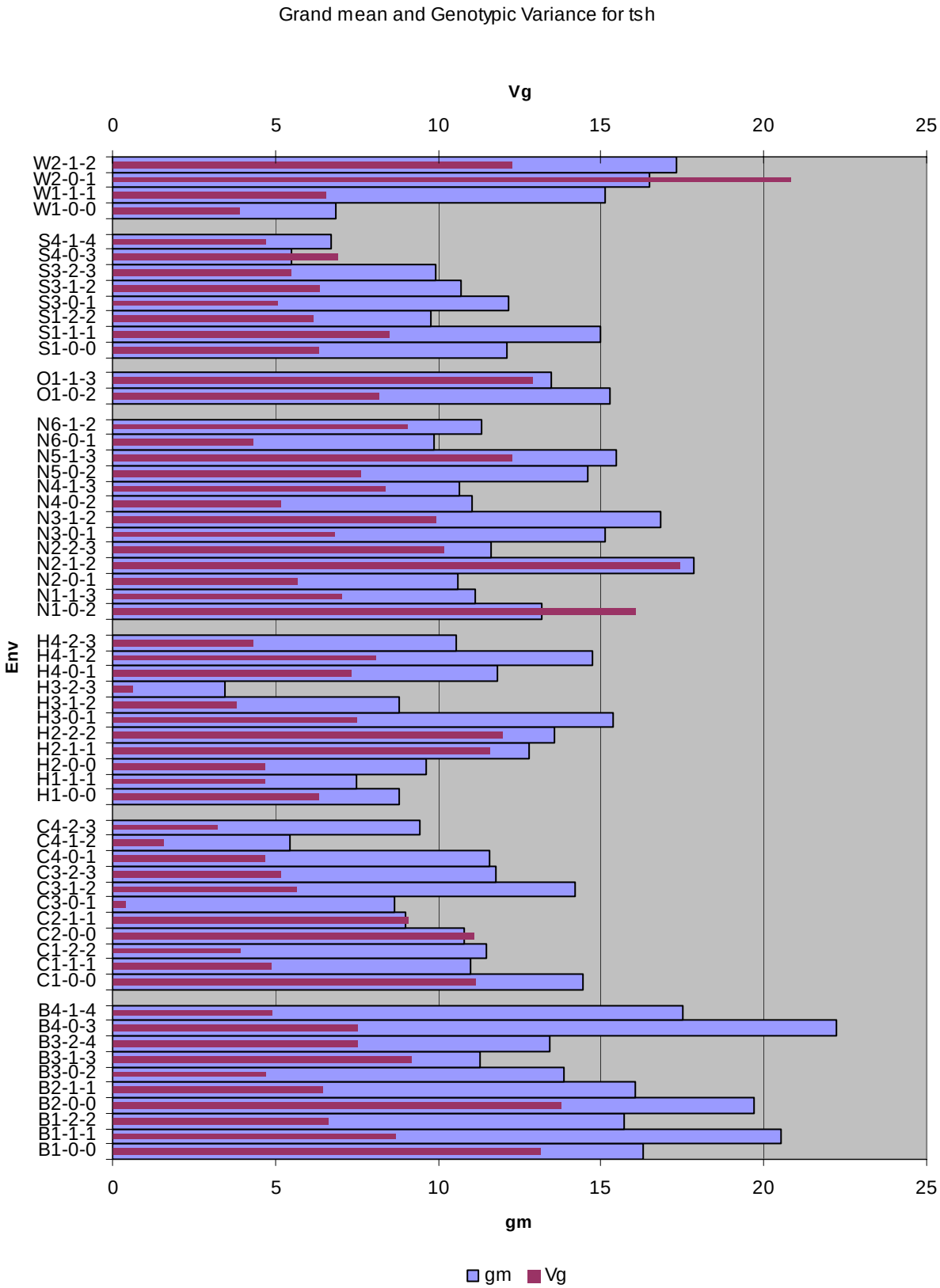


Figure 4-10 Grand mean (gm) and genotypic variance (Vg) for TSH in each trial.

Table 4-11 Mean trial values and estimates of trial residual variance components for TCH (t^2 ha^{-1}) and CCS (CCS units^2). In the GxE analysis within and across regions, a heterogeneous error model was used (i.e. each trial was fitted). These data are the average trial residual error variance from individual analyses of each trial.

Region	*TCH*		*CCS*	
	mean	Var	Mean	Var
North	89	161	14.7	0.88
Herbert	71	107	15.1	0.62
Burdekin	128	414	13	1.52
Central	68	112	15.8	0.38
South	71	134	14.3	0.35
NSW	118	409	11.6	0.47
Ord	129	186	11.2	3.03

4.3. Comparison of commercial checks (Q canes) with unselected clones at trial, location and region levels

4.3.1. Averaged over entries, commercial checks ('Q canes') had higher tch and ccs than unselected clones in all trials

Method

Taking the BLUEs data derived from the AOVF model above, the values of tch and ccs were averaged for the unselected clones (ca. 40 to 48 entries per trial) and the Q canes (ca. 4 to 8 entries). The means for the unselected clones were regressed against the Q canes.

Result

For both tch and ccs, the mean value for unselected clones was around 90% that of the Q canes in most of the trials (Figure 4-11). The largest deviations for tch were in the coolest site, W2, where the tch of unselected clones was < 70% of the Q canes and for ccs in B1 (ca. 80%).

4.3.2. Averaged over entries and either trials, locations or regions, the top 10% of unselected clones were equal to or superior to Q canes

Method

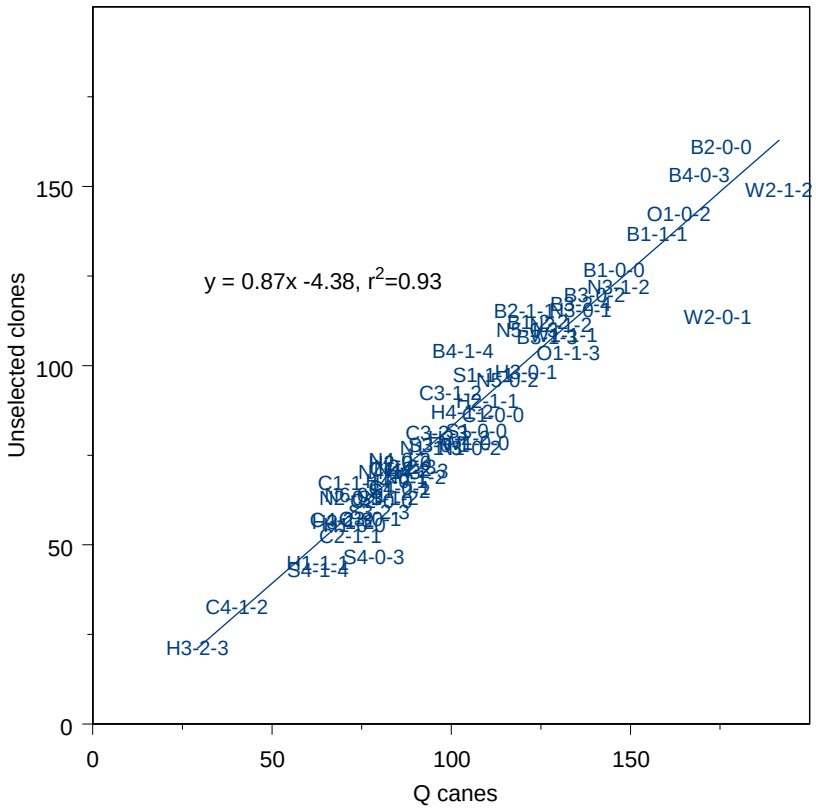
Using the data described above, the unselected clones and Q canes were averaged over locations or regions. For the same aggregations, the top 10% of the 40 to 50 unselected clones (i.e. 4 or 5 entries for each location or region) for either tch, ccs or tsh were also averaged. Regressions were fitted to compare unselected clones against Q canes.

Result

The lower line in the panels of Figure 4-12 is the same as in Figure 4-11. The upper line showed that the top 10% unselected clones were slightly superior to the Q canes (ca. 5%) for tch and tsh. At lower levels of ccs, there was 2-3 unit advantage of the top 10% clones.

However, inspection of this data indicates that the high ccs clones tend to be poor for tch cf. the Q canes (not shown).

When selected at the level of mean performance in a location (Figure 4-13) or region (Figure 4-14), the differences between the Q canes and top 10% clones were smaller. In both cases, the clonal performance was poorer in the highest tsh and tch location (W2). The two-year plant crop at this site experienced substantial lodging, and was quite variable (see above section on error variances).



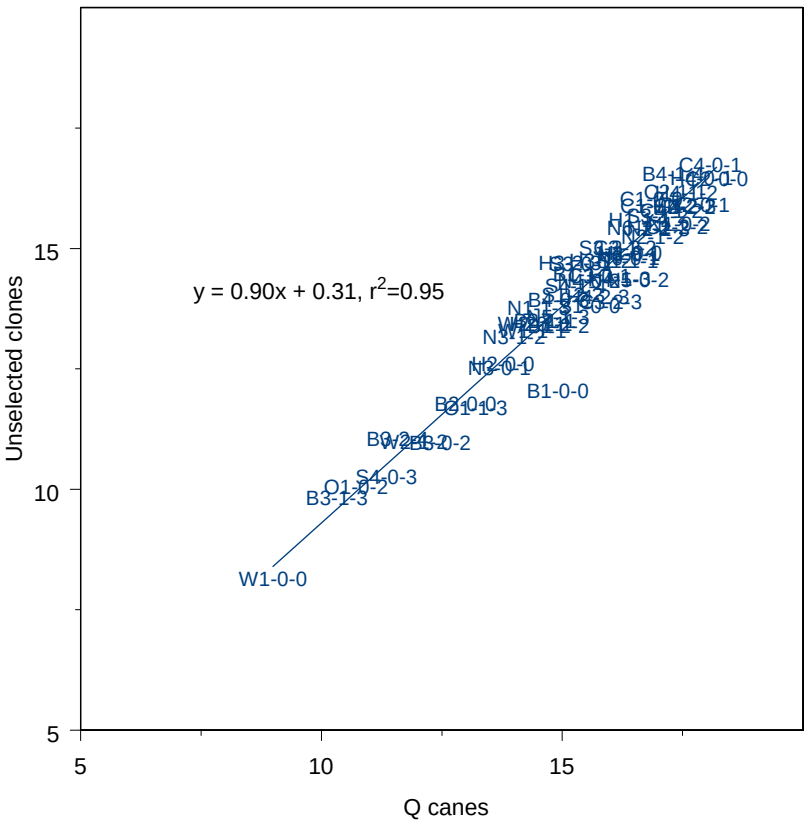


Figure 4-11 Plot of trial mean tch (top) or ccs (bottom) for commercial checks (Q canes) vs unselected clones

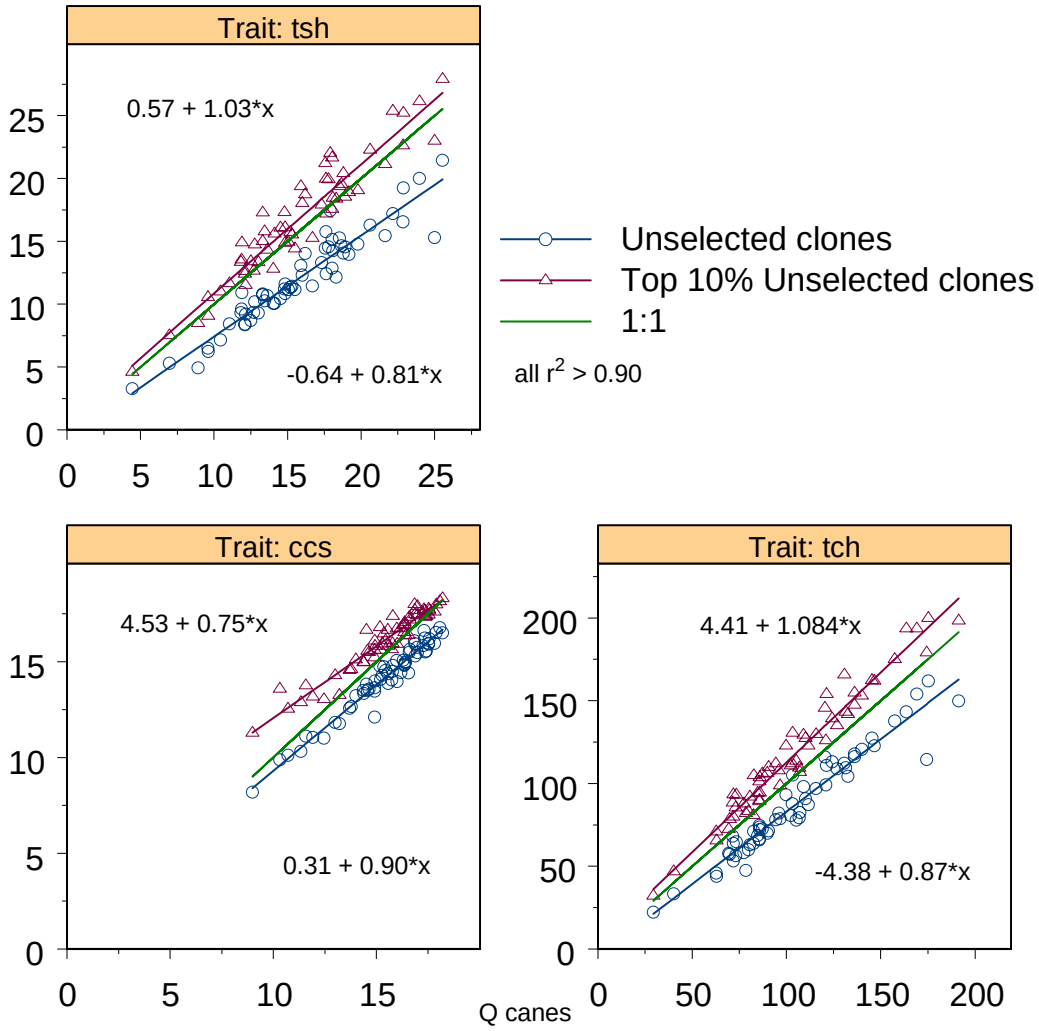


Figure 4-12 For each trial and trait, relative performance of Q canes vs unselected clones (see Figure 4-11) for trial refs) or top 10% of unselected clones. Top 10% is usually from 4 clones (3 to 5), depending on number of entries per trial, which ranged from 36 to 56, but was nominally 48.

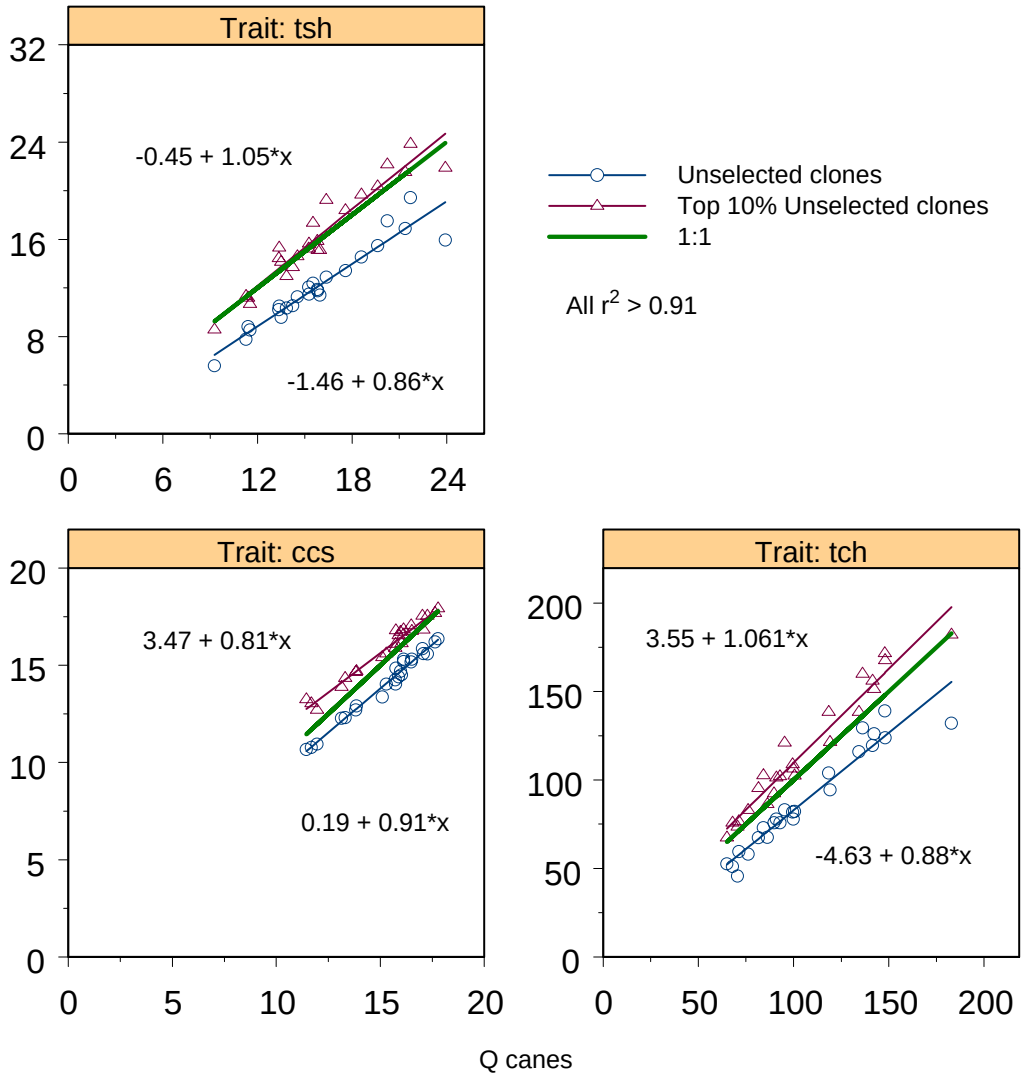


Figure 4-13 For each location and trait, relative performance of Q canes vs unselected clones or top 10% of unselected clones. Top 10% is usually from 4 clones (3 to 5), depending on number of entries per trial.

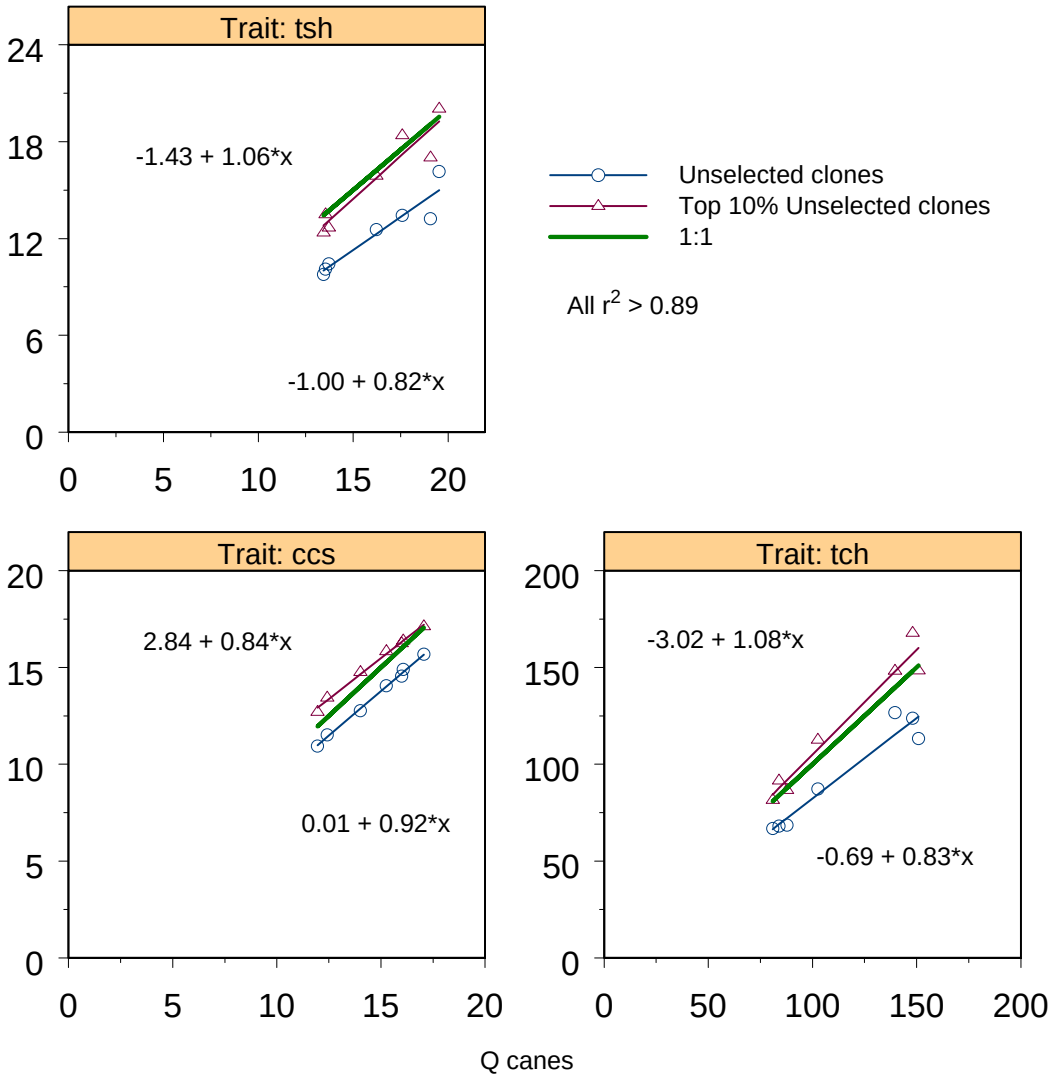


Figure 4-14 For each region and trait, relative performance of Q canes vs unselected clones or top 10% of unselected clones. Top 10% is usually from 4 clones (3 to 5), depending on number of entries per trial.

Table 4-12 For each trait analysed in each environment the z.ratio for the random effect of genotype. Lightly shaded values (> 2.0) are considered 'significant' in a mixed model context, while the darker shaded values are considered not significant. NA indicates that the trait was not observed in a trial.

Env	arr	brx	brxe	ccs	ccse	con	dia	dmc	fib	len	lod	Pol	pole	pur	pure	sfw	ssh	stc	stp	sts	suw	tch	tsh
B1-0-0	3.16	2.10	NA	3.43	NA	3.31	4.38	NA	NA	3.74	3.23	3.29	NA	3.51	NA	4.44	6.89	3.18	1.13	3.05	2.41	2.34	3.39
B1-1-1	NA	3.66	NA	3.11	NA	NA	NA	NA	NA	NA	3.77	3.32	NA	1.96	NA	NA	0.01	NA	6.48	1.83	1.69	2.18	2.85
B1-2-2	6.89	3.68	NA	3.43	NA	3.47	NA	4.79	4.79	NA	2.72	3.57	NA	2.83	NA	NA	0.02	NA	2.40	2.22	0.82	2.19	2.84
B2-0-0	4.47	4.18	4.35	4.13	4.22	4.23	4.43	4.34	4.34	3.75	3.67	4.19	4.28	NA	NA	4.58	0.31	4.05	1.98	3.36	2.62	3.60	3.84
B2-1-1	3.46	2.85	NA	3.21	NA	NA	4.57	4.39	4.39	4.11	4.37	3.16	NA	NA	NA	4.37	4.45	3.69	3.25	NA	3.23	3.84	3.69
B3-0-2	0.01	3.60	NA	3.73	NA	NA	3.95	NA	NA	2.85	2.72	3.83	NA	3.47	NA	NA	6.89	NA	NA	2.27	2.13	1.40	2.14
B3-1-3	0.01	3.18	NA	3.49	NA	3.79	2.89	0.70	2.73	1.29	2.56	3.56	NA	3.31	NA	4.09	5.90	2.49	NA	0.01	NA	2.21	3.45
B3-2-4	NA	NA	NA	3.26	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.67	3.02
B4-0-3	NA	3.03	NA	1.38	NA	3.67	2.36	1.97	1.71	2.67	1.24	2.20	NA	1.56	NA	3.36	NA	1.60	NA	NA	6.67	2.31	1.85
B4-1-4	NA	NA	NA	3.80	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	2.90	3.05
C1-0-0	4.21	4.28	4.43	4.37	4.21	3.58	NA	NA	4.47	NA	6.48	4.26	4.48	4.34	4.35	NA	NA	NA	NA	1.12	0.46	3.99	4.05
C1-1-1	4.64	4.06	0.64	4.04	0.09	NA	NA	NA	NA	NA	6.89	3.95	3.48	2.54	0.29	NA	NA	NA	NA	3.90	3.23	3.52	3.68
C1-2-2	0.00	4.46	4.10	4.42	4.12	4.44	3.77	NA	3.75	4.28	2.97	4.50	4.13	3.13	4.03	4.26	NA	3.82	NA	2.18	1.93	3.81	3.70
C2-0-0	4.00	3.57	NA	3.88	NA	2.79	NA	NA	4.22	NA	2.33	3.77	NA	3.23	NA	NA	NA	NA	NA	1.15	0.43	4.01	4.00
C2-1-1	4.67	4.20	NA	4.41	NA	NA	NA	NA	NA	NA	3.62	4.30	NA	3.22	NA	NA	NA	NA	NA	3.40	2.73	4.20	4.20
C3-0-1	4.55	4.07	NA	4.13	NA	NA	NA	NA	NA	NA	4.19	4.08	NA	3.46	NA	NA	NA	NA	NA	0.92	0.60	2.47	1.81
C3-1-2	0.27	4.07	NA	4.26	NA	4.44	3.95	NA	4.22	3.61	1.29	4.30	NA	3.04	NA	4.44	1.36	3.68	0.25	NA	1.29	2.67	3.09
C3-2-3	4.66	4.07	NA	4.08	NA	4.44	3.95	NA	3.57	3.61	1.79	4.30	NA	3.04	NA	4.44	4.28	3.07	NA	2.55	3.98	3.90	3.82
C4-0-1	4.71	3.11	3.56	3.12	3.87	3.31	NA	NA	4.38	NA	3.15	2.75	3.91	1.67	3.51	NA	NA	NA	NA	6.89	6.32	3.75	3.71
C4-1-2	3.21	4.13	3.85	4.60	3.78	4.62	4.00	NA	4.30	4.07	NA	4.69	3.80	3.81	3.70	4.41	NA	3.47	NA	5.91	6.48	3.29	3.39
C4-2-3	4.08	NA	NA	4.41	NA	NA	NA	NA	3.50	NA	6.86	NA	NA	NA	NA	NA	NA	NA	NA	1.89	0.43	4.16	4.13
H1-0-0	NA	4.35	3.57	4.31	4.10	4.65	4.71	4.66	4.66	3.97	7.00	4.46	4.18	0.62	3.11	4.58	0.00	3.92	NA	4.44	2.48	4.53	4.50
H1-1-1	4.42	4.36	1.66	4.40	2.11	4.46	3.77	3.51	3.69	2.61	7.00	4.22	2.42	2.48	0.88	2.95	4.10	3.46	NA	NA	3.62	3.81	3.71
H2-0-0	4.51	4.61	NA	4.58	NA	4.18	4.25	4.39	4.39	4.36	4.75	4.64	NA	2.78	NA	4.51	NA	3.24	NA	3.63	3.86	4.06	4.28
H2-1-1	4.40	3.99	NA	4.32	NA	3.44	4.28	3.71	3.71	3.46	3.31	4.30	NA	3.64	NA	4.17	2.95	3.91	7.45	4.24	1.46	4.77	4.76
H2-2-2	3.37	4.36	NA	3.00	NA	4.57	4.37	3.62	3.62	3.83	3.37	3.72	NA	0.12	NA	4.04	1.64	3.76	1.24	1.63	1.48	4.37	4.49
H3-0-1	4.24	4.84	NA	4.73	NA	4.84	4.77	3.47	3.75	2.94	2.87	4.75	NA	3.59	NA	4.84	1.30	3.69	0.66	NA	0.42	3.47	3.76
H3-1-2	4.70	3.36	3.73	3.97	4.07	3.83	4.38	4.00	4.00	3.75	NA	3.95	3.98	3.62	4.14	4.44	NA	4.31	NA	NA	NA	4.21	3.94
H3-2-3	4.91	3.72	2.51	3.44	2.27	2.65	4.42	4.54	4.54	3.78	NA	3.58	2.54	2.20	2.10	4.40	NA	2.88	NA	2.20	2.26	4.08	3.65
H4-0-1	4.52	3.99	1.42	3.98	1.13	4.00	4.08	4.33	4.33	3.48	4.28	3.98	1.26	3.50	0.65	3.65	4.18	2.75	1.53	3.29	3.94	3.89	3.95
H4-1-2	4.11	3.76	NA	3.95	NA	4.44	4.06	4.04	4.02	3.78	3.31	3.99	NA	1.39	NA	4.39	4.09	3.37	3.30	0.32	0.22	3.04	3.48
H4-2-3	4.53	3.50	NA	3.45	NA	2.77	3.88	4.02	4.05	3.17	3.60	3.59	NA	2.48	NA	4.26	0.00	3.62	6.89	NA	2.02	4.02	3.76
N1-0-2	4.54	4.44	NA	4.08	NA	4.02	4.02	NA	4.42	4.04	3.49	4.13	NA	NA	NA	4.30	NA	3.23	NA	4.07	3.70	3.91	4.04

Env	arr	brx	brxe	ccs	ccse	con	dia	dmc	fib	len	lod	Pol	pole	pur	pure	sfw	ssh	stc	stp	sts	suw	tch	tsh
N1-1-3	NA	3.81	NA	4.17	NA	3.63	4.41	NA	4.48	4.37	3.70	4.24	NA	3.80	NA	4.65	NA	3.95	NA	3.12	2.46	4.41	3.85
N2-0-1	2.24	3.71	3.98	3.73	3.94	3.49	4.01	NA	4.28	3.69	3.37	3.69	3.96	NA	3.76	3.46	4.02	3.55	NA	6.48	1.01	2.66	2.57
N2-1-2	4.39	2.62	NA	2.22	NA	2.70	4.19	NA	4.32	3.12	4.10	2.57	NA	NA	NA	4.49	4.00	4.01	NA	0.68	3.27	4.05	3.82
N2-2-3	3.21	3.79	NA	3.64	NA	4.13	3.83	NA	4.29	3.42	2.80	3.83	NA	2.13	NA	4.23	NA	3.51	NA	0.98	3.60	3.81	3.96
N3-0-1	0.53	3.77	NA	3.81	NA	3.28	4.33	NA	4.64	4.10	6.63	3.91	NA	NA	NA	4.11	6.89	3.39	NA	6.63	6.63	3.42	3.51
N3-1-2	3.29	3.19	NA	3.35	NA	NA	4.49	NA	2.49	4.24	3.96	3.66	NA	2.86	NA	4.26	NA	3.33	NA	NA	NA	3.12	3.36
N4-0-2	4.59	3.67	3.01	3.77	3.05	NA	4.41	NA	4.56	3.93	NA	3.95	3.07	NA	2.70	4.26	NA	3.82	NA	4.16	3.55	3.65	3.84
N4-1-3	NA	4.07	3.86	4.29	NA	3.45	3.54	NA	4.41	4.13	NA	4.26	3.96	NA	NA	4.05	NA	3.64	NA	NA	NA	4.14	4.21
N5-0-2	4.48	3.19	NA	3.58	NA	3.14	4.47	NA	4.29	3.09	4.03	3.46	NA	NA	NA	4.32	NA	3.43	NA	3.94	3.02	3.68	3.61
N5-1-3	4.24	4.25	NA	4.15	NA	2.75	4.24	NA	4.31	3.49	4.11	4.25	NA	3.68	NA	3.80	NA	3.41	NA	3.84	4.20	4.06	3.83
N6-0-1	4.83	3.75	NA	3.70	NA	2.34	2.57	NA	4.48	4.02	0.83	3.80	NA	NA	NA	3.07	NA	2.05	NA	3.03	3.56	3.70	3.76
N6-1-2	4.53	4.04	NA	3.77	NA	3.08	3.56	NA	3.90	4.20	3.85	3.81	NA	NA	NA	4.27	NA	3.45	NA	2.78	5.90	4.13	3.96
O1-0-2	NA	2.80	NA	2.11	NA	2.73	3.69	3.25	3.02	3.04	NA	2.40	NA	1.16	NA	3.66	0.86	3.20	NA	NA	0.27	3.51	2.80
O1-1-3	NA	2.34	NA	2.82	NA	NA	NA	NA	3.62	NA	NA	2.69	NA	1.66	NA	NA	NA	NA	NA	NA	NA	3.65	3.61
S1-0-0	0.47	4.30	4.16	4.36	4.23	NA	4.48	4.34	4.34	3.85	0.07	4.30	4.24	4.01	4.14	4.32	4.49	3.95	NA	2.84	4.09	3.42	3.83
S1-1-1	6.32	4.25	4.32	4.16	4.30	3.35	4.56	4.15	4.15	3.98	6.89	4.17	4.33	3.56	4.03	4.37	NA	3.93	3.57	4.57	4.48	3.22	3.61
S1-2-2	0.64	3.42	NA	3.51	NA	3.41	4.42	4.19	4.19	4.12	5.92	3.34	NA	3.53	NA	4.09	2.73	3.27	NA	0.03	2.16	3.70	3.81
S3-0-1	3.67	NA	3.78	3.83	3.69	3.41	3.94	3.84	3.84	3.95	3.50	NA	3.74	NA	3.46	3.63	NA	3.45	NA	5.96	5.20	3.47	3.56
S3-1-2	NA	3.96	3.93	3.92	3.84	3.84	3.88	3.99	3.99	3.86	3.68	3.94	3.87	2.97	3.61	3.64	NA	3.25	NA	3.49	3.29	3.50	3.58
S3-2-3	3.43	3.88	NA	3.87	NA	3.49	3.83	3.74	3.74	3.85	3.01	3.88	NA	3.82	NA	3.69	0.00	2.72	5.54	0.29	0.67	3.59	3.51
S4-0-3	NA	3.78	NA	3.95	NA	NA	3.91	4.15	4.15	3.88	2.02	3.92	NA	3.91	NA	4.20	NA	2.82	6.00	1.95	5.92	3.38	3.66
S4-1-4	NA	3.95	NA	3.74	NA	NA	NA	NA	NA	NA	NA	3.86	NA	3.47	NA	NA	NA	NA	NA	NA	NA	3.64	3.74
W1-0-0	NA	4.42	4.14	4.27	4.19	NA	3.17	NA	NA	3.03	1.46	4.39	4.17	3.82	4.20	NA	NA	NA	NA	NA	NA	3.13	4.05
W1-1-1	NA	3.65	4.35	3.97	4.26	NA	3.41	NA	NA	2.09	3.86	3.87	4.30	3.63	4.00	4.11	2.67	3.86	2.43	NA	4.54	4.03	3.82
W2-0-1	0.00	3.90	3.89	3.79	3.97	NA	4.13	NA	NA	3.20	2.93	3.85	3.97	2.97	3.80	3.45	6.89	2.62	2.55	1.83	1.28	3.44	3.44
W2-1-2	NA	3.38	3.56	3.73	3.88	NA	3.80	NA	4.34	2.70	2.09	3.60	3.89	3.04	3.58	3.80	NA	2.61	NA	1.54	1.60	3.61	3.30

4.3.3. Values of tch and ccs were largely independent across clones

Method

Values of ccs and tch were compared at trial (not shown) and region level.

Results

While the NSW and Burdekin regions had a greater tch and lower ccs than the other regions, there was no relationship between clone values of ccs and tch when averaged at the region level (Figure 4-15). The somewhat 'shotgun-like' relationship suggests that the highest (and lowest) tch clones are likely to have moderate ccs and similarly that high (or low) ccs clones have moderate tch.

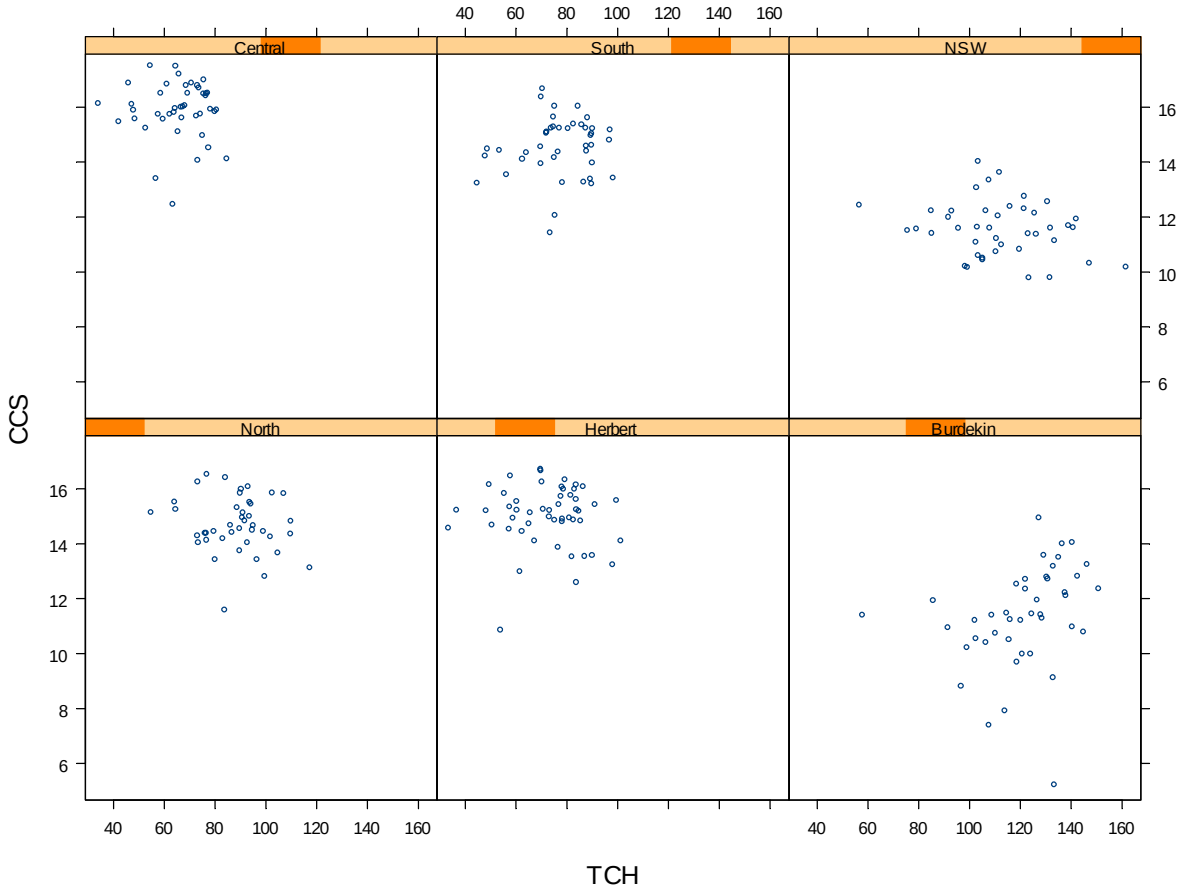


Figure 4-15 Averaged over trials within each region, the tch plotted against ccs for all clones (Ord not shown).

4.4. Averaged over trials, relationships of secondary traits to genotypic variation for TCH and CCS

Method

There are a number of secondary traits that are frequently included in selection indices for sugarcane because there is a perception or reasonable expectation that they are of value for adaptation. Some are selected against to improve harvesting or milling qualities, e.g. reduced trash or reduced stool suckering. Given the difficulty of quantifying many of these traits precisely and in the same population, the heritability of these traits and their direct effects on TCH and CCS have rarely been tested. The additional data observed on the population studied here allows some of these theories to be checked.

In this section, clonal values for secondary traits and either TCH or CCS are averaged over trials where there was substantial expression of the secondary trait. In the next section (4.5), genetic correlations are estimated for each trial. That section shows that while there may not be correlations between traits and TCH or CCS over trials, there is are some trials in which a positive genetic correlation exists.

For each trait discussed in this section, trials were first filtered to select a set of trials that had substantial expression for the trait being measured or scored. The clone trait values (or scores) were averaged over the selected trials and then compared to their mean TCH or CCS for the same trials and regressions fitted. Note that while there was slight variation (ca 5-10%) in the number of trials being averaged for some clones that weren't in all trials of a subset, but these were checked to make sure they didn't bias the interpretation.

Result

To summarise the below information, positive relationships existed for early CCS with late CCS and for stalk number and length with TCH. While number of check lines was only small (6), it is of interest to note their values relative to the unselected clones. The check lines were biased upward for early CCS, stalk number (density) and stalk length and so some positive selection seems to have occurred for these traits. Reduced arrowing was the only other trait where the checks were biased compared to the clones (in this case, biased lower), but the trait was not related to mean clonal TCH or CCS averaged over about 20 trials. For the remaining traits examined (apart from orange rust – see below), lodging, stool suckering, sucker weight and stalk diameter, the checks were intermediate and relationships with TCH and CCS were neutral.

4.4.2. Over trials, early CCS of clones was strongly correlated with their harvest CCS

A CCS sample was taken early in the season (Feb to April) from two trials in every region (B2, C1, C4, H1, H3, N2, N4, S1, S3, W1 and W2) on one or two occasions. In these 12 to 16 instances, CCSe was found to be highly correlated with CCS when averaged over trials (Figure 4-16). While the Q canes averaged 10.3%, the clones ranged from 7.3 to 12.7%. This finding is not novel, but helps to verify that the relationship holds in this type of unselected germplasm, while it is already being exploited in other selection programs.

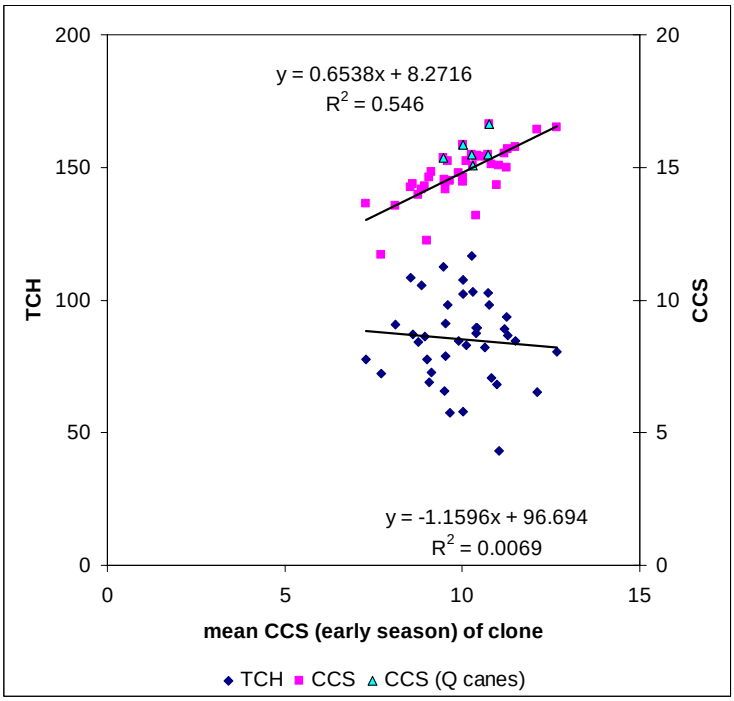


Figure 4-16 Averaged over trials, the relationship between mean early season CCS of clones and either TCH or CCS of clones at harvest. Q canes are identified separately.

4.4.3. Over trials, arrowing of clones was not correlated with TCH or CCS

Arrowing (flowering) has been thought to have a negative effect on cane yield as it may indicate the maturation or halting of stalk growth and sugar filling. It is visually scored at harvest as the % plants arrowed per plot. The 10 locations (C1, C2, H1, H2, H3, H4, N1, N2, N5, S1) in which average arrowing was >20% (20 trials in all) were taken as a subset. In all locations, arrowing occurred during the year of harvest of the plant crop year, and except for C1, C2 and H3, arrowing occurred also during ratoon harvest years. For clones that had been observed in > 15 trials of the trials, mean clonal values of arrowing were calculated and regressed against mean clonal TCH and CCS (Figure 4-17).

Across the clones, mean arrowing ranged from 0 to 90% and was about 22% in check lines (Q canes). Some selection against arrowing has been employed, particularly in the North and may account for the lower arrowing proportion in the Q cane checks. However, no relationship was found between mean arrowing % and either TCH or CCS in these trials where mean arrowing had been > 20%.

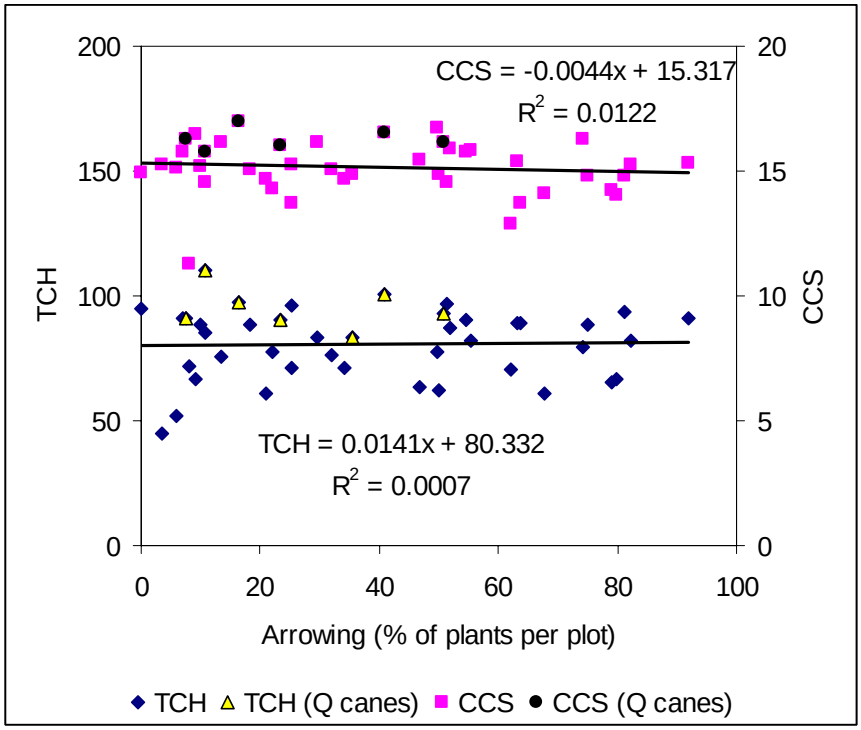


Figure 4-17 Averaged over trials, the relationship between mean arrowing (% of plants) of clones and either TCH or CCS of clones at harvest. Q canes are identified separately.

4.4.4. Over trials, lodging of clones was not correlated with TCH or CCS

For this analysis, trials with more than 20% plants lodged were retained, many of which were > 100 t ha^{-1} (Figure 4-2) for cane yield. It was found that the clonal mean lodging scores averaged over 17 to 20 trials in B1, B2, B3, B4, H2, H4, N2, N5, S1 and W2 ranged from 15 to 65% with the check lines averaging 46%. These clonal scores were not related to either TCH or CCS averaged over the trials. Interpretation of genetic relationships between lodging and cane yield is difficult. On the one hand, the clones which produce high cane yields would normally be expected to be more prone to lodging because weight of cane is a factor which promotes lodging. On the other hand, after lodging occurs it can have a negative impact on further growth of such canes, so this analysis was not able to separate the effects of lodging intensity (% lodging) and its interaction with the timing of lodging relative to harvest. The results of SRDC project CTA030 have previously shown that there is an effect of lodging on TCH, CCS and TSH in high rainfall and irrigated crops. However, the trials here are not able to answer whether there is a direct genotypic variation for lodging vs yield effects.

4.4.5. Over trials, sucker weight of clones was not correlated with TCH or CCS

The proportion of harvest weight that comprised suckers was estimated visually. In 5 trials (B1, C3, H1, H4, N2), this estimate was > 5% for the trial and was 17% in the check lines. While the clones varied from 2 to 23% over these trials, the scores were not related to either TCH or CCS averaged over these trials.

4.4.6. Over trials, stool suckering of clones was not correlated with TCH or CCS

In plant and some ratoon trials (19 to 23 in total) conducted in B1, C1, C2, C3, H1, H2, H4, N1, N2 N4, N5, N6, S3, S4 and W2 the clone means for % stools with suckering ranged from 15 to 90%. Checks (4 Q canes) averaged 50%. However, there was no relationship with TCH or CCS.

4.4.7. Over trials, a small weak negative relationship exists between clonal score for orange rust and TCH

Trials with average orange rust scores > 1% were found in about 18 instances in locations B2, B4, C1, C2, C3, C4, H2, H3, H4, N2, N4, N6, S3, S4 with the susceptible check, Q124, recording a mean value of 15% over a range of 5 to 70% infection where it was grown and scored. When the large values of Q124 and two susceptible clones (> 12% average infection) were removed, there still existed a weak relationship between increased rust score and reduced TCH (Figure 4-18).

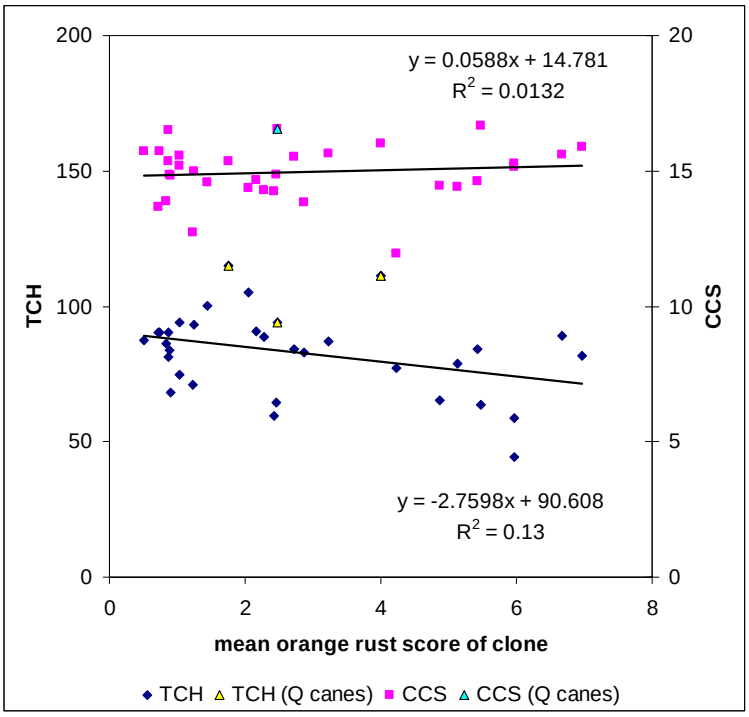


Figure 4-18 Averaged over trials, the relationship between mean orange rust score (% infection) of clones and either TCH or CCS of clones at harvest. Q canes are identified separately. Note that susceptible check (Q124) is not shown and had a mean score of 17%.

4.4.8. Over trials, small positive relationships exist between TCH of clones and their stalk length or stalk density

With clones ranging from 1.8 to 2.6m (checks = 2.5m) and 7.7 to 8.1 stalks per m2 (checks = 8), TCH increased slightly with changes in these clonal values, averaged across > 30 trials. Stalk diameter at chest height averaged 26 mm in checks and 19 to 32 mm in unselected clones and was positively correlated with TCH.

4.4.9. No combinations of soil, location, weather or pathology variables yet tested had a significant impact on genotype by environment interaction variances

The environment variables listed in section Table 4.12 have been tested in mixed models as fixed covariates to see if they can explain part of the observed genotype by environment interactions (Appendix 6). However, thus far they do not. Further work is on-going in the new project BS267 to investigate other combinations of these factors.

4.4.10. PPO activity in juice was correlated between two sites

Several research projects have studied the relationships between colour development in juice (an unwanted quality trait) and the levels of the enzyme poly-phenol oxidase. However, this has rarely been studied in random clones. Dr. Joan Vickers used juice samples from the H1 and H2 harvests to measure the levels of PPO. Details of the protocols etc can be found in that SRDC project.

The PPO activities from the two sites were found to be highly correlated. The commercial clones generally had low PPO activities, relative to the range observed. There was no clear correlation between PPO activity and either TCH or CCS, though those several clones with high PPO (> 2.5) were among the lowest yielding for TCH.

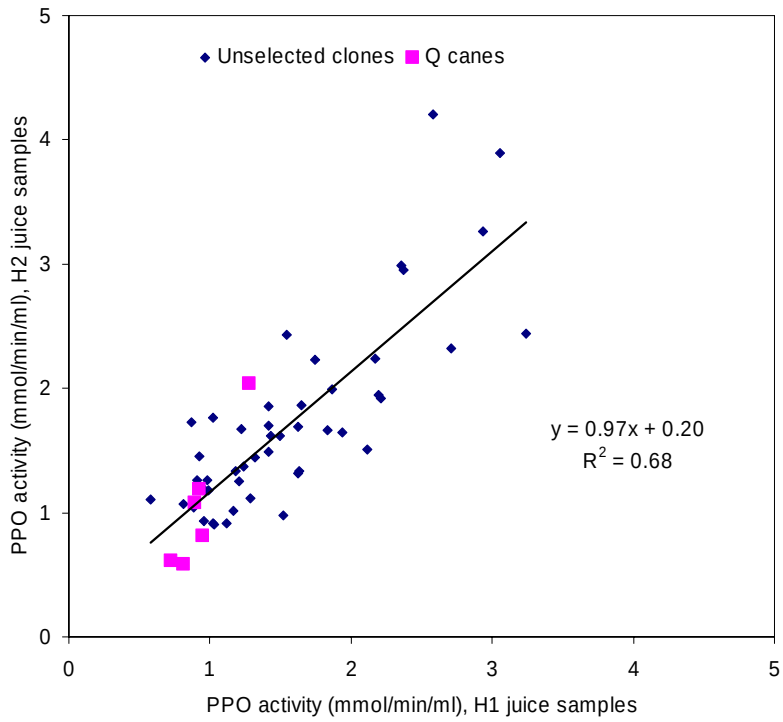


Figure 4-19 Poly-phenol oxidase activity in sites H1 and H2 from juice samples taken at harvest

4.5. Genetic correlations between secondary traits and TCH or CCS

This section reports on genetic correlations between traits. Note that there were also some strong correlations between the mean trial value of primary and secondary traits when compared across environments. These are reported separately at the end of Appendix 6.

4.5.1. Calculation of genetic correlations

The data were first filtered to select only trials where the secondary trait had been observed. For some datasets where the secondary trait was observed to be quite low in expression (e.g. arrowing < 10% maximum), the dataset was not analysed.

Genetic correlations (r_g) were estimated on a per trial basis from:

$r_g = covg_{xy}/sqrt(Vg_x * Vg_y)$

where x and y are two traits being compared. The genotypic covariance (cov_{xy}) was derived from the generic relationship between variance components for two traits or loci and the variance of the sum of the effects (e.g. as in Falconer and Mackay 1996):

$Vg_{x+y} = Vg_x + Vg_y + 2 * covg_{xy}$

The phenotypic correlations (r_p) were estimated as for r_g after calculating the phenotypic variance components (Vp) for x, y and x+y as:

$Vp = Vg/h^2$

where h^2 is the broad sense heritability, i.e. line mean repeatability for a trial. From a random model h^2 was estimated as:

$h^2 = 1-(avsed^2/(2*Vg))$ with a standard error of

$h^2se = Vgse/Vp$

where avsed is the average standard error of the difference for genotype BLUPs and Vgse is the standard error of the genotypic variance component estimated by the random model.

The standard error for r_g was estimated according to Reeve (1955) and Robertson (1959) using the formula of Falconer and Mackay (1996):

$r_gse = (1-r_g^2)/sqrt(2) * sqrt(h_x^2se * h_y^2se/h_x^2 * h_y^2)$

For each x:y contrast (e.g. tch:lod, for TCH vs lodging), a random model was applied to the raw data to estimate genotypic variance, i.e. Vg_x and Vg_y for two traits and their sum (Vg_{x+y}). The same random model was used for each of the three analyses: Genotype + Rep. Comparisons with genetic correlations from a random model that included column and row effects were similar, so the simpler model was used (data not presented). In addition to the heritabilities, correlations and standard errors, another genetic (rank) correlation was estimated according to Burdon (1977):

$r_grank = r_{pxy}/sqrt(h_x^2 * h_y^2)$

This r_grank is the one that was used to compare regressions for the same traits in different environments (see section 0) and is useful when the raw data cannot be used for these comparisons because the designs are unbalanced across environments.

Genetic correlations that were estimated as >1 or less than 1 were set to 0.999 or -0.999, respectively and were eliminated from the following interpretations. Other points that were eliminated were those where the genotypic variance component for either trait was < 2 times its standard error – a standard test in using random or mixed models.

As our interest is in the degree to which secondary traits can predict response to selection, this was also estimated. Response to selection is given by:

$R_x = i_x * h_x * sqrt(Vp_x)$

where i is the selection differential (units of standard deviation), h is the square root of the heritability and Vp is the phenotypic variance component. The correlated response to selection, given a secondary trait y, can be shown to be:

$CR_x = i_x * h_x * hy * r_g * sqrt(Vp_x)$

Assuming the same selection differential is used, then the ratio of correlated to direct selection can be estimated as:

$CRx/Rx = h_x * h_y * r_g/h_x^2 = r_g * h_y/h_x$

This ratio therefore indicates the expected response of the primary trait if selection is made on the secondary trait, rather than directly on the primary trait.

When employing indirect selection, one option is to increase the selection differential compared to what would be used in direct selection. The magnitude of this required increase can be estimated by assuming that a CRx/Rx ratio of 1 is required, i.e.

$CR_x/R_x = 1 = i_{xi}/i_{xd} * rg * h_y/h_x$

$i_{xi}/i_{xd} = 1/(r_g*h_y/h_x) = h_x/(h_y*r_g)$

or more simply, the ratio requires is equal to R_x/CR_x.

4.5.2. Summary of results

Fifteen important genetic correlations between secondary traits and CCS or TCH are discussed here, following elimination of points as described above. Other correlations were considered but were less relevant to this analysis. The correlations examined included those with the secondary traits of:

arr: arrowing (percentage of plants per plot that had arrowed (flowered))

brx: brix of juice from 8 stalk sample at harvest

dia: diameter of stalks at chest height, measured on 8 stalk sample at harvest

fib: fibre (percentage of stalk sample that is fibre, measured on 8 stalk sample at harvest)

len: length of stalks, measured on 8 stalk sample at harvest

lod: lodging (percentage of plants per plot that had lodged at harvest)

pol: pol of juice at harvest

stc: stalk count per m^2, estimated by counting stalks in 5m of row at harvest

sts: stool suckering (percentage of cane stools per plot with suckers)

4.5.3. Repeatability of secondary traits was generally independent of the precision for TCH and CCS

For most of these correlations, the repeatabilities (broad sense line mean heritabilities) were not correlated (Figure 4-20). The exceptions were where a trait (CCS) was derived from a calculation of other variables (brix and pol). Hence, in general, over many trials, the precision with which a secondary trait was measured was not related to the precision of measurement of TCH or CCS. Note that the mean standard error for these heritabilities was about 0.2 for all comparisons (data not presented).

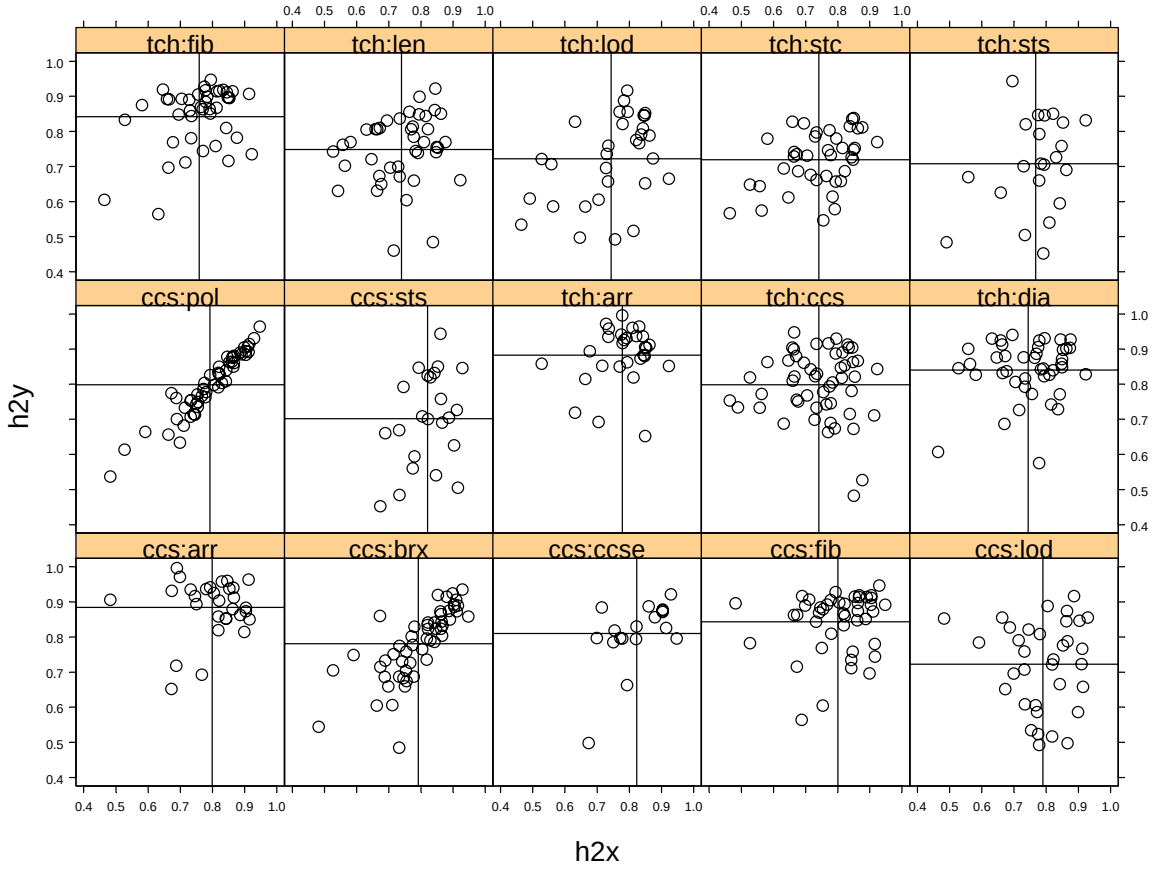


Figure 4-20 For correlations between CCS or TCH (x) and secondary traits (y), the relationship between the heritability (i.e. ratio of genotypic to phenotypic variance) for x and y. Each point is from a single environment and all 59 environments (harvests) are represented only in the TCH:CCS comparison as the secondary traits were not observed in every environment. The solid lines represent the mean values across trials.

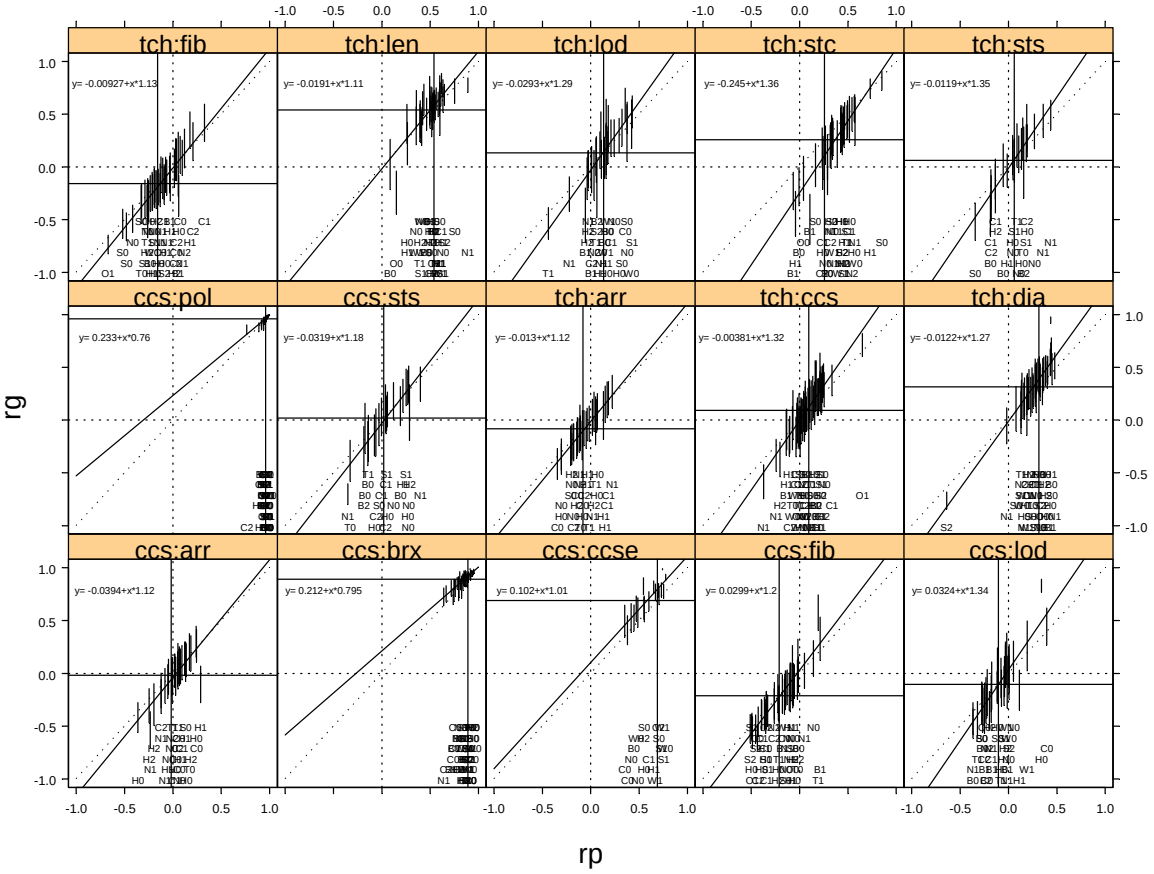


Figure 4-21 Phenotypic (r_p) vs genetic (r_g) correlation for secondary traits and CCS or TCH. Reference lines are indicated for origin and 1:1 line (dotted) and for linear fit (solid) and mean values of correlations. Vertical symbol lines are values r_g +/- standard error.

The mean genetic correlations over trials were >0 for many trials in the comparisons ccs:brx, ccs:ccse, ccs:pol, tch:dia, tch:len and tch:stc. For ccs:fib and tch:fib, the mean correlation was –ve.

For most trait comparisons, the genetic correlations were 10 to 30% larger than the phenotypic correlations, with an intercept close to 0 (Figure 4-21). Exceptions included tch:stc where the intercept was -0.25 and for the comparisons of ccs with brix, ccse or pol, where the r_g and r_p were effectively the same for the range of r_g and r_p observed.

For all trait comparisons, there were harvests for which the r_g differed from 0. While the effects of region seemed to be relatively inconsistent, careful examination of shows some interesting interactions. For example, for tch:ccs, most correlations were not significant, but it was +ve for the Ord ratoon and negative for two ratoon crops in the North.

The only +ve correlations for ccs:fib and tch:fib were in ratoon trials (two in Burdekin and Tableland) and two in Central, respectively. For ccs:fib, there were numerous –ve correlations, especially in the South, Central and Herbert. The –ve correlations for tch:fib were in all regions except Central.

Most of the significant +ve correlations (4 of 5) for ccs:arr were plant crops (i.e. 0) while most (5/6) –ve correlations were ratoon crops. This effect was reversed for the tch:arr comparison with slight –ve correlations existing for several plant crops (7/9), but +ve correlations for several ratoons (4/4). There were several +ve correlations for tch:lod in plant crops (10/12) and some -ve correlations (6/6) only in ratoon crops.

About 5 trials (mainly Burdekin and Tableland) had –ve correlations for ccs:sts (stool suckering) and the same number (mainly in Herbert and North) had +ve correlations. Significant

correlations of tch:sts were few, with 3 +ve correlations in the North and –ve correlations in 3 Central trials and 1 each in South, Burdekin and Herbert.

Detail

The following statements (from examination of Figure 4-21 and standard errors) summarise the observations of how genetic correlation varied with region when averaged for trials in a region:

ccs:arr ~ 0, but -.13 in N

ccs:brx > 0.9 in all regions

ccs:ccse > 0.7 in H, S, W; < 0.6 in rest

ccs:lod ~ 0 except -.2 in B/C

ccs:pol > 0.95 all reg

ccs:sts ~ 0 except -.3 in T

tch:arr ~ 0 but -.15 in C/T (no obs in B)

tch:ccs ~ 0, but slightly positive in 3 regions 0.2 in B, 0.35 in O, 0.2 in S

tch:dia 0.6 in B, > 0.3 in C H O, 0.2 in N W

tch:fib ~ 0, but -.5 O, -0.35 in S T, -.2 W

tch:len >= .5 except B (0.36) & O (-.24)

tch:lod ~ 0 except >.2 C S W

tch:stc -.3 B, > 0.3 H N S W

tch:sts ~ 0 except >.2 N T & <-.2 S W

When compared on the average for crop class, the following were observed:

ccs:lod increases from 0 to -.2 between cclass 0 and 1 or 2 (effect of harvest time?)

tch:lod decreases from 0.3 to 0 between cclass 0 and 1 or 2

tch:fib increases from -.2 to 0 from cclass 0 through 1 to 2

4.5.4. Genetic correlations were similar when computed by standard or rank correlation methods

For most correlations, the $r_g$rank, computed only from phenotypic variance and heritabilities was quite similar to that r_g derived by the standard method (Figure 4-22). The standard error of rg was < 0.05 for ccs:brx and ccs:pol, 0.09 for ccs:ccse and between 0.13 and 0.20 for the remaining comparisons, i.e. for most cases, the $r_g$rank was within the standard error for r_g. When heritabilities were high (for CCS, brix and pol), many of the values of $r_g$rank were > 1 or < -1 and are not shown. In these cases, $r_g$rank was obviously a poor predictor.

In fact, in this data set, stool suckering was positively correlated with TCH in the North and Tableland. Note, however, that we measure CCS from a sample of ‘sound stalks’ which does not include the dilution effect of sucker weight on the net CCS for a harvested crop. In the crops we saw, sucker weight was a small component of TCH, yet it can be 20-30% in some areas. Arrowing had a small negative effect on TCH in plant crops, especially in the South, but not in the north. This indicates that we need to be careful in the use of arrowing to discard clones which have been transferred between regions. BS267 will review this in the light of the economic weights assigned to arrowing.

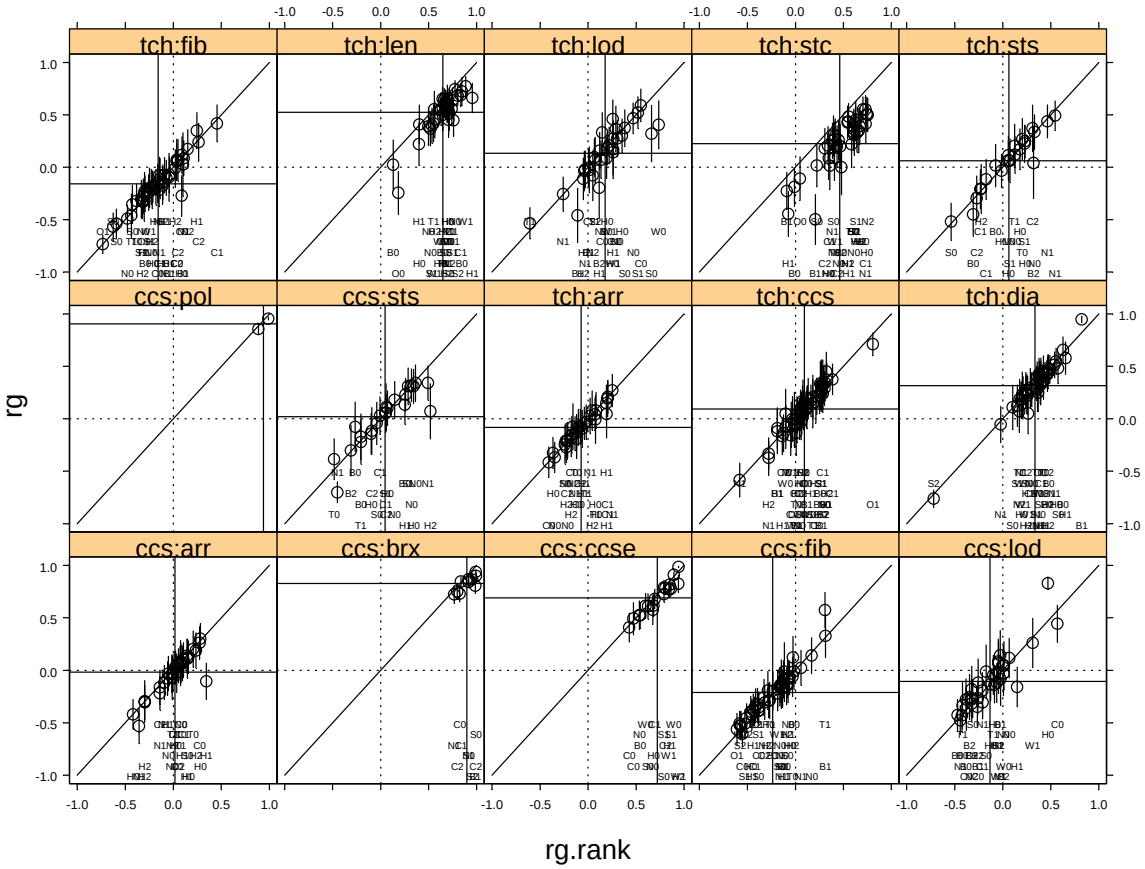


Figure 4-22 Relationship between genetic correlation calculated from phenotypic correlation and heritability ($r_g$rank) and genetic correlation (r_g) calculated directly from genotypic variances and covariance. Standard errors are shown for rg while other reference lines show mean values and 1:1 line (solid) or origin (dotted). Codes below points indicate region and crop class (0=plant; 1= 1st ratoon; 2=2nd ratoon) for the harvest. Points where rg.rank > 1 or < -1 have been removed.

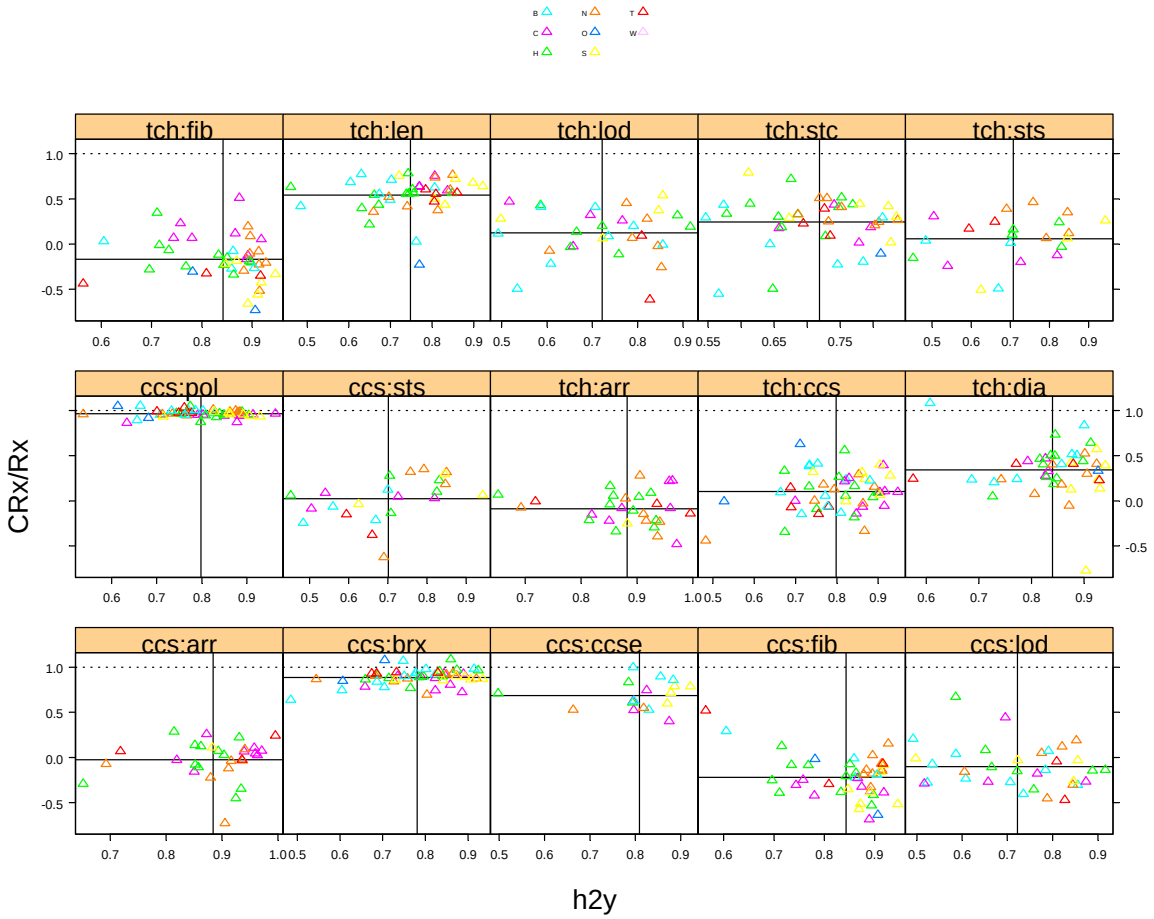


Figure 4-23 Relationships between heritability of a secondary trait (h_y^2) and the ratio of correlated response (change in trait x, given y) and direct response to selection

Table 4-13 CRx/Rx ratios (see text) averaged over regions or crop class

Reg	B	C	H	N	O	S	T	W	Plant	1st ratoon	2nd ratoon
ccs:arr	NA	0.05	-0.04	-0.16	NA	0.11	0.10	NA	0.06	-0.08	-0.10
ccs:brx	0.86	0.85	0.92	0.86	0.96	0.88	0.94	0.93	0.90	0.88	0.89
ccs:ccse	0.53	0.57	0.72	0.54	NA	0.72	NA	0.84	0.60	0.81	0.73
ccs:fib	0.02	-0.37	-0.22	-0.11	-0.33	-0.37	0.05	-0.19	-0.21	-0.19	-0.29
ccs:lod	-0.24	-0.11	-0.02	-0.09	NA	-0.08	-0.26	0.11	-0.05	-0.13	-0.16
ccs:pol	0.98	0.93	0.96	0.98	0.98	0.95	0.99	0.98	0.96	0.97	0.95
ccs:sts	-0.10	0.02	0.11	0.11	NA	0.11	-0.26	NA	0.05	0.03	-0.05
len:dia	0.20	-0.05	0.25	0.06	0.45	-0.07	0.08	0.06	0.11	0.10	0.07
tch:arr	NA	-0.08	-0.07	-0.11	NA	-0.25	-0.06	NA	-0.20	0.06	-0.14
tch:ccs	0.23	0.09	0.09	-0.01	0.31	0.23	-0.03	0.02	0.13	0.08	0.11
tch:dia	0.73	0.38	0.40	0.26	0.33	0.16	0.32	0.27	0.39	0.36	0.21
tch:fib	-0.11	0.09	-0.14	-0.14	-0.52	-0.40	-0.37	-0.26	-0.28	-0.13	-0.03
tch:len	0.48	0.66	0.53	0.54	-0.23	0.62	0.55	0.59	0.50	0.58	0.57
tch:lod	-0.04	0.26	0.16	0.08	NA	0.31	-0.26	0.24	0.34	0.02	-0.07
tch:stc	-0.24	0.20	0.30	0.34	-0.11	0.38	0.24	0.34	0.23	0.23	0.30
Tch:sts	-0.15	-0.06	0.06	0.28	NA	-0.06	0.21	NA	0.03	0.12	-0.01

The above values can be inverted to estimate the relative relaxation in selection intensity (relative to direct selection) required to achieve a CRx/Rx ratio of 1. As a guide: 1/0.9 = 1.1; 1/0.8 = 1.25; 1/0.7 = 1.43; 1/0.6 = 1.67; 1/0.5 = 2; 1/0.4 = 2.5; 1/0.2 = 5

4.5.5. Indirect selection for early generation germplasm; early season CCS is a good predictor of CCS while stalk length, diameter and lodging were good predictors for TCH especially in plant crops

Detailed comments on the CR/R ratios from Table 4-13 are given here. Note that the averages in the table are effectively for r_g as the ratio of h_y/h_x was almost always close to 1.0 when averaged over trials within regions or crop classes (data not shown).

ccs:arr close to 0

ccs:brx ca 0.88

ccs:ccse 0.6 to 0.8; best in H S W > 0.7

ccs:fib -0.2 but some +ve. always -ve in S and C (-.4)

ccs:lod -0.2 in B and T

ccs:pol 0.95

ccs:sts -.3 in T

tch:arr -0.2 in plant crop but some +ve inc in 1st ratoon

tch:dia +ve 0.35-0.40 exc. one 2nd ratoon crop

tch:fib -.3 in plant crop; always +ve in ratoon; always -ve in O -.5 S -.4 T -.4 W -.3

tch:len +ve CRx/Rx 0.5 to 0.6 (exc. two crops in B and O)

tch:lod +ve CRx/Rx 0.34 for plant crops, decreases in later crops; +ve in C S W

tch:stc 0.25 over all; +ve in most reg

tch:sts 0.3 +ve in N and T 0.2

Apart from the high value of brix and pol as predictors of CCS, the most obvious points of interest are that:

1. early CCS can be best used for indirect selection in Herbert, South and NSW regions;
2. fibre always had a –ve correlation with CCS in South and Central
3. fibre was –ve for TCH in plant crop, +ve in ratoon
4. about 50 to 60% of gain in TCH could come through selection for stalk length and about 30% (potentially overlapping) for stalk diameter
5. selection for arrowing would decrease TCH in plant crops in South
6. selection for stool suckering was +vely associated with TCH in North and Tableland and –ve for CCS in Tableland
7. selection for lodging in plant crops was +ve for TCH especially in Central and South, but negative for CCS in Burdekin and Tableland

4.6. Variance components and principal component analysis of TCH and CCS

4.6.1. Across the whole dataset, Genotype by location effects for TCH and CCS were greater than interactions associated with crop class

Table 4-14 shows that the genotype by crop class (i.e. plant, ratoon etc) effects was 0 for CCS and relatively about ¼ of the genotype by location effect for TCH. For TCH, the 3-way interaction of these effects was similar to the genotype by crop class effect, while for CCS it was similar to the genotype by location effect. In confirmation of section 4.5
, the table demonstrates that it is more important to sample environments as locations for TCH, compared with CCS where locations and crop classes are equally important.

Table 4-14 Variance components and standard errors for TCH and CCS for entire dataset with environments fixed and genotypes and interaction effects with location and crop class as random.

Source	TCH	TCHse	CCS	CCSse
Gen	161.5	27.9	0.82	0.13

Gen:Loc	73.8	5.3	0.22	0.02
Gen:Cclass	15.0	2.8	0.00	NA
Gen:Loc:Cclass	12.4	3.1	0.17	0.02

4.6.2. Genotype by region effects were only a relatively small proportion of total genotype by environment effects

In pooled analysis of cane yield across regions (Appendix 4, summarised in Table 4-15), it can be seen that genotype x region interaction, while significant, is only about 4% of the size of genotype main effects, and less than 1/10 of the average genotype x location within region interaction, and about the same as the averaged genotype x crop x location within region interaction.

The size of the genotype x location or crop class interaction components, indicate that selection in even a highly variable, unselected population of clones as used in this project, would benefit from evaluation across multiple environments. However, the relatively small size of the genotype x region interaction effect indicates that environmental factors driving GE interaction are not strongly associated with regional differences, and a large proportion of GE interactions can be sampled from multiple sites and crop-years within regions.

An analysis was also done on the top 50% of clones based on performance of clones in one region (with the Herbert region arbitrarily chosen) to simulate a population more representative of later stages of selection. In this case, as expected, the genotype main effect was smaller, but the genotype x environment interaction variance components were of similar magnitude. The larger size of the interaction components relative to the genotype main effects in this selected population highlights the even greater importance of evaluating genotypes across sites at later stages of selection. Note, this is a preliminary analysis that will be re-examined in BSS267.

For CCS, the regional effect was relatively larger (about 9% of the genotype main effect), but nevertheless quite small. The interaction with crop class was again negligible, and the 3 way interaction averaged across regions was similar to the location effect.

Table 4-15 Results from analysis of variance of the random clones across all environments for cane yield and CCS. For cane yield, the analysis is also shown for the top 50% of clones (selected based on performance in the Herbert region

Source of variation	Cane yield (t/ha) All clones	Cane yield (t/ha) Top 50% of clones	CCS
Genotypes (G)	175±32	49.7±20	0.789
G x region (R)	22±6	22.0±9.2	0.071
G x location within R	76±7	58.3±10.3	0.167
G x crop	19±4	8.7±4.3	0
G x crop x location within R	70±5	63.8±7.8	0.168
Residual variance	178.5	178.5	

4.6.3. Genetic correlations among environments were similar within and between regions

Genetic correlations are a useful statistic because gain from indirect selection in one environment for performance in another is directly proportional to this statistic. The relative similarity of trial results within and between regions can therefore be further illustrated by genetic correlations among the unselected clones (i.e. Q canes removed) in Table 4-16, Table 4-17 and Table 4-18. Table 4-16 shows, the average of all genetic correlations between different trials within each region (diagonal) in comparison with the average of genetic correlations between trials from different regions. Overall, the mean genetic correlation for CCS was 0.53 and for TCH was 0.52.

When the Q-canes were removed, these mean correlations increased by about 0.03 for CCS and 0.07 for TCH (data not shown). The other two tables (summarised by principal component analysis in the next section) show all of the genetic correlations among all of the 59 harvests, for CCS and TCH, respectively. In these tables, blocks of green (dark) text going down the left-right diagonal indicate good correlations between trials within a region. Other blocks indicate regions with good correlations between each other for more than one environment.

From Table 4-16, one can see that in most cases, trials within regions have a higher genetic correlation with each other (the correlations given along the diagonal), compared with their correlation with trials from other regions (correlations away from the diagonal). However, in many cases this difference is not large, and in some cases, especially for CCS, the results suggest that similar gains could be achieved from selection in other regions. For example, for CCS, the genetic correlation between any given region (except the Ord) and either the Central or South regions was often greater than or similar to the genetic correlation within the given region, i.e. clones selected for CCS in either the Central or South should be the same clones that would be chosen within any other region, except the Ord. Overall these results suggest that, apart from the Ord, for any given region, indirect selection for CCS in some other regions could be just as effective as selection within the target region itself. The Burdekin was notable in also having a generally poor genetic correlation within and among regions. However, it seems that at least part of these poor average correlations was related to poor correlation between B1 and B2 vs B3 and B4 (Table 4-18). Recall that B1 and B2 were partially compromised by problems with propagation which reduced the number of clones available for comparison with other trials.

For cane yield, selection within the region is generally most effective, but gains of up to 90% in most cases could be made from selection in some other regions. The relative advantages of selecting within a region compared with other regions are greatest for the Herbert and North regions, although indirect selection in either region for the other would be almost as good (0.68 and 0.74 for within-region correlations, versus 0.65 – or >91% relative gain – for between-region correlations). The Ord and the Atherton Tableland are well correlated with each other for TCH. The Herbert and Burdekin were the best existing breeding regions for prediction of TCH in the Ord and Tableland. In fact, the Burdekin trials B2, B3, B4 had a mean correlation of ca 0.9 for TCH with the Ord plant crop (Table 4-18). The Herbert was the best predictor of performance in most other regions.

Overall, these results reinforce the conclusions based on the variance components (section 4.6.3) that variation among locations (regions) is greater for TCH than for CCS and that sampling of locations is more important for the former. .The results obviously highlight that data collected in most regions could be used for making gains in all other regions.

4.6.4. No locations were well correlated with the Ord for CCS

The Ord clearly had low correlations with environments in all other regions, especially for CCS (Table 4-16). However, as indicated previously, the limited number of clones in this trial and the fact that only a single trial was conducted limits the level of confidence in any conclusions drawn from this result.

Table 4-16 The average of genetic correlations (for CCS and cane yield, TCH) between environments in each region versus (i) all independent environments (i.e. different sites) in the same region (along the diagonal) and (ii) all environments in each other region. Figures in bold are correlations of 0.5 or greater while those in italics are less than 0.3 (i.e. non-significant at p< 0.05, n = 40 genotypes). Note that the Ord comparison is of only a plant and ratoon trial in one location.

CCS

	North-coast	North-Tableland	Herbert	Burdekin	Central	South	NSW	Ord[1]
North-coast	**0.74**	**0.62**	**0.65**	0.48	**0.73**	**0.76**	**0.60**	*0.13*
North-	**0.62**	**0.75**	**0.68**	**0.53**	**0.73**	**0.71**	**0.61**	*0.17*

tableland								
Herbert	**0.65**	**0.68**	**0.68**	0.49	**0.78**	**0.78**	**0.50**	*0.19*
Burdekin	0.48	**0.53**	0.49	0.50	**0.52**	**0.53**	0.45	*-0.11*
Central	**0.73**	**0.73**	**0.78**	**0.52**	**0.82**	**0.87**	**0.59**	*0.22*
Southern	**0.76**	**0.71**	**0.78**	**0.53**	**0.87**	**0.88**	**0.69**	*0.15*
NSW	**0.60**	**0.61**	**0.50**	0.45	**0.59**	**0.69**	**0.67**	*-0.02*
Ord	*0.13*	*0.17*	*0.19*	*-0.11*	*0.22*	*0.15*	*-0.02*	**0.58**

TCH

	North-coast	North-Tableland	Herbert	Burdekin	Central	South	NSW	Ord[1]
North-coast	**0.74**	0.40	**0.67**	**0.57**	0.45	0.46	**0.51**	0.49
North-tableland	0.40	**0.59**	0.46	0.48	0.43	0.41	0.46	**0.68**
Herbert	**0.67**	0.46	**0.75**	**0.60**	**0.54**	**0.53**	**0.58**	**0.54**
Burdekin	**0.57**	0.48	**0.60**	**0.67**	0.43	**0.55**	**0.52**	**0.59**
Central	0.45	0.43	**0.54**	0.43	**0.63**	0.47	**0.53**	0.40
South	0.46	0.41	**0.53**	**0.55**	0.47	**0.53**	**0.64**	0.39
NSW	**0.51**	0.46	**0.58**	**0.52**	**0.53**	**0.64**	**0.80**	*0.29*
Ord	0.49	**0.68**	**0.54**	**0.59**	0.40	0.39	*0.29*	**0.74**

Table 4-17 Genetic correlations for CCS among all trials, ordered geographical from North to NSW (and Ord at end). Note that N3 and N6 were on the Atherton Tableland. Non-significant correlations (between -0.3 and 0.3) are shaded yellow, large positive correlations (> 0.7) are shaded green. (will be updated)

ccs	N1-0-2	N1-1-3	N2-0-1	N2-1-2	N2-2-3	N4-0-2	N4-1-3	N5-0-2	N5-1-3	N3-0-1	N3-1-2	N6-0-1	N6-1-2	H1-0-0	H1-1-1	H2-0-0	H2-1-1	H2-2-2	H3-0-1	H3-1-2	H3-2-3	H4-0-1	H4-1-2	H4-2-3	B1-0-0	B1-1-1	B1-2-2	B2-0-0	B2-1-1
N1-0-2	1.17	0.67	0.98	0.82	0.61	0.78	0.71	0.70	0.65	0.56	0.51	0.48	0.53	0.59	0.40	0.59	0.68	1.03	0.67	0.50	0.58	0.51	0.64	0.83	0.19	0.46	0.29	0.20	0.19
N1-1-3	0.67	1.15	0.79	0.80	0.68	0.65	0.57	0.61	0.58	0.49	0.57	0.59	0.45	0.56	0.38	0.57	0.60	0.67	0.63	0.69	0.89	0.68	0.33	0.49	0.58	0.80	0.63	0.43	0.78
N2-0-1	0.98	0.79	1.27	1.02	0.79	0.86	0.77	0.79	0.74	0.63	0.63	0.59	0.54	0.71	0.54	0.69	0.71	1.16	0.79	0.78	0.72	0.58	0.67	0.81	0.66	0.93	0.40	0.44	0.71
N2-1-2	0.82	0.80	1.02	1.94	1.10	0.66	0.86	0.58	0.59	0.43	0.34	0.60	0.48	0.74	0.51	0.52	0.47	0.81	0.60	0.61	0.41	0.40	0.49	0.71	0.59	0.64	0.24	0.25	0.62
N2-2-3	0.61	0.68	0.79	1.10	1.28	0.71	0.56	0.39	0.53	0.37	0.47	0.53	0.38	0.55	0.31	0.39	0.50	0.58	0.56	0.50	0.51	0.26	0.48	0.45	0.41	0.40	0.31	0.21	0.51
N4-0-2	0.78	0.65	0.86	0.66	0.71	1.26	0.92	0.78	0.92	0.92	0.76	0.81	0.63	0.62	0.48	0.90	0.99	1.00	0.98	0.81	0.92	0.46	0.45	0.47	0.61	0.70	0.32	0.50	0.59
N4-1-3	0.71	0.57	0.77	0.86	0.56	0.92	1.12	0.73	0.84	0.86	0.65	0.80	0.65	0.61	0.65	0.82	0.92	0.95	0.88	0.80	0.84	0.56	0.56	0.55	0.72	0.58	-0.08	0.46	0.74
N5-0-2	0.70	0.61	0.79	0.58	0.39	0.78	0.73	1.32	0.91	0.81	0.62	0.64	0.86	0.77	0.59	0.92	0.85	0.98	0.85	0.81	0.71	0.45	0.46	0.48	0.27	0.66	0.38	0.11	0.16
N5-1-3	0.65	0.58	0.74	0.59	0.53	0.92	0.84	0.91	1.16	0.81	0.67	0.83	0.73	0.62	0.44	0.90	0.87	0.88	0.84	0.78	0.81	0.42	0.51	0.44	0.40	0.49	0.21	0.24	0.29
N3-0-1	0.56	0.49	0.63	0.43	0.37	0.92	0.86	0.81	0.81	1.25	0.65	0.80	0.71	0.56	0.38	0.95	1.03	0.72	0.91	0.78	0.89	0.62	0.47	0.62	0.55	0.61	0.17	0.48	0.65
N3-1-2	0.51	0.57	0.63	0.34	0.47	0.76	0.65	0.62	0.67	0.65	1.40	0.75	0.61	0.44	0.58	0.74	0.84	0.82	0.51	0.59	0.58	0.54	0.33	0.51	0.62	0.78	0.22	0.51	0.61
N6-0-1	0.48	0.59	0.59	0.60	0.53	0.81	0.80	0.64	0.83	0.80	0.75	1.27	0.97	0.55	0.57	0.78	0.99	0.75	0.64	0.73	0.94	0.63	0.65	0.64	0.51	0.74	0.44	0.39	0.50
N6-1-2	0.53	0.45	0.54	0.48	0.38	0.63	0.65	0.86	0.73	0.71	0.61	0.97	1.26	0.68	0.61	0.74	0.83	0.64	0.61	0.74	0.69	0.63	0.67	0.66	0.23	1.08	0.55	0.25	0.37
H1-0-0	0.59	0.56	0.71	0.74	0.55	0.62	0.61	0.77	0.62	0.56	0.44	0.55	0.68	1.20	0.78	0.73	0.68	0.76	0.72	0.65	0.56	0.77	0.61	0.71	0.48	0.82	0.56	0.26	0.63
H1-1-1	0.40	0.38	0.54	0.51	0.31	0.48	0.65	0.59	0.44	0.38	0.58	0.57	0.61	0.78	1.18	0.60	0.57	0.85	0.61	0.68	0.57	0.52	0.45	0.40	0.76	1.00	0.40	0.42	0.81
H2-0-0	0.59	0.57	0.69	0.52	0.39	0.90	0.82	0.92	0.90	0.95	0.74	0.78	0.74	0.73	0.60	1.13	0.97	0.79	0.98	0.95	0.80	0.53	0.40	0.54	0.54	0.24	0.19	0.38	0.47
H2-1-1	0.68	0.60	0.71	0.47	0.50	0.99	0.92	0.85	0.87	1.03	0.84	0.99	0.83	0.68	0.57	0.97	1.19	0.83	0.87	0.89	0.97	0.64	0.53	0.57	0.57	0.38	0.21	0.50	0.57
H2-2-2	1.03	0.67	1.16	0.81	0.58	1.00	0.95	0.98	0.88	0.72	0.82	0.75	0.64	0.76	0.85	0.79	0.83	1.59	0.95	0.88	0.66	0.47	0.88	0.69	0.49	0.37	-0.11	0.16	0.26
H3-0-1	0.67	0.63	0.79	0.60	0.56	0.98	0.88	0.85	0.84	0.91	0.51	0.64	0.61	0.72	0.61	0.98	0.87	0.95	1.11	0.91	0.74	0.52	0.56	0.46	0.44	0.32	0.06	0.26	0.46
H3-1-2	0.50	0.69	0.78	0.61	0.50	0.81	0.80	0.81	0.78	0.78	0.59	0.73	0.74	0.65	0.68	0.95	0.89	0.88	0.91	1.31	0.96	0.54	0.39	0.33	0.75	0.53	0.10	0.33	0.64
H3-2-3	0.58	0.89	0.72	0.41	0.51	0.92	0.84	0.71	0.81	0.89	0.58	0.94	0.69	0.56	0.57	0.80	0.97	0.66	0.74	0.96	1.46	0.75	0.36	0.38	0.76	0.76	0.47	0.49	0.89
H4-0-1	0.51	0.68	0.58	0.40	0.26	0.46	0.56	0.45	0.42	0.62	0.54	0.63	0.63	0.77	0.52	0.53	0.64	0.47	0.52	0.54	0.75	1.19	0.68	0.87	0.58	1.08	0.60	0.59	1.03
H4-1-2	0.64	0.33	0.67	0.49	0.48	0.45	0.56	0.46	0.51	0.47	0.33	0.65	0.67	0.61	0.45	0.40	0.53	0.88	0.56	0.39	0.36	0.68	1.22	0.93	0.21	0.59	0.08	0.21	0.37
H4-2-3	0.83	0.49	0.81	0.71	0.45	0.47	0.55	0.48	0.44	0.62	0.51	0.64	0.66	0.71	0.40	0.54	0.57	0.69	0.46	0.33	0.38	0.87	0.93	1.36	0.47	0.90	0.69	0.57	0.67
B1-0-0	0.19	0.58	0.66	0.59	0.41	0.61	0.72	0.27	0.40	0.55	0.62	0.51	0.23	0.48	0.76	0.54	0.57	0.49	0.44	0.75	0.76	0.58	0.21	0.47	1.35	0.63	0.60	0.92	0.77
B1-1-1	0.46	0.80	0.93	0.64	0.40	0.70	0.58	0.66	0.49	0.61	0.78	0.74	1.08	0.82	1.00	0.24	0.38	0.37	0.32	0.53	0.76	1.08	0.59	0.90	0.63	1.47	0.87	0.64	0.72
B1-2-2	0.29	0.63	0.40	0.24	0.31	0.32	-0.08	0.38	0.21	0.17	0.22	0.44	0.55	0.56	0.40	0.19	0.21	-0.11	0.06	0.10	0.47	0.60	0.08	0.69	0.60	0.87	1.34	0.61	0.42
B2-0-0	0.20	0.43	0.44	0.25	0.21	0.50	0.46	0.11	0.24	0.48	0.51	0.39	0.25	0.26	0.42	0.38	0.50	0.16	0.26	0.33	0.49	0.59	0.21	0.57	0.92	0.64	0.61	1.21	0.76
B2-1-1	0.19	0.78	0.71	0.62	0.51	0.59	0.74	0.16	0.29	0.65	0.61	0.50	0.37	0.63	0.81	0.47	0.57	0.26	0.46	0.64	0.89	1.03	0.37	0.67	0.77	0.72	0.42	0.76	1.51
B3-0-2	0.68	0.69	0.78	0.64	0.73	1.00	0.88	0.76	0.77	0.97	0.65	0.77	0.46	0.52	0.46	0.85	0.98	0.92	0.90	0.77	0.97	0.44	0.36	0.38	0.43	0.21	-0.06	0.26	0.49
B3-1-3	0.37	0.61	0.36	0.42	0.24	0.57	0.45	0.38	0.40	0.65	0.41	0.60	0.23	0.35	0.21	0.40	0.53	0.26	0.34	0.60	0.87	0.59	0.10	0.31	0.55	0.65	0.33	0.35	0.40
B3-2-4	0.58	0.77	0.65	0.48	0.69	0.96	0.78	0.74	0.77	0.89	0.67	0.77	0.55	0.48	0.32	0.74	0.93	0.49	0.69	0.79	1.13	0.53	0.20	0.32	0.46	0.48	0.38	0.39	0.48
B4-0-3	0.36	0.55	0.32	0.01	0.29	0.03	0.23	0.18	0.10	0.08	0.62	0.34	0.31	0.25	0.41	0.21	0.23	0.20	0.06	-0.05	0.67	0.59	0.29	0.36	0.15	-0.04	0.24	0.05	-0.03
B4-1-4	0.36	0.39	0.44	0.32	0.22	0.40	0.62	0.43	0.28	0.42	0.48	0.43	0.48	0.51	0.60	0.24	0.31	0.49	0.34	0.29	0.56	0.61	0.58	0.59	0.63	0.75	0.33	0.46	0.78
C1-0-0	0.57	0.69	0.69	0.40	0.47	0.77	0.63	0.63	0.58	0.67	0.38	0.33	0.28	0.71	0.64	0.72	0.73	0.71	0.91	0.82	0.93	0.64	0.36	0.40	0.66	0.63	0.55	0.50	0.85
C1-1-1	0.63	0.61	0.81	0.60	0.72	0.94	0.97	0.80	0.87	1.10	0.83	0.85	0.79	0.78	0.58	0.87	0.98	0.74	0.95	0.85	0.80	0.83	0.77	0.74	0.57	0.63	-0.02	0.56	0.87
C1-2-2	0.85	0.61	0.84	0.52	0.57	0.96	0.92	0.93	0.87	1.01	0.71	0.72	0.78	0.88	0.71	0.91	0.96	0.94	1.03	0.85	0.87	0.82	0.73	0.71	0.34	0.42	0.01	0.33	0.67
C2-0-0	0.76	0.62	0.91	0.52	0.55	1.00	0.90	1.00	0.91	0.93	0.73	0.82	0.82	0.72	0.59	0.89	0.93	0.93	0.96	0.92	1.00	0.77	0.66	0.75	0.42	0.35	0.25	0.37	0.67
C2-1-1	0.87	0.65	0.99	0.72	0.68	1.09	1.03	0.99	0.92	1.05	0.91	0.75	0.73	0.85	0.69	1.01	1.00	1.00	1.09	0.92	0.76	0.77	0.70	0.79	0.55	0.61	0.07	0.50	0.71
C3-0-1	0.74	0.67	0.90	0.59	0.65	0.95	0.93	0.81	0.80	1.01	0.75	0.81	0.71	0.66	0.62	0.93	0.96	0.82	0.97	0.86	0.81	0.65	0.48	0.57	0.47	0.31	-0.03	0.42	0.88
C3-1-2	0.72	0.63	0.78	0.41	0.49	0.94	0.79	0.83	0.71	0.85	0.58	0.55	0.55	0.83	0.73	0.85	0.91	0.97	1.04	0.84	0.80	0.77	0.61	0.64	0.53	0.62	0.35	0.46	0.83
C3-2-3	0.74	0.80	0.98	0.55	0.64	0.86	0.77	0.91	0.71	0.76	0.52	0.51	0.52	0.86	0.70	0.79	0.83	0.95	0.96	0.87	0.85	0.71	0.57	0.56	0.60	0.76	0.41	0.47	0.95
C4-0-1	0.65	0.33	0.50	0.38	0.32	0.76	0.75	0.61	0.70	0.93	0.66	0.72	0.76	0.70	0.53	0.74	0.77	0.63	0.72	0.55	0.81	0.81	0.68	0.73	0.20	0.53	-0.12	0.39	0.87
C4-1-2	0.93	0.57	0.86	0.58	0.47	0.89	0.87	0.86	0.74	0.80	0.64	0.59	0.69	0.81	0.68	0.77	0.88	0.97	0.85	0.62	0.74	0.81	0.68	0.74	0.31	0.67	0.14	0.43	0.85
C4-2-3	0.74	0.40	0.73	0.42	0.46	0.83	0.86	0.83	0.80	0.95	0.66	0.62	0.72	0.72	0.59	0.76	0.82	0.72	0.82	0.64	0.73	0.71	0.65	0.76	0.45	0.68	0.12	0.53	0.90
S1-0-0	0.62	0.56	0.71	0.70	0.63	0.88	0.90	0.80	0.83	0.93	0.52	0.79	0.79	0.78	0.50	0.78	0.78	0.71	0.89	0.72	0.77	0.75	0.71	0.69	0.37	0.43	-0.01	0.37	0.82
S1-1-1	0.76	0.61	0.82	0.66	0.57	1.00	1.00	0.98	0.91	1.05	0.59	0.74	0.79	0.85	0.59	0.90	1.01	0.90	1.04	0.85	0.89	0.78	0.74	0.68	0.54	0.62	-0.02	0.44	0.84
S1-2-2	0.72	0.50	0.83	0.60	0.60	0.86	0.86	0.83	0.83	0.74	0.49	0.72	0.69	0.88	0.72	0.85	0.84	0.96	0.95	0.76	0.80	0.64	0.79	0.71	0.49	0.64	0.00	0.48	1.15
S3-0-1	0.62	0.63	0.74	0.26	0.55	0.80	0.84	0.83	0.71	0.76	0.44	0.48	0.52	0.87	0.68	0.76	0.86	0.81	0.96	0.72	0.97	0.79	0.71	0.55	0.55	0.42	0.11	0.41	0.98
S3-1-2	0.85	0.61	0.89	0.57	0.66	0.97	1.06	0.98	0.88	0.93	0.52	0.71	0.80	0.90	0.67	0.86	0.95	0.96	1.04	0.77	0.99	0.84	0.87	0.69	0.37	0.38	-0.18	0.28	0.80
S3-2-3	0.80	0.70	0.92	0.68	0.79	1.01	1.00	0.93	0.87	0.95	0.44	0.83	0.85	0.94	0.62	0.86	0.99	0.99	1.08	0.84	0.98	0.90	0.89	0.69	0.31	0.38	-0.08	0.24	0.69
S4-0-3	0.78	0.74	1.01	0.77	0.75	0.84	0.95	0.69	0.68	0.94	0.65	0.83	0.73	0.63	0.50	0.71	0.87	0.83	0.83	0.78	0.95	0.75	0.73	0.74	0.55	0.65	0.20	0.48	0.78
S4-1-4	0.65	0.42	0.77	0.46	0.65	0.74	0.86	0.69	0.75	0.79	0.56	0.60	0.51	0.51	0.51	0.67	0.71	0.77	0.77	0.58	0.67	0.36	0.48	0.52	0.24	-0.10	-0.06	0.11	0.20
W1-0-0	0.50	0.46	0.60	0.86	0.50	0.58	0.74	0.60	0.58	0.81	0.47	0.71	0.56	0.37	0.26	0.56	0.60	0.43	0.51	0.63	0.72	0.38	0.40	0.50	0.32	0.21	-0.09	0.16	0.33
W1-1-1	0.47	0.61	0.59	0.58	0.20	0.56	0.71	0.69	0.58	0.71	0.49	0.45	0.47	0.48	0.42	0.58	0.60	0.56	0.57	0.59	0.78	0.52	0.26	0.28	0.41	0.46	-0.09	0.30	0.77
W2-0-1	0.63	0.60	0.81	0.78	0.62	0.69	0.80	0.50	0.51	0.70	0.57	0.61	0.58	0.47	0.46	0.48	0.67	0.82	0.60	0.61	0.57	0.42	0.45	0.45	0.44	0.78	-0.04	0.37	0.55
W2-1-2	0.41	0.51	0.61	0.82	0.54	0.57	0.78	0.51	0.62	0.64	0.60	0.80	0.48	0.26	0.26	0.50	0.66	0.45	0.43	0.64	0.73	0.41	0.44	0.41	0.66	0.25	-0.15	0.39	0.60
O1-0-2	-0.18	-0.25	-0.18	-0.21	-0.05	0.09	0.07	0.25	0.17	0.19	0.15	0.29	0.41	0.14	0.21	0.36	0.37	0.23	0.20	0.15	0.01	0.11	0.21	-0.01	-0.49	-1.03	-0.53	-0.51	-0.39
O1-1-3	0.33	0.01	0.43	0.49	0.30	0.32	0.34	0.29	0.20	-0.06	0.09	0.20	0.09	0.21	0.19	0.11	0.31	0.34	0.10	0.03	0.26	0.17	0.22	0.32	0.40	0.28	0.33	0.35	0.39

ccs	B3-0-2	B3-1-3	B3-2-4	B4-0-3	B4-1-4	C1-0-0	C1-1-1	C1-2-2	C2-0-0	C2-1-1	C3-0-1	C3-1-2	C3-2-3	C4-0-1	C4-1-2	C4-2-3	S1-0-0	S1-1-1	S1-2-2	S3-0-1	S3-1-2	S3-2-3	S4-0-3	S4-1-4	W1-0-0	W1-1-1	W2-0-1	W2-1-2	O1-0-2	O1-1-3
N1-0-2	0.68	0.37	0.58	0.36	0.36	0.57	0.63	0.85	0.76	0.87	0.74	0.72	0.74	0.65	0.93	0.74	0.62	0.76	0.72	0.62	0.85	0.80	0.78	0.65	0.50	0.47	0.63	0.41	-0.18	0.33
N1-1-3	0.69	0.61	0.77	0.55	0.39	0.69	0.61	0.61	0.62	0.65	0.67	0.63	0.80	0.33	0.57	0.40	0.56	0.61	0.50	0.63	0.61	0.70	0.74	0.42	0.46	0.61	0.60	0.51	-0.25	0.01
N2-0-1	0.78	0.36	0.65	0.32	0.44	0.69	0.81	0.84	0.91	0.99	0.90	0.78	0.98	0.50	0.86	0.73	0.71	0.82	0.83	0.74	0.89	0.92	1.01	0.77	0.60	0.59	0.81	0.61	-0.18	0.43
N2-1-2	0.64	0.42	0.48	0.01	0.32	0.40	0.60	0.52	0.52	0.72	0.59	0.41	0.55	0.38	0.58	0.42	0.70	0.66	0.60	0.26	0.57	0.68	0.77	0.46	0.86	0.58	0.78	0.82	-0.21	0.49
N2-2-3	0.73	0.24	0.69	0.29	0.22	0.47	0.72	0.57	0.55	0.68	0.65	0.49	0.64	0.32	0.47	0.46	0.63	0.57	0.60	0.55	0.66	0.79	0.75	0.65	0.50	0.20	0.62	0.54	-0.05	0.30
N4-0-2	1.00	0.57	0.96	0.03	0.40	0.77	0.94	0.96	1.00	1.09	0.95	0.94	0.86	0.76	0.89	0.83	0.88	1.00	0.86	0.80	0.97	1.01	0.84	0.74	0.58	0.56	0.69	0.57	0.09	0.32
N4-1-3	0.88	0.45	0.78	0.23	0.62	0.63	0.97	0.92	0.90	1.03	0.93	0.79	0.77	0.75	0.87	0.86	0.90	1.00	0.86	0.84	1.06	1.00	0.95	0.86	0.74	0.71	0.80	0.78	0.07	0.34
N5-0-2	0.76	0.38	0.74	0.18	0.43	0.63	0.80	0.93	1.00	0.99	0.81	0.83	0.91	0.61	0.86	0.83	0.80	0.98	0.83	0.83	0.98	0.93	0.69	0.69	0.60	0.69	0.50	0.51	0.25	0.29
N5-1-3	0.77	0.40	0.77	0.10	0.28	0.58	0.87	0.87	0.91	0.92	0.80	0.71	0.71	0.70	0.74	0.80	0.83	0.91	0.83	0.71	0.88	0.87	0.68	0.75	0.58	0.58	0.51	0.62	0.17	0.20
N3-0-1	0.97	0.65	0.89	0.08	0.42	0.67	1.10	1.01	0.93	1.05	1.01	0.85	0.76	0.93	0.80	0.95	0.93	1.05	0.74	0.76	0.93	0.95	0.94	0.79	0.81	0.71	0.70	0.64	0.19	-0.06
N3-1-2	0.65	0.41	0.67	0.62	0.48	0.38	0.83	0.71	0.73	0.91	0.75	0.58	0.52	0.66	0.64	0.66	0.52	0.59	0.49	0.44	0.52	0.44	0.65	0.56	0.47	0.49	0.57	0.60	0.15	0.09
N6-0-1	0.77	0.60	0.77	0.34	0.43	0.33	0.85	0.72	0.82	0.75	0.81	0.55	0.51	0.72	0.59	0.62	0.79	0.74	0.72	0.48	0.71	0.83	0.83	0.60	0.71	0.45	0.61	0.80	0.29	0.20
N6-1-2	0.46	0.23	0.55	0.31	0.48	0.28	0.79	0.78	0.82	0.73	0.71	0.55	0.52	0.76	0.69	0.72	0.79	0.79	0.69	0.52	0.80	0.85	0.73	0.51	0.56	0.47	0.58	0.48	0.41	0.09
H1-0-0	0.52	0.35	0.48	0.25	0.51	0.71	0.78	0.88	0.72	0.85	0.66	0.83	0.86	0.70	0.81	0.72	0.78	0.85	0.88	0.87	0.90	0.94	0.63	0.51	0.37	0.48	0.47	0.26	0.14	0.21
H1-1-1	0.46	0.21	0.32	0.41	0.60	0.64	0.58	0.71	0.59	0.69	0.62	0.73	0.70	0.53	0.68	0.59	0.50	0.59	0.72	0.68	0.67	0.62	0.50	0.51	0.26	0.42	0.46	0.26	0.21	0.19
H2-0-0	0.85	0.40	0.74	0.21	0.24	0.72	0.87	0.91	0.89	1.01	0.93	0.85	0.79	0.74	0.77	0.76	0.78	0.90	0.85	0.76	0.86	0.86	0.71	0.67	0.56	0.58	0.48	0.50	0.36	0.11
H2-1-1	0.98	0.53	0.93	0.23	0.31	0.73	0.98	0.96	0.93	1.00	0.96	0.91	0.83	0.77	0.88	0.82	0.78	1.01	0.84	0.86	0.95	0.99	0.87	0.71	0.60	0.60	0.67	0.66	0.37	0.31
H2-2-2	0.92	0.26	0.49	0.20	0.49	0.71	0.74	0.94	0.93	1.00	0.82	0.97	0.95	0.63	0.97	0.72	0.71	0.90	0.96	0.81	0.96	0.99	0.83	0.77	0.43	0.56	0.82	0.45	0.23	0.34
H3-0-1	0.90	0.34	0.69	0.06	0.34	0.91	0.95	1.03	0.96	1.09	0.97	1.04	0.96	0.72	0.85	0.82	0.89	1.04	0.95	0.96	1.04	1.08	0.83	0.77	0.51	0.57	0.60	0.43	0.20	0.10
H3-1-2	0.77	0.60	0.79	-0.05	0.29	0.82	0.85	0.85	0.92	0.92	0.86	0.84	0.87	0.55	0.62	0.64	0.72	0.85	0.76	0.72	0.77	0.84	0.78	0.58	0.63	0.59	0.61	0.64	0.15	0.03
H3-2-3	0.97	0.87	1.13	0.67	0.56	0.93	0.80	0.87	1.00	0.76	0.81	0.80	0.85	0.81	0.74	0.73	0.77	0.89	0.80	0.97	0.99	0.98	0.95	0.67	0.72	0.78	0.57	0.73	0.01	0.26
H4-0-1	0.44	0.59	0.53	0.59	0.61	0.64	0.83	0.82	0.77	0.77	0.65	0.77	0.71	0.81	0.81	0.71	0.75	0.78	0.64	0.79	0.84	0.90	0.75	0.36	0.38	0.52	0.42	0.41	0.11	0.17
H4-1-2	0.36	0.10	0.20	0.29	0.58	0.36	0.77	0.73	0.66	0.70	0.48	0.61	0.57	0.68	0.68	0.65	0.71	0.74	0.79	0.71	0.87	0.89	0.73	0.48	0.40	0.26	0.45	0.44	0.21	0.22
H4-2-3	0.38	0.31	0.32	0.36	0.59	0.40	0.74	0.71	0.75	0.79	0.57	0.64	0.56	0.73	0.74	0.76	0.69	0.68	0.71	0.55	0.69	0.69	0.74	0.52	0.50	0.28	0.45	0.41	-0.01	0.32
B1-0-0	0.43	0.55	0.46	0.15	0.63	0.66	0.57	0.34	0.42	0.55	0.47	0.53	0.60	0.20	0.31	0.45	0.37	0.54	0.49	0.55	0.37	0.31	0.55	0.24	0.32	0.41	0.44	0.66	-0.49	0.40
B1-1-1	0.21	0.65	0.48	-0.04	0.75	0.63	0.63	0.42	0.35	0.61	0.31	0.62	0.76	0.53	0.67	0.68	0.43	0.62	0.64	0.42	0.38	0.38	0.65	-0.10	0.21	0.46	0.78	0.25	-1.03	0.28
B1-2-2	-0.06	0.33	0.38	0.24	0.33	0.55	-0.02	0.01	0.25	0.07	-0.03	0.35	0.41	-0.12	0.14	0.12	-0.01	-0.02	0.00	0.11	-0.18	-0.08	0.20	-0.06	-0.09	-0.09	-0.04	-0.15	-0.53	0.33
B2-0-0	0.26	0.35	0.39	0.05	0.46	0.50	0.56	0.33	0.37	0.50	0.42	0.46	0.47	0.39	0.43	0.53	0.37	0.44	0.48	0.41	0.28	0.24	0.48	0.11	0.16	0.30	0.37	0.39	-0.51	0.35
B2-1-1	0.49	0.40	0.48	-0.03	0.78	0.85	0.87	0.67	0.67	0.71	0.88	0.83	0.95	0.87	0.85	0.90	0.82	0.84	1.15	0.98	0.80	0.69	0.78	0.20	0.33	0.77	0.55	0.60	-0.39	0.39
B3-0-2	1.27	0.72	1.08	0.69	0.37	0.70	0.86	0.85	0.83	0.92	0.90	0.87	0.80	0.69	0.72	0.72	0.84	0.93	0.74	0.98	1.00	1.07	0.99	1.07	0.78	0.59	0.83	0.64	0.07	-0.04
B3-1-3	0.72	1.34	0.87	0.28	0.15	0.28	0.37	0.35	0.30	0.43	0.22	0.29	0.19	0.39	0.18	0.25	0.42	0.51	0.11	0.17	0.29	0.35	0.45	0.22	0.74	0.39	0.33	0.67	-0.09	0.00
B3-2-4	1.08	0.87	1.43	0.81	0.43	0.84	0.94	0.82	0.79	0.83	0.73	0.79	0.87	0.63	0.69	0.71	0.81	0.84	0.57	0.88	0.86	0.91	0.89	0.86	0.77	0.55	0.79	0.72	-0.13	0.05
B4-0-3	0.69	0.28	0.81	2.83	0.85	0.32	0.47	0.41	0.30	0.22	0.13	0.26	0.34	0.47	0.39	0.34	0.36	0.22	0.10	0.67	0.59	0.53	0.79	0.89	0.48	0.52	0.48	0.25	-0.18	-0.30
B4-1-4	0.37	0.15	0.43	0.85	1.20	0.50	0.59	0.58	0.53	0.44	0.30	0.60	0.58	0.70	0.56	0.66	0.63	0.61	0.52	0.83	0.76	0.61	0.67	0.72	0.43	0.64	0.57	0.43	-0.41	0.05
C1-0-0	0.70	0.28	0.84	0.32	0.50	1.10	0.65	0.79	0.78	0.60	0.55	0.85	0.90	0.66	0.71	0.68	0.51	0.71	0.64	0.90	0.76	0.79	0.50	0.40	0.25	0.54	0.45	0.22	-0.13	0.25
C1-1-1	0.86	0.37	0.94	0.47	0.59	0.65	1.18	0.96	0.80	0.91	0.89	0.81	0.77	0.85	0.78	0.90	0.96	1.04	0.81	0.95	1.06	1.11	1.01	0.81	0.72	0.78	0.84	0.81	-0.21	-0.01
C1-2-2	0.85	0.35	0.82	0.41	0.58	0.79	0.96	1.09	0.94	0.93	0.91	0.90	0.91	0.94	0.94	0.98	0.90	1.03	0.90	0.98	1.11	1.11	0.81	0.74	0.58	0.77	0.67	0.53	0.20	0.18
C2-0-0	0.83	0.30	0.79	0.30	0.53	0.78	0.80	0.94	1.23	0.89	0.79	0.84	0.77	0.79	0.80	0.90	0.84	0.98	0.92	0.95	1.07	1.07	0.77	0.73	0.65	0.78	0.38	0.60	0.50	0.83
C2-1-1	0.92	0.43	0.83	0.22	0.44	0.60	0.91	0.93	0.89	1.10	0.92	0.80	0.80	0.65	0.79	0.83	0.91	1.03	0.94	0.81	0.98	0.97	0.89	0.83	0.71	0.78	0.72	0.69	0.31	0.44
C3-0-1	0.90	0.22	0.73	0.13	0.30	0.55	0.89	0.91	0.79	0.92	1.15	0.73	0.79	0.70	0.74	0.78	0.86	0.91	0.90	0.83	0.96	0.94	0.92	0.81	0.62	0.78	0.73	0.72	0.53	0.18
C3-1-2	0.87	0.29	0.79	0.26	0.60	0.85	0.81	0.90	0.84	0.80	0.73	1.13	0.93	0.70	0.86	0.80	0.81	0.96	0.85	1.00	0.98	1.03	0.64	0.66	0.32	0.62	0.55	0.30	0.14	0.17
C3-2-3	0.80	0.19	0.87	0.34	0.58	0.90	0.77	0.91	0.77	0.80	0.79	0.93	1.18	0.61	0.88	0.77	0.69	0.80	0.84	0.95	0.90	0.93	0.68	0.58	0.33	0.56	0.72	0.31	0.09	0.29
C4-0-1	0.69	0.39	0.63	0.47	0.70	0.66	0.85	0.94	0.79	0.65	0.70	0.70	0.61	1.47	0.87	1.00	0.95	0.99	0.85	0.85	1.04	0.99	0.72	0.57	0.60	0.76	0.57	0.55	-0.05	0.01
C4-1-2	0.72	0.18	0.69	0.39	0.56	0.71	0.78	0.94	0.80	0.79	0.74	0.86	0.88	0.87	1.05	0.89	0.84	0.95	0.94	0.88	1.05	1.02	0.69	0.57	0.34	0.61	0.65	0.35	0.18	0.44
C4-2-3	0.72	0.25	0.71	0.34	0.66	0.68	0.90	0.98	0.90	0.83	0.78	0.80	0.77	1.00	0.89	1.09	0.90	1.02	0.87	0.95	1.07	1.00	0.76	0.76	0.56	0.73	0.59	0.52	0.10	0.45
S1-0-0	0.84	0.42	0.81	0.36	0.63	0.51	0.96	0.90	0.84	0.91	0.86	0.81	0.69	0.95	0.84	0.90	1.11	0.98	0.95	0.86	1.03	1.08	0.78	0.72	0.72	0.77	0.62	0.68	0.18	0.25
S1-1-1	0.93	0.51	0.84	0.22	0.61	0.71	1.04	1.03	0.98	1.03	0.91	0.96	0.80	0.99	0.95	1.02	0.98	1.16	0.93	0.96	1.11	1.12	0.84	0.72	0.73	0.90	0.64	0.72	0.15	0.39
S1-2-2	0.74	0.11	0.57	0.10	0.52	0.64	0.81	0.90	0.92	0.94	0.90	0.85	0.84	0.85	0.94	0.87	0.95	0.93	1.34	0.93	1.12	1.08	0.69	0.59	0.50	0.64	0.45	0.53	0.33	0.63
S3-0-1	0.98	0.17	0.88	0.67	0.83	0.90	0.95	0.98	0.95	0.81	0.83	1.00	0.95	0.85	0.88	0.95	0.86	0.96	0.93	1.09	0.93	0.88	0.67	0.78	0.34	0.78	0.57	0.43	-0.07	0.07
S3-1-2	1.00	0.29	0.86	0.59	0.76	0.76	1.06	1.11	1.07	0.98	0.96	0.98	0.90	1.04	1.05	1.07	1.03	1.11	1.12	0.93	1.06	1.01	0.80	0.80	0.60	0.86	0.66	0.63	0.27	0.47
S3-2-3	1.07	0.35	0.91	0.53	0.61	0.79	1.11	1.11	1.07	0.97	0.94	1.03	0.93	0.99	1.02	1.00	1.08	1.12	1.08	0.88	1.01	1.10	0.85	0.77	0.57	0.78	0.76	0.59	0.12	0.34
S4-0-3	0.99	0.45	0.89	0.79	0.67	0.50	1.01	0.81	0.77	0.89	0.92	0.64	0.68	0.72	0.69	0.76	0.78	0.84	0.69	0.67	0.80	0.85	1.14	0.79	0.93	0.87	0.95	0.88	-0.45	0.10
S4-1-4	1.07	0.22	0.86	0.89	0.72	0.40	0.81	0.74	0.73	0.83	0.81	0.66	0.58	0.57	0.57	0.76	0.72	0.72	0.59	0.78	0.80	0.77	0.79	1.18	0.72	0.72	0.81	0.59	-0.33	-0.07
W1-0-0	0.78	0.74	0.77	0.48	0.43	0.25	0.72	0.58	0.65	0.71	0.62	0.32	0.33	0.60	0.34	0.56	0.72	0.73	0.50	0.34	0.60	0.57	0.93	0.72	1.13	0.75	0.55	0.92	0.05	0.18
W1-1-1	0.59	0.39	0.55	0.52	0.64	0.54	0.78	0.77	0.78	0.78	0.78	0.62	0.56	0.76	0.61	0.73	0.77	0.90	0.64	0.78	0.86	0.78	0.87	0.72	0.75	1.20	0.59	0.71	-0.11	0.07
W2-0-1	0.83	0.33	0.79	0.48	0.57	0.45	0.84	0.67	0.38	0.72	0.73	0.55	0.72	0.57	0.65	0.59	0.62	0.64	0.45	0.57	0.66	0.76	0.95	0.81	0.55	0.59	1.25	0.50	-0.40	-0.28
W2-1-2	0.64	0.67	0.72	0.25	0.43	0.22	0.81	0.53	0.60	0.69	0.72	0.30	0.31	0.55	0.35	0.52	0.68	0.72	0.53	0.43	0.63	0.59	0.88	0.59	0.92	0.71	0.50	1.27	-0.01	0.36
O1-0-2	0.07	-0.09	-0.13	-0.18	-0.41	-0.13	-0.21	0.20	0.50	0.31	0.53	0.14	0.09	-0.05	0.18	0.10	0.18	0.15	0.33	-0.07	0.27	0.12	-0.45	-0.33	0.05	-0.11	-0.40	-0.01	1.87	0.58
O1-1-3	-0.04	0.00	0.05	-0.30	0.05	0.25	-0.01	0.18	0.83	0.44	0.18	0.17	0.29	0.01	0.44	0.45	0.25	0.39	0.63	0.07	0.47	0.34	0.10	-0.07	0.18	0.07	-0.28	0.36	0.58	1.41

Table 4-18 Genetic correlations for TCH among all trials, ordered geographical from North to NSW (and Ord at end). Non-significant correlations (between -0.3 and 0.3) are shaded yellow, large positive correlations (> 0.7) are shaded green. (will be updated)

tch	N1-0-2	N1-1-3	N2-0-1	N2-1-2	N2-2-3	N4-0-2	N4-1-3	N5-0-2	N5-1-3	N3-0-1	N3-1-2	N6-0-1	N6-1-2	H1-0-0	H1-1-1	H2-0-0	H2-1-1	H2-2-2	H3-0-1	H3-1-2	H3-2-3	H4-0-1	H4-1-2	H4-2-3	B1-0-0	B1-1-1	B1-2-2	B2-0-0	B2-1-1	B3-0-2	B3-1-3	B3-2-4	B4-0-3	B4-1-4	C1-0-0	C1-1-1	C1-2-2	C2-0-0	C2-1-1	C3-0-1	C3-1-2	C3-2-3	C4-0-1	C4-1-2	C4-2-3	S1-0-0	S1-1-1	S1-2-2	S3-0-1	S3-1-2	S3-2-3	S4-0-3	S4-1-4	W1-0-0	W1-1-1	W2-0-1	W2-1-2	O1-0-2	O1-1-3
N1-0-2	1.20	0.80	0.50	0.29	0.39	0.72	0.60	0.59	0.65	0.42	-0.05	0.49	0.35	0.34	0.25	0.60	0.50	0.42	0.47	0.67	0.68	0.60	0.62	0.35	0.53	0.67	0.47	0.32	0.28	0.81	0.54	0.83	0.49	0.32	0.20	0.44	0.16	0.61	0.43	0.18	0.02	0.21	0.34	0.38	0.42	0.53	0.47	0.42	0.34	0.23	0.24	0.67	0.59	0.75	0.48	0.54	0.60	0.25	0.27
N1-1-3	0.80	1.09	0.71	0.73	0.79	0.76	0.87	0.77	0.94	0.57	0.39	0.53	0.54	0.53	0.58	0.70	0.68	0.75	0.53	0.71	0.76	0.65	0.92	0.78	1.01	0.62	0.38	0.39	0.44	1.09	0.73	0.88	0.79	0.78	0.38	0.56	0.68	0.55	0.44	0.55	0.48	0.49	0.46	0.51	0.56	0.64	0.62	0.68	0.36	0.33	0.39	0.32	0.46	0.53	0.62	0.59	0.76	0.83	0.50
N2-0-1	0.50	0.71	1.59	0.92	0.97	0.77	0.78	0.64	0.73	0.45	0.15	0.52	0.57	0.80	0.99	0.67	0.62	0.68	0.49	0.73	0.65	0.82	0.71	0.62	0.11	0.66	0.52	0.24	0.32	0.54	0.51	0.71	0.56	0.76	0.61	0.56	0.49	0.63	0.73	0.54	0.35	0.31	0.45	0.42	0.29	0.62	0.64	0.50	0.46	0.62	0.64	0.51	0.48	0.45	0.39	0.83	0.69	0.56	0.09
N2-1-2	0.29	0.73	0.92	1.18	1.05	0.62	0.85	0.57	0.74	0.32	0.39	0.05	0.21	0.68	0.75	0.48	0.61	0.94	0.43	0.58	0.55	0.43	0.77	0.71	0.60	0.35	0.26	0.39	0.21	0.66	0.52	0.44	0.80	0.81	0.43	0.39	0.74	0.25	0.37	0.54	0.64	0.53	0.14	0.30	0.33	0.49	0.49	0.60	0.14	0.26	0.32	-0.06	0.13	0.07	0.28	0.40	0.55	0.59	0.11
N2-2-3	0.39	0.79	0.97	1.05	1.24	0.53	0.76	0.56	0.73	0.31	0.33	0.11	0.23	0.49	0.66	0.44	0.60	0.76	0.35	0.44	0.50	0.32	0.59	0.72	0.73	0.29	0.09	0.29	0.14	0.45	0.35	0.34	0.69	0.71	0.47	0.19	0.70	0.40	0.29	0.58	0.55	0.50	0.31	0.44	0.53	0.46	0.53	0.65	0.17	0.24	0.36	-0.04	0.12	0.13	0.38	0.44	0.52	0.38	-0.10
N4-0-2	0.72	0.76	0.77	0.62	0.53	1.29	1.02	0.98	0.81	0.60	0.19	0.44	0.61	0.65	0.59	0.75	0.48	0.69	0.68	0.66	0.83	0.78	0.89	0.50	0.17	0.51	0.47	0.36	0.31	1.19	0.57	0.60	0.73	0.71	0.40	0.71	0.56	0.46	0.55	0.65	0.48	0.56	0.51	0.41	0.47	0.83	0.46	0.58	0.54	0.37	0.34	0.51	0.54	0.48	0.40	0.66	0.61	0.76	0.59
N4-1-3	0.60	0.87	0.78	0.85	0.76	1.02	1.16	0.81	0.95	0.45	0.29	0.35	0.47	0.60	0.75	0.75	0.69	0.85	0.63	0.70	0.77	0.63	0.80	0.67	0.60	0.73	0.61	0.41	0.46	1.07	0.54	0.71	0.70	0.70	0.33	0.61	0.65	0.44	0.48	0.45	0.42	0.44	0.35	0.44	0.50	0.63	0.51	0.66	0.29	0.27	0.39	0.22	0.33	0.40	0.48	0.63	0.73	0.73	0.38
N5-0-2	0.59	0.77	0.64	0.57	0.56	0.98	0.81	1.28	0.90	0.81	0.42	0.49	0.70	0.72	0.62	0.88	0.68	0.80	0.90	0.77	0.93	0.90	1.03	0.70	0.49	0.33	0.07	0.41	0.40	1.33	0.75	0.59	1.00	0.83	0.52	0.64	0.56	0.44	0.37	0.51	0.73	0.60	0.54	0.40	0.42	0.94	0.75	0.62	0.53	0.39	0.22	0.46	0.60	0.50	0.48	0.57	0.54	1.01	0.69
N5-1-3	0.65	0.94	0.73	0.74	0.73	0.81	0.95	0.90	1.18	0.36	0.22	0.45	0.54	0.64	0.75	0.71	0.71	0.91	0.56	0.72	0.82	0.64	0.85	0.72	0.50	0.75	0.48	0.47	0.48	1.07	0.69	0.71	0.88	0.88	0.25	0.60	0.56	0.41	0.43	0.24	0.27	0.36	0.32	0.42	0.51	0.57	0.70	0.69	0.44	0.51	0.54	0.41	0.55	0.45	0.45	0.48	0.65	0.80	0.40
N3-0-1	0.42	0.57	0.45	0.32	0.31	0.60	0.45	0.81	0.36	1.36	0.88	0.51	0.72	0.44	0.21	0.76	0.53	0.23	0.71	0.59	0.47	0.82	0.54	0.43	1.06	0.55	0.29	0.27	0.17	0.97	0.44	0.53	0.68	0.62	0.46	0.28	0.39	0.59	0.33	0.78	0.76	0.52	0.71	0.20	0.16	0.99	0.31	0.36	0.64	0.46	0.23	0.22	0.28	0.59	0.46	0.51	0.52	0.70	0.90
N3-1-2	-0.05	0.39	0.15	0.39	0.33	0.19	0.29	0.42	0.22	0.88	1.45	0.20	0.40	0.34	0.34	0.45	0.46	0.38	0.41	0.36	0.37	0.41	0.32	0.43	0.85	0.37	0.17	0.19	0.02	0.75	0.38	0.53	0.56	0.64	0.46	0.27	0.57	0.35	0.39	0.69	0.87	0.41	0.49	0.21	0.01	0.32	0.16	0.36	0.32	0.31	0.18	0.00	0.22	0.23	0.43	0.33	0.34	0.84	0.60
N6-0-1	0.49	0.53	0.52	0.05	0.11	0.44	0.35	0.49	0.45	0.51	0.20	1.28	0.85	0.31	0.40	0.67	0.40	0.17	0.38	0.43	0.25	0.64	0.36	0.30	0.64	0.88	0.62	0.28	0.42	0.69	0.03	0.29	0.24	0.26	0.11	0.34	0.15	0.48	0.51	0.53	0.32	0.20	0.60	0.42	0.20	0.49	0.39	0.16	0.53	0.55	0.44	0.57	0.53	0.56	0.43	0.49	0.34	0.55	0.57
N6-1-2	0.35	0.54	0.57	0.21	0.23	0.61	0.47	0.70	0.54	0.72	0.40	0.85	1.15	0.45	0.59	0.59	0.54	0.34	0.63	0.69	0.55	0.79	0.53	0.40	0.74	0.63	0.48	0.28	0.35	0.65	0.17	0.37	0.41	0.61	0.36	0.54	0.38	0.52	0.65	0.58	0.59	0.45	0.51	0.36	0.12	0.64	0.48	0.38	0.58	0.66	0.51	0.43	0.47	0.47	0.48	0.61	0.50	0.64	0.59
H1-0-0	0.34	0.53	0.80	0.68	0.49	0.65	0.60	0.72	0.64	0.44	0.34	0.31	0.45	1.15	0.85	0.66	0.53	0.70	0.84	0.75	0.72	0.84	0.84	0.46	0.67	0.42	0.30	0.49	0.45	0.98	0.58	0.44	0.75	0.63	0.64	0.63	0.46	0.58	0.71	0.52	0.63	0.42	0.50	0.46	0.27	0.63	0.64	0.52	0.46	0.55	0.47	0.58	0.63	0.42	0.36	0.44	0.33	0.59	0.38
H1-1-1	0.25	0.58	0.99	0.75	0.66	0.59	0.75	0.62	0.75	0.21	0.34	0.40	0.59	0.85	1.34	0.66	0.69	0.67	0.73	0.76	0.77	0.76	0.69	0.62	0.42	0.68	0.38	0.26	0.41	0.71	0.41	0.66	0.54	0.77	0.62	0.69	0.55	0.35	0.70	0.43	0.46	0.36	0.30	0.59	0.30	0.39	0.84	0.75	0.25	0.59	0.67	0.36	0.50	0.30	0.50	0.61	0.55	0.63	0.07
H2-0-0	0.60	0.70	0.67	0.48	0.44	0.75	0.75	0.88	0.71	0.76	0.45	0.67	0.59	0.66	0.66	1.25	0.84	0.54	0.99	0.80	0.75	0.79	0.62	0.62	0.73	0.50	0.35	0.55	0.56	1.00	0.48	0.57	0.42	0.59	0.62	0.54	0.42	0.76	0.56	0.75	0.64	0.45	0.72	0.49	0.31	0.74	0.64	0.47	0.46	0.30	0.33	0.39	0.35	0.72	0.73	0.60	0.61	0.68	0.45
H2-1-1	0.50	0.68	0.62	0.61	0.60	0.48	0.69	0.68	0.71	0.53	0.46	0.40	0.54	0.53	0.69	0.84	1.08	0.69	0.73	0.85	0.76	0.64	0.59	0.70	0.82	0.21	-0.07	0.28	0.31	0.71	0.48	0.74	0.46	0.66	0.41	0.60	0.56	0.52	0.54	0.34	0.58	0.38	0.28	0.43	0.22	0.55	0.69	0.52	0.31	0.50	0.47	0.15	0.22	0.46	0.69	0.56	0.64	0.50	0.27
H2-2-2	0.42	0.75	0.68	0.94	0.76	0.69	0.85	0.80	0.91	0.23	0.38	0.17	0.34	0.70	0.67	0.54	0.69	1.17	0.64	0.72	0.74	0.62	0.98	0.66	0.61	0.20	-0.12	0.45	0.19	1.01	0.98	0.84	0.97	0.92	0.50	0.67	0.78	0.26	0.47	0.48	0.79	0.56	0.20	0.38	0.35	0.60	0.85	0.65	0.03	0.24	0.25	0.13	0.38	0.13	0.41	0.34	0.54	0.81	0.30
H3-0-1	0.47	0.53	0.49	0.43	0.35	0.68	0.63	0.90	0.56	0.71	0.41	0.38	0.63	0.84	0.73	0.99	0.73	0.64	1.44	0.92	0.84	0.95	0.75	0.56	0.86	0.27	0.14	0.70	0.57	1.12	0.54	0.52	0.66	0.64	0.94	0.64	0.58	0.74	0.73	0.77	0.88	0.69	0.77	0.58	0.38	0.85	0.94	0.60	0.21	0.41	0.32	0.33	0.52	0.54	0.66	0.71	0.64	0.61	0.38
H3-1-2	0.67	0.71	0.73	0.58	0.44	0.66	0.70	0.77	0.72	0.59	0.36	0.43	0.69	0.75	0.76	0.80	0.85	0.72	0.92	1.24	0.96	0.89	0.83	0.67	0.81	0.54	0.32	0.53	0.52	0.85	0.70	0.80	0.54	0.75	0.57	0.77	0.57	0.59	0.81	0.37	0.58	0.38	0.33	0.60	0.29	0.63	0.73	0.53	0.44	0.61	0.48	0.62	0.63	0.69	0.67	0.81	0.85	0.57	0.35
H3-2-3	0.68	0.76	0.65	0.55	0.50	0.83	0.77	0.93	0.82	0.47	0.37	0.25	0.55	0.72	0.77	0.75	0.76	0.74	0.84	0.96	1.27	0.87	0.89	0.72	0.37	0.34	0.38	0.36	0.51	0.87	0.74	0.80	0.73	0.76	0.63	0.82	0.65	0.56	0.65	0.42	0.70	0.51	0.50	0.54	0.49	0.56	0.70	0.53	0.36	0.39	0.33	0.52	0.68	0.55	0.70	0.81	0.68	0.73	0.34
H4-0-1	0.60	0.65	0.82	0.43	0.32	0.78	0.63	0.90	0.64	0.82	0.41	0.64	0.79	0.84	0.76	0.79	0.64	0.62	0.95	0.89	0.87	1.24	0.95	0.60	0.59	0.75	0.63	0.34	0.58	1.07	0.93	0.90	0.80	0.86	0.72	0.92	0.56	0.76	0.94	0.69	0.63	0.53	0.57	0.45	0.24	0.86	0.78	0.47	0.85	0.88	0.76	0.79	0.80	0.76	0.62	0.89	0.75	0.75	0.63
H4-1-2	0.62	0.92	0.71	0.77	0.59	0.89	0.80	1.03	0.85	0.54	0.32	0.36	0.53	0.84	0.69	0.62	0.59	0.98	0.75	0.83	0.89	0.95	1.54	0.78	0.57	0.19	0.10	0.31	0.44	1.33	1.34	0.94	1.10	0.99	0.57	0.90	0.79	0.39	0.56	0.72	0.75	0.70	0.36	0.57	0.49	0.85	0.77	0.54	0.60	0.57	0.48	0.58	0.79	0.45	0.42	0.56	0.69	0.98	0.70
H4-2-3	0.35	0.78	0.62	0.71	0.72	0.50	0.67	0.70	0.72	0.43	0.43	0.30	0.40	0.46	0.62	0.62	0.70	0.66	0.56	0.67	0.72	0.60	0.78	1.18	0.68	0.35	0.24	0.47	0.53	0.53	0.63	0.64	0.75	0.87	0.44	0.45	0.62	0.26	0.38	0.30	0.49	0.40	0.16	0.24	0.20	0.40	0.48	0.40	0.41	0.48	0.44	0.18	0.30	0.37	0.66	0.53	0.68	0.84	0.45
B1-0-0	0.53	1.01	0.11	0.60	0.73	0.17	0.60	0.49	0.50	1.06	0.85	0.64	0.74	0.67	0.42	0.73	0.82	0.61	0.86	0.81	0.37	0.59	0.57	0.68	1.88	0.76	0.71	0.93	0.65	0.85	0.25	0.82	0.54	0.60	0.26	0.04	0.72	0.38	0.02	0.65	0.51	0.16	0.20	0.45	0.03	0.94	0.28	0.97	0.54	0.28	0.30	0.41	0.75	0.22	0.68	0.53	0.40	0.58	0.16
B1-1-1	0.67	0.62	0.66	0.35	0.29	0.51	0.73	0.33	0.75	0.55	0.37	0.88	0.63	0.42	0.68	0.50	0.21	0.20	0.27	0.54	0.34	0.75	0.19	0.35	0.76	1.90	1.05	0.50	0.93	0.50	0.23	1.36	0.81	0.60	0.13	0.40	0.20	0.18	0.67	0.21	0.03	0.08	0.22	0.61	0.21	0.68	0.59	1.18	0.78	0.42	0.73	0.98	1.00	0.69	0.50	1.08	0.60	0.35	0.12
B1-2-2	0.47	0.38	0.52	0.26	0.09	0.47	0.61	0.07	0.48	0.29	0.17	0.62	0.48	0.30	0.38	0.35	-0.07	-0.12	0.14	0.32	0.38	0.63	0.10	0.24	0.71	1.05	1.94	0.88	0.86	0.08	0.18	0.39	0.14	0.32	-0.02	0.18	-0.08	0.54	0.79	0.34	-0.06	0.03	0.46	0.42	0.35	0.07	-0.07	0.11	0.65	0.30	0.60	0.71	0.42	0.72	0.31	0.79	0.49	0.29	0.30
B2-0-0	0.32	0.39	0.24	0.39	0.29	0.36	0.41	0.41	0.47	0.27	0.19	0.28	0.28	0.49	0.26	0.55	0.28	0.45	0.70	0.53	0.36	0.34	0.31	0.47	0.93	0.50	0.88	1.37	0.91	0.30	0.42	0.12	0.31	0.41	0.18	0.02	0.24	0.22	0.31	0.34	0.07	0.13	0.24	0.26	0.20	0.37	0.15	0.10	0.40	0.51	0.42	0.57	0.44	0.26	0.30	0.28	0.31	0.84	0.40
B2-1-1	0.28	0.44	0.32	0.21	0.14	0.31	0.46	0.40	0.48	0.17	0.02	0.42	0.35	0.45	0.41	0.56	0.31	0.19	0.57	0.52	0.51	0.58	0.44	0.53	0.65	0.93	0.86	0.91	1.30	0.16	0.36	0.21	0.39	0.53	0.15	0.45	0.12	0.32	0.43	0.28	0.18	0.21	0.21	0.56	0.29	0.27	0.36	0.21	0.55	0.44	0.58	0.70	0.64	0.41	0.42	0.74	0.53	0.69	0.30
B3-0-2	0.81	1.09	0.54	0.66	0.45	1.19	1.07	1.33	1.07	0.97	0.75	0.69	0.65	0.98	0.71	1.00	0.71	1.01	1.12	0.85	0.87	1.07	1.33	0.53	0.85	0.50	0.08	0.30	0.16	2.84	1.26	1.38	1.18	0.89	0.70	1.11	1.13	0.63	0.78	0.87	0.98	0.73	0.90	0.91	0.87	1.23	1.11	0.90	0.50	0.34	0.16	0.41	0.69	0.48	0.58	0.50	0.53	1.20	0.93
B3-1-3	0.54	0.73	0.51	0.52	0.35	0.57	0.54	0.75	0.69	0.44	0.38	0.03	0.17	0.58	0.41	0.48	0.48	0.98	0.54	0.70	0.74	0.93	1.34	0.63	0.25	0.23	0.18	0.42	0.36	1.26	1.98	1.55	1.05	0.92	0.68	1.05	1.02	0.30	0.63	0.57	0.62	0.53	0.21	0.59	0.53	0.70	0.68	0.29	0.70	0.50	0.47	0.54	0.52	0.37	0.44	0.45	0.73	0.89	0.60
B3-2-4	0.83	0.88	0.71	0.44	0.34	0.60	0.71	0.59	0.71	0.53	0.53	0.29	0.37	0.44	0.66	0.57	0.74	0.84	0.52	0.80	0.80	0.90	0.94	0.64	0.82	1.36	0.39	0.12	0.21	1.38	1.55	2.44	1.00	0.81	0.62	1.02	1.07	0.18	0.67	0.16	0.47	0.37	0.14	0.47	0.26	0.72	0.82	0.78	0.45	0.26	0.33	0.59	0.64	0.51	0.70	0.73	0.79	0.79	0.27
B4-0-3	0.49	0.79	0.56	0.80	0.69	0.73	0.70	1.00	0.88	0.68	0.56	0.24	0.41	0.75	0.54	0.42	0.46	0.97	0.66	0.54	0.73	0.80	1.10	0.75	0.54	0.81	0.14	0.31	0.39	1.18	1.05	1.00	1.84	1.13	0.58	0.50	0.72	0.08	0.27	0.55	1.06	0.89	0.23	0.37	0.43	0.84	0.75	0.67	0.43	0.42	0.31	0.19	0.66	0.03	0.25	0.56	0.59	0.98	0.65
B4-1-4	0.32	0.78	0.76	0.81	0.71	0.71	0.70	0.83	0.88	0.62	0.64	0.26	0.61	0.63	0.77	0.59	0.66	0.92	0.64	0.75	0.76	0.86	0.99	0.87	0.60	0.60	0.32	0.41	0.53	0.89	0.92	0.81	1.13	1.51	0.41	0.84	0.81	0.24	0.60	0.69	0.70	0.71	0.11	0.29	0.26	0.81	0.84	0.78	0.60	0.68	0.64	0.25	0.55	0.23	0.50	0.66	0.84	0.94	0.45
C1-0-0	0.20	0.38	0.61	0.43	0.47	0.40	0.33	0.52	0.25	0.46	0.46	0.11	0.36	0.64	0.62	0.62	0.41	0.50	0.94	0.57	0.63	0.72	0.57	0.44	0.26	0.13	-0.02	0.18	0.15	0.70	0.68	0.62	0.58	0.41	1.20	0.41	0.51	0.66	0.55	0.63	0.77	0.53	0.81	0.68	0.39	0.43	0.50	0.32	0.18	0.33	0.33	0.16	0.19	0.36	0.57	0.61	0.41	0.44	0.17
C1-1-1	0.44	0.56	0.56	0.39	0.19	0.71	0.61	0.64	0.60	0.28	0.27	0.34	0.54	0.63	0.69	0.54	0.60	0.67	0.64	0.77	0.82	0.92	0.90	0.45	0.04	0.40	0.18	0.02	0.45	1.11	1.05	1.02	0.50	0.84	0.41	1.34	0.70	0.47	0.81	0.20	0.42	0.61	0.17	0.54	0.40	0.74	1.06	0.61	0.59	0.63	0.63	0.21	0.39	0.39	0.80	0.77	0.75	0.71	0.49
C1-2-2	0.16	0.68	0.49	0.74	0.70	0.56	0.65	0.56	0.56	0.39	0.57	0.15	0.38	0.46	0.55	0.42	0.56	0.78	0.58	0.57	0.65	0.56	0.79	0.62	0.72	0.20	-0.08	0.24	0.12	1.13	1.02	1.07	0.72	0.81	0.51	0.70	1.23	0.44	0.62	0.72	0.93	0.80	0.46	0.72	0.64	0.82	0.91	0.80	0.42	0.46	0.47	0.01	0.33	0.15	0.75	0.50	0.58	0.80	0.38
C2-0-0	0.61	0.55	0.63	0.25	0.40	0.46	0.44	0.44	0.41	0.59	0.35	0.48	0.52	0.58	0.35	0.76	0.52	0.26	0.74	0.59	0.56	0.76	0.39	0.26	0.38	0.18	0.54	0.22	0.32	0.63	0.30	0.18	0.08	0.24	0.66	0.47	0.44	1.19	0.82	0.70	0.53	0.46	0.81	0.67	0.52	0.65	0.54	0.33	0.66	0.65	0.65	0.47	0.32	0.98	0.84	0.76	0.63	0.11	0.20
C2-1-1	0.43	0.44	0.73	0.37	0.29	0.55	0.48	0.37	0.43	0.33	0.39	0.51	0.65	0.71	0.70	0.56	0.54	0.47	0.73	0.81	0.65	0.94	0.56	0.38	0.02	0.67	0.79	0.31	0.43	0.78	0.63	0.67	0.27	0.60	0.55	0.81	0.62	0.82	1.14	0.51	0.53	0.51	0.48	0.68	0.39	0.57	0.78	0.46	0.68	0.86	0.82	0.63	0.52	0.75	0.87	0.93	0.72	0.26	0.16
C3-0-1	0.18	0.55	0.54	0.54	0.58	0.65	0.45	0.51	0.24	0.78	0.69	0.53	0.58	0.52	0.43	0.75	0.34	0.48	0.77	0.37	0.42	0.69	0.72	0.30	0.65	0.21	0.34	0.34	0.28	0.87	0.57	0.16	0.55	0.69	0.63	0.20	0.72	0.70	0.51	1.75	1.13	0.78	0.91	0.68	0.59	0.89	0.43	0.52	0.64	0.45	0.53	0.35	0.35	0.57	0.75	0.62	0.54	0.54	0.43
C3-1-2	0.02	0.48	0.35	0.64	0.55	0.48	0.42	0.73	0.27	0.76	0.87	0.32	0.59	0.63	0.46	0.64	0.58	0.79	0.88	0.58	0.70	0.63	0.75	0.49	0.51	0.03	-0.06	0.07	0.18	0.98	0.62	0.47	1.06	0.70	0.77	0.42	0.93	0.53	0.53	1.13	1.67	1.10	0.75	0.76	0.44	0.81	0.69	0.51	0.18	0.16	0.05	0.00	0.44	0.08	0.52	0.54	0.29	0.79	0.56
C3-2-3	0.21	0.49	0.31	0.53	0.50	0.56	0.44	0.60	0.36	0.52	0.41	0.20	0.45	0.42	0.36	0.45	0.38	0.56	0.69	0.38	0.51	0.53	0.70	0.40	0.16	0.08	0.03	0.13	0.21	0.73	0.53	0.37	0.89	0.71	0.53	0.61	0.80	0.46	0.51	0.78	1.10	1.23	0.51	0.63	0.53	0.79	0.80	0.61	0.43	0.35	0.37	-0.09	0.34	0.17	0.44	0.45	0.43	0.50	0.49
C4-0-1	0.34	0.46	0.45	0.14	0.31	0.51	0.35	0.54	0.32	0.71	0.49	0.60	0.51	0.50	0.30	0.72	0.28	0.20	0.77	0.33	0.50	0.57	0.36	0.16	0.20	0.22	0.46	0.24	0.21	0.90	0.21	0.14	0.23	0.11	0.81	0.17	0.46	0.81	0.48	0.91	0.75	0.51	1.26	0.82	0.71	0.61	0.36	0.27	0.32	0.32	0.27	0.28	0.27	0.54	0.56	0.41	0.16	0.37	0.51
C4-1-2	0.38	0.51	0.42	0.30	0.44	0.41	0.44	0.40	0.42	0.20	0.21	0.42	0.36	0.46	0.59	0.49	0.43	0.38	0.58	0.60	0.54	0.45	0.57	0.24	0.45	0.61	0.42	0.26	0.56	0.91	0.59	0.47	0.37	0.29	0.68	0.54	0.72	0.67	0.68	0.68	0.76	0.63	0.82	1.41	1.01	0.54	0.81	0.49	0.37	0.52	0.60	0.30	0.52	0.29	0.58	0.62	0.32	0.23	0.19
C4-2-3	0.42	0.56	0.29	0.33	0.53	0.47	0.50	0.42	0.51	0.16	0.01	0.20	0.12	0.27	0.30	0.31	0.22	0.35	0.38	0.29	0.49	0.24	0.49	0.20	0.03	0.21	0.35	0.20	0.29	0.87	0.53	0.26	0.43	0.26	0.39	0.40	0.64	0.52	0.39	0.59	0.44	0.53	0.71	1.01	1.16	0.60	0.73	0.52	0.18	0.18	0.31	-0.05	0.13	0.24	0.53	0.36	0.34	0.28	0.20
S1-0-0	0.53	0.64	0.62	0.49	0.46	0.83	0.63	0.94	0.57	0.99	0.32	0.49	0.64	0.63	0.39	0.74	0.55	0.60	0.85	0.63	0.56	0.86	0.85	0.40	0.94	0.68	0.07	0.37	0.27	1.23	0.70	0.72	0.84	0.81	0.43	0.74	0.82	0.65	0.57	0.89	0.81	0.79	0.61	0.54	0.60	1.37	0.87	0.84	0.55	0.43	0.35	0.24	0.34	0.62	0.70	0.70	0.68	0.67	0.60
S1-1-1	0.47	0.62	0.64	0.49	0.53	0.46	0.51	0.75	0.70	0.31	0.16	0.39	0.48	0.64	0.84	0.64	0.69	0.85	0.94	0.73	0.70	0.78	0.77	0.48	0.28	0.59	-0.07	0.15	0.36	1.11	0.68	0.82	0.75	0.84	0.50	1.06	0.91	0.54	0.78	0.43	0.69	0.80	0.36	0.81	0.73	0.87	1.44	0.97	0.20	0.42	0.48	0.12	0.44	0.45	0.70	0.67	0.72	0.59	0.25
S1-2-2	0.42	0.68	0.50	0.60	0.65	0.58	0.66	0.62	0.69	0.36	0.36	0.16	0.38	0.52	0.75	0.47	0.52	0.65	0.60	0.53	0.53	0.47	0.54	0.40	0.97	1.18	0.11	0.10	0.21	0.90	0.29	0.78	0.67	0.78	0.32	0.61	0.80	0.33	0.46	0.52	0.51	0.61	0.27	0.49	0.52	0.84	0.97	1.27	0.27	0.22	0.41	0.22	0.45	0.50	0.59	0.68	0.63	0.44	-0.02
S3-0-1	0.34	0.36	0.46	0.14	0.17	0.54	0.29	0.53	0.44	0.64	0.32	0.53	0.58	0.46	0.25	0.46	0.31	0.03	0.21	0.44	0.36	0.85	0.60	0.41	0.54	0.78	0.65	0.40	0.55	0.50	0.70	0.45	0.43	0.60	0.18	0.59	0.42	0.66	0.68	0.64	0.18	0.43	0.32	0.37	0.18	0.55	0.20	0.27	1.18	0.90	0.87	0.70	0.50	0.91	0.59	0.63	0.55	0.31	0.68
S3-1-2	0.23	0.33	0.62	0.26	0.24	0.37	0.27	0.39	0.51	0.46	0.31	0.55	0.66	0.55	0.59	0.30	0.50	0.24	0.41	0.61	0.39	0.88	0.57	0.48	0.28	0.42	0.30	0.51	0.44	0.34	0.50	0.26	0.42	0.68	0.33	0.63	0.46	0.65	0.86	0.45	0.16	0.35	0.32	0.52	0.18	0.43	0.42	0.22	0.90	1.19	1.05	0.57	0.54	0.73	0.59	0.70	0.63	0.48	0.69
S3-2-3	0.24	0.39	0.64	0.32	0.36	0.34	0.39	0.22	0.54	0.23	0.18	0.44	0.51	0.47	0.67	0.33	0.47	0.25	0.32	0.48	0.33	0.76	0.48	0.44	0.30	0.73	0.60	0.42	0.58	0.16	0.47	0.33	0.31	0.64	0.33	0.63	0.47	0.65	0.82	0.53	0.05	0.37	0.27	0.60	0.31	0.35	0.48	0.41	0.87	1.05	1.14	0.52	0.46	0.81	0.63	0.80	0.74	0.25	0.41
S4-0-3	0.67	0.32	0.51	-0.06	-0.04	0.51	0.22	0.46	0.41	0.22	0.00	0.57	0.43	0.58	0.36	0.39	0.15	0.13	0.33	0.62	0.52	0.79	0.58	0.18	0.41	0.98	0.71	0.57	0.70	0.41	0.54	0.59	0.19	0.25	0.16	0.21	0.01	0.47	0.63	0.35	0.00	-0.09	0.28	0.30	-0.05	0.24	0.12	0.22	0.70	0.57	0.52	1.31	1.01	1.05	0.23	0.74	0.40	0.14	-0.09
S4-1-4	0.59	0.46	0.48	0.13	0.12	0.54	0.33	0.60	0.55	0.28	0.22	0.53	0.47	0.63	0.50	0.35	0.22	0.38	0.52	0.63	0.68	0.80	0.79	0.30	0.75	1.00	0.42	0.44	0.64	0.69	0.52	0.64	0.66	0.55	0.19	0.39	0.33	0.32	0.52	0.35	0.44	0.34	0.27	0.52	0.13	0.34	0.44	0.45	0.50	0.54	0.46	1.01	1.23	0.68	0.18	0.76	0.34	0.62	0.17
W1-0-0	0.75	0.53	0.45	0.07	0.13	0.48	0.40	0.50	0.45	0.59	0.23	0.56	0.47	0.42	0.30	0.72	0.46	0.13	0.54	0.69	0.55	0.76	0.45	0.37	0.22	0.69	0.72	0.26	0.41	0.48	0.37	0.51	0.03	0.23	0.36	0.39	0.15	0.98	0.75	0.57	0.08	0.17	0.54	0.29	0.24	0.62	0.45	0.50	0.91	0.73	0.81	1.05	0.68	1.46	0.76	0.75	0.83	0.21	0.26
W1-1-1	0.48	0.62	0.39	0.28	0.38	0.40	0.48	0.48	0.45	0.46	0.43	0.43	0.48	0.36	0.50	0.73	0.69	0.41	0.66	0.67	0.70	0.62	0.42	0.66	0.68	0.50	0.31	0.30	0.42	0.58	0.44	0.70	0.25	0.50	0.57	0.80	0.75	0.84	0.87	0.75	0.52	0.44	0.56	0.58	0.53	0.70	0.70	0.59	0.59	0.59	0.63	0.23	0.18	0.76	1.19	0.72	0.79	0.47	0.18
W2-0-1	0.54	0.59	0.83	0.40	0.44	0.66	0.63	0.57	0.48	0.51	0.33	0.49	0.61	0.44	0.61	0.60	0.56	0.34	0.71	0.81	0.81	0.89	0.56	0.53	0.53	1.08	0.79	0.28	0.74	0.50	0.45	0.73	0.56	0.66	0.61	0.77	0.50	0.76	0.93	0.62	0.54	0.45	0.41	0.62	0.36	0.70	0.67	0.68	0.63	0.70	0.80	0.74	0.76	0.75	0.72	1.36	0.93	0.45	0.06
W2-1-2	0.60	0.76	0.69	0.55	0.52	0.61	0.73	0.54	0.65	0.52	0.34	0.34	0.50	0.33	0.55	0.61	0.64	0.54	0.64	0.85	0.68	0.75	0.69	0.68	0.40	0.60	0.49	0.31	0.53	0.53	0.73	0.79	0.59	0.84	0.41	0.75	0.58	0.63	0.72	0.54	0.29	0.43	0.16	0.32	0.34	0.68	0.72	0.63	0.55	0.63	0.74	0.40	0.34	0.83	0.79	0.93	1.31	0.47	0.26
O1-0-2	0.25	0.83	0.56	0.59	0.38	0.76	0.73	1.01	0.80	0.70	0.84	0.55	0.64	0.59	0.63	0.68	0.50	0.81	0.61	0.57	0.73	0.75	0.98	0.84	0.58	0.35	0.29	0.84	0.69	1.20	0.89	0.79	0.98	0.94	0.44	0.71	0.80	0.11	0.26	0.54	0.79	0.50	0.37	0.23	0.28	0.67	0.59	0.44	0.31	0.48	0.25	0.14	0.62	0.21	0.47	0.45	0.47	1.14	0.74
O1-1-3	0.27	0.50	0.09	0.11	-0.10	0.59	0.38	0.69	0.40	0.90	0.60	0.57	0.59	0.38	0.07	0.45	0.27	0.30	0.38	0.35	0.34	0.63	0.70	0.45	0.16	0.12	0.30	0.40	0.30	0.93	0.60	0.27	0.65	0.45	0.17	0.49	0.38	0.20	0.16	0.43	0.56	0.49	0.51	0.19	0.20	0.60	0.25	-0.02	0.68	0.69	0.41	-0.09	0.17	0.26	0.18	0.06	0.26	0.74	1.09

4.6.5. Principal component analysis of correlations showed that there was little structure associated with regions, locations or crop classes

PCA is used to reduce the dimensionality of complex data. Plots of loadings from these analyses can be interpreted to describe general relationships that are difficult to discern from tables like Table 4-17. Angles between vectors are proportional to the correlations among loadings. i.e. loadings (drawn as vectors from the origin) that are close to each other infer are well correlated, while vectors at 90° represent no correlation and at 180° represent a negative correlation.

The following figures summarise a large proportion of the relationships in the complex tables above into two components. For CCS, TCH and TSH, these dimensions explain 57, 48 and 47% of the variation, respectively. The lower graph in each pair is simply the upper graph re-drawn to separate out regions and crop classes (plant vs ratoon 1 or 2).

It can be seen that there is substantial overlap across regions and locations in the positioning of the vectors. Apart from the Ord plant crop and B1-2-2, the total spread of the vectors for CCS is less than for TCH or TSH.

For CCS, the Ord plant crop is a clear outlier and is almost directly opposite (i.e. negatively correlated) with the B1 crops. B1/2 and B3/4 contrast with each other. The South, Tableland and NSW are perhaps the most similar within regions. Central, Herbert and North are spread across 90 degrees within each region, but with no consistency w.r.t. location.

For TCH, the vectors tend to have a greater spread within regions cf. CCS. The three most obvious contrasts are S1 vs the other South locations, and C2 vs the other C locations and B1/B2 vs B3/B4. T3 (N3) and T6 (N6) also contrasted similarly in the plant and ratoon crops. The relationships for TSH were quite similar to those for TCH.

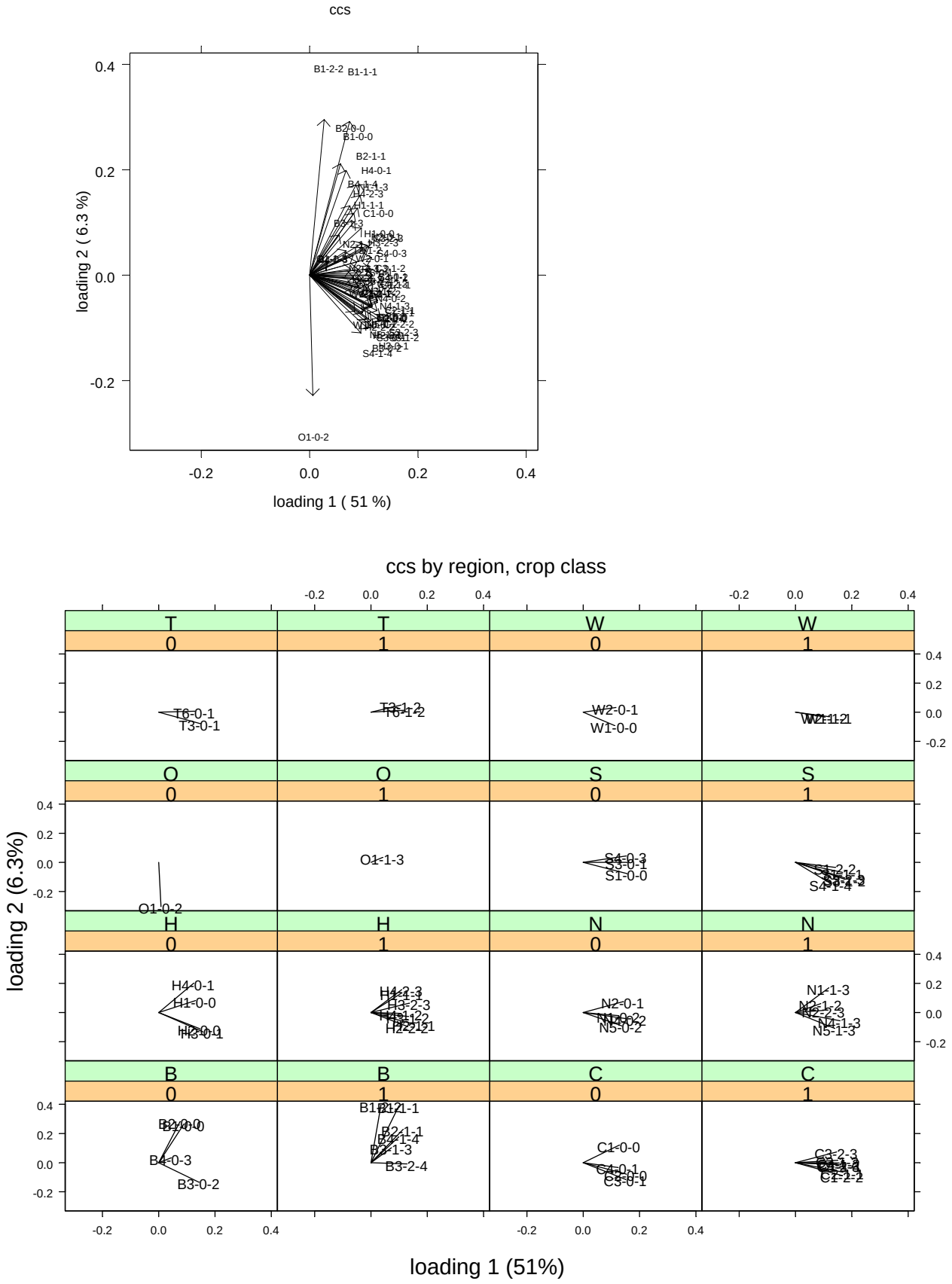


Figure 4-24 Loadings from a principal components analysis of CCS using the correlation matrix from all environments

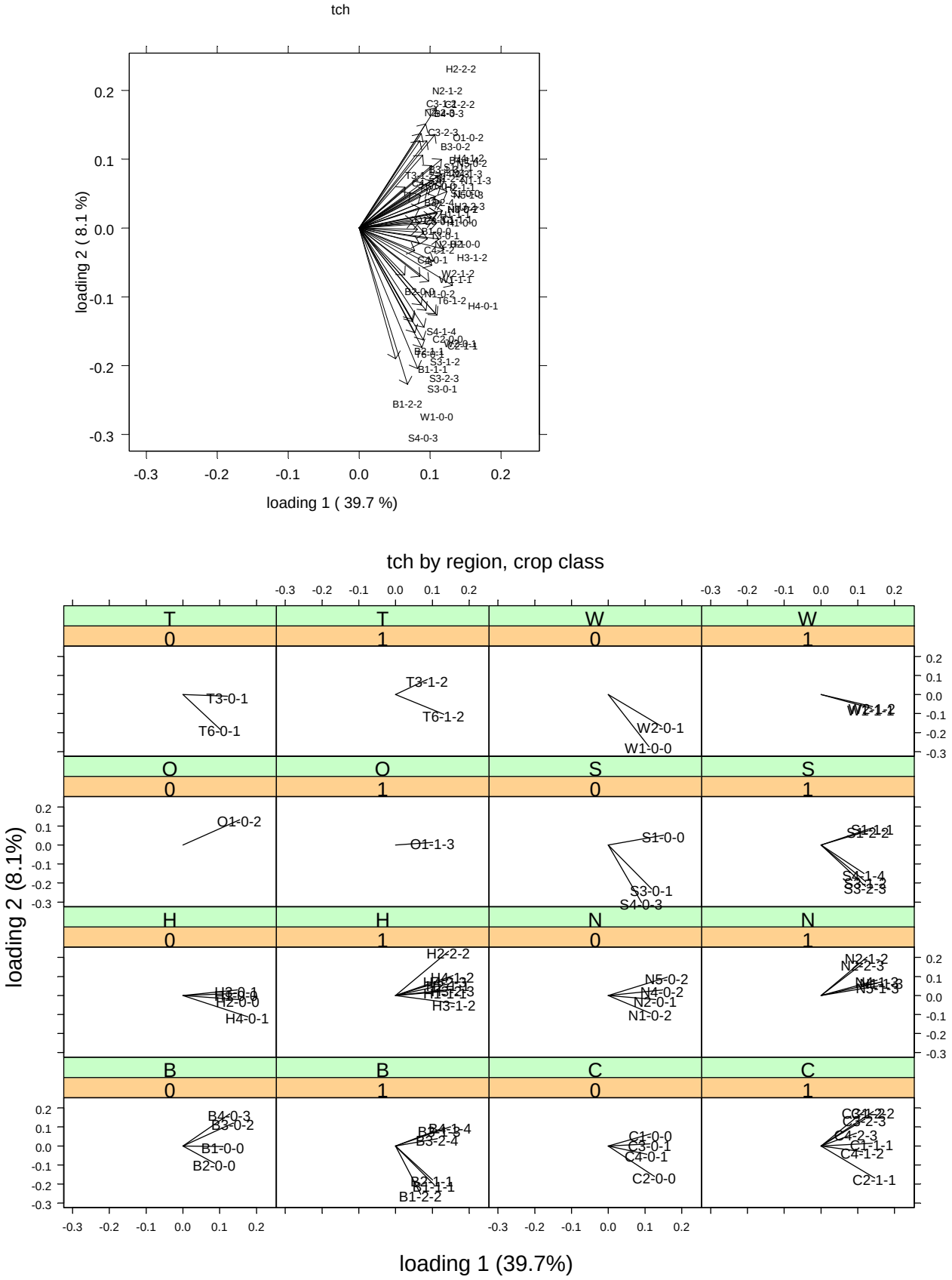
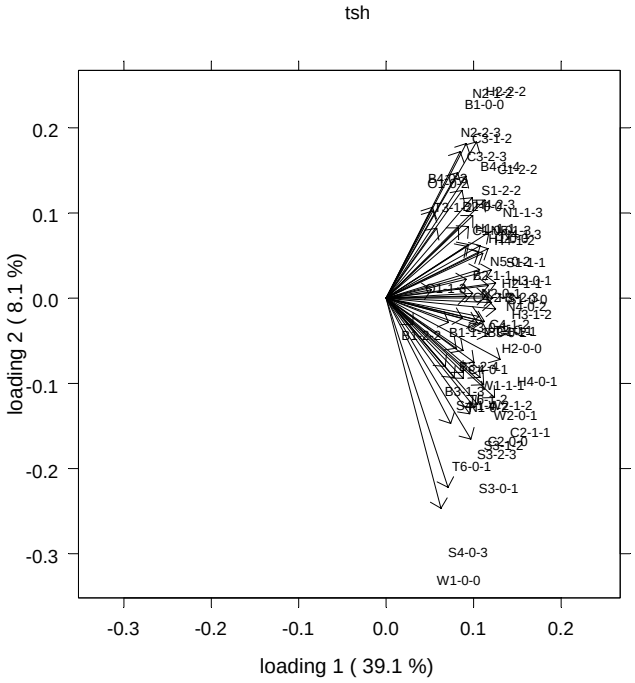


Figure 4-25 Loadings from a principal components analysis of TCH using the correlation matrix from all environments



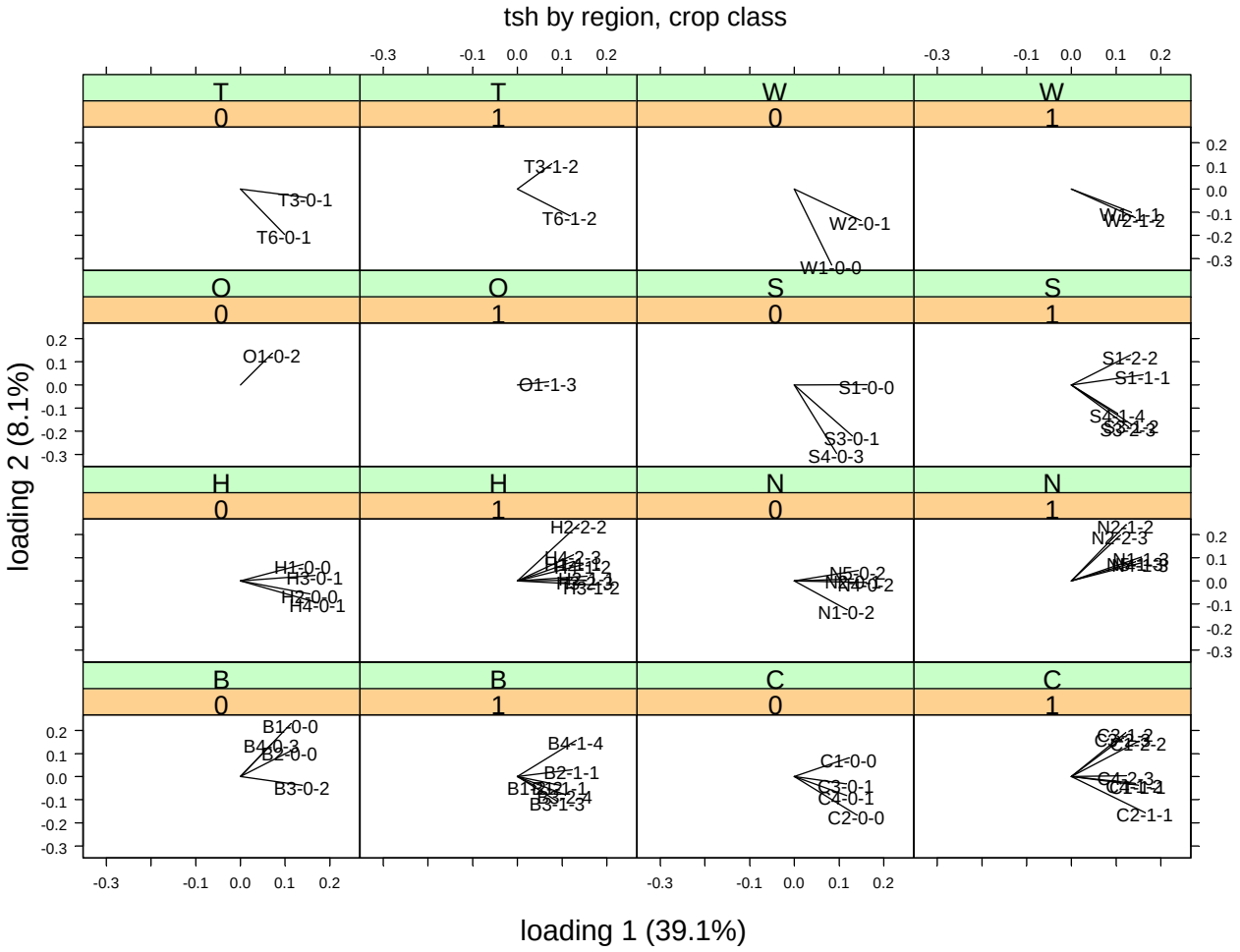


Figure 4-26 Loadings from a principal components analysis of TSH using the correlation matrix from all environments

4.6.6. Selection efficiency at the trial level was maximised at moderate trial means for TCH and moderate to high trial means for CCS

Method

The data on the relationship between G and error variances with mean value of TCH or CCS indicate that selection efficiency might be associated with the mean level of these traits achieved in trials. This can be tested by calculating repeatabilities (H^2) for several levels of the traits using all of the trial data. The value of H2 is an indicator of how efficiently selection is likely to work.

The trials were ranked by mean value, and then split into 5 equal size groups (i.e. 59 trials = 4x12 + 1x11) based on mean value for TCH, CCS or TSH. Within each group, the variance components for G (V_g) and GxE (V_{ge}) and residual trial variance (V_{err}) were estimated by ASREML.

Then, the repeatability at the plot level was calculated:

$H^2 = V_g/(V_g + V_{ge}/ne + V_{err}/(ne \times nr)$.

Several scenarios were examined with the number of environments (ne) was varied from 2 to 8 per group (e.g. representing 1 to 4 locations per group with 2 years of data taken) and the number of reps was set to 2.

Results

The results clearly illustrate the point made in section 4.2.3 where it was suggested that slower advance due to poorer estimates of performance would occur for CCS where trial CCS was outside the range of 14 to 16 units and for TCH where trial TCH was < ca. 70 t/ha or > ca. 110 t/ha. The response surface for TSH was a little flatter, though H2 also decreased in the extreme low or high trial mean groups.

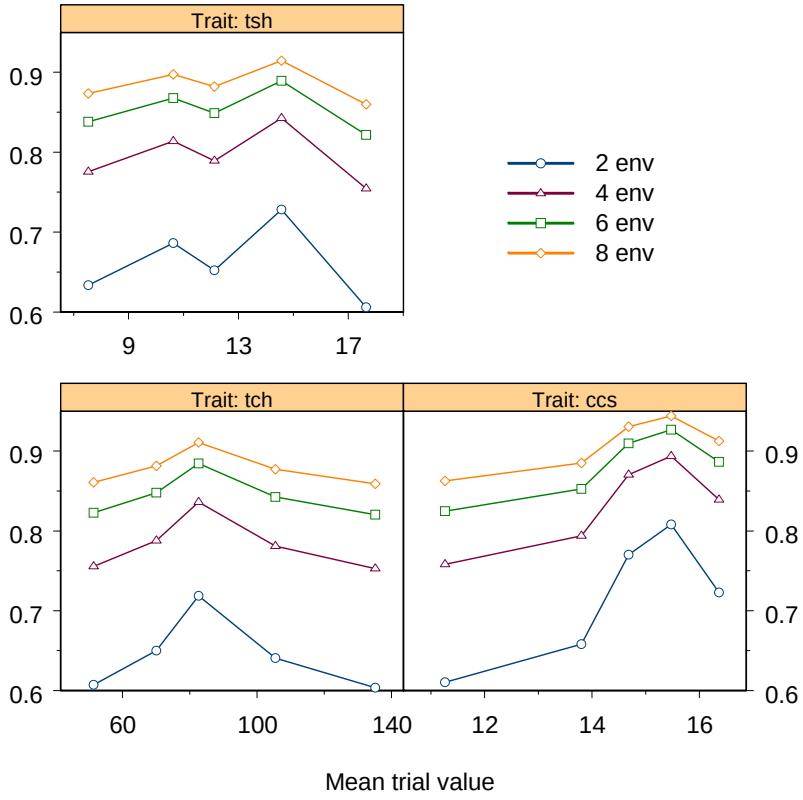


Figure 4-27 Repeatabilities for 3 traits, calculated within each of 5 equal size groups of trials using estimated variance components for Genotype, Genotype x Environment and residual error. Examples are given for different numbers of environments (2 to 8) and 2 replicates per trial

Appendix 5. Trial data summaries

Table of Contents

The Word version of this file ("cta028 Final report Appendix 05 Trial data.doc") contains links to PowerPoint presentations that contain dozens of graphs detailing the raw data and data summaries from the MegaGxE trials. Double-click on the graphs in the Word document or right-click and choose from options to start the slide viewer.

Note that this figures are **not** printed in the report (as they would comprise several hundred pages), but can be viewed in the electronic version and the figures allow readers to see all of the collected raw data.

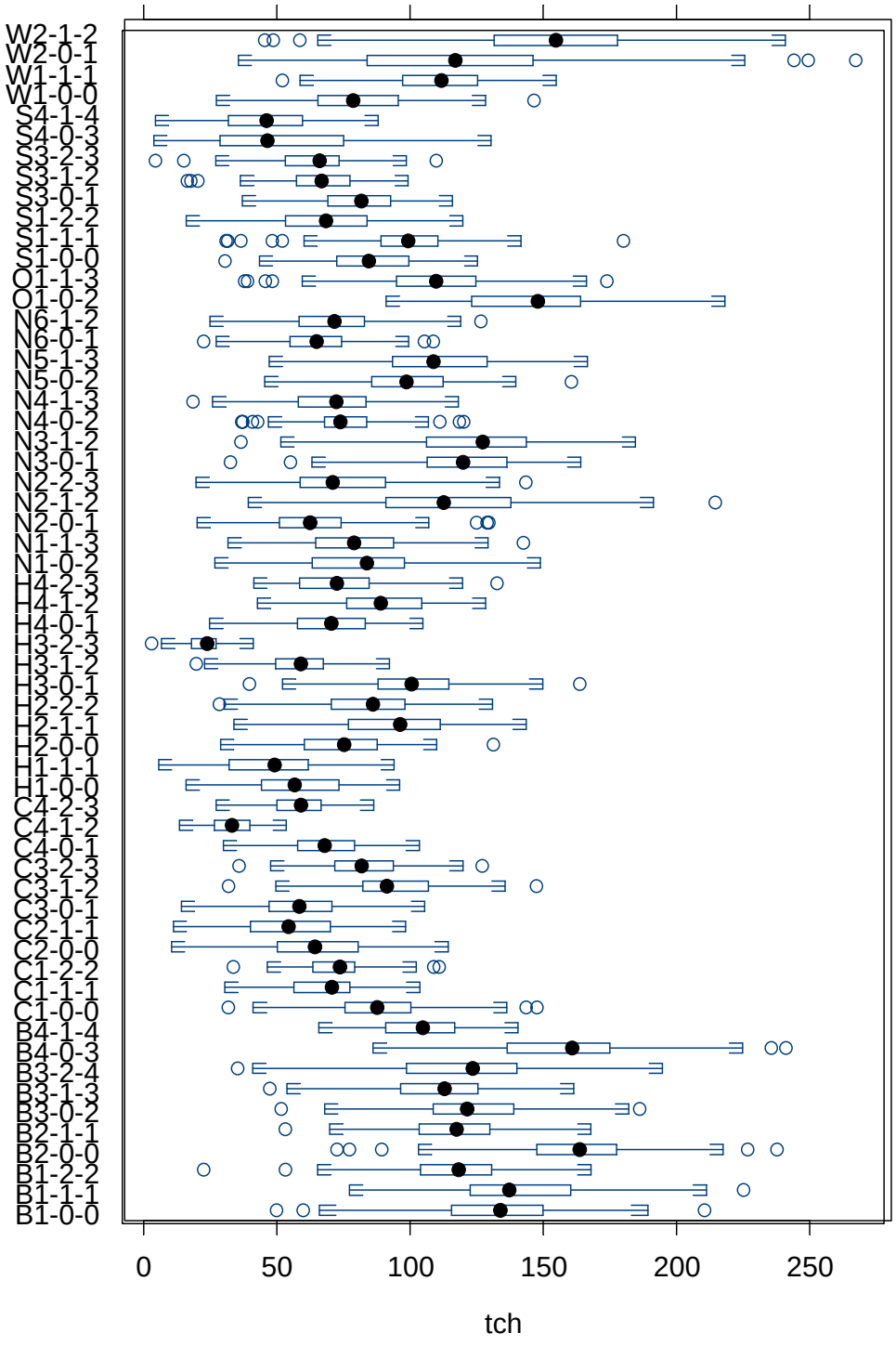


Figure 5-1 Box plots of all variables in all trials

Box plots all crop variables.ppt

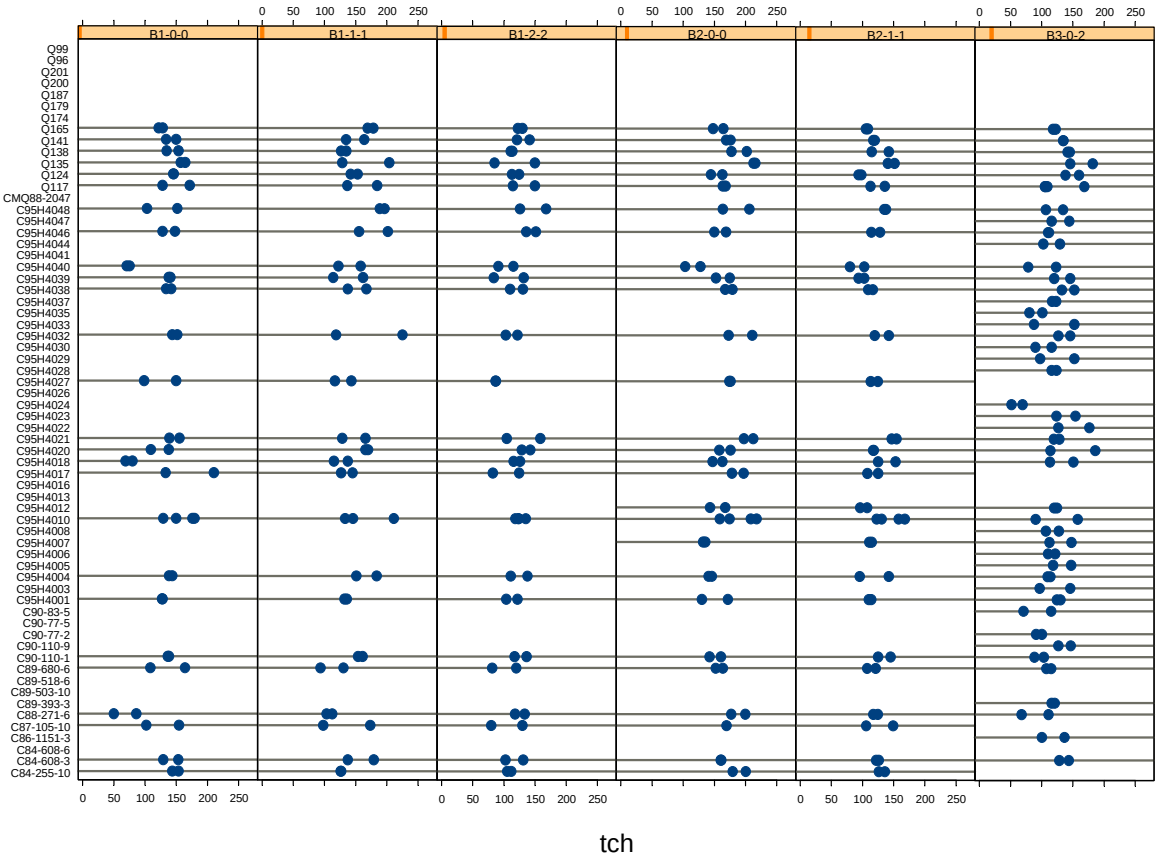


Figure 5-2 Dot plots of all variables in all trials

Dot plots all crop variables.ppt

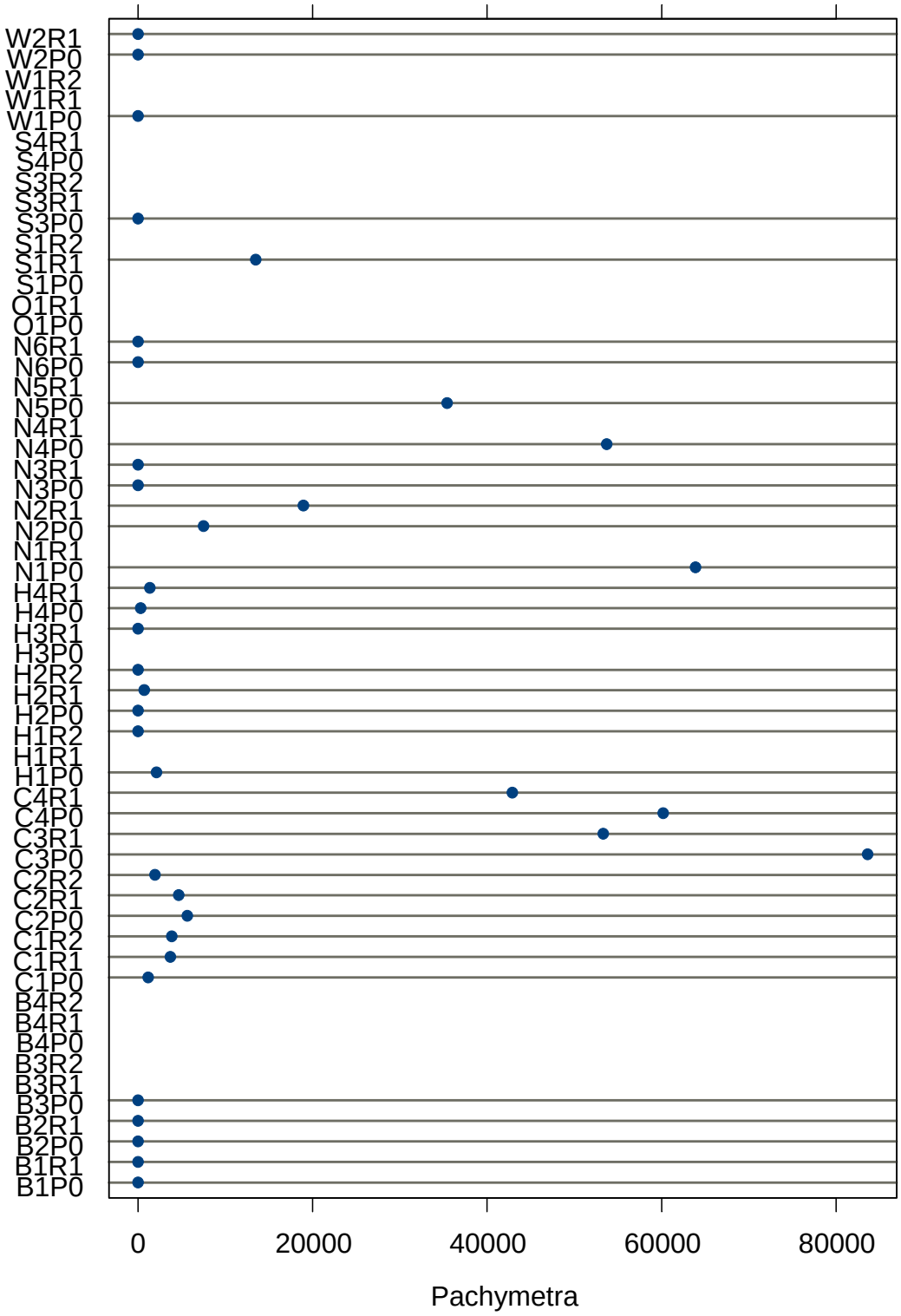


Figure 5-3 Dot plots of soil pathology data

Dot plots soil pathology.ppt

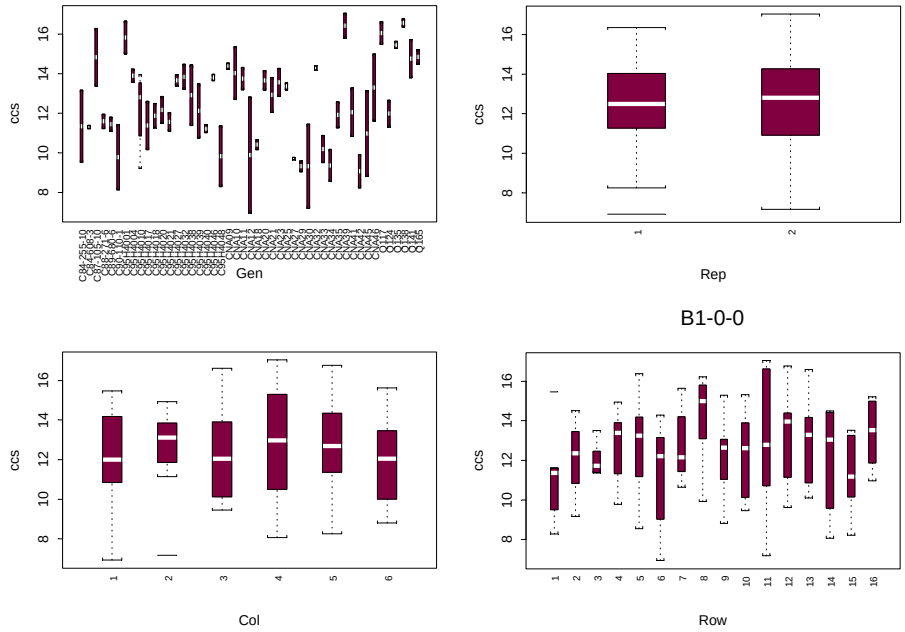


Figure 5-4 Factor plots of all CCS data (by trial)

Factor plots ccs.ppt

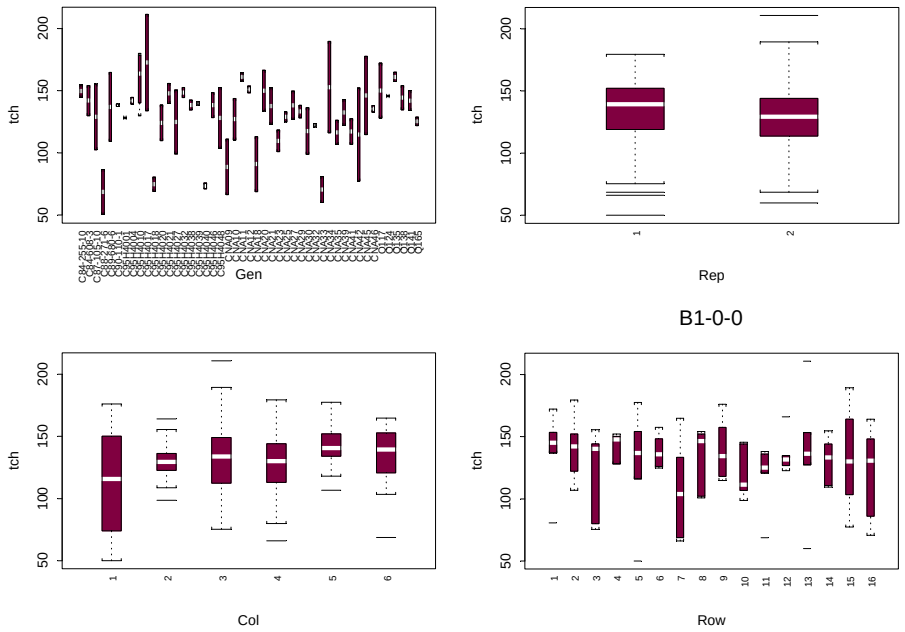


Figure 5-5 Factor plots of all TSH data (by trial)

Factor plots tch.ppt

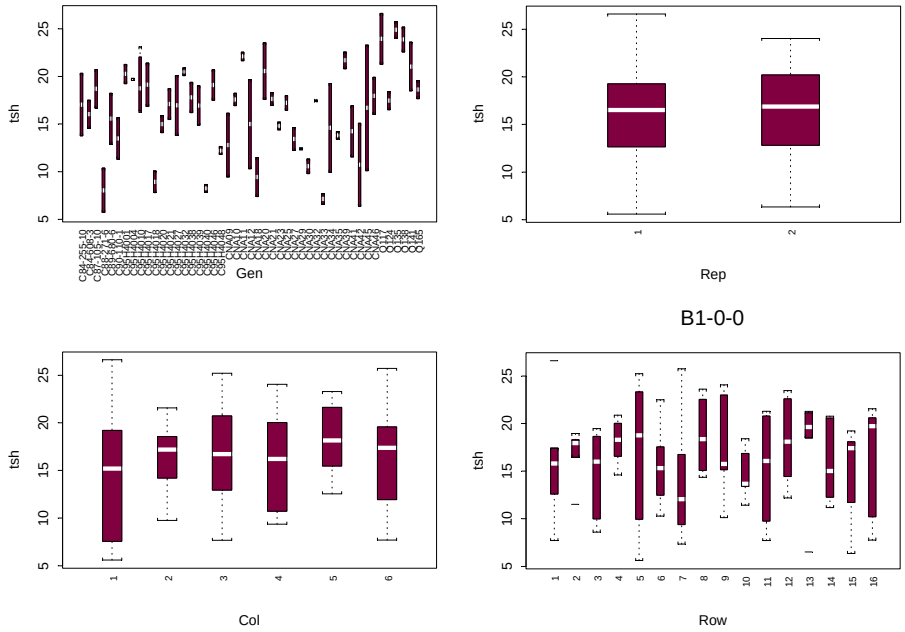


Figure 5-6 Factor plots of all TSH data (by trial)

Factor plots tsh.ppt

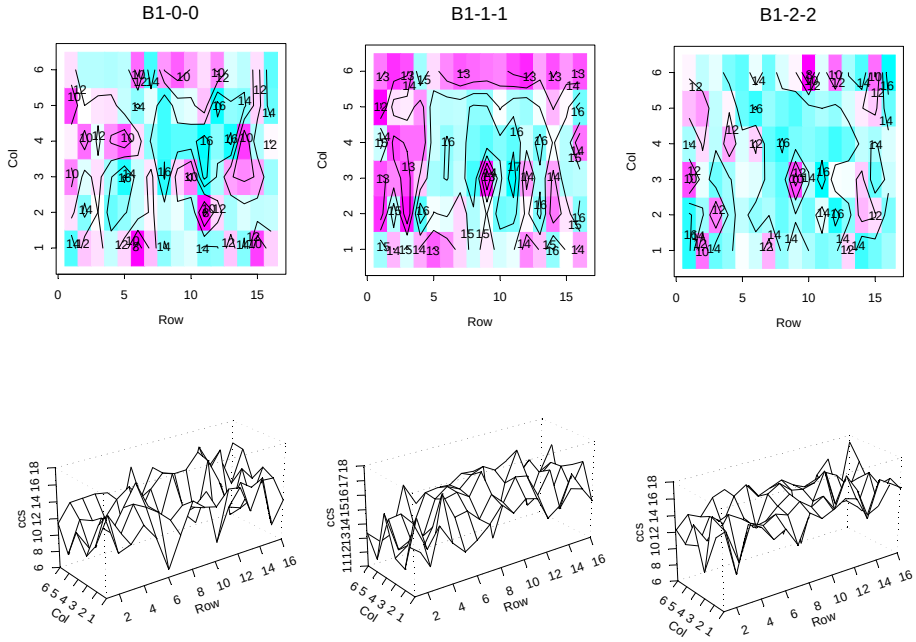


Figure 5-7 Field maps of all CCS data (by trial)

Field maps ccs.ppt

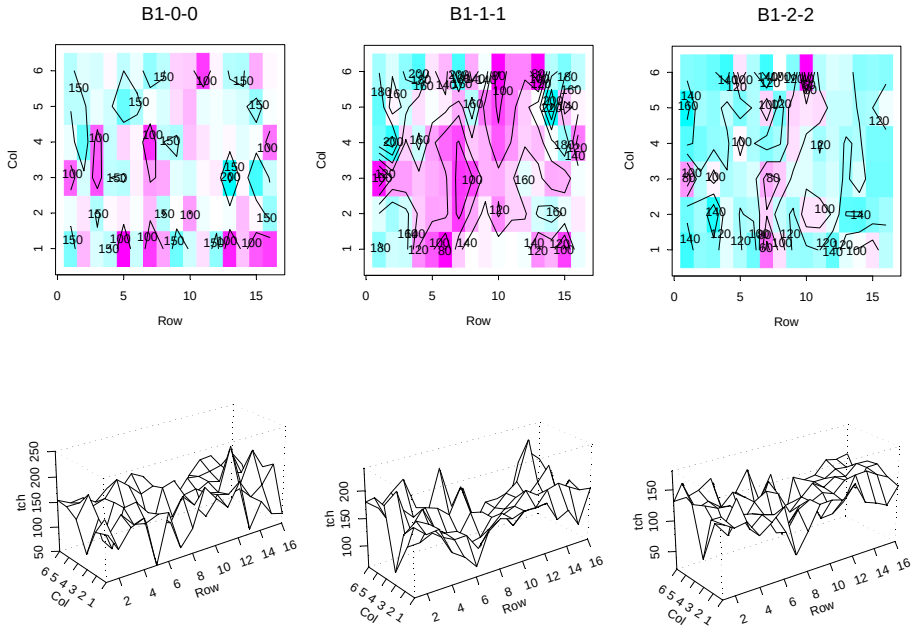


Figure 5-8 Field maps of all TCH data (by trial)

Field maps tch.ppt

Appendix 6. Location and environment covariates and interpretation

Table of contents

6.1. Overview

This section was prepared as a presentation for the July 2004 workshop, with additional notes added. The data are not all presented here (they are on the CD), but rather are presented as results in bi-plots etc. The aim of this analysis is to guide the selection of variables to be used in explaining variation in clonal rankings between trials and locations.

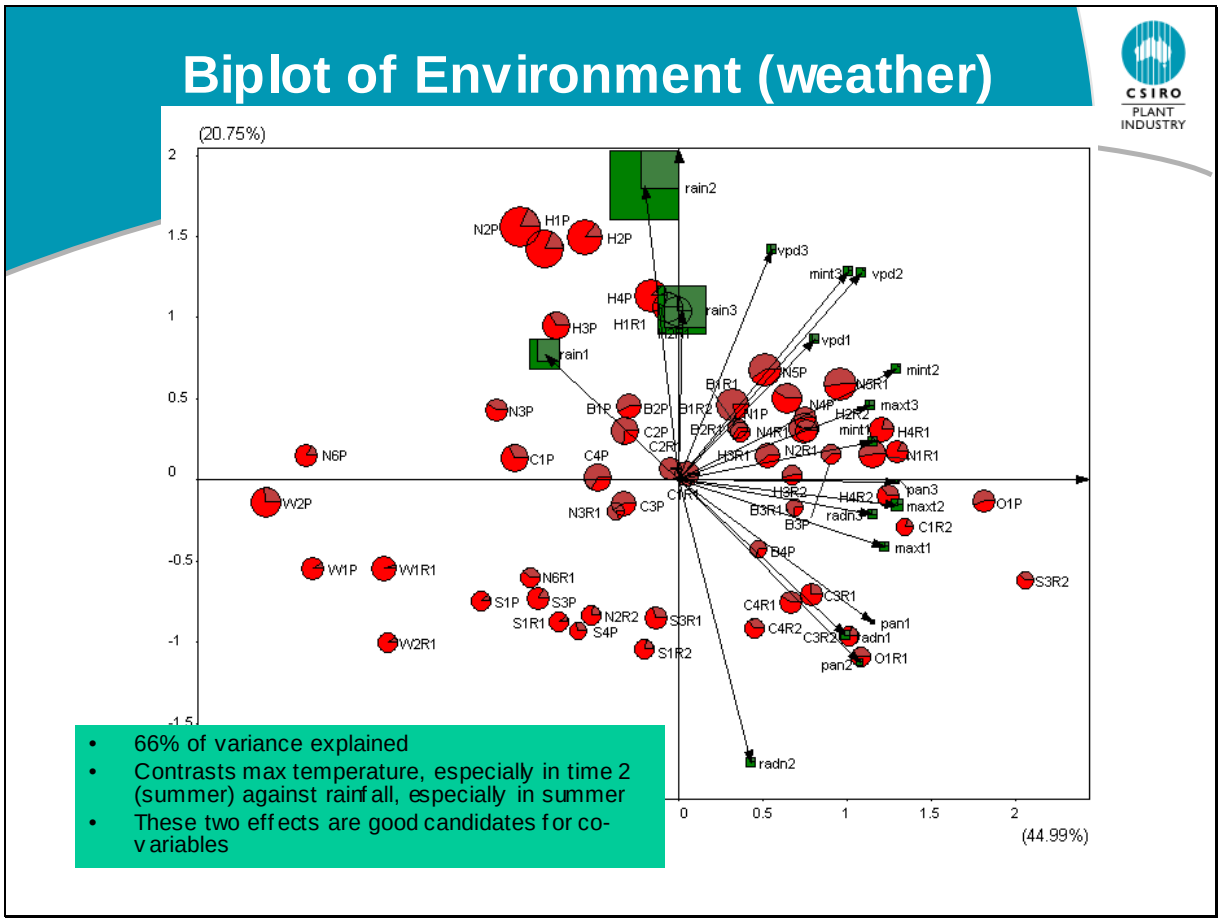
First, each variable in the matrix being considered was standardised (subtract mean and divide by standard deviation) to remove scaling effects of the different units. Then a principal component analysis was applied to the scaled matrix. The bi-plot was prepared with the trials or locations being points and the vectors or loadings representing the variables. Through inspection of the bi-plot and discussion with those conducting trials, suitable variables were chosen for later use as fixed covariates in the ASREML analyses. Generally, several explanatory variables are chosen such that they are orthogonal (at 90°) to each other and therefore explain as much of the observed variation as possible.

At the end of this report is a summary of the results of the comparison of different covariates against tch, ccs and tsh.

6.2. Environment variates (weather and geographical coordinates)

Summary of Environment data

- Collated weather data from nearest weather station for all trials
- Separated into 3 periods:
  - 1: Plant/ratoon to Nov 15 (establishment)
  - 2: Nov 15 to Mar15 (growth)
  - 3: Mar 15 to harvest (maturation)
- Standardised data and analysed in bi-plot



i.e. maxt2 and rain2 are useful to be considered in the fixed effect analysis. See appendix 4 trial results

6.3. Location variables – soil chemical attributes

The average pH of the soils across all locations planted was 5.8 (Table 6-1). The highest pHs were in the Burdekin (6.8 to 7.5) and Ord (8.4). In most soils, the aluminium saturation percentage was less than 20 (Table 6-1 and Figure 6-1). The exceptions were N2, N4, N5, S4 (ca. 40%) and H2, W1, N1 (>60%). Organic carbon was a little low (0.5%) in N3 and S4.

Over all locations, cation exchange capacity (CEC) ranged from 2 to 35 meq $100g^{-1}$ with a mean of 9. It was greatest in the 4 Burdekin sites and the Ord which were had substantial clay contents (>35%) and had an average CEC of 21 meq $100g^{-1}$ compared with the remaining locations (5.6 meq $100g^{-1}$).

Sodium was high (1.58 meq $100g^{-1}$) in B4, relative to the average of 0.24. This site as well as H1 and S1 had Na/CEC ratios of between 6 and 7%, while the rest were < 4%. The ratio of Mg/CEC was <30% in all sites except H1, N3, O1, S1, S3.

Fertiliser was applied to all crops, and mostly comprised N, P and K. Regarding the elements often applied in fertiliser, there were several sites where an element (macro or trace) was low in chemical analyses and where fertiliser was not applied and therefore the crop may have been deficient in these. These were (averaged for 0-60cm):

Sulphur: B3 and S1 where S was 4 and 4.5 mg kg^{-1} in the plant crop;

Zinc: B4, N2, S3 where Zn was 0.1, 0.2 and 0.07 mg kg^{-1};

Copper: N5 where Cu was 0.15 mg kg^{-1};

Potassium: C4 and S3 where K was 0.11 meq $100g^{-1}$.

The potassium to potassium (nitric extraction) ratios were >25% in B4, C1, C3, C4, N6 and S3, indicating strong potential in these soils to bind potassium. The relationships between CEC and the various cations (Figure 6-2) show that magnesium and calcium dominated in most soils, including that with the highest CEC (Ord), but that B4 had high sodium and potassium as noted above.

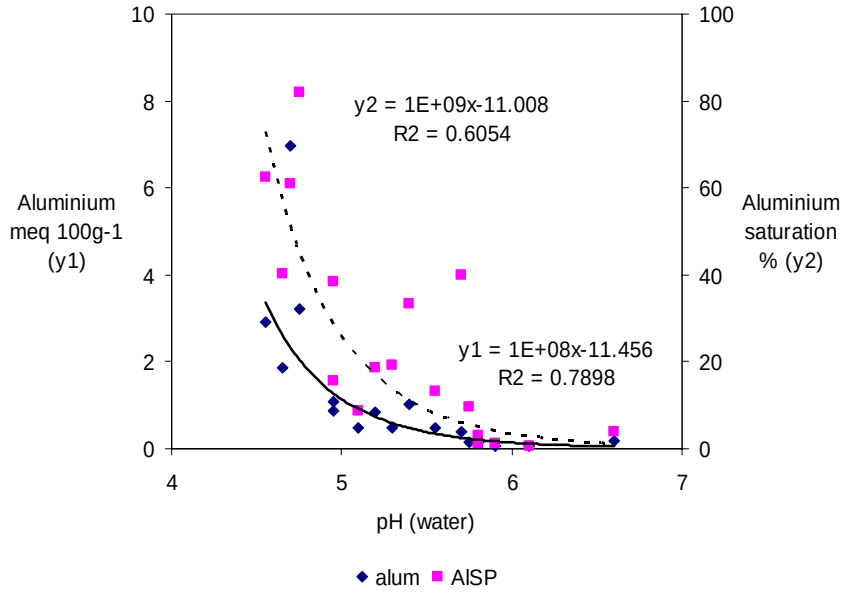


Figure 6-1 Aluminium content and saturation (% of cation exchange capacity) against pH for the acidic soil locations in the MegaGxE project (all sites except Burdekin and Ord).

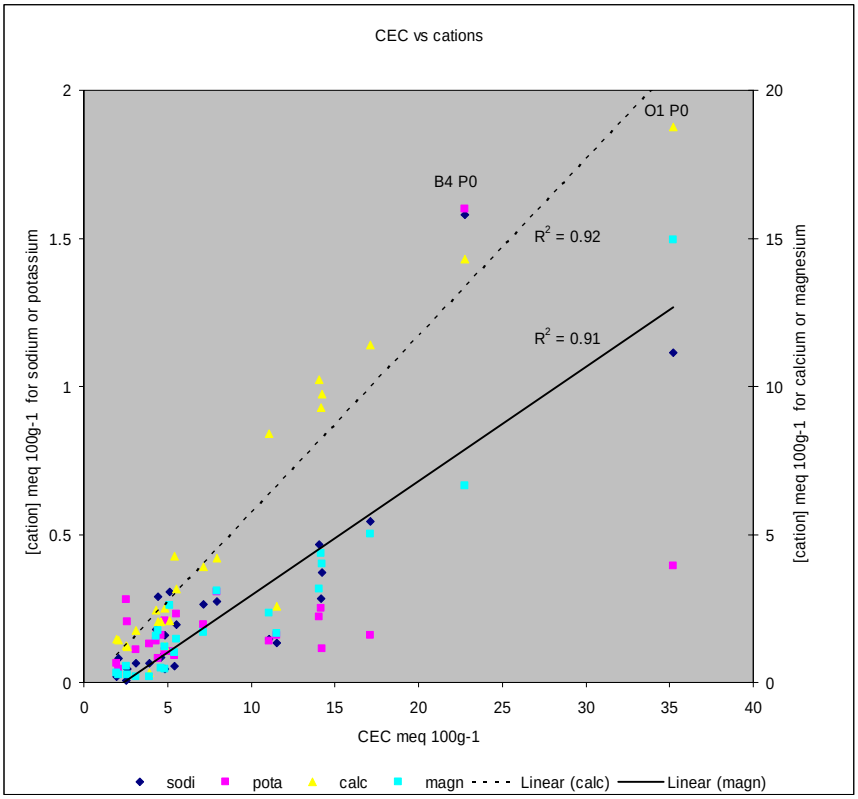


Figure 6-2 Cation exchange capacity (CEC) vs [cations] averaged for 0-60cm samples

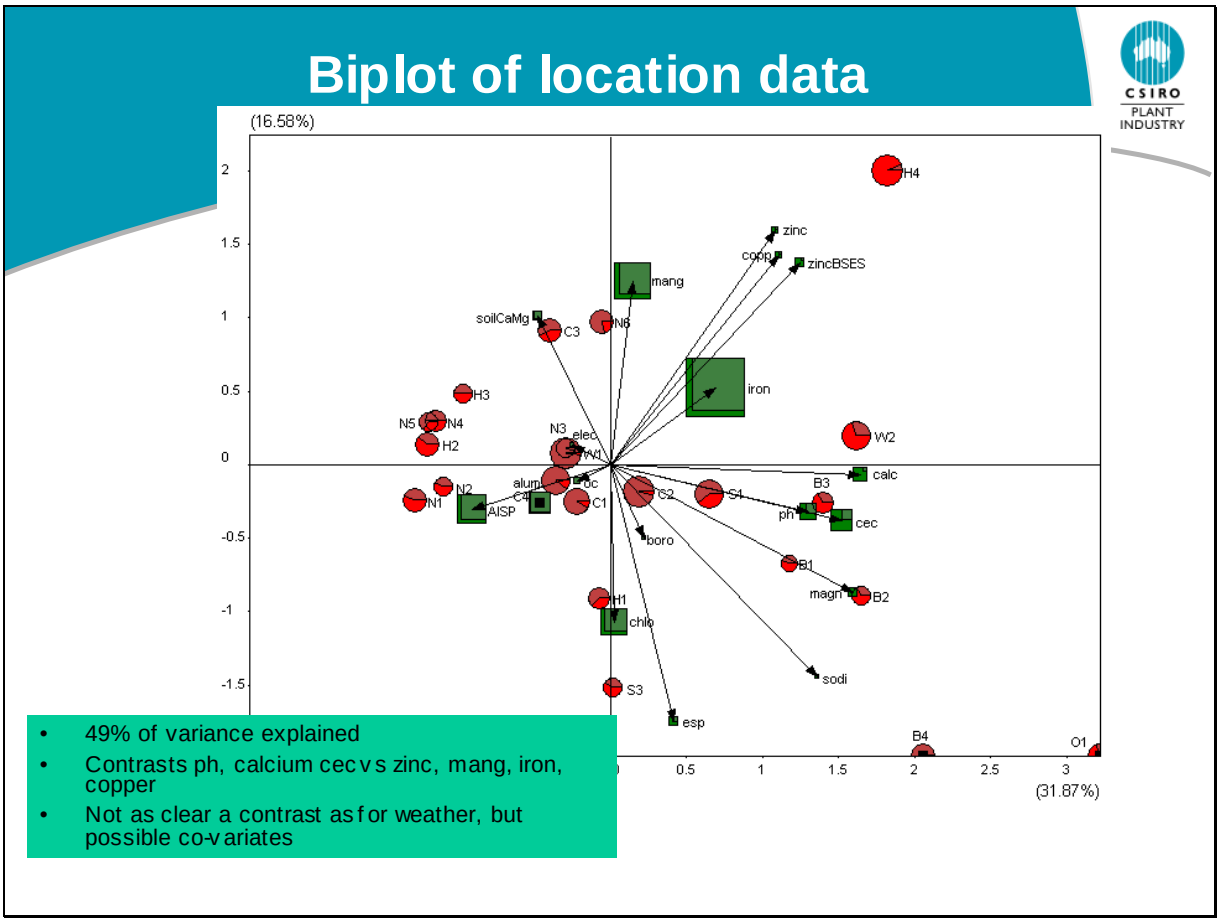
Summary of Location data

- Collated Incitec soil data for all locations
- Averaged data for 0-30 and 30-60 cm
- Only used ‘non-fertiliser’ variables, usually taken in plant crop after planting (some in ratoons)
- Standardised data and analysed in bi-plot

Table 6-1 Results of soil test results (Incitec) taken before or after planting in the plant crop (Note that fertiliser applications will have changed these)

Loc	B1	B2	B3	B4	C1	C2	C3	C4	H1	H2	H3	H4
latitude	-19.55	-19.52	-19.55	-19.78	-21.21	-20.4	-21.15	-21.42	-18.65	-18.44	-18.95	-18.54
longitude	147.35	147.42	147.35	147.23	149.16	148.58	148.94	149.17	146.16	145.92	146.29	146.25
ph	7.45	6.75	7.05	NA	5.1	4.95	5.75	5.2	5.55	4.55	5.3	6.1
phCaCl	NA	NA	5.9	6.6	NA	NA	5.05	4.3	4.55	4.35	4.6	5.2
phbuffer	NA	6.1	NA	NA	5.85	5.75	6.25	5.85	5.95	5.4	6.15	6
oc	0.95	1	1.1	0.9	0.65	0.7	0.6	0.7	0.85	0.75	0.6	0.8
no3ppm	1.85	0.85	0.35	9.3	4.35	2.3	5	11.95	3.85	5.4	5.35	12.75
sulf	2.5	27	4	19	16	15	14	15.5	4	31	27.5	7.5
phosBSES	80.5	116.5	121	28	48	108.5	39.5	14.5	5.5	17.5	7	115.5
phos	8.5	26.5	49.5	17	43	110.5	31.5	8	4.5	12	4.5	98.5
pota	0.115	0.16	0.22	1.6	0.23	0.195	0.065	0.105	0.08	0.21	0.28	0.14
calc	9.73	11.39	10.235	14.3	3.165	3.92	1.47	2.5	2.05	1.23	1.23	8.42
magn	4.02	5.015	3.165	6.63	1.46	1.68	0.32	1.22	1.75	0.45	0.545	2.335
alum	NA	NA	NA	NA	0.49	1.075	0.14	0.85	0.485	2.925	0.47	0.06
sodi	0.37	0.545	0.465	1.58	0.195	0.265	0.02	0.16	0.29	0.045	0.005	0.145
chlo	7.5	5	12.5	25	25	25	10	22.5	12.5	7.5	5	10
copp	0.75	0.7	1.3	1.4	0.7	0.9	0.35	0.75	0.55	0.45	0.25	2.75
zinc	0.65	0.95	1.65	0.1	0.75	1.5	2.85	0.65	0.5	0.25	0.6	4.3
mang	10	9.5	39	16	67	29	11	80	15.5	33.5	63.5	76
iron	12	32.5	49	35	66.5	189.5	101.5	85	78.5	33.5	18.5	153
boro	0.35	0.7	0.2	1	0.3	0.3	0.25	0.35	0.35	0.3	0.3	0.3
zincBSES	2.3	3.3	3	0.7	1.15	1.75	3.95	1	1	0.55	1.05	9.55
potanitric	2.84	3.59	2.675	1.6	0.805	1.635	0.255	0.36	1.38	2.615	2.36	2.28
siliBSES	NA	NA	465	NA	NA	NA	35	110	125	125	110	1100
cec	14.24	17.115	14.085	22.75	5.545	7.13	1.94	4.835	4.45	4.86	2.54	11.07
soilCaMg	2.425	2.29	3.24	2.16	2.16	2.325	4.355	2.04	1.195	2.565	2.335	3.63
AlSP	NA	NA	NA	NA	8.7	15.6	9.5	18.6	13.3	62.4	19.1	0.6
esp	2.635	3.155	3.325	6.94	3.465	3.525	1.105	3.3	6.37	1.02	0.4	1.3
elec	0.25	0.5	0.35	0.6	0.35	0.4	0.35	0.4	0.2	0.25	0.25	0.35

Loc	N1	N2	N3	N4	N5	N6	O1	S1	S3	S4	W1	W2
latitude	-17.75	-17.93	-17.13	-17.09	-17.34	-17.27	-15.77	-24.87	-25.54	-25.18	-28.32	-29.42
longitude	146.02	145.92	145.34	145.79	145.92	145.48	128.74	152.35	152.7	152.45	153.43	153.24
ph	4.75	4.65	6.6	4.95	5.4	5.8	8.4	5.95	5.9	5.7	4.7	5.8
phCaCl	4.2	4.55	5.6	4.4	4.6	5.35	7.3	5.4	5	5.05	4.25	4.9
phbuffer	5.5	5.7	NA	5.8	5.95	6.1	105	6.05	6.2	NA	4.7	5.7
oc	1.3	2.2	0.45	1	1.3	1.35	0.36	1	1.1	0.51	3.8	1.15
no3ppm	8.7	21.1	0.75	11.7	6.25	8.4	0.55	5.5	9.7	4.125	8.65	3.2
sulf	27.5	23	7.5	94	13.5	113	5.9	4.5	61	6.5	196	6.5
phosBSES	94	76.5	26	53.5	77.5	54	23	93	43	NA	150.5	69
phos	39	18	10	40	35.5	52.5	18	47.5	22	56.5	60.5	63
pota	0.13	0.16	0.14	0.205	0.11	0.09	0.395	0.305	0.105	0.045	0.16	0.25
calc	0.32	2.045	2.44	1.21	1.76	4.26	18.75	4.195	2.07	1.425	2.575	9.28
magn	0.19	0.475	1.565	0.255	0.18	1.005	14.96	3.08	2.61	0.275	1.665	4.365
alum	3.22	1.855	NA	0.88	1.03	0.15	NA	NA	0.065	0.4	6.975	0.17
sodi	0.065	0.085	0.18	0.045	0.065	0.055	1.115	0.275	0.305	0.08	0.135	0.285
chlo	10	10	12.5	7.5	7.5	5	21.5	12.5	32.5	12.4	10	10
copp	0.25	0.2	0.45	0.8	0.15	2.1	1.07	1.05	0.225	0.69	0.4	1.2
zinc	0.45	0.2	0.55	0.45	0.3	0.85	1.32	1.5	0.065	0.48	1.2	2.35
mang	0.75	2	42	23.5	1.5	114	13.5	11.5	5.75	2.8	5	13.5
iron	43	42.5	25.5	34.5	34.5	11.5	18.5	176	41.5	54	158.5	189
boro	0.55	0.6	0.2	0.3	0.25	0.9	0.945	0.4	0.7	0.235	0.5	0.6
zincBSES	1.05	1.2	1.25	0.85	1.1	1.65	3.25	2.9	1.15	NA	3.75	4.95
potanitric	3.325	2.825	0.74	3.075	1.775	0.265	NA	2.675	0.255	NA	0.99	3.275
siliBSES	300	565	115	90	190	430	1200	240	155	NA	380	345
cec	3.93	4.62	4.32	2.605	3.14	5.41	35.215	7.94	5.155	2.05	11.515	14.175
soilCaMg	1.79	4.3	2.16	4.115	10.3	4.26	1.26	1.395	0.9	6	1.535	2.15
AlSP	81.95	40.2	4.02	38.35	33.35	2.95	NA	NA	1.25	40	60.95	1.25
esp	1.705	1.85	0.25	1.965	2.135	1.035	NA	3.355	5.69	4.6	1.215	2.01
elec	0.3	0.45	0.55	0.7	0.25	0.45	0.54	0.3	0.4	0.4	0.55	0.2



As for weather variables, these variables selected from the biplot were tested as covariates in the ASREML analyses.

6.4. Soil pathology variables

Summary of soil pathology data

- Soil samples taken each year (usually Feb, sometimes May-June)
- Analysed at Tully for Pachymetra (oospores/kg) and nematode counts:
  - Pratylenchus, Helicotylenchus, Meloidogyne, Tylenchorhynchus, Paratrichodorus, Criconemella, Xiphinema

    (and some other rarer ones: Rotyl?, Tylenchus?, Paratyl?, Achlysiella?)

Background information on Nematodes

(from R. Magarey, BSES Limited Tully)

Soil samples (0-30 cm) were collected in late summer (normally February) or in autumn from the replicate plots of the check clones: Q117, Q124, Q138. These samples were kept cool and sent to the BSES Limited pathology laboratory at Tully for analysis. Following standard procedures, counts were made of the various nematode species and of *Pachymetra* spp oospores per unit mass of soil.

Table 6-2 Critical nematode threshold levels used to establish whether nematodes are likely to have an effect on cane growth and yield (Source: R. Magarey, BSES Limited, Tully March 2001).

Species	Abb. Name	Common Name	Threshold Plant &1R	Threshold 2R, 3R ….
Pratylenchus	Praty.	root lesion	300	900-1000
Achlysiella	Achly.	root lesion		400
Meloidogyne	Mel.	root knot	200	600-1000
Helicotylenchus	Helico.	spiral	500	1500-2000
Paratrichodorus	Para.	stubby root	300	500
Tylenchorhynchus	Tyl.	root stunt	500	1500-2000
Xiphinema	Xip.	lance dagger		400
Criconemella	Crico.	ring		

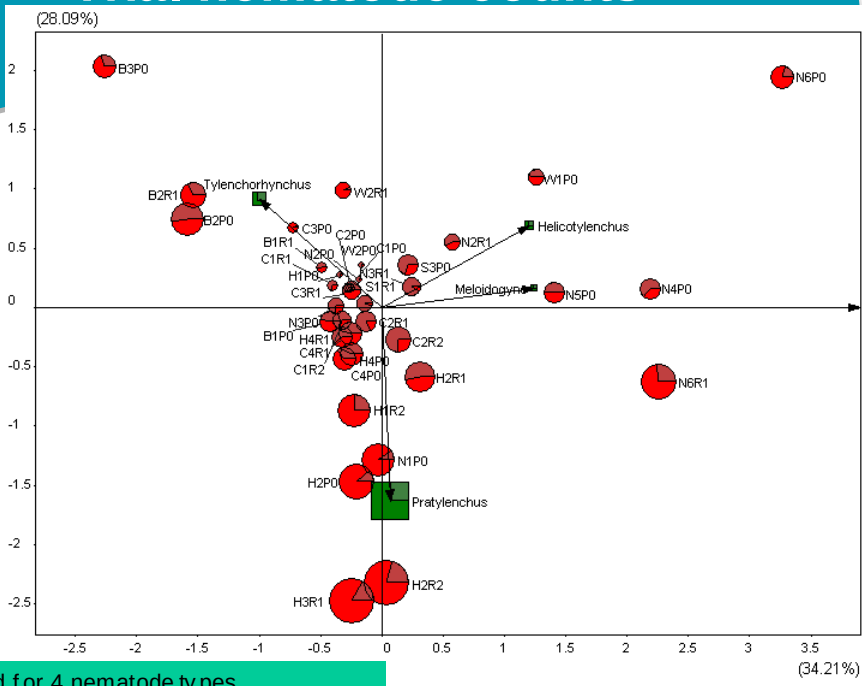
Notes:

- Sub-critical levels of nematodes may still cause a problem particularly on sandy soils.
- Soil fertility and water situation are vitally important considerations.
- Keep grass out of fallows. Legume break crop is the best way to control nematodes.

Table 6-3 Pachymetra and nematode counts (per g soil). Note that some environments were not sampled, and in some cases the data were interpreted following averaging over crops.

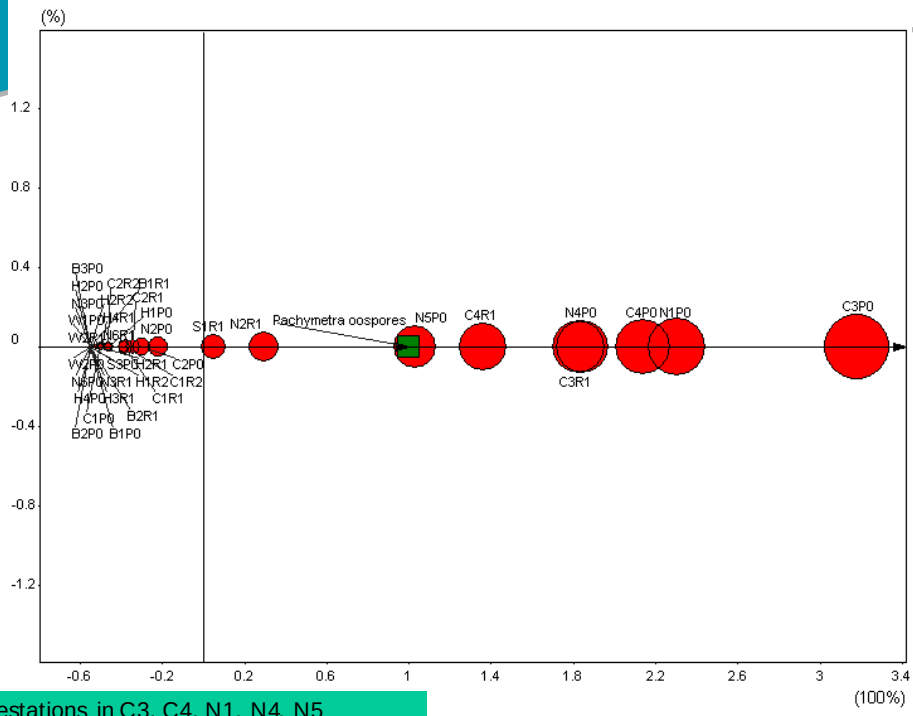
Env	Loc	Pachymetra	Pratylenchus	Helicotylenchus	Meloidogyne	Tylenchorhynchus
B1P0	B1	0.00	1319.83	0.00	0.00	155.83
B1R1	B1	0.00	294.50	4.00	0.00	209.17
B2P0	B2	0.00	2308.17	62.33	0.00	1408.67
B2R1	B2	0.00	1192.67	0.00	0.00	1231.33
B3P0	B3	0.00	80.83	0.00	0.00	1905.83
C1P0	C1	1160.64	339.17	19.67	0.00	32.00
C1R1	C1	3692.00	450.17	0.00	0.00	120.33
C1R2	C1	3862.17	1183.67	17.17	0.00	91.67
C2P0	C2	5632.58	281.83	12.50	2.17	14.50
C2R1	C2	4661.67	1392.67	81.00	12.00	91.67
C2R2	C2	1910.83	2134.83	244.00	0.00	69.50
C3P0	C3	83568.67	108.17	24.17	0.00	465.67
C3R1	C3	53289.17	1115.50	126.83	0.00	207.17
C4P0	C4	60171.67	1824.50	31.83	0.00	49.50
C4R1	C4	42860.83	1678.17	71.67	0.00	126.00
H1P0	H1	2101.50	76.83	0.00	0.00	58.17
H1R2	H1	0.00	3654.00	58.17	23.50	258.00
H2P0	H2	0.00	4683.67	44.83	0.00	85.83
H2R1	H2	679.67	3022.00	309.33	0.00	29.33
H2R2	H2	0.00	6905.17	121.67	0.00	31.83
H3R1	H3	0.00	7097.67	0.00	0.00	87.67
H4P0	H4	294.00	1871.50	0.00	0.00	56.00
H4R1	H4	1340.67	1427.67	0.00	0.00	67.00
N1P0	N1	63854.83	4143.17	99.00	0.00	0.00
N2P0	N2	7483.50	171.75	49.50	0.00	0.00
N2R1	N2	18927.50	458.33	452.83	2.17	2.33
N3P0	N3	0.00	865.50	1.83	0.00	102.83
N3R1	N3	0.00	981.17	0.00	116.17	225.17
N4P0	N4	53690.83	1124.50	25.67	379.00	18.33
N5P0	N5	35389.83	1173.83	153.17	217.17	4.00
N6P0	N6	0.00	320.83	1461.17	155.00	155.17
N6R1	N6	0.00	3984.33	469.50	249.17	0.00
S1R1	S1	13480.17	864.50	59.33	11.67	51.00
S3P0	S3	0.00	1043.83	347.00	0.00	156.33
W1P0	W1	0.00	69.00	830.83	0.00	0.00
W2P0	W2	0.00	26.33	84.00	0.00	34.50
W2R1	W2	0.00	171.50	270.33	4.17	537.67

Trial nematode counts



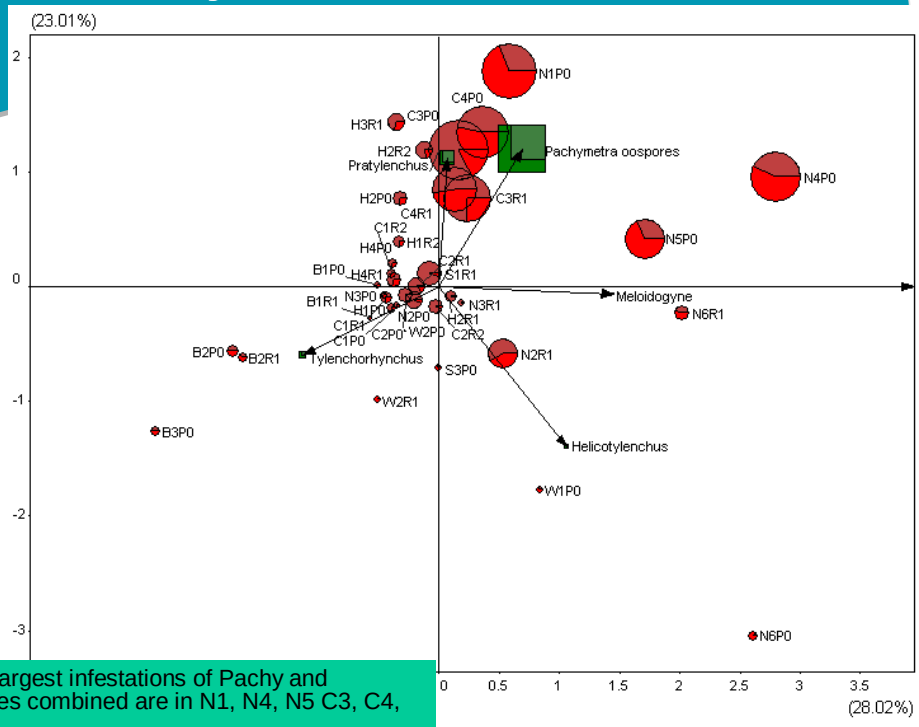
- 62% explained for 4 nematode types
- H2, H3, H1, N1 heavy infestation of Pratylenchus
- B2, B3 Tylenchorhynchus

Pachymetra



- Heavy infestations in C3, C4, N1, N4, N5

Pachymetra + Nematodes



- Overall, largest infestations of Pachy and nematodes combined are in N1, N4, N5 C3, C4, H2, H3

Summary of Environment and Location covariates

- Potential orthogonal covariates
  - Weather – maximum temperature and rainfall during summer period
  - Soil chemistry – ph and soil Cu or Zn
  - Soil path – pachymetra

6.5. Environmental correlations among covariates across trials

Source: covariates across trials.xls

Method

Many of the traits observed in experiments are correlated with each other. Frequently, these correlations are examined between traits across genotypes. However, the traits are also correlated when examined across trials, e.g. high tch trials will often have high tsh. So, in that case, either might be suitable for use as covariates in an across environment analysis. This should not be confused with interpretation of the genetic correlations done elsewhere in this project.

Here we have calculated the correlation matrix among trials for all of the traits observed in trials. The mean trial value for each trait was first calculated. Each correlation is based on all of the trials for which a given pair of traits was observed, as some traits were not taken in all trials.

Results

The environmental correlations are shown in a table below, and summarised in another table. Note that these correlations are not all assumed to be causal, though some are obviously related. For example, arrowing is related to stool suckering, but both of these traits are more common at the northern latitudes. The major correlations observed are:

- mean tch of trials positively correlated with tsh, lodging, stalk length, single stalk fw and stalk count
- mean tch negatively correlated with ccs
- sucker weight is correlated with gaps and stalk breakage;
- arrowing with suckering and side shoots and yellow spot;
- stool tipping with lodging, stalk breakage and single stalk fw;
- fibre with early ccs.

Table 6-4 Trait names and abbreviations

Abbr	Trait
TCH	TONNES CANE (fresh) per HA
CCS	COMMERCIAL CANE SUGAR %
TSH	TONNES SUGAR per HA
WFI	WET FIBRE WT (g)
DFI	DRY FIBRE WT (g)
DMC	DRY/WET FIBRE
CON	JUICE CONDUCTIVITY
FIB	FIBRE t/ha
LOD	LODGING SCORE
SUW	SUCKER WT %
ARR	ARROWING %
STP	STOOL TIPPING %
STS	STOOL SUCKERING %
SSH	SIDE SHOOTS %
GPS	NO. GAPS>1M
RAT	RAT DAMAGE %
SBR	STALK BREAKAGE %
LEN	STALK LENGTH (M)
DIA	STALK DIA (MM)
SFW	SINGLE STALK FW (KG)

Abbr	Trait
STC	STALKS PER M ROW at harvest
STCe	STALKS PER M ROW early
CCSe	CCS EARLY
CRU	COMMON RUST %
ORU	ORANGE RUST %
TRT	TOP ROT %
YSP	YELLOW SPOT %
CONe	JUICE CONDUCTIVITY early
BRXe	JUICE BRIX early
POLe	JUICE POL early
PURe	JUICE PURITY early
BRX	JUICE BRIX
OL	JUICE POL
PUR	JUICE PURITY

Table 6-5 Environmental correlations among pairs of observed traits (averaged across genotypes within trials). Colours indicate significant correlations (cf. signif. r of 0.38, n=59). Note that not all traits were observed in all trials, so n varies for different comparisons.

	Tch	ccs	tsh	wfi	dfi	con	dmc	fib	lod	suw	arr	stp	sts	ssh	gps	sbr	len	dia	sfw	stce	ccse	cru	oru	trt	ysp	stc
tch	1.00	-0.51	0.91	-0.11	0.07	0.11	0.43	0.14	0.65	0.02	0.00	0.38	0.07	-0.05	-0.12	0.36	0.72	0.49	0.87	0.40	-0.37	0.01	-0.05	0.23	0.17	0.81
ccs	-0.51	1.00	-0.13	-0.05	0.10	-0.27	-0.39	0.00	-0.13	0.08	0.23	-0.12	0.08	0.22	-0.06	-0.09	-0.15	-0.45	-0.42	-0.41	0.54	-0.02	0.27	-0.22	-0.04	-0.30
tsh	0.91	-0.13	1.00	-0.17	0.05	0.00	0.22	0.15	0.70	0.06	0.11	0.38	0.15	0.03	-0.11	0.41	0.76	0.38	0.78	0.31	-0.16	0.02	0.07	0.12	0.20	0.80
wfi	-0.11	-0.05	-0.17	1.00	-0.28	-0.06	-0.03	-0.18	-0.11	0.20	-0.02	0.17	0.05	-0.27	-0.32	0.42	0.06	-0.03	0.15	0.01	-0.98	0.13	0.22	-0.04	0.20	-0.42
dfi	0.07	0.10	0.05	-0.28	1.00	-0.19	0.42	0.21	0.12	0.06	0.49	-0.02	0.49	0.86	-0.18	-0.10	0.25	-0.11	0.16	-0.21	0.40	0.62	-0.05	0.40	0.07	-0.04
con	0.11	-0.27	0.00	-0.06	-0.19	1.00	0.35	-0.02	0.02	-0.06	-0.19	0.01	-0.54	-0.17	0.03	0.05	0.03	0.14	0.23	0.11	-0.40	-0.35	-0.02	0.18	-0.31	0.04
dmc	0.43	-0.39	0.22	-0.03	0.42	0.35	1.00	0.30	0.09	0.10	0.24	0.01	0.11	0.05	-0.12	-0.13	0.37	0.10	0.46	-0.09	0.14	-0.05	0.06	1.09	0.02	0.24
fib	0.14	0.00	0.15	-0.18	0.21	-0.02	0.30	1.00	0.06	0.10	0.00	0.07	0.12	0.15	-0.06	0.00	0.14	-0.23	0.10	-0.03	0.56	-0.03	-0.13	0.00	-0.13	0.10
lod	0.65	-0.13	0.70	-0.11	0.12	0.02	0.09	0.06	1.00	0.13	0.08	0.55	0.20	0.05	-0.07	0.53	0.61	0.19	0.45	0.31	-0.18	0.07	0.06	0.16	0.24	0.58
suw	0.02	0.08	0.06	0.20	0.06	-0.06	0.10	0.10	0.13	1.00	-0.04	0.25	0.04	0.01	0.56	0.47	0.01	-0.37	-0.01	-0.21	0.04	-0.12	0.08	0.01	-0.02	-0.08
arr	0.00	0.23	0.11	-0.02	0.49	-0.19	0.24	0.00	0.08	-0.04	1.00	-0.16	0.49	0.54	-0.11	-0.10	0.34	0.11	0.15	-0.39	0.28	0.21	0.09	0.15	0.42	-0.09
stp	0.38	-0.12	0.38	0.17	-0.02	0.01	0.01	0.07	0.55	0.25	-0.16	1.00	0.00	0.00	0.16	0.51	0.24	0.20	0.43	0.34	-0.53	-0.02	0.11	0.03	-0.01	0.15
sts	0.07	0.08	0.15	0.05	0.49	-0.54	0.11	0.12	0.20	0.04	0.49	0.00	1.00	0.30	-0.13	0.11	0.23	0.07	0.09	-0.04	0.21	0.30	-0.13	0.12	0.59	0.05
ssh	-0.05	0.22	0.03	-0.27	0.86	-0.17	0.05	0.15	0.05	0.01	0.54	0.00	0.30	1.00	-0.06	-0.03	0.24	0.07	0.15	-0.28	0.46	0.31	0.04	-0.05	0.15	-0.23
gps	-0.12	-0.06	-0.11	-0.32	-0.18	0.03	-0.12	-0.06	-0.07	0.56	-0.11	0.16	-0.13	-0.06	1.00	0.19	-0.24	-0.24	-0.23	-0.13	0.15	-0.15	-0.09	-0.05	-0.07	-0.03
rat	-0.14	0.17	-0.09	0.37	-0.07	-0.36	-0.07	0.09	-0.03	-0.01	0.21	0.09	0.06	-0.01	-0.10	0.12	-0.04	-0.02	-0.12	-0.07	0.23	0.37	-0.13	0.00	0.18	-0.21
sbr	0.36	-0.09	0.41	0.42	-0.10	0.05	-0.13	0.00	0.53	0.47	-0.10	0.51	0.11	-0.03	0.19	1.00	0.22	0.04	0.20	0.18	-0.13	0.06	0.00	-0.08	0.22	0.17
len	0.72	-0.15	0.76	0.06	0.25	0.03	0.37	0.14	0.61	0.01	0.34	0.24	0.23	0.24	-0.24	0.22	1.00	0.36	0.77	-0.04	-0.08	-0.03	0.16	0.28	0.38	0.42
dia	0.49	-0.45	0.38	-0.03	-0.11	0.14	0.10	-0.23	0.19	-0.37	0.11	0.20	0.07	0.07	-0.24	0.04	0.36	1.00	0.53	0.50	-0.57	0.11	0.12	0.07	0.06	0.32
sfw	0.87	-0.42	0.78	0.15	0.16	0.23	0.46	0.10	0.45	-0.01	0.15	0.43	0.09	0.15	-0.23	0.20	0.77	0.53	1.00	0.16	-0.52	-0.12	0.27	0.28	0.17	0.38
stce	0.40	-0.41	0.31	0.01	-0.21	0.11	-0.09	-0.03	0.31	-0.21	-0.39	0.34	-0.04	-0.28	-0.13	0.18	-0.04	0.50	0.16	1.00	-0.43	0.05	-0.08	-0.12	-0.12	0.54
ccse	-0.37	0.54	-0.16	-0.98	0.40	-0.40	0.14	0.56	-0.18	0.04	0.28	-0.53	0.21	0.46	0.15	-0.13	-0.08	-0.57	-0.52	-0.43	1.00	-0.02	0.06	-0.16	0.09	-0.02
cru	0.01	-0.02	0.02	0.13	0.62	-0.35	-0.05	-0.03	0.07	-0.12	0.21	-0.02	0.30	0.31	-0.15	0.06	-0.03	0.11	-0.12	0.05	-0.02	1.00	-0.21	0.08	0.08	0.02
oru	-0.05	0.27	0.07	0.22	-0.05	-0.02	0.06	-0.13	0.06	0.08	0.09	0.11	-0.13	0.04	-0.09	0.00	0.16	0.12	0.27	-0.08	0.06	-0.21	1.00	-0.06	-0.19	-0.12
trt	0.23	-0.22	0.12	-0.04	0.40	0.18	1.09	0.00	0.16	0.01	0.15	0.03	0.12	-0.05	-0.05	-0.08	0.28	0.07	0.28	-0.12	-0.16	0.08	-0.06	1.00	0.11	0.13
ysp	0.17	-0.04	0.20	0.20	0.07	-0.31	0.02	-0.13	0.24	-0.02	0.42	-0.01	0.59	0.15	-0.07	0.22	0.38	0.06	0.17	-0.12	0.09	0.08	-0.19	0.11	1.00	0.08
stc	0.81	-0.30	0.80	-0.42	-0.04	0.04	0.24	0.10	0.58	-0.08	-0.09	0.15	0.05	-0.23	-0.03	0.17	0.42	0.32	0.38	0.54	-0.02	0.02	-0.12	0.13	0.08	1.00

Table 6-6 Summary of significant across-environment correlations between traits

Trait	+ve correlations	-ve correlations
Tch	tsh, lod, len, sfw, stc	Ccs
Ccs	ccse & components	tch, dia, sfw, stce
Fib	ccse & components	
Lod	tch, tsh, stp, sbr, len, stc	
Suw	gps, sbr	
Arr	sts, ssh, ysp	Cone
Stp	lod, sbr, sfw	Ccse
Wfi	sbr	Ccse
Dfi	ssh, arr, ssh. ccse	

```
[1] "covar.lod" "covar.suw" "covar.arr" "covar.stp" "covar.sts" "covar.ssh" "covar.gps"
   "covar.rat" "covar.sbr" were all transformed by arcsin
```

6.6. Relationships between explanatory covariates and tch, ccs, tsh principal component analyses

These results are being re-analysed as part of BSS267 and are not discussed in detail here. In Appendix 4, the principal component analyses of TCH, CCS and TSH were described. As noted in that section, the PCAs did not reveal any consistent differences among regions, locations or crop classes for discrimination among clones for these traits. There was a slight tendency for the 2nd axis to separate out plant crop and ratoon trials, more so for Northern, Herbert and Central trials. The analysis below considers other explanatory effects in the data, based on observed variables described in this appendix 6.

Table 6-7 shows the regression of PCA loadings against covariates, for each trial. Most of the correlations were below the significant level ($r = 0.38$, $p = 0.05$). Higher loadings in component 1 for TCH were associated with higher seasonal minimum temperatures (e.g. mint0), more so during the pre-summer period (mint1) and ripening period (mint3). In component 2 for TCH, there was a negative association with temperature and evaporative demand (pan), i.e. the trials with higher component 2 loadings were slightly cooler. There was also a positive association with Helicotylenchus for component 2.

For CCS, there were negative correlations between component 1 and soil variables such as CEC. Component 2 was negatively correlated with harvest month, temperature in pre-summer and the trial mean CCS (cover.CCS) and positively correlated with Tylenchorhynchus (which occurred mostly in the Burdekin).

Table 6-7 The correlations between the scores (components 1 to 3) from the PC analyses (for TCH, CCS or TSH) correlated against observed explanatory covariates. Significant scores are *not* shaded.

	TCH				CCS				TSH		
Covariate	Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord		
	Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3
plantmonth	0.04	0.04	0.08		0.20	-0.28	0.26		0.12	-0.11	-0.23
harvestmonth	0.04	-0.09	-0.05		0.03	-0.50	0.31		0.06	-0.23	-0.29
croplengthdays	0.01	0.05	-0.04		-0.26	-0.01	0.11		-0.03	0.01	0.05
croplengthmths	0.01	0.05	-0.04		-0.25	-0.01	0.11		-0.03	0.01	0.05
totalirrig	-0.25	-0.30	0.01		-0.45	0.33	0.15		-0.50	-0.08	0.38
totaln	-0.44	-0.01	-0.20		-0.35	0.29	0.14		-0.45	0.03	-0.11
radn0	-0.17	-0.50	0.01		0.04	-0.19	0.05		-0.19	-0.40	0.20
maxt0	0.24	-0.59	0.31		-0.10	-0.18	-0.06		0.03	-0.51	0.47
mint0	0.49	-0.52	0.32		-0.05	-0.15	-0.18		0.31	-0.50	0.35
pan0	0.07	-0.63	0.27		-0.10	-0.03	0.05		-0.09	-0.50	0.38
vpd0	0.45	-0.45	0.18		-0.05	-0.15	-0.24		0.30	-0.45	0.22
rain0	0.35	0.06	0.01		0.02	-0.19	-0.17		0.30	-0.08	-0.13
rainirrig0	0.23	-0.07	0.00		-0.20	-0.05	-0.09		0.07	-0.12	0.02
radn1	0.00	-0.32	0.07		0.12	-0.31	0.15		-0.02	-0.38	-0.03
maxt1	0.16	-0.47	0.19		0.07	-0.43	0.07		0.06	-0.51	0.18
mint1	0.42	-0.41	0.22		0.18	-0.47	0.01		0.38	-0.53	0.08
pan1	0.06	-0.41	0.20		0.06	-0.26	0.17		-0.01	-0.44	0.08
vpd1	0.41	-0.37	0.11		0.09	-0.44	-0.06		0.35	-0.47	0.04
rain1	0.20	0.27	-0.03		0.02	0.02	-0.04		0.23	0.21	-0.07
irrig1	0.28	-0.46	0.37		-0.79	0.41	0.59		-0.36	-0.17	0.37
rainirrig1	-0.02	0.00	-0.05		-0.35	0.25	0.09		-0.17	0.09	0.16
radn2	-0.30	-0.24	0.01		0.04	-0.02	0.16		-0.28	-0.14	0.12
maxt2	0.07	-0.40	0.30		0.06	-0.19	-0.08		-0.03	-0.35	0.36
mint2	0.34	-0.42	0.27		0.09	-0.24	-0.22		0.24	-0.41	0.34
pan2	-0.10	-0.44	0.23		-0.05	0.00	0.11		-0.22	-0.31	0.39
vpd2	0.38	-0.32	0.13		0.08	-0.24	-0.31		0.32	-0.34	0.20
rain2	0.30	0.11	-0.15		0.09	-0.27	-0.26		0.31	-0.02	-0.16
irrig2	0.27	-0.32	0.31		-0.41	0.42	0.13		-0.22	-0.10	0.26
rainirrig2	0.22	0.05	-0.14		0.02	-0.20	-0.25		0.18	-0.02	-0.09
radn3	-0.08	-0.35	-0.03		0.07	-0.39	0.04		-0.04	-0.37	0.03
maxt3	0.14	-0.29	0.27		0.08	-0.09	-0.17		0.05	-0.25	0.35

	TCH				CCS				TSH		
Covariate	Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord		
	Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3
mint3	0.41	-0.30	0.31		0.01	-0.03	-0.22		0.28	-0.29	0.36
pan3	0.09	-0.38	0.20		0.06	-0.16	-0.03		0.04	-0.35	0.20
vpd3	0.39	-0.33	0.14		-0.07	0.02	-0.25		0.24	-0.28	0.32
rain3	0.35	-0.09	0.22		-0.07	-0.16	0.01		0.23	-0.21	0.02
irrig3	-0.27	-0.13	0.06		-0.07	0.09	0.14		-0.33	-0.06	0.13
rainirrig3	0.29	-0.14	0.26		-0.12	-0.14	0.05		0.13	-0.24	0.05
water	-0.04	-0.27	0.06		-0.42	0.25	0.05		-0.33	-0.12	0.36
covar.tch	-0.08	-0.33	0.02		-0.46	0.37	0.11		-0.25	-0.15	0.11
covar.ccs	0.20	-0.12	-0.18		0.21	-0.74	0.09		0.32	-0.35	-0.27
covar.tsh	0.00	-0.41	-0.05		-0.40	0.05	0.18		-0.14	-0.35	0.02
covar.wfi	0.24	-0.31	-0.18		0.00	0.06	-0.37		0.15	-0.35	-0.04
covar.dfi	0.48	0.16	0.01		-0.09	-0.13	0.13		0.36	0.12	0.06
covar.con	0.15	-0.13	-0.01		0.25	0.03	-0.27		0.25	-0.09	-0.04
covar.dmc	-0.12	0.01	0.03		-0.16	-0.62	0.54		-0.14	-0.17	-0.05
covar.fib	-0.10	-0.24	0.01		-0.12	-0.32	0.50		-0.12	-0.29	-0.02
covar.lod	0.12	-0.39	0.13		-0.29	0.01	0.22		-0.08	-0.32	0.17
covar.suw	0.00	-0.19	-0.17		0.11	-0.18	-0.11		0.01	-0.25	-0.07
covar.arr	0.46	-0.21	0.04		0.03	-0.36	-0.15		0.41	-0.35	-0.04
covar.stp	0.10	-0.07	-0.06		0.01	-0.09	0.00		0.14	-0.12	0.04
covar.sts	0.25	0.12	0.34		0.05	0.01	0.15		0.20	0.05	0.15
covar.ssh	0.36	-0.05	0.06		-0.02	-0.22	0.16		0.31	-0.12	0.13
covar.gps	-0.19	0.10	0.09		0.28	0.00	-0.02		-0.05	0.07	0.11
covar.rat	0.21	-0.15	0.28		-0.16	-0.11	0.09		0.05	-0.23	0.10
covar.sbr	0.16	-0.20	0.03		0.01	-0.07	-0.17		0.13	-0.22	0.11
covar.len	0.09	-0.40	-0.15		-0.28	-0.06	-0.07		-0.06	-0.34	0.17
covar.dia	-0.04	0.34	0.24		-0.25	0.51	0.10		-0.10	0.42	0.14
covar.sfw	0.02	-0.13	-0.25		-0.24	0.24	-0.11		0.02	-0.05	0.04
covar.stce	-0.25	0.17	0.19		-0.40	0.46	0.38		-0.38	0.22	0.00
covar.ccse	-0.05	-0.08	-0.03		0.38	-0.63	0.21		0.11	-0.18	-0.28
covar.cru	0.15	0.06	0.19		-0.19	0.09	0.22		0.04	0.10	0.13
covar.oru	-0.23	0.13	-0.52		0.24	-0.22	-0.28		0.01	0.06	-0.30
covar.trt	0.18	-0.05	0.08		-0.01	0.01	-0.24		0.08	-0.02	0.14
covar.ysp	0.29	-0.21	0.24		0.02	0.02	-0.20		0.16	-0.24	0.05
covar.brx	0.13	-0.25	-0.20		0.06	-0.58	0.05		0.16	-0.38	-0.10
covar.pol	0.19	-0.21	-0.15		0.17	-0.76	0.08		0.26	-0.39	-0.14

	TCH				CCS				TSH		
Covariate	Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord		
	Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3
covar.pur	0.19	0.06	-0.01		0.36	-0.64	0.04		0.35	-0.19	-0.23
covar.brxe	0.14	-0.07	0.00		0.21	-0.68	0.05		0.23	-0.21	-0.10
covar.pole	0.07	-0.07	0.03		0.32	-0.63	0.21		0.19	-0.18	-0.20
covar.pure	-0.13	0.02	-0.01		0.30	-0.35	0.35		0.00	-0.01	-0.33
covar.cone	0.35	0.07	0.21		0.36	0.88	-0.48		0.60	0.42	0.32
covar.stc	-0.26	-0.29	0.02		-0.42	0.32	0.31		-0.44	-0.15	-0.11
latitude	0.21	-0.44	0.03		-0.14	-0.15	-0.19		0.08	-0.45	0.11
longitude	-0.26	0.44	-0.05		0.25	0.08	0.16		-0.08	0.44	-0.13
ph	-0.27	0.01	0.02		-0.12	0.14	0.04		-0.29	0.18	0.26
phCaCl	-0.23	-0.17	0.07		-0.33	0.14	0.28		-0.40	-0.03	0.32
phbuffer	-0.08	-0.10	-0.08		0.35	-0.46	-0.20		0.09	-0.18	0.16
oc	0.00	0.13	0.10		-0.27	0.35	0.25		-0.19	0.17	-0.18
sulf	-0.10	0.36	-0.02		0.00	0.22	0.07		-0.11	0.37	-0.29
calc	-0.02	-0.18	0.19		-0.55	0.19	0.48		-0.26	0.00	0.33
magn	-0.06	-0.04	0.14		-0.39	0.07	0.46		-0.20	0.06	0.16
alum	0.07	0.04	0.00		-0.26	0.38	0.09		-0.12	0.12	-0.21
sodi	-0.09	-0.19	0.16		-0.44	0.04	0.44		-0.32	-0.11	0.27
chlo	-0.29	0.24	-0.12		0.22	-0.31	0.14		-0.09	0.18	-0.17
swcon	-0.14	-0.10	0.15		-0.25	0.02	0.46		-0.27	-0.09	0.10
copp	0.04	0.02	0.12		-0.34	-0.08	0.48		-0.06	0.09	0.15
zinc	0.04	-0.01	-0.15		-0.14	-0.12	0.20		0.02	0.03	0.02
mang	-0.04	0.04	-0.27		-0.01	-0.18	-0.04		0.08	0.05	-0.18
iron	0.10	0.19	-0.19		0.02	-0.10	0.24		0.15	0.17	-0.25
boro	-0.15	0.16	0.17		-0.31	0.02	0.51		-0.26	0.10	-0.05
zincBSES	0.07	0.08	0.05		-0.24	-0.07	0.39		-0.01	0.12	0.11
potanitric	0.55	-0.32	0.54		-0.25	0.35	0.06		0.32	-0.22	0.45
siliBSES	0.16	0.00	0.34		-0.53	0.04	0.66		-0.06	0.06	0.25
cec	0.00	-0.12	0.19		-0.57	0.24	0.52		-0.27	0.05	0.23
soilCaMg	0.07	-0.19	0.20		-0.04	0.13	-0.08		-0.08	-0.15	0.28
AlSP	0.20	-0.17	0.26		-0.13	0.31	-0.01		0.03	-0.09	0.17
esp	-0.13	0.10	0.25		-0.01	-0.22	0.29		-0.17	0.07	0.23
elec	-0.31	0.03	-0.07		-0.14	0.18	0.28		-0.31	0.06	-0.11
Pachymetra	-0.18	-0.28	-0.25		0.17	-0.19	-0.07		-0.10	-0.28	-0.07
Pratylenchus	0.37	-0.01	0.12		0.11	-0.13	-0.30		0.39	-0.09	0.15
Helicotylenchus	-0.26	0.47	-0.02		-0.12	0.23	0.26		-0.32	0.45	-0.30

	TCH				CCS				TSH		
Covariate	Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord				Excluding B1 and B2 and Ord		
	Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3		Comp. 1	Comp. 2	Comp. 3
Meloidogyne	0.12	-0.07	0.20		0.10	0.10	-0.14		0.10	-0.07	0.05
Tylenchorhynchus	-0.21	-0.20	0.10		-0.20	0.43	-0.17		-0.34	0.12	0.46
NemTotal	0.31	0.00	0.16		0.05	0.01	-0.33		0.29	0.00	0.23
LocPathol	-0.05	-0.22	-0.18		0.19	-0.16	-0.25		0.02	-0.21	-0.02
LocPatholNem	0.21	0.04	0.14		-0.02	0.08	-0.21		0.17	0.02	0.13
LocPatholPachy	-0.14	-0.23	-0.19		0.16	-0.18	-0.11		-0.07	-0.21	-0.04

Appendix 7. Project meetings and workshops

Table of contents

7.1. 26 Nov 1999, BSES, Indooroopilly (see milestone 4 report)

At this meeting, a formal decision was made to modify the experiment schedule (following discussions earlier in 1999). The schedule was restructured to spread the work-load more evenly over 3 years of testing. Slightly more than half of the trials (Series 1) were to be planted in 1999. In 2000, these trials were to be ratooned and the next series planted. In 2001, Series 2 trials were to be ratooned.

Consequently, damage to the propagations in the north by Cyclone Rhona (Feb 1999) resulted in further delays to planting these trials.

7.2. 15 Feb 2001, CSIRO, Townsville (see milestone 8 report)

A one day workshop meeting was attended by Scott Chapman, Phil Jackson, Mike Cox, Nils Berding, Collins Kimbeng, Allan Rattey and Mac Hogarth. As well as planning for 2001 planting and harvesting activities, this meeting dealt with the issues arising from the propagation problems discovered in the Burdekin. We decided to sample all of the genotypes from at least one trial in each region, and for a random subset of genotypes in each trial in each region. This required quite an effort from the field staff in collecting leaf material for DNA extraction, and for CSIRO casual staff in Brisbane, who undertook the extraction and analysis using CSIRO resources.

7.3. 8-9 June 2004 (see milestone 11)

At the workshop, we presented a summary of all of the results collected in the project including environment, soil chemistry, yield performance, disease and trait scores (see appendix). The analyses completed included the effects of region, location and crop class (i.e. plant, ratoon) on genotype by environment interaction; analyses of correlations within and between regions. Many of the data were summarised in an ASSCT paper presented in May 2004. Powerpoint presentations from the workshop were submitted with milestone 11 and as a separate ZIP file and are included on the CD for this report. During the workshop, the strong general correlations amongst regions in terms of performance were recognised. Options to make use of this data include utilising inter-regional data when evaluating clones in new regions where they haven't previously been tested. There may also be options to rationalise the initial testing of clones, given that their performance at this stage of selection is likely to be well-correlated among regions. These impressions as well as further ones regarding the importance of locations vs years and the effects of pathogens (especially *Pachymetra* in Herbert and Central trials) are still to be interpreted for the final report. The agenda for this workshop is given below.

7.3.1. Agenda 8-9 June 2004, BSES Meringa station, Cairns

Scott Chapman, Phillip Jackson, Xianming Wei, Mike Cox, Nils Berding, Jo Stringer, Robert Troedson

Tuesday

1330-1345 Overview of workshop/project (Scott)

1345-1415 Historical background on breeding in BSES related to GxE (Allan)

1415-1430 Historical background on breeding in CSR related to GxE (Phil)

1430:1500 Presentation on GxE and what to do about it (Scott)

- GxE framework (Byth and Cooper's)
- estimating Vg, etc
- calculating H2 and rg

1530-1600 Details and intent of CC028 and description/summaries of overlap in
climate, weather, soil types, pathogens of the Mega GxE trials (Scott)
1600-1630 Summaries of observed harvest and scoring data for mega dataset (Scott)
- performance of the random clones vs checks in each region for all traits
1630-1700 Comparisons of variances within regions (Scott)
- estimated VCs from final stage variety trials
- comparison with VCs from mega trials
- how many locs do you need within a region?

Wed
0900-1000 Variances across regions for mega GxE dataset for various models and traits
- Estimates of rg and heritability from random clones
- within and between regions
- G+ GxE
- G + L + Y + LxY
- G + Gxregion effects
- effect of covariates, XFA models...
1030-1200 Estimates of effect of between/within region rg on selection and
direct/indirect selection based on subdividing regions (based on Atlin's paper) for subsets of region combinations
- N vs H
- C vs (S+W)
- Northern vs Southern (exc Bkin)
- Bkin vs Tableland
(above not all presented on basis that correlations are largely close to 1. Further analyses to be done on these)))).
1330-1530 Discussion of options to modify programs (Phil, Scott, Al) and analyses

Appendix 8. Press release

Below is a copy of the article written by Phillip Jackson and Mike Cox to be distributed to industry publications providing more information about the GxE project.

8.1. Improving selection efficiency and decreasing time to release of new varieties across regions.

by BSES and CSIRO staff.

Currently, BSES conduct distinct variety selection programs in different regions. These include the northern region (Tully-Mossman), Herbert, Burdekin, Central (around Mackay), southern (Rocky point to Bundaberg) and NSW regions. The aim is to select varieties adapted to environments within each region. Promising clones identified toward the latter stages of selection in each region are transferred to other regions to assess if they also perform well elsewhere.

However, it is not known whether conducting separate selection programs on a regional basis as is currently done leads to maximum genetic gains given the available limited resources for variety selection. In addition, there may also be ways to decrease time to release of varieties across all environments to which they are suited. It is important that varieties showing promise in any particular selection trial anywhere in Australia are quickly sent for testing and possible release in other locations where they could be of commercial value. However there are limited available resources in breeding programs. Therefore the process of transfer of selections between regions needs to be carefully managed and targeted for maximum success, rather than simply transferring and testing large numbers of promising varieties between all regions largely at random.

It is possible that selection across Australia could be structured more around environmental groupings relating to variety response rather than on a regional basis. For example, if wet or poorly drained sites in the central, Herbert and Northern regions were found to produce similar rankings of varieties then perhaps a selection program could be developed to address this type of targeted environment. The early stages of such a program could be based in one of these regions and then selections transferred to similar environments in the latter stages for further testing. It is possible that changes like these could be introduced that could deliver better value per dollar spent on selection and speed up release of varieties across all locations to which they are suited.

A research project being conducted by BSES and CSIRO with funding from SRDC aims to examine such issues. The end goal is to decrease time to release of promising varieties and improve efficiency of resource use in selection. The project, nicknamed “The mega G by E project”, involves planting a common set of around 50 unselected varieties across a wide range of environments in Australia. The project is utilises unselected clones in order to address questions like how effective would selection in one environment be for discarding poor clones or picking elite clones for many other environments and regions. The first series of trials in this project were established in NSW, the southern region, the central region, the Burdekin, the Herbert and the northern region in 1999. A further series will be established in 2000. The trial sites will be monitored in terms of weather and soil characteristics and for several pathogens. This will assist in interpreting and extrapolating the results obtained.

Trials are also being established on the tablelands and possibly the Ord region. The results will help determine from where selected clones should be sourced for these newer regions in the industry.

Altogether around 25 large field trials are being conducted as part of the project. This represents a large amount of work for BSES and CSIRO technical staff. However, it is hoped that the end result will be a more streamlined and efficient selection process across the whole country that will deliver even better returns than now from the annual investment by the industry in variety selection.

Appendix 9. Extract from milestone 8 report - clone identification following 1st year results

Table of contents

Following discussion of the 1st year results at the Feb 2001 meeting, we were concerned by the poor correlation of sugar and cane yields between the two Burdekin trials and the other six trials that were harvested in 2000. Clustering and principal component analysis had immediately revealed this distinction. It had therefore been useful for the project plan to make immediate provision for preliminary reporting of results in December 2000.

The obvious conclusion from the data was that the Burdekin environments provided a unique challenge to the clones that resulted in differential performance cf. other sites. However, the results were so striking that we had to consider the possibility that there may have been some mix-up in the clones during the transfer and/or propagation of seed cane for the Burdekin. As both Burdekin trials had been propagated from the same plots, such an event could have explained the poor correlation between the Burdekin trials and the other regions, as well as the high correlation observed between the two Burdekin trials. The Burdekin field staff were asked to check the identities of some of the clones by comparing them visually with plots in the Herbert, where the initial propagations were done. This seemed to indicate a problem with the propagation and/or multiplication in the Burdekin for the sites coded B1 and B2. Consequently, the germplasm for sites B3 and B4 were sourced from the Herbert.

To confirm the identities of the clones, we requested the help of Lynne McIntyre (CSIRO). Leaf samples were collected from replicate 1 of the H2 (Herbert CSR Abergowrie) and B2 (Burdekin CSR Kalamia) trials. They were frozen and transferred to Brisbane to be processed by Vicki Whan and Scott Chapman and Lynne McIntyre during May 2001. Leaves were freeze-dried, DNA extracted and gels run for the clones, pairing the H2, B2 trials for a clone. We used three micro-satellite markers (#21, 26 and 36) and scored 10 to 15 alleles for each marker.

Based on 3 markers, all of the commercial clones were correct (Appendix 2). This would be expected, given that the source material for these was separate to the propagation nursery. Of the 48 random clones, 23 from the B2 trial were identified as matches with H2. Two of the 48 are conclusively non-matches. Three of the 23 matches are being checked again, due to insufficient DNA in the sample. Of the 23 matches, 4 clones had been correctly assigned and 4 clones had been directly swapped. Finally, all 23 putative matches are in the process of being checked against an additional 2 micro-satellite markers. This may result in several more miss-matches.

From the marker results, it seems that two things have happened:

1. a systematic error (related to the 4 correct and 4 swapped assignments – unlikely chance events) during propagation or cutting of planting material
2. at least 25 clones in the B2 trial do not appear to be in the H2 trial and were possibly sourced or cut from incorrect plots at some stage during propagation.

As we have only just completed the fingerprinting, there has not yet been time to consult at length with staff in the Herbert and Burdekin. The results of the fingerprinting are being sent to the field staff for comparison with field plans to see if the source of error can be determined. While it may not assist in interpreting the results of the Burdekin trials, we hope that it will assist breeding programs in avoiding similar errors in future.

Table 9-1 Milestone 8 extract (June 2001) to identify clones in trial B2

Assignments

A (Herbert H2?)	B (Burdekin 2)	Comments		
4001			would have been 4016 except for marker 36.9!	
4003	84-25510	#36, no DNA for 21 or 26	GREEN = TO CHECK	
4004	4004	3 markers	YELLOW = SAME	RESENT
4005				
4006	4048			
4007				
4008				
4010	4010	3 markers		RESENT
4012	4017		CYAN = FLIP	
4013				
4016				
4017	4012			
4018				
4020	84-6083			
4021	4021	3 markers		RESENT
4022				
4023				
4024	4046	3 markers	ORANGE = FOUND	
4027				
4028				
4029				
4030				
4032	89-6806	#36		
4033	4010	But we already have 4010		
4035	4027	#36,21, but no DNA in 26		RESENT
4037				
4038				
4039	4040	3 markers		
4040	4039	3 markers		
4044				
4046				
4047				
4048	4018	3 markers		
84-25510	4007	#36, no DNA for 21 or 26		
84-6083	4020	3 markers		
84-6086				
86-151				
87-10510	87-10510	3 markers		RESENT
88-271				
89-3933	4038			
89-50310	90-1101	3 markers		
89-518	no match			
89-6806	4032			
90-1101	88-271	3 markers		
90-1109	no match			
90-77-5 ??			not sure what diff is here….	
90-77-2	4001	3 markers, re-extr DNA to chk if 90-77-2 or 90-77-5		
90-83				
Q117	Q117	3 markers		

Q124	Q124	3 markers
Q124	Q124	3 markers
Q135	Q135	3 markers
Q138	Q138	3 markers
Q141	Q141	3 markers
Q165	Q165	3 markers

Table 9-2 Final marker screen results based on bands from two micro-satellite markers (21SA and 19) from CSIRO PI laboratory. Within a marher and across rows, numbers indicate a marker class (i.e. same identity). Note that about half the B2 clones had been re-assigned and the remainder were not known to be part of the original study set.

MARKER	21SA	21SA	21SA	21SA	21SA	21SA	21SA	19	19	19	19	19	19	19
Clone	H1	H2	B2	B3	C1	S4	N4	H1	H2	B2	B3	C	ISIS	N4
84-255-10	1	1	2	NP	3	NP	NP	1	1	2	NP	3	NP	NP
84-608-3	1	1	2	1	0	1	1	1	1	2	1	0	1	1
84-608-6	1	1	2	NP	1	1	1	1	1	2	NP	1	0	1
86-1151-3	1	1	2	1	1	1	1	1	1	2	1	1	1	1
87-105-10	1	1	1	2	3	3	1	1	1	1	2	3	3	1
88-271-6	1	1	2	1	1	1	1	1	1	2	1	1	1	1
89-393-3	1	1	2	1	1	1	1	1	1	2	1	1	1	1
89-503-10	1	1	2	1	1	1	1	1	1	2	1	1	1	1
89-518-6	1	1	2	NP	NP	NP	NP	1	1	2	NP	NP	NP	NP
89-680-6	1	1	2	1	0	1	1	1	1	2	1	0	1	1
90-110-1	1	1	2	1	3	3	1	1	1	2	1	3	3	1
90-110-9	1	1	2	1	0	1	1	1	1	2	1	0	1	1
90-77-2	1	0	0	1	1	1	1	1	0	0	1	1	1	1
90-77-5	1	0	0	NP	0	NP	NP	1	0	0	NP	0	NP	NP
90-83-5	1	1	2	1	NP	1	1	1	1	2	1	NP	1	1
95H4001	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4003	0	1	2	1	1	1	1	0	1	2	1	1	1	1
95H4004	0	1	0	1	0	1	1	0	1	1	1	0	1	1
95H4005	0	1	2	1	1	3	1	0	1	2	1	1	3	1
95H4006	0	0	2	1	0	1	1	0	0	2	1	0	1	1
95H4007	1	0	2	1	1	1	1	1	0	2	1	0	1	1
95H4008	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4010	1	1	1	1	1	1	1	1	1	1	1	1	1	1
95H4012	1	1	2	1	0	1	1	1	1	2	1	0	1	1
95H4013	1	1	2	NP	1	NP	NP	1	1	2	NP	1	NP	NP
95H4016	1	1	2	NP	0	NP	NP	1	1	2	NP	0	NP	NP
95H4017	1	1	2	NP	NP	NP	NP	1	1	2	NP	NP	NP	NP
95H4018	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4020	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4021	1	1	1	1	2	2	1	1	1	1	1	2	2	1
95H4022	1	1	2	1	1	1	1	1	1	2	1	1	1	?
95H4023	1	1	2	1	0	1	1	1	1	2	1	0	1	1
95H4024	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4026	1	NP	NP	NP	NP	NP	NP	1	NP	NP	NP	NP	NP	NP
95H4027	1	1	2	3	1	1	1	1	1	2	3	1	1	1
95H4028	1	0	0	1	1	1	1	1	0	0	1	1	1	?
95H4029	1	1	2	1	NP	0	0	1	1	2	1	NP	0	1
95H4030	1	1	0	1	1	1	1	0	1	0	1	1	1	1
95H4032	1	1	2	1	NP	1	1	0	1	2	1	NP	1	1
95H4033	1	3	2	1	4	1	1	1	3	2	1	4	1	1
95H4035	1	1	2	1	1	1	1	1	1	0	1	2	1	1
95H4037	1	1	2	1	1	1	1	1	1	1	0	1	1	1
95H4038	1	3	2	1	1	1	1	1	3	2	?	?	1	?
95H4039	1	1	2	1	1	1	4	1	1	2	1	1	1	4
95H4040	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4041	1	NP	NP	NP	NP	NP	NP	1	NP	NP	NP	NP	NP	NP

MARKER	21SA	21SA	21SA	21SA	21SA	21SA	21SA	19	19	19	19	19	19	19
Clone	H1	H2	B2	B3	C1	S4	N4	H1	H2	B2	B3	C	ISIS	N4
95H4044	1	1	2	1	0	1	1	1	1	2	1	0	1	1
95H4046	1	1	2	1	1	1	1	1	1	2	1	1	1	1
95H4047	1	1	2	1	1	3	1	1	1	2	1	1	3	1
95H4048	1	1	2	1	1	1	1	1	1	2	1	1	1	1
MQ88-2047														
Q117	1	1	1	1	0	1	?	1	1	1	1	1	1	1
Q124	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Q135	1	1	1	1	0	1	1	1	1	1	0	0	1	1
Q138	0	0	1	1	1	1	1	0	0	1	1	1	1	0
Q141	1	1	1	1	NP	1	1	1	1	1	0	NP	1	1
Q165	1	1	1	1	2	1	0	1	1	1	1	2	1	0

Appendix 11. Draft paper on G and GxE interaction across sugarcane regions

Genotypic and genotype by environment variation in sucrose content and cane yield across Australian sugarcane production regions

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11.1. Figure captions

Fig. 1. For both datasets, from single trial analyses, trial mean versus estimated residual variance for (a) TCH and (b) CCS. Linear regressions are fitted with no outlier trials removed. At significance of $p = 0.05$ and $n = 50$; significant $r = 0.27$, i.e. $r^2 = 0.07$.

Fig. 2. Mean CCS against mean TCH for each trial in both datasets.

Fig. 3 For each dataset, (a) trial mean TCH against estimated genetic variance after removal of 3 outliers each in MegaGxE (S4 plant crop (52 t ha^{-1}, 433 t^2 ha^{-2}); W2 plant (123 t ha^{-1}, 1042 t^2 ha^{-2}) and 1st ratoon (155 t ha^{-1}, 804 t^2 ha^{-2})) and in BSES FATs (Macknade plant (56 t ha^{-1}, 269 t^2 ha^{-2}) and ratoon (96 t ha^{-1}, 435 t^2 ha^{-2}) and Harwood plant (128 t ha^{-1}, 830 t^2 ha^{-2})) and (b) data for CCS with no outliers removed.

Fig. 4 For each harvest in the MegaGxE dataset, lodging scores (% of plants lodged) against total cane yield (t ha-1). Trials excluded as in Fig. 1 and not recorded for two other trials (1st ratoons in N4 and O1, see Table 1). The dotted line is the mean trial yield for the entire dataset.

Fig. 5 BLUP estimates for CCS plotted against those for TCH for each region within the two datasets. None of the correlations are significant.

11.2. Abstract

Each year, each of six (now four) regional breeding programs makes approximately 250 crosses to initially test about 25 000 sugarcane seedlings in total across the industry. Over two to four years, clones from each screen are culled in single location trials and propagated for three year multi-location trials of about 100 clones for final-stage testing. Clones for potential release are evaluated for other disease and quality criteria with multiplication and regional release occurring within 2-3 years of the final testing. Crossing and field testing is currently undertaken separately for each regional program, although there is exchange of germplasm between regions as part of the later stages of selection. Our aim was to (1) determine the magnitude and differences of genotypic main effect (variance) and genotype by site and year effects contribute to variation among genotypes and (2) investigate the degree of change in genetic variance of the germplasm between early and late stages of selection.

For CCS (commercial cane sugar %), genotypic variance was similar across regions for clones from early (random clones) or late stages ('selected' clones) of selection. However, genotypic and genotype by environment interaction (GEI) variances were twice as large for the random clones as for the selected clones. In both datasets, the high GEI variances for CCS were largely associated with site and site by crop-year interaction effects, rather than year interactions. The genotypic variance of TCH (fresh weight of tonnes cane per ha) varied more across regions than that for CCS, and was 2 to 4 fold greater for random clones than for selected clones. The GEI variance generally decreased between the random and selected clone datasets, and the interaction between genotype and year was greater than for CCS.

…..still some bits to add… re h2 etc….

11.3. Keywords:

Genetic variance, correlation, CCS, TCH, lodging

11.4. Introduction

Among other maintenance, harvestability and quality traits, sugarcane breeders strive to improve fresh cane yield per ha (TCH) and the sucrose content of cane which, in Australia, is measured by a formula that converts brix and pol observations to Commercial Cane Sugar (CCS). The Australian industry currently operates 5 regional breeding programs along a coastal growing region of almost 2000 km (Hogarth and Mullins, 1989). Two major reasons for the existence of regional programs are quarantine requirements to limit the spread of several diseases, and the logisitics of managing sugarcane planting material (i.e. stalks) compared to other crops where seed is used and is much easier to multiple and transfer.

Over 8-10 years, these regional programs create, test and release new cultivars (also described as clones), with limited exchange of germplasm occurring among the programs both pre- and post-release. While some released clones have been shown to have broad adaptation to the entire region or specific adaptation outside their original region, this is normally discovered through transfers and later testing, often following their release. The breeding programs are interested to determine whether broad adaptation in the germplasm might be detected more easily, and also whether there are correlations among different regions for specific adaptation. If this is the case, then re-structuring of the breeding program activities could increase the rate of release of broadly adapted clones.

Apart from a the improvement of yield and disease tolerance, the breeding programs have visual and measured observations of other crop characteristics to filter selection. These observations include measures of the degree of lodging, suckering, arrowing (flowering) and other traits thought to be related to crop performance and/or suitability for harvesting and processing. Hence, there is also an interest in determining which of these traits have genetic variability and how they relate to the major selection traits.

Globally, all commercial sugarcane is derived from a relatively narrow genetic base of less than 20 interspecific hybrids produced in the 1930s (reference??). Released clones in Australia are based on derivatives from these hybrids that have been identified here and elsewhere in the world, particularly South Africa, Florida, the West Indies and India??. An industry owned company, BSES Limited, coordinates six (soon to be four) regional breeding programs in Australia that are undertaken in association with CSIRO (a Commonwealth Government research agency) and CSR Limited (a public company which also owns milling operations). Each regional breeding program makes ca 250 crosses between ‘proven parents (i.e. as demonstrated by past performance of their respective progeny) and tests the 20 000 to 30 000 seedlings in PATs (Progeny Assessment Trials) grown as single-row families, i.e. multiple rows per cross, but with each row comprising stools of individual genotypes (seedlings). In the plant (1st year) crop, TCH and CCS are determined for each family and together with other visual scores, 2000 to 3000 seedlings are selected from the 1st ratoon (2nd year) rows for planting as single-row plots into the next stage of trials: CATs (Clonal Assessment Trials). Following two years of assessment and selection as plant and 1st ratoon crops, about 100 clones are then evaluated in 3 to 6 sites in replicated multi-row plots for 3 years: FATs (Final Assessment Trials). Other traits are considered before clones are registered for release and distribution by regional productivity boards.

From past research, there has developed a reasonable understanding of the performance and genotype by environment interactions for either unselected or advanced selection stage genotypes within particular regions, e.g. Southern (Mirzawan *et al.*, 1993); Central (Kimbeng *et al.*, 2002); Herbert (Jackson and Hogarth, 1992; Jackson *et al.*, 1995); Burdekin (Rattey and Kimbeng, 2001); Northern (Pollock, 1979). The majority of these studies had found substantial GEI variance component effects within regions, often greater than was observed for Genotype main effects.

There has been little research to explore GxE interactions across different regions. Such research should enable plant breeders to utilise indirect selection between different regions, especially in early selection stages and in progeny performance for parent and cross evaluation. Further, most of the trials were focussed on the last stage of selection and therefore underestimate the genotypic variance that exists in an initial cross. This variance and its interaction with the environment must be known if we wish to determine repeatability and genetic correlations among and within regions and allow the potential for plant breeders to utilise indirect selection between different regions.

To address these issues, a series of trials was planned over the entire Australian sugarcane growing area with between 3 and 6 sites planted per region and grown for 2 to 4 successive harvests, i.e. plant crop plus 1, 2 or 3 ratoon crops. Apart from commercial checks, the genotypes used were propagated from seedlings from randomly chosen crosses. The objective of the study was to determine, for TCH and CCS of 'random clones', the genotypic and genotype by environment (location, region, year) variance components and the genetic relationships within and between regions. Within regions, these results are compared with a set of experiments undertaken within regions (FATs) during the same years, where the entries comprise 'selected clones' that have already undergone 5 to 10 years of selection. A secondary objective was a preliminary evaluation of some of the secondary selection traits, such as lodging, and their relationship to variation in TCH and CCS.

11.5. Materials and Methods

Two sets of data are analysed here. The first data set is from experiments, labelled as the MegaGxE study, where the same set of 48 unselected clones was grown across all regions. The second set is the results of FATs conducted by BSES Limited during 1999 and 2000 within each breeding region. These are final assessment trials for clones that have been heavily selected as described in the introduction (i.e. about 100 clones from an original set of ca. 25 000 seedlings) for performance within the region. Across regions these trials have in common only a small number of check and test clones.

In 1997, when the project was initiated, there were six breeding programs in place (Fig 1): from north to south termed as Northern, Herbert, Burdekin, Central, Southern (all in Queensland) and NSW. The Southern and NSW programs were combined in 1998, and the Northern and Herbert programs are being combined during 2004. Given the structure of the crosses in the FAT data set, the results are presented here for six breeding programs.

11.5.1 Propagation and planting times

All seed material was ensured to be free of ratoon stunting disease. For the MegaGxE study, stalks derived from the seedlings (see below) were transferred to the CSR Limited experiment station at Macknade near Ingham. These were planted out in 1997 to provide stalks that were transferred to other regions in 1998 and 1999. Following another year of propagation to provide sufficient planting material, trials were planted over 1999, 2000, 2001and 2002. The imbalance in planting time was partially deliberate, in order to distribute the workload and to sample a greater number of years, but was otherwise imposed by problems caused by cyclones and several sampling errors during propagation.

The BSES FATs were grown as part of the normal breeding program within each region, and so germplasm for these had been propagated prior following selection in regional CATs. The results have been collated from trials planted in 2000 and harvested as plant (2001) and 1st ratoon (2002) crops. In NSW, the crops were planted in late 1999 and grown through to a 2nd year before the plant harvest in 2001 and 1st ratoon in 2002.

11.5.2 Sites

Each dataset encompassed the breeding regions in the states of Queensland and NSW (Tables 1 and 2). In the MegaGxE dataset, 56 harvests were made in 2000-2003 over 24 locations. In the BSES FATs dataset, 52 harvests were taken in 2001 and 2002 only, over 26 locations. In the MegaGxE study, an additional trial was also planted in the Ord irrigation region in the north of Western Australia (Table 1). This trial had only about 50% of the clones, as they were pre-screened to remove smut-susceptible clones when that disease established itself in the Ord just before the first round of germplasm was prepared for transfer there.

Note that the two datasets have several site names in common. These names refer to the nearest locality and trials with the same site name may not have been planted in the same field and managed exactly the same way. Hence, the comparison of results from MegaGxE with the FATs should be constrained to the regional level (i.e. to compare relative magnitude of variances) rather than as direct site comparisons or direct estimates of average performance in any region, i.e. in both datasets, the trials are regarded as ‘samples’ of the production environment within each region.

11.5.3 Germplasm

Table 3 shows the pedigrees and abbreviated names of the ‘random’ clones used in the MegaGxE study. Excluding commercial checks (Q canes) and excepting errors (see below), 51 clones were harvested on at least four occasions. Each random clone had been randomly chosen from a random cross in either of the existing Herbert breeding programs, run by CSR Limited and BSES. In most sites, 48 clones were planted, including four to six Q canes (Table 1). The number of entries varied slightly from this in several trials and was lower in the Ord (35) due to smut-screening and S3 (36), due to propagation problems. In such a large sugarcane experiment over this many locations, with distribution of large quantities of seed material (stalks), there is the possibility of error during propagation and planting of trials. During an early stage of analysis, we noticed poor correlations between the first Burdekin trials and the other locations. With the assistance of Lynne McIntyre (CSIRO), two microsatellite DNA probes (mSSCIR19 and SMS21SA) from the International Sugarcane Microsatellite Consortium (Cordeiro et al 2000) were used to screen DNA extracted from leaf material of all clones at sites B1 and B2, and from clones grown in the first trial within each region. As sugarcane is a polyploid, each microsatellite marker generates a large number of allelic bands that can be used to fingerprint clones. The markers indicated that errors apparently occurred during propagation in the Burdekin, such that 20 clones in the B1 and B2 locations could not be correctly identified as being part of the core set. Any errors found in other regions (there were 7 in Central and Southern trials) were checked further by screening the same clones from other trials in the region. In most cases, the errors had occurred during propagation and so the errors were also ‘propagated’ through the region. Any genotypes that were found to be incorrect were assigned a new name to distinguish them from all others in the dataset. These ‘unknown’ clones are not listed in Table 3. In the worst cases (B1 and B2), the number of random clones was as low as 24, while in almost all other trials, there were at least 40 random clones from the original set, plus the additional checks. When computing correlations and relationships among the B1 and B2 trials, the ‘unknown’ clones are kept in the dataset, as they are still effectively to be random selections from the nursery block, but they are dropped from cross-regional analyses as they were not grown elsewhere.

In the FAT experiments, the clone sets differed among regions, depending on the selection history with little overlap apart from some check genotypes (details not presented here). The check genotypes (Q canes) used were the best adapted commercial clones across regions with some additional checks within each region.

11.5.4 Management, design and measurements

Experiments were planted on grower's properties or on research land owned by either BSES Limited or CSR Limited (Tables 1 and 2). The trials were managed using standard grower practices with regard to fertiliser, irrigation and control of weeds, insects and diseases. Cane setts were treated with fungicide to prevent sett rotting caused by *Ceratocystis* paradoxa. In Burdekin experiments, a controlled release formulation of chlorpyrifos (suSCon Blue) was incorporated to control the white larvae of *Lepidiota* and *Dermolepida* genera (cane grub). Trials in the Burdekin region were fully irrigated (up to 7 ML ha^{-1} per season), while most trials in the Central and Southern regions received supplementary irrigation in early to mid-summer (usually <0.5 ML ha^{-1}). Diseases that did affect the trials to varying degrees, due to their endemic nature in mono-cropped cane lands include *Pachymetra chaunorhiza* (root rot), root nematodes, common and/or orange rust and yellow-spot virus. These effects were monitored in the MegaGxE trials by soil sampling for *Pachymetra* and nematodes and by visual scoring for foliar disease at harvest or earlier. In each trial, other observations were made to be later used as explanatory variables: visual percentage scores for lodging, suckering, arrowing (flowering), stool-tipping (i.e. stool lodging), stalk breakage, rat damage and existence of gaps in plots; measurement of average length, diameter and single stalk fresh weight of the stalks taken for CCS determination (see below). Only the scores related to lodging at discussed in this paper.

All experiments were row-column (latinized in the column direction) designs with two replicates (three in the Ord). Plots were 4 rows by 10m long, with observations taken only on the two central rows. For many of the locations in the BSES FAT trials, the clones were actually split across two adjacent trials planted on the same day. This occurred for logistical reasons related to propagation, as one trial contained clones derived from selection within the region, while the other trial included new clones that had been introduced from other regions. Both trials contained check lines.

Just prior to the harvest of each plot area, a sub-sample of 8 sound stalks was hand-harvested from the observation rows. The remaining stalks were machine-harvested and their fresh mass determined by a weigh-bin to estimate TCH (tonnes of fresh cane per ha). The sub-sample was processed in a BSES or CSR laboratory to estimate sucrose concentration by fresh weight (CCS = commercial cane sugar) from observations of brix, pol and fibre, according to standard protocols, (REF??.)

In two of the MegaGxE trials (plant crops of H1 and H2, see Table 1), additional observations of stalk characteristics were made in 2000 (18^{th} April in H1 and 6^{th} April in H2). In each plot, a spring balance was attached to each of 5 stalks at 1.5m above the ground to determine the amount of horizontal force (kg) required to deflect a stalk by 20cm. The stalk diameter at 1.5m and the stalk height were also recorded.

11.5.5 Analysis

Variance components and standard errors were estimated for CCS and TCH for the effects of genotype and interactions with either environment (trial) or with the location, crop year (i.e. plant or ratoon 1, 2 or 3) and location x crop year effect.

Insert model etc here:

Random row and column:rep and residual effects were fitted to each environment, i.e. using a heterogenous error model. For both datasets, environments were regarded as fixed effects, as were regions, locations or crop years, when fitted. In the MegaGxE study, check genotypes and ones that had been identified as errors by the DNA analysis, were fitted as fixed effects. The effects for the remaining clones and their interactions were assumed to be random. Similarly for the FAT trials, clone effects were assumed to be random and those for environments fixed. BLUPs were computed for each clone across regions.

Finally, using the variance component estimates for each region, and the average residual trial errors for each region, repeatability was computed for both traits and each region:

Etc…

11.6. Results and Discussion

11.6.1 Trial yields and residual error variance

In the plant and 1st ratoon crops of both datasets, the TCH averaged close to 90 t ha^{-1} (Tables 1 and 2), with a similar range of mean trial TCH for each region. Within regions, the average CCS in the BSES FAT trials was 1.7 (plant crop) to 1.3 (1st ratoon) units higher than in the MegaGxE trials. Averaged across regions, much of the difference in CCS between the datasets seemed to be related to higher CCS in the Northern region. Recall that the clones in the BSES FAT trials vary between regions, so it seems that the Northern region BSES trials, in comparison to the MegaGxE trials, either contained a larger proportion of high CCS clones or, in general that the locations and harvest times were more favourable than for the MegaGxE. Direct comparison of the data means is not the major interest here, though it is useful to realise that the trials were sampling a similar diversity of yield performance conditions.

Table 4 shows the average trial error variances within regions (and across regions for the MegaGxE dataset) for TCH and CCS. Similar patterns of TCH error variance occurred across regions in both datasets (Tables 1, 2) and across trials (Fig. 1a) with the largest average values occurring in the highest yielding regions (Burdekin and NSW). The average trial error variance for CCS was greatest in the Burdekin, NSW and the Ord where the lowest CCS values were recorded (Tables 1, 2, Fig. 1b). The existence of these relationships for error variance would initially indicate that at TCH levels above 110 t ha^{-1} and CCS levels below about 13, there is an increased chance of encountering large residual variance, perhaps double the size of the mean of the dataset (Table 4). For any given TCH, there is a tendency for CCS to be greater in the BSES FAT trials than in the MegaGxE trials (Fig. 2).

While the data fits are similar for both datasets, there are a large number of high variance trials in the MegaGxE set that appear to be compensated by a similar number of lower yielding trials. Overall, we can say that, given similar experimental designs, we should expect similar mean yield/error relationships in both the early and late stages of selection. It has been well established that plot size (Jackson and McRae 2001) and associated inter-plot competition (Stringer and Cullis 2002) are important constraints on the precision of early-stage selection in sugarcane. For example, Jackson and McRae (2001) found that the genetic correlation between TCH in 1 row and 6 row plots was only 0.49, though the correlation for CCS was 0.91. While this is clearly an issue for selection, the data we show here suggest that there is no intrinsic difference in the error structure of early stage germplasm in comparison to later stage germplasm. This information is of use when estimating repeatabilities or variance components in quantitative genetic models to examine alternative selection strategies.

11.6.2 Genotypic variance within trials

While the relationships between residual trial variance and trial mean for either TCH or CCS seem to be rather similar for early and late stage trials, this is not the case for genotypic variance. In the MegaGxE trials, the genotypic variance of any single trial was correlated with the mean of the trial (Fig. 3a). The relationship was improved after removing the three harvests with highest genetic variance: S4, which was the shortest duration plant crop (Table 1) and the two harvests at W2 (Harwood) which is the coldest site and in which the plant crop was a 2 year crop. The

mean/variance relationship was only just significant for the BSES FAT trials, with a similar distribution of genotypic variance occurring for the entire range between 75 and 140 t ha^{-1}. While there was no obvious explanation for the high genetic variance in the BSES FATs at Macknade (Fig. 3a caption), the largest genetic variance in this dataset was also recorded for a two-year crop at Harwood. Obviously, the reduction in genotypic variance at the trial level was to be expected in comparing the datasets, given that the clones being tested in the BSES FATs have been through several stages of selection.

Of the 19 MegeGxE trials that yielded greater than the overall mean of the dataset (89.1 t ha^{-1}), the degree of lodging was greater than 30% in all but 5 of the trials (Fig. 2). Singh et al (2002) have demonstrated that lodging can reduce cane yields substantially in large cane crops. A preliminary study of possible selectable traits was made in two trials. In the H1 and H2 trials, the stem deflection force averaged 4.1 kg m^{-1} and 6.9 kg m^{-1}, respectively, with a correlation between the trials of 0.64. The phenotypic correlation between TCH and the stem deflection force was 0.65 (H1) and 0.53 (H2). In both trials, this correlation was greater than 0.7 if clones with less than average stalk numbers were dropped from the analysis (i.e. clones that may have had strong stalks simply because the stools had only initiated few stalks). Correlations of TCH with stem diameter and height were both positive, but small. The mean yields of these trials were not high (Table 1), so trial mean lodging scores were also relatively low at 2 and 13% respectively. However, in both trials the best 15 cultivars for TCH all had a stem deflection force of greater than the trial mean. Across trial correlations of TCH with other traits (such as suckering and arrowing) were generally insignificant and these traits are being further investigated within specific trials where trait expression was greatest (data not shown). These data show that mean TCH (Fig. 2) and also genetic variance for TCH (Fig. 1) may be partially related to lodging, and therefore that it should be possible to select clones with improved characteristics for performance under lodging conditions. In demonstrating the existence of poor correlations between single row and 6 rows plots, Jackson and McRae (2001) indicated that this effect could well be related to relative differences in the effects of lodging associated with plot size, i.e. in small plots, tall thin canes could dominate more sturdy types that could well be better yielding in pure stands. Here we have discussed only the association between trial yield and propensity to lodge leading to increased genotypic variance. Studies into the within trial genotypic variation and its association with degrees of lodging are ongoing.

For CCS, genetic variance increases as trial CCS decreases (Fig. 1b). Again the variance was generally larger in the MegaGxE trials, particularly as CCS decreased below about 14 or 15 units. The three largest variances for CCS were in high cane yielding trials in the Burdekin (B1 plant and B3 1st ratoon) and in the Ord (plant crop). When BLUPs were computed for each trial (data not shown) or region (Fig. 5), the values for TCH and CCS were not correlated, so the large variances observed at the extremes (high TCH, low CCS) in Fig. 3 were unlikely to be caused by the same genotypes for both traits.

11.6.3 Genotype and Genotype by environment effects within and between regions

Within each region, for both TCH and CCS, the genotypic variance component was larger in the MegaGxE dataset compared with the BSES FATs (Table 5). For TCH, the genotypic variance in the FAT trials was, on average, 41% of that in the Mega trials, while for CCS, this figure was 60%. Similar ratios exist (slightly higher for TCH) when comparing the sum of G and GE for the two sets of trials. These results would be expected, given that the entries in the BSES FATs had already undergone both family selection (in small plots in one location within a region) and preliminary selection in 2 row plots in one or two locations. However, for TCH there was greater variability between regions for these dataset ratios when compared with CCS (Table 5). Notably, for the Burdekin and Central regions, the G variance component of the FAT trials was only about 20% of that in the Mega trials, while for the Herbert it was 70% and for other regions, between 40 and 53%, i.e. there was relatively less G or G+GE variance for TCH in later stage trials

(FATs) in the Burdekin and Central regions. This could indicate a stronger degree of selection pressure on the clones for TCH in these regions (and lower selection in the Herbert), though this cannot be confirmed here, given that the FAT trial entries are not directly derived from the Mega trial entries. For CCS, the most notable observation with regard to the dataset comparisons is that the G variance component ratio was relatively larger for NSW, although it also had the lowest G variance in the Mega trial dataset.

A large ratio of genotypic to genotype by environment interaction variance indicates that GE is less likely to complicate the ranking of genotypes and that 'average' TCH (or CCS) from a sample of trials will be a good indicator of future relative genotype performance. During selection for broad adaptation (i.e. by averaging data over trials within a region), this ratio will tend to decrease as the genetic variance is reduced, assuming that genotype by environment interactions (specific adaptation) will become more evident. On average and within each region (except South), this effect was apparent for TCH where G/GE was larger in the Mega trials compared with the FAT trials, and to the greatest degree in the Burdekin and Central regions. In contrast, the average G/GE ratio for CCS was the same in both datasets, though it varied between regions. In Central, South and NSW, the ratio decreased substantially, with small increases in the North and Herbert region and a substantial increase in the Burdekin, i.e. in the Burdekin FAT trials, almost all genetic variation for CCS was associated with the main effect of genotype, and the GE component was relatively small.

11.6.4 Repeatability

Fig. 6 demonstrates the integrated effect of the genetic (Table 5) and experimental (Table 4) sources of variation on the repeatability (h^2) of TCH and CCS within each dataset and region. A high h^2 is needed if a strong response to selection is to be realised. Considering TCH, the h^2 for all regions was greater in the Mega trials than the FAT trials. The difference was greatest when computed for only one site, and with six sites, the difference between the datasets was not as great, especially if the Central data in the BSES trials was ignored. In the FAT trials, there were relatively small differences between regions for h^2, excepting the low values for Central. The highest h^2 in the Mega trials were in the Herbert and Burdekin, the lowest in the North and South, with Central and NSW being intermediate. Given high genetic correlations between regions, this would indicate that the Herbert and Burdekin are the best regions in which to evaluate TCH in early stage selection, while any region except Central would be better in late stages of selection, and four sites would double the repeatability compared with one site. The increment in h^2 with crop year was generally less in the Mega dataset compared with the FAT trials, though in both datasets, the was relatively little increment in h^2 when site number was increased from four to six.

For CCS h^2, there was again only one poor region (NSW), and only a small difference between using 2 vs 3 crop years or 4 vs 6 sites. However, h^2 for NSW was relatively high in the Mega dataset (especially when 4 to 6 sites were used), with the Burdekin being the poorest region for h^2, and Central and South being the best. The Herbert and North were intermediate.

In the case of CCS, the ranking of h^2 in each dataset was strongly associated with experimental error (Table 4). Therefore minimising experimental error (cf GE interaction) is most important to obtain high repeatability for this trait. There is an advantage of having two or more sites and crop-years, especially in the later stage of selection. For TCH, the influence of the ratio of G/GE variance was more important in determining the h^2 than was experimental error. Compared to other sites, Central had a relatively low genotypic variance for TCH in the FAT trials (and low h^2) while the Herbert and Burdekin sites had relatively lower variances for Genotype by Crop Year effects in particular.

11.6.5 Further discussion being written

11.7. Acknowledgments

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11.8. References

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Table 1 For the MegaGxE dataset, trial locations, planting and harvest dates for plant and ratoon (R) crops, fresh cane yield (TCH = 'tonnes cane per ha') and commercial sugar content (CCS %). There were 24 locations used and 54 harvests (trials).

Region	*Location*	*Trial code*	*Number of clones*	*Planting date*	*Plant crop harvest*	*1st R harvest*	*2nd R harvest*	*TCH Plant*	*1st R*
North	Silkwood	N1	48	01/08/2001	07/10/2002	20/10/2003		82	81
	Tully BSES	N2	48	18/06/2000	20/09/2001	18/11/2002	30/10/2003	65	115
	Arriga (Tablelan d north)	N3	48	04/05/2000	14/06/2001	27/06/2002		119	126
	Mulgrave	N4	48	21/05/2001	17/07/2002	23/08/2003		76	73
	Babinda	N5	48	09/07/2001	06/09/2002	15/09/2003		99	112
	Atherton (Tablelan d south)	N6	48	25/05/2000	29/08/2001	07/10/2002		66	72
	Average							85	97
Herbert	Ingham BSES	H1	56	29/06/1999	31/08/2000	06/09/2001		58	48
	Abergowrie CSR	H2	56	24/06/1999	07/08/2000	17/09/2001	12/11/2002	75	93
	Mutarnee BSES	H3	56	01/06/2000	14/06/2001	22/08/2002	18/08/2003	102	59
	Macknade CSR	H4	48	06/07/2000	17/09/2001	04/11/2002	29/09/2003	71	90
	Average							77	73
Burdekin	Ayr BSES	B1	48	05/05/1999	26/07/2000	19/07/2001	08/08/2002	130	141
	Kalamia CSR	B2	54	07/05/1999	24/07/2000	17/07/2001		164	117
	Brandon BSES	B3	48	18/05/2001	17/06/2002	12/06/2003	7/6/2004	123	112
	Clare	B4	45	04/04/2002	08/09/2003	21/09/2004		157	105

	Average							144	123
Central	Baker's Creek	C1	48	09/06/1999	19/09/2000	26/09/2001	01/10/2002	89	68
	Proserpine	C2	48	25/08/1999	14/09/2000	29/08/2001		64	55
	Marian	C3	48	11/08/2000	04/09/2001	10/10/2002	24/10/2003	60	94
	Plane Creek	C4	48	24/08/2000	10/10/2001	01/10/2002	15/10/2003	68	34
	Average							70	63
South	Bundaberg	S1	48	08/09/1999	07/09/2000	13/09/2001	08/09/2002	86	100
	Maryborough	S3	36	30/08/2000	01/11/2001	31/10/2002	27/11/2003	82	67
	Isis	S4	42	03/09/2002	23/07/2003	3/8/2004		52	47
	Average							73	71
NSW	Condong	W1	48	16/09/1999	03/08/2000	15/10/2001		83	112
	Harwood	W2	48	22/10/1999	17/08/2001	13/10/2002		121	153
	Average							102	133
Ord	Kununurra	O1	35	31/05/2001	10/07/2002	15/09/2003		148	110
All trials	*Average*							93	91

Table 2 For the BSES FAT (Final Assessment Trials) for harvests in 2001 (plant) and 2002 (1st ratoon (R)) seasons: location, planting and harvest dates, number of entries and mean tonnes cane per ha (TCH) and commercial cane sugar (CCS). * indicates locations where clones were planted in two adjacent trials (on the same date).

Region	Location	Number of clones	Planting date	Plant harvest	1st R harvest	TCH Plant	TCH 1st R	CCS Plant	CCS 1st R
North	Babinda	100	17/07/2000	23/08/2001	27/08/2002	58	90	16.4	16.5
	Gordonvale	96	16/06/2000	20/08/2001	19/08/2002	104	75	17.2	17.0
	Mourilyan	96	24/07/2000	8/10/2001	2/10/2002	84	101	17.7	17.1
	Sth. Johnstone	90	26/05/2000	28/08/2001	17/09/2002	75	93	15.3	17.0
	Tully	98	31/07/2000	19/09/2001	5/11/2002	98	114	15.6	16.7
	Average					84	95	16.4	16.9
Herbert	Abergowrie	64	8/06/2000	1/10/2001	29/08/2002	99	112	16.8	14.5
	Bambaroo*	110	6/06/2000	29/08/2001	5/08/2002	92	75	16.1	16.1
	Coldwater*	90	1/08/2000	8/09/2001	3/09/2002	82	87	16.9	15.3
	Ingham*	98	20/07/2000	4/09/2001	7/10/2002	90	104	16.5	15.9
	Macknade	98	25/07/2000	13/09/2001	23/09/2002	56	96	17.0	15.6
	Average					84	95	16.6	15.7
Burdekin	Ayr*	112	19/05/2000	7/09/2001	17/09/2002	134	139	15.5	15.5
	Brandon*	108	23/05/2000	10/07/2001	2/07/2002	130	132	14.6	13.4
	Clare*	96	23/08/2000	24/09/2001	25/09/2002	78	109	16.9	16.5
	Average					114	127	15,7	15.1
Central	Bakers Creek*	70	21/07/2000	26/09/2001	27/10/2002	76	83	17.1	17.8
	Farleigh*	126	8/06/2000	26/07/2001	23/08/2002	76	80	15.1	17.0
	Marian	71	10/08/2000	3/09/2001	14/10/2002	86	104	15.2	15.8
	Mirani*	132	13/09/2000	10/09/2001	18/07/2002	37	51	16.0	16.0
	Oakenden	36	18/08/2000	21/09/2001	3/10/2002	91	66	15.5	17.2
	Sarina	62	23/08/2000	11/10/2001	22/10/2002	72	80	17.5	17.9

	Average					73	77	16.1	17
South	Bingera*	112	8/03/2000	9/07/2001	22/07/2002	97	46	14.3	15.0
	Bundaberg*	114	16/03/2000	15/08/2001	31/07/2002	124	69	13.8	14.4
	Childers*	112	16/08/2000	15/10/2001	16/08/2002	78	101	15.2	14.2
	Maryborough*	112	23/08/2000	1/11/2001	30/10/2002	84	75	15.3	16.3
	Average					96	73	14.7	15
NSW	Broadwater*	110	30/09/1999	12/10/2001	23/10/2002	113	105	14.4	13.3
	Harwood*	104	2/12/1999	24/08/2001	12/08/2002	126	67	11.0	9.9
	Average					120	86	12.7	11.6
All Trials	*Average*					90	90	15.7	15.7

Table 3 Pedigree of clones used in the MegaGxE dataset and number of trials (of 54) in which they were harvested. 'Q' canes are commercially released while the other clones were randomly selected from random crosses (one clone per cross) in either the CSR Limited or BSES Limited (95H) breeding programs. Three additional random clones were planted in several Herbert trials, and, in fewer than five trials, up to six additional Q canes were planted.

Clone	Female parent	Male parent	Number of trials	Clone	Female parent	Male parent	Number of trials
84-255-10	MQ57-728	CASSIUS	13	95H4018	Q179[A]	CP74-2005	54
84-608-3	MQ67-494	Unknown	54	95H4020	80N1042	77N405	54
84-608-6	MQ67-494	Unknown	43	95H4021	80N4350	MQ75-1000	39
86-1151-3	H56-752	66C760	49	95H4022	80N4422	74C82	52
87-105-10	MQ55-2160	POLYCROSS	37	95H4023	81N289	77N676	51
88-271-6	MQ73-584	H49-3666	51	95H4024	82N300	73C214	48
89-393-3	MQ80-968	POLYCROSS	51	95H4027	84N4500	78F1025	55
89-503-10	PELORUS	MQ79-1123	49	95H4028	85N774	88B78	46
89-518-6	GEMINI	MQ57-540	11	95H4029	85N799	84C275	38
89-680-6	CENTAUR	MQ77-281	54	95H4030	85N2169	79N587	52
90-110-1	TS68-830	MQ79-141	36	95H4032	86N1833	83N976	46
90-110-9	TS68-830	MQ79-141	47	95H4033	88N5000	79N1283	29
90-77-2	CP70-1547	TS64-375	52	95H4035	Q96	85N2522	38
90-77-5	CP70-1547	TS64-375	19	95H4037	Q115	82N238	46
90-83-5	MQ68-203	MQ79-212	37	95H4038	Q117	MEX59-1828	51
95H4001	78A383	90N6006	57	95H4039	Q120	VMC67-315	44
95H4003	88B71	83N947	52	95H4040	Q125	Q165	54
95H4004	ARRIS	85N511	57	95H4044	Q138	F168	52
95H4005	73C214	87S7427	42	95H4046	Q160	71C413	54
95H4006	75C87	75C553	44	95H4047	R573	85N1647	45
95H4007	83C623	86A3050	54	95H4048	81S1049	Q170	57
95H4008	83C627	79N96	49	Q117	Q77	58N829	56
95H4010	F177	Q135	65	Q124	NCO310	54N7096	57
95H4012	H52-663	Q161	48	Q135	NCO310	54N7096	57
95H4013	M1819-63	Q142	19	Q138	58N829	66N2008	57
95H4016	Q167[A]	87S7181	19	Q141	NCO310	54N7096	43
95H4017	77N557	76N1544	13	Q165	Q117	CP33-372	43

Table 4 For regions in two datasets, estimates of trial residual variance components for TCH (t2 ha-1) and CCS (%2). In the GxE analysis within and across regions, a heterogeneous error model was used (i.e. each trial was fitted). These data are the average trial residual error variance and standard deviation of that value (in italic font) from individual analyses of each trial. These can be approximately used in repeatability calculations together with data in Table 5.

Trait and region	MegaGxE		BSES FATs	
TCH				
North	161	*81*	112	*37*
Herbert	107	*46*	164	*59*
Burdekin	426	*146*	250	*88*
Central	112	*67*	122	*52*
South	142	*80*	96	*31*
NSW	409	*291*	513	*383*
Ord	186	*36*		
(average)	194	*159*	173	*157*
CCS				
North	0.88	*0.40*	0.48	*0.18*
Herbert	0.62	*0.32*	0.50	*0.32*
Burdekin	1.56	*0.78*	1.03	*0.72*
Central	0.38	*0.17*	0.55	*0.29*
South	0.35	*0.17*	0.35	*0.21*
NSW	0.47	*0.15*	1.24	*0.86*
Ord	3.03	*1.47*		
(average)	0.81	*0.72*	0.61	*0.47*

Table 5 For regions in two datasets, variance components for TCH (t2 ha-1) and CCS (%2) for effects of genotype (Gen, G) and genotype interaction with Site, Crop year (plant, 1st, 2nd ratoon) or Site and Crop year. For the MegaGxE dataset, where the same genotypes were grown in all regions, variance components are also estimated for all regions combined. G/GE is the ratio of the Genotypic variance to the sum of the interaction variances. Averages for variance components and G/GE ratio are given (excluding the Ord where only one site was grown), as are ratios for G and G + GE between the FAT and Mega trials. Standard errors are given in italic font.

Trait and site	Mega GxE									BSES FATs								Ratio of G	Ratio of G + GE
	Gen		G:Site		G:Crop		G:Site:Crop		G/GE	Gen		G:Site		G:Crop		G:Site:Crop		G/GE	FATs/ Mega	FATs/ Mega
TCH																				
North	136	*36*	20	*7*	131	*17*	19	*10*	0.80	60	*12*	35	*7*	27	*6*	23	*6*	0.71	0.44	0.47
Herbert	131	*28*	10	*6*	21	*7*	39	*9*	1.84	93	*19*	44	*9*	32	*8*	18	*7*	0.99	0.71	0.93
Burdekin	226	*53*	31	*19*	56	*23*	0	*0*	2.59	47	*13*	34	*11*	3	*6*	4	*10*	1.15	0.21	0.28
Central	93	*25*	23	*7*	46	*9*	23	*8*	1.02	17	*5*	34	*6*	8	*3*	6	*5*	0.35	0.18	0.35
South	107	*39*	24	*9*	108	*25*	0	*0*	0.81	57	*11*	36	*5*	15	*4*	7	*4*	0.98	0.53	0.48
NSW	245	*89*	29	*31*	161	*59*	0	*0*	1.29	99	*27*	0	*0*	0	*0*	95	*27*	1.04	0.40	0.45
Ord	785	*268*																		
ALL	178	*32*	21	*4*	97	*7*	13	*5*	1.36											
(average)	156		23		87		14			62		31		14		26		0.87	0.41	0.49
CCS																				
North	0.88	*0.20*	0.01	*0.03*	0.29	*0.06*	0.27	*0.07*	1.57	0.47	*0.07*	0.11	*0.03*	0.03	*0.02*	0.10	*0.03*	2.00	0.53	0.49
Herbert	0.79	*0.17*	0.00	*0.03*	0.17	*0.04*	0.18	*0.05*	2.22	0.46	*0.07*	0.10	*0.02*	0.04	*0.02*	0.04	*0.02*	2.49	0.58	0.56
Burdekin	0.89	*0.26*	0.29	*0.15*	0.50	*0.17*	0.30	*0.17*	0.81	0.56	*0.10*	0.16	*0.04*	0.00	*0.00*	0.00	*0.00*	3.50	0.63	0.36
Central	1.00	*0.22*	0.00	*0.00*	0.01	*0.03*	0.26	*0.04*	3.59	0.59	*0.08*	0.15	*0.03*	0.04	*0.02*	0.03	*0.02*	2.63	0.59	0.64
South	0.91	*0.21*	0.00	*0.00*	0.13	*0.05*	0.11	*0.04*	3.88	0.46	*0.07*	0.02	*0.02*	0.01	*0.02*	0.24	*0.03*	1.71	0.51	0.63
NSW	0.74	*0.19*	0.00	*0.00*	0.00	*0.00*	0.44	*0.09*	1.67	0.56	*0.14*	0.22	*0.09*	0.13	*0.07*	0.09	*0.07*	1.28	0.76	0.85
Ord	0.90	*0.70*																		

ALL	0.86	*0.14*	0.00	*0.01*	0.26	*0.03*	0.29	*0.03*	1.58							
(average)[1]	0.87		0.05		0.18		0.26		1.76	0.52	0.13	0.04	0.08	2.27	0.60	0.59

[1] Exc. Ord

Figure captions

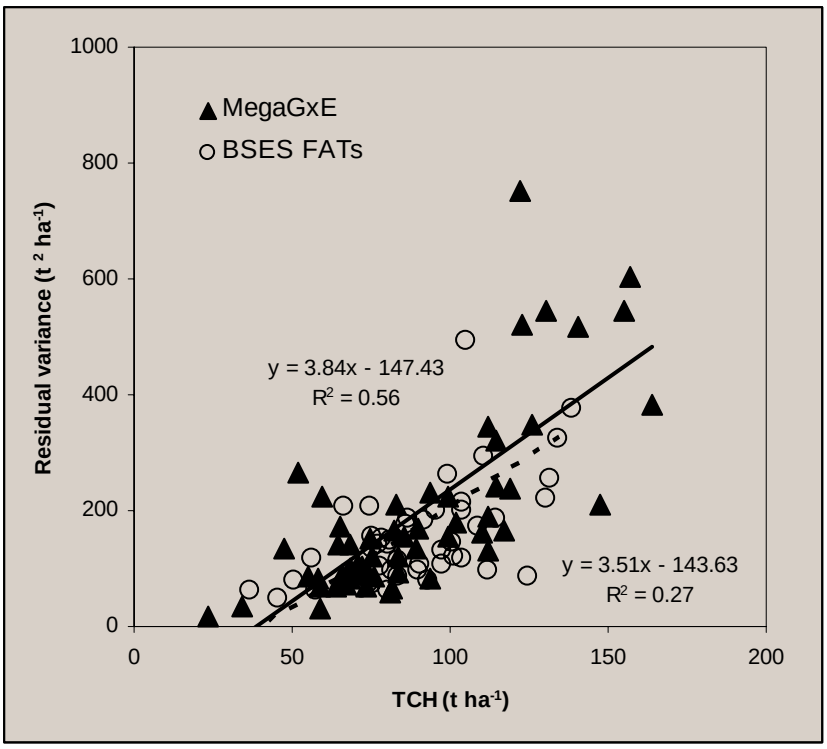
Fig. 1. For both datasets, from single trial analyses, trial mean versus estimated residual variance for (a) TCH and (b) CCS. Linear regressions are fitted with no outlier trials removed. At significance of $p = 0.05$ and $n = 50$; significant $r = 0.27$, i.e. $r^2 = 0.07$.

Fig. 2. Mean CCS against mean TCH for each trial in both datasets.

Fig. 3 For each dataset, (a) trial mean TCH against estimated genetic variance after removal of 3 outliers each in MegaGxE (S4 plant crop (52 t ha^{-1}, 433 t^2 ha^{-2}); W2 plant (123 t ha^{-1}, 1042 t^2 ha^{-2}) and 1st ratoon (155 t ha^{-1}, 804 t^2 ha^{-2})) and in BSES FATs (Macknade plant (56 t ha^{-1}, 269 t^2 ha^{-2}) and ratoon (96 t ha^{-1}, 435 t^2 ha^{-2}) and Harwood plant (128 t ha^{-1}, 830 t^2 ha^{-2})) and (b) data for CCS with no outliers removed.

Fig. 4 For each harvest in the MegaGxE dataset, lodging scores (% of plants lodged) against total cane yield (t ha-1). Trials excluded as in Fig. 1 and not recorded for two other trials (1st ratoons in N4 and O1, see Table 1). The dotted line is the mean trial yield for the entire dataset.

Fig. 5 BLUP estimates for CCS plotted against those for TCH for each region within the two datasets. None of the correlations are significant.


MegaGxE
BSES FATs
Residual variance (t ² ha-1)
TCH (t ha-1)
y = 3.84x - 147.43
R2 = 0.56
y = 3.51x - 143.63
R2 = 0.27
0
200
400
600
800
1000
0
50
100
150
200

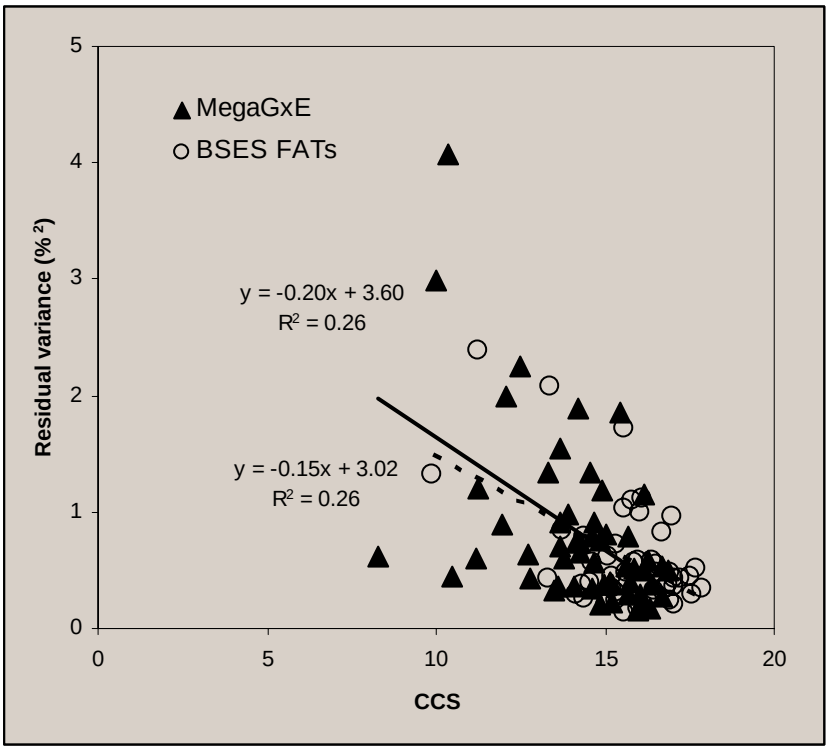

MegaGxE
BSES FATs
Residual variance (% ²)
CCS
y = -0.20x + 3.60
R2 = 0.26
y = -0.15x + 3.02
R2 = 0.26
0
1
2
3
4
5
0
5
10
15
20

Fig. 1 a and b

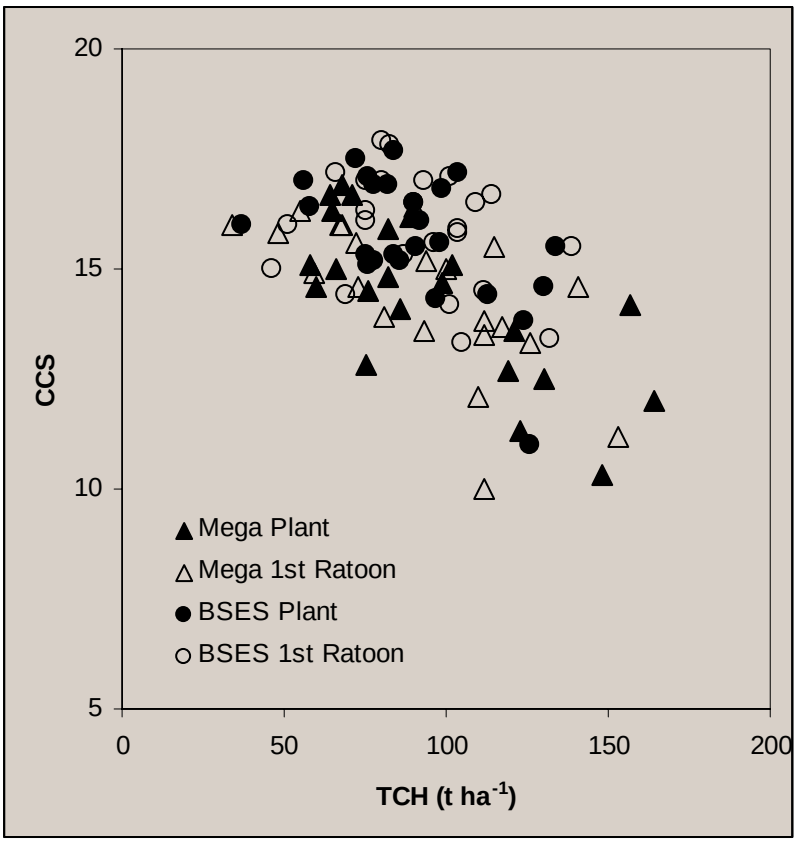

20
15
10
5
CCS
0
50
100
150
200
TCH (t ha-1)
Mega Plant
Mega 1st Ratoon
BSES Plant
BSES 1st Ratoon

Fig. 2

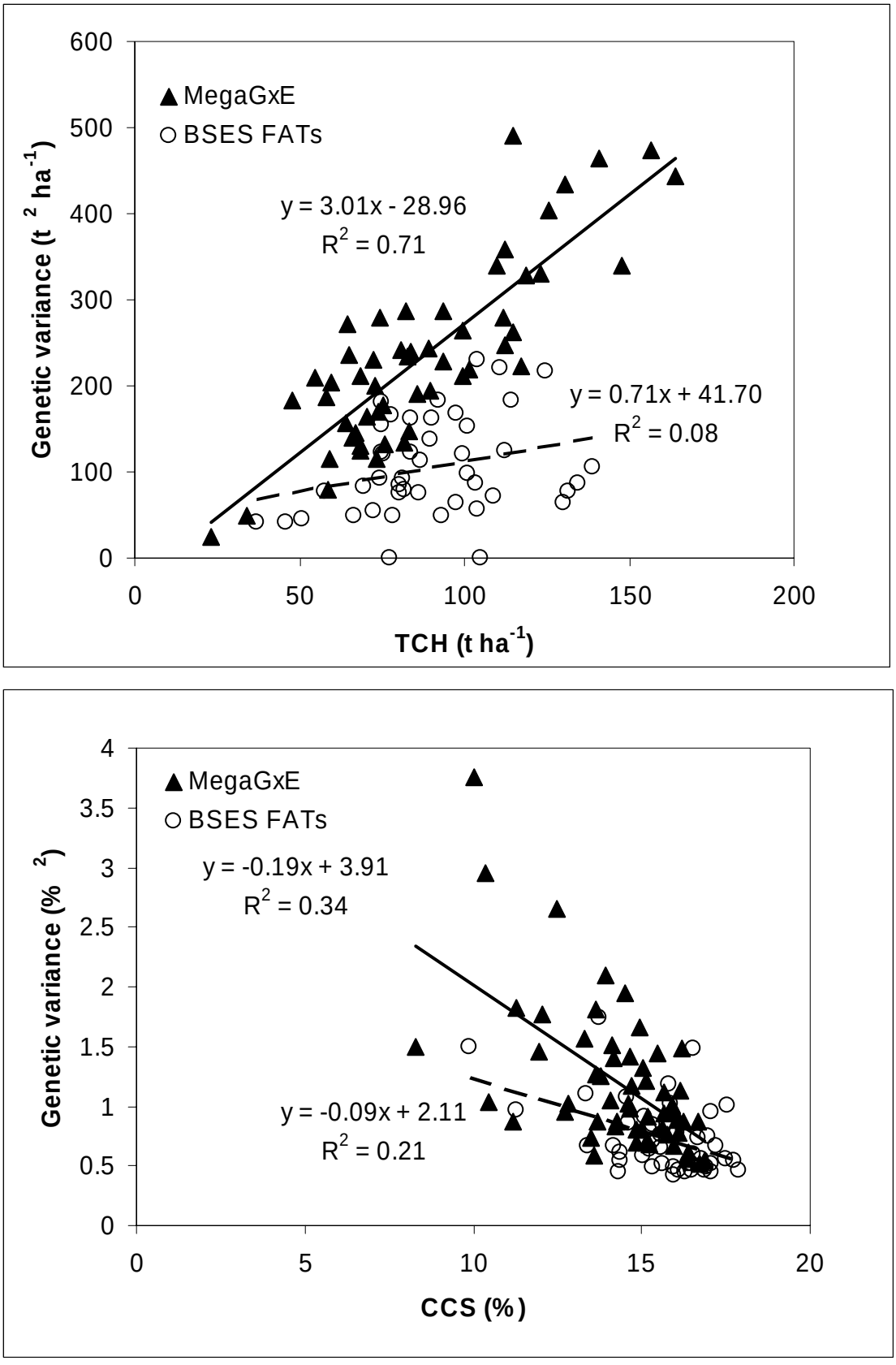

MegaGxE
BSES FATs
y = 3.01x - 28.96
R2 = 0.71
y = 0.71x + 41.70
R2 = 0.08
Genetic variance (t 2 ha-1)
TCH (t ha-1)
0
100
200
300
400
500
600
0
50
100
150
200
MegaGxE
BSES FATs
y = -0.19x + 3.91
R2 = 0.34
y = -0.09x + 2.11
R2 = 0.21
Genetic variance (% 2)
CCS (%)
0
0.5
1
1.5
2
2.5
3
3.5
4
0
5
10
15
20

Fig. 3 a and b

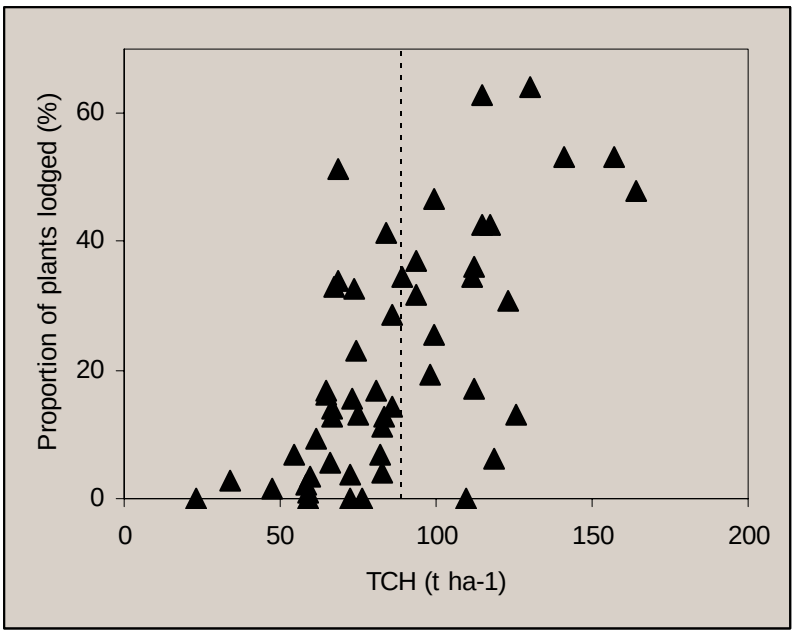
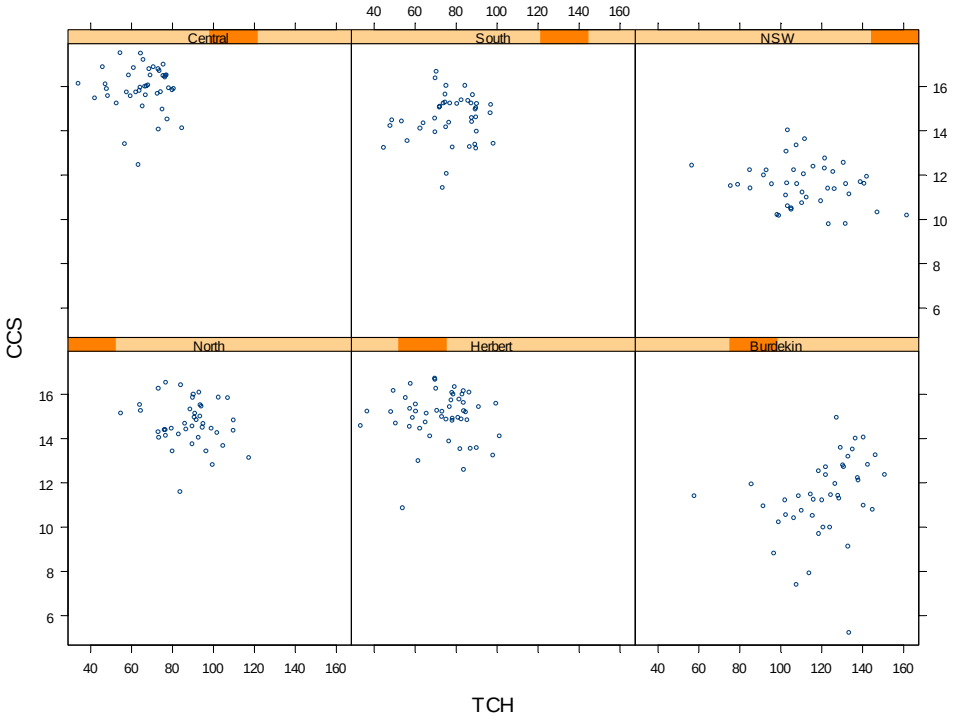

Proportion of plants lodged (%)
60
40
20
0
0
50
100
150
200
TCH (t ha-1)

Fig. 4

(a) MegaGxE



(b) BSES FATs

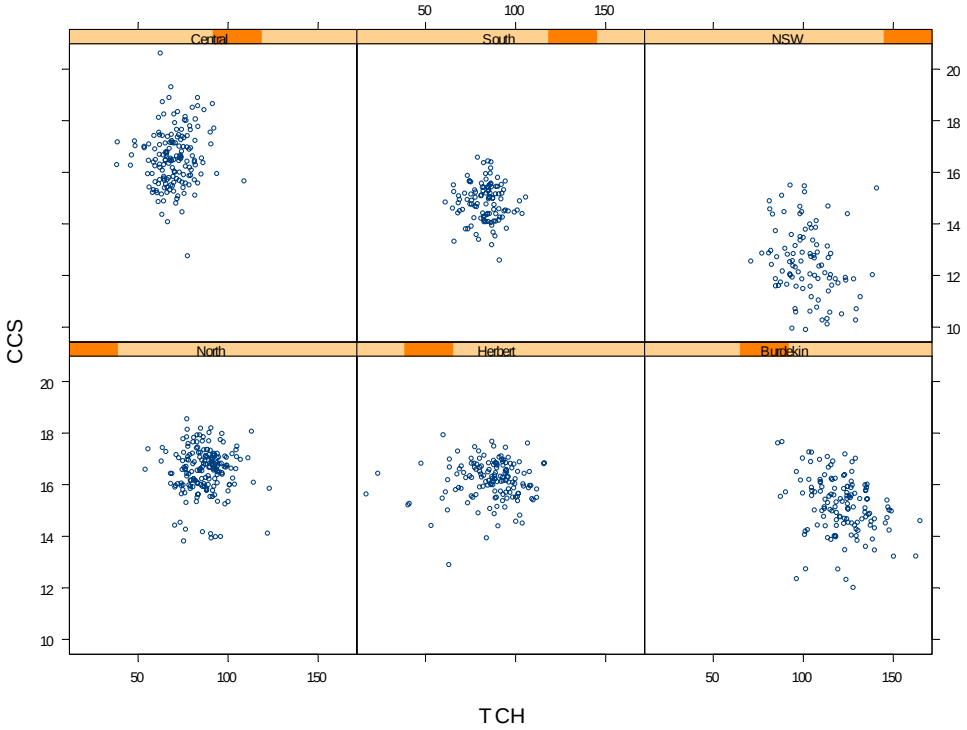


Fig 5

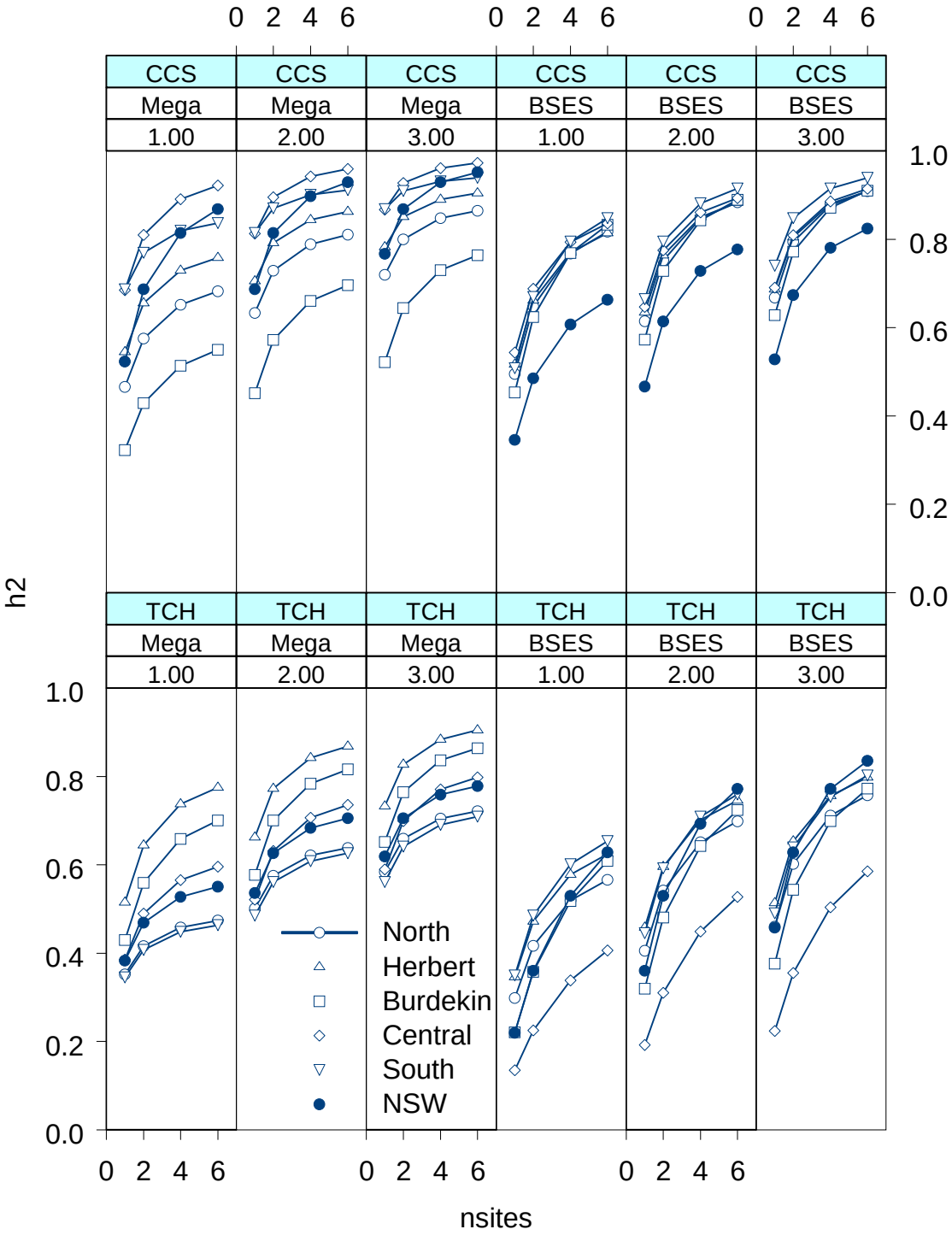

CCS
Mega
1.00
CCS
Mega
2.00
CCS
Mega
3.00
CCS
BSES
1.00
CCS
BSES
2.00
CCS
BSES
3.00
TCH
Mega
1.00
TCH
Mega
2.00
TCH
Mega
3.00
TCH
BSES
1.00
TCH
BSES
2.00
TCH
BSES
3.00
h2
nsites
0 2 4 6
0.0
0.2
0.4
0.6
0.8
1.0
North
Herbert
Burdekin
Central
South
NSW

Fig. 6

Appendix 12. Collation and analysis of regional clone results from BSES-FATs series 2000

In this project, our objective was particularly to examine the characteristics of data collected on unselected clones across the industry. Part of our interest was to therefore compare the analyses of this data against collected data from selected clones, i.e. at later stages of the selection process. This has implications for how the genetic parameters might be used for further simulation of alternative breeding program scenarios. However, after collation of prior published and internal analyses, it was apparent that there had been few attempts to conduct this type of analysis in all of the regions. Therefore, when Allan Rattey joined the project in 2001, he collated a large dataset from the BSES final assessment trials (FATs) that were harvested in 2001 and 2002 to coincide with major seasons of the CTA028 harvests. These are final assessment trials for clones that have been heavily selected as described in the introduction (i.e. about 100 clones from an original set of ca. 25 000 seedlings) for performance within the region. Across regions these trials have in common only a small number of check and test clones. These data provided useful 'within-region' estimates of variance components, given selected clones, cf. 'unselected clones' as used in our experiments (see below).

12.1. Methodology

12.1.1. Propagation and harvest times

The BSES FATs were grown as part of the normal breeding program within each region, and so germplasm for these had been propagated prior following selection in regional PATs and CATs. The results have been collated from trials planted in 2000 and harvested as plant (2001) and 1st ratoon (2002) crops. In NSW, the crops were planted in late 1999 and grown through to a 2nd year before the plant harvest in 2001 and 1st ratoon in 2002.

12.1.2. Locations and germplasm

For this dataset, 52 harvests were taken in 2001 and 2002 only, over 26 locations (Table 12-1). While the BSES-FATs and MegaGxE have several site names in common, these names refer to the nearest locality and trials with the same site name may not have been planted in the same field and managed exactly the same way. Hence, the comparison of results from MegaGxE with the FATs should be constrained to the regional level (i.e. to compare relative magnitude of variances) rather than as direct site comparisons or direct estimates of average performance in any region, i.e. in both datasets, the trials are regarded as 'samples' of the production environment within each region.

In the FAT experiments, the clone sets differed among regions, depending on the selection history with little overlap between regions apart from some check genotypes (details not presented here). About 90 clones were grown in most of the trials, with check genotypes (cultivars- Q canes) used as the best adapted cultivars within each region.

12.1.3. Management and monitoring

These trials were grown on experiment stations and grower's properties and were managed in a way similar to the MegaGxE trials (see below). While data on diseases etc were collected for the original purposes in each region (i.e. selection of clones for potential release), these data vary with region and were not collated as part of the dataset. In the MegaGxE these data were collected using consistent protocols (see below).

12.1.4. Design

All experiments were row-column (latinized in the column direction) designs with two replicates Plots were 4 rows by 10m long, with observations taken only on the two central rows. For many of the locations in the BSES FAT trials, the clones were actually split across two adjacent trials planted on the same day to limit bias due to field variation. Both trials contained the same check cultivars and were harvested on the same day.

12.1.5. Measurements

Just prior to the harvest of each plot area, a sub-sample of 6 sound stalks was hand-harvested from the observation rows. The remaining stalks were machine-harvested and their fresh mass determined by a weigh-bin to estimate TCH (tonnes of fresh cane per ha). The sub-sample was processed in a BSES or CSR laboratory to estimate sucrose concentration by fresh weight (CCS = commercial cane sugar) from observations of brix and pol, according to standard protocols. Fibre content used during CCS analysis were generally an estimate based on previous within region and crop class history. Analysis methods were the same as for the MegaGxE 'within-region' analysis. For the BSES-FATs we estimated variance components and correlations (within regions) as described for the MegaGxE.

12.1.6. Data analysis

As for the CTA028 trials (Appendix 3), clone effects were assumed to be random and those for environments fixed. Best Linear Unbiased Predictors (BLUPs) were computed for each clone within regions. These are effectively 'means' that have been weighted by the precision of the trials.

Models 1 and 2 of Appendix 3 were applied to these data to compute within region variance component estimates for genotype effects and their interactions with environments (site, crop-year and site by crop-year). This enabled comparison of the relative sizes of within region variance components for clones having undergone prior selection, cf. the project trials where no selection had been performed.

12.2. Results

For CCS, the relative sizes of the variance components for Gen and Gen:Env were similar across regions (Table 12-2). On average Gen was 3 times the size of GxE for CCS. This multiplier was 2 times, when the GxE was extended into location, crop class and location by crop class interactions with genotype (this model was also a better fit to the data). Apart from the South, most of the GxE was derived from interactions of Gen with location or crop class. In the South the 3-way interaction dominated.

In the case of TCH, GxE was relatively less than G (ratio of 1.4 for G/GxE) in all regions except Central, where a small G was observed in these two years. The G main effect was relatively greater in the Herbert and NSW regions in this dataset, and GxLocation was the most important interaction except in NSW where the 3-way interaction was the largest. G:Crop effects were greatest in the North and Herbert regions.

These results indicate that interactions with site and crop class are more important in contributing to clonal yields for TCH than for CCS. Within-region G and GxE effects were correlated across regions for TCH ($r = 0.81$), but not for CCS ($r = -0.56$).

The implications from these results are that it is more important to sample additional locations and years when comparing clones for TCH than for CCS.

Table 12-1 For the BSES FAT (Final Assessment Trials) for harvests in 2001 (plant) and 2002 (1st ratoon (R)) seasons: location, planting and harvest dates, number of entries and mean tonnes cane per ha (TCH) and commercial cane sugar (CCS). * indicates locations where clones were planted in two adjacent trials (on the same date).

Region	Location	Number of clones	Planting date	Plant harvest	1st R harvest	TCHPlant		CCS	
							1st R	Plant	1st R
North	Babinda	100	17/07/2000	23/08/2001	27/08/2002	58	90	16.4	16.5
	Gordonvale	96	16/06/2000	20/08/2001	19/08/2002	104	75	17.2	17.0
	Mourilyan	96	24/07/2000	8/10/2001	2/10/2002	84	101	17.7	17.1
	Sth. Johnstone	90	26/05/2000	28/08/2001	17/09/2002	75	93	15.3	17.0
	Tully	98	31/07/2000	19/09/2001	5/11/2002	98	114	15.6	16.7
	Average					84	95	16.4	16.9
Herbert	Abergowrie	64	8/06/2000	1/10/2001	29/08/2002	99	112	16.8	14.5
	Bambaroo*	110	6/06/2000	29/08/2001	5/08/2002	92	75	16.1	16.1
	Coldwater*	90	1/08/2000	8/09/2001	3/09/2002	82	87	16.9	15.3
	Ingham*	98	20/07/2000	4/09/2001	7/10/2002	90	104	16.5	15.9
	Macknade	98	25/07/2000	13/09/2001	23/09/2002	56	96	17.0	15.6
	Average					84	95	16.6	15.7
Burdekin	Ayr*	112	19/05/2000	7/09/2001	17/09/2002	134	139	15.5	15.5
	Brandon*	108	23/05/2000	10/07/2001	2/07/2002	130	132	14.6	13.4
	Clare*	96	23/08/2000	24/09/2001	25/09/2002	78	109	16.9	16.5
	Average					114	127	15.7	15.1
Central	Bakers Creek*	70	21/07/2000	26/09/2001	27/10/2002	76	83	17.1	17.8
	Farleigh*	126	8/06/2000	26/07/2001	23/08/2002	76	80	15.1	17.0
	Marian	71	10/08/2000	3/09/2001	14/10/2002	86	104	15.2	15.8
	Mirani*	132	13/09/2000	10/09/2001	18/07/2002	37	51	16.0	16.0
	Oakenden	36	18/08/2000	21/09/2001	3/10/2002	91	66	15.5	17.2
	Sarina	62	23/08/2000	11/10/2001	22/10/2002	72	80	17.5	17.9
	Average					73	77	16.1	17

Region	Location	Number of clones	Planting date	Plant harvest	1st R harvest	TCHPlant	1st R	CCS Plant	1st R
South	Bingera*	112	8/03/2000	9/07/2001	22/07/2002	97	46	14.3	15.0
	Bundaberg*	114	16/03/2000	15/08/2001	31/07/2002	124	69	13.8	14.4
	Childers*	112	16/08/2000	15/10/2001	16/08/2002	78	101	15.2	14.2
	Maryborough*	112	23/08/2000	1/11/2001	30/10/2002	84	75	15.3	16.3
	Average					96	73	14.7	15
NSW	Broadwater*	110	30/09/1999	12/10/2001	23/10/2002	113	105	14.4	13.3
	Harwood*	104	2/12/1999	24/08/2001	12/08/2002	126	67	11.0	9.9
	Average					120	86	12.7	11.6
All Trials	*Average*					90	90	15.7	15.7

Table 12-2 For CCS and TCH in each region of the BSES FATS-2000 series, variance components for two random effects models (Genotype main effect + GxE interaction and Gen+Gen:Site + Gen:Crop class + Gen:Site:CropClass). Environments were fixed in the model.

Trait	*Region*	*Gen*	*Gen:Env*	*G/GxE*	*G/(G+GxE)*
CCS	North	0.53	0.19	2.70	0.73
	Herbert	0.49	0.16	3.05	0.75
	Burdekin	0.61	0.13	4.85	0.83
	Central	0.65	0.18	3.54	0.78
	South	0.46	0.27	1.68	0.63
	NSW	0.67	0.28	2.41	0.71
	avg	*0.57*	*0.20*	*2.80*	*0.74*
TCH	North	78.01	67.73	1.15	0.54
	Herbert	122.50	73.89	1.66	0.62
	Burdekin	57.42	31.10	1.85	0.65
	Central	26.47	38.45	0.69	0.41
	South	69.26	44.52	1.56	0.61
	NSW	106.31	97.49	1.09	0.52
	avg	*59.04*	*42.65*	1.38	0.58

		Gen	*G:Loc*	*G:Crop*	*G:Loc:Crop*	G/GxE	G/(G+GxE)
CCS	North	0.45	0.13	0.03	0.10	1.77	0.64
	Herbert	0.44	0.10	0.07	0.04	2.09	0.68
	Burdekin	0.54	0.22	0.00	0.00	2.47	0.71
	Central	0.62	0.15	0.04	0.04	2.65	0.73
	South	0.46	0.01	0.01	0.26	1.65	0.62
	NSW	0.55	0.20	0.13	0.07	1.39	0.58
	avg	*0.51*	*0.13*	*0.04*	*0.09*	1.92	*0.66*

		Gen	*G:Loc*	*G:Crop*	*G:Loc:Crop*	G/GxE	G/(G+GxE)
TCH	North	59.10	36.25	26.05	24.40	0.68	0.41
	Herbert	90.39	47.30	32.80	20.95	0.89	0.47
	Burdekin	44.38	35.06	3.31	4.52	1.03	0.51
	Central	16.15	35.47	8.25	7.07	0.32	0.24
	South	57.00	35.09	16.21	7.18	0.97	0.49
	NSW	103.62	0.00	8.55	91.81	1.03	0.51
	avg	*61.77*	*31.53*	*15.86*	*25.99*	0.84	*0.46*

Appendix 13. BSES-Across Analysis: results from analysis of 40 genotypes planted across regions between plant years 1991 and 2002

Table of contents

13.1. Abstract

From this data it can be said that for advanced stage (commercial) clones, Genotype by Environment interactions are large relative to Genotype main effects. In the case of ccs, the interaction effect is about 2 times the main effect (Table 3), while for tch and tsh, the interaction is 6 and 9 times the main effect, respectively. While the Genotype by region effect for tsh is relatively larger cf the main effect, for all three traits, the Genotype by Environment interaction dominates through the two-way interaction with locations and three-way interaction with locations and crop class. The two-way interaction with crop class is relatively small compared with other forms of interaction.

13.2. Method

Genotype mean data from the BSES Limited trial database for trials planted in 1989 to 2002 in all regions (except Ord) were filtered to find genotypes that had been grown in trials in at least three regions in trials at any stage of the breeding program. After inspection of the dataset, trials were further filtered to meet the following criteria so that extremely unbalanced factors were removed:

- Deleted years with < 14 genotypes planted (> 24 all years except 1991)
- Deleted trials where plot size was 1 row/plot
- Deleted genotypes that were planted < 5 years of the set

The dataset therefore comprised of 7867 observations from 12 plant years for 40 genotypes distributed across 730 location-plant year combinations and harvested in plant and 1st ratoon and sometimes in 2nd ratoon (Tables 1 and 2). Almost all of the genotypes analysed here were commercial clones (Table 1), and having passed through the selection process, there is expected to be relatively low genotypic variances in the dataset. Note that the South region trials included trials from NSW.

Given the imbalance in this dataset (genotypes over locations and years), the data were not suitable for comparisons of correlations between locations and years etc. Hence, the analysis was done only to examine the relative size of variance components associated with genotypes and interactions with environments. From the dataset, we initially had only standard errors for the trait tsh. For tch and ccs, we had to estimate weights from the mean values of tch and ccs for each trial. This was done using the large BSES-FATs dataset, where models had been fitted for the residual variances as a function of trial mean (Appendix 11).

For tch: EMS = 3.5 * tch – 143 (lower limit of 20) and

For ccs: EMS = -0.15ccs + 3 (lower limit to 0.15)

For each trait, the weight was calculated as:

Wt = 2* avg standard error over all trials/std error of each genotype BLUE

ASREML was used to estimate variance components for several models for that trait tsh (Table 4). In all cases, trials (environments) were considered to be fixed effects, and the appropriate errors were used to weight the genotype estimates.

13.3. Results

Model 1 demonstrates that over the entire dataset, GxE interactions were between about 2 times (ccs) and 6 (tch) to 9 (tsh) times the size of G main effects. For all three traits, the major interactions are associated with location and location by crop class effects, whereas the interaction of genotype and crop class is relatively small. In model 2, the interaction effects were partitioned between genotype by region (Gen.Reg) and genotype by environment (plant-year by crop class) within region, averaged over regions (Gen.Reg.Env). While the Gen.Reg term was of the same order as the Gen main effect, it was only 20% (tch) to 41% (ccs) of the

Gen.Reg.Env effect, i.e. variation due to environments within regions had a greater interaction with genotype than did regions themselves.

Model 2 was further partitioned in Model 3 to reveal that for tch and ccs, the majority of the within region variation between environments was related to the 3 way interaction within regions of genotype with location and crop class. For tsh, the within region interaction with environment was about the same as the within region 3 way interaction. The Gen.Cclass interaction was relatively small (i.e. as seen in Model 1) and was left in with the Gen.Reg.Loc.Cclass component. This was because experiments are generally grown for 2-3 crop classes and, within regions, the number of locations is more likely to vary than is number of crop classes.

The final model has plant year added to Model 3. Given that the occurrence of clones in multiple regions is relatively small, the data had to be collated over 12 plant years, and there was concern that variation in climate from year to year may interact with Genotype. This does seem to be the case for tch and ccs more than tsh, with Gen.Pyear being larger than Gen.Reg, i.e. some of the Gen.Reg effect observed in model 3 was partly related to the fact that not all regions were evenly represented in each plant year and that their relationships between each other varied with plant year.

These results are in contrast to those from the analyses of the within-region analyses of the MegaGxE and BSES-FAT trials (Table 4). These show that the G main effect in this analysis for tch was half that observed in the FAT trials, and for ccs was less than 1/3 that in the FAT trials. The increase in total interaction effect is clearly evident compared to the other levels of trials. Collective comparison of variance components estimated from the three populations indicate that the importance of GxE interactions increases as the tested genotypes become more selected, and this increased importance of GxE is more so for TCH than CCS (Table 13-4).

Table 13-1 For plant years 1991 to 2002 in the BSES-Across dataset, the number of observations (location x harvest) per genotype and region. Regions are Burdekin (B), Central (C), Herbert (H), North (N) and South (S, including NSW trials).

Gen	Reg B	C	H	N	S	Total
77N792	6	6	14	15		41
84N1750	5	15	11	12	9	52
84N2976	6	11	7	25		49
86N1833	8	15	8	18		49
H56-752	12	129	43	84	26	294
Q117	157	20	67	112		356
Q124	41	271	234	120	364	1030
Q135	13	296	34	86	22	451
Q138	9	168	50	198	229	654
Q141	1	5	6	7	325	344
Q147	13		8	17	5	43
Q150		28	16	18	38	100
Q151	8	35	6	22	238	309
Q152	10	21	51	220		302
Q153		31	8	17	14	70
Q154	8	12	25	19	25	89
Q155	12	30	8	27	294	371
Q157	8	23	128	15	16	190
Q158	8	32	177	182	13	412
Q159	8	93		17	46	164
Q160	8	16	12	47	8	91
Q161		15	20	45	15	95
Q162	12	19	87	32	16	166
Q164	4	28	61	18		111
Q165	32	26	32	33	13	136
Q167		21	12	43	56	132
Q170	7	63	9	33	212	324
Q171	38	18	12	17		85
Q174	8	23	52	101		184
Q175	5		6	56	9	76
Q176	25	13	8	12		58
Q177	29	17	10	12	20	88
Q179	8	3	88	15		114
Q183	41	9	8	12	6	76
Q185		98	17	9	11	135
Q186	7	3	44	56		110
Q189	20	14	6	10	1	51
Q190		109	9	10	28	156
Q196		29	15	5	39	88
Q209		17	23	17	11	68
Total	577	1782	1432	1814	2109	7714

Table 13-2 For genotypes in the BSES-Across dataset, the number of location-genotype combinations per plant-year in each region with harvests in plant crop, 1st ratoon or 2nd ratoon.

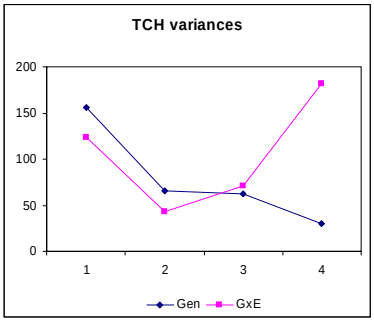
Pyear	Reg B	C	H	N	S	Total
1991	36	67	15	117	20	255
1992		186	102	117	29	434
1993	42	117	128	244	162	693
1994	102	203	139	247	172	863
1995	102	67	97	201	135	602
1996	22	265	20	267	174	748
1997	76	136	152	196	256	816
1998	72	228	120	112	368	900
1999	19	109	240	88	245	701
2000	44	166	223	122	228	783
2001	38	154	134	76	190	592
2002	24	84	62	27	130	327
Total	577	1782	1432	1814	2109	7714

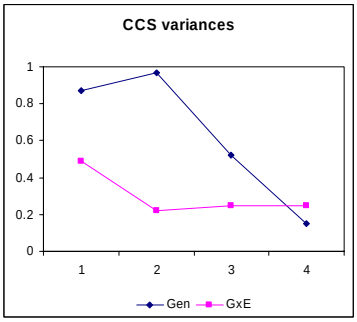
Table 13-3 From the BSES-Across dataset for cane yield (tonnes per ha), ccs (%) and sugar yield (tonnes sugar per ha), variance components (VC) and their standard errors for a series of different random effects models.

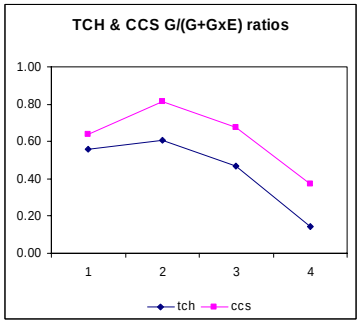
Model	Source	Number of terms	tch		ccs		tsh	
			VC	VCse	VC	VCse	VC	VCse
Model 1	Gen	40	33.43	*9.04*	0.151	0.036	0.51	0.15
	Gen.Cclass	120	6.84	*1.63*	0.002	0.002	0.15	0.04
	Gen.Loc	29240	80.37	*3.78*	0.131	0.010	1.90	0.09
	Gen.Cclass.Loc	87720	95.50	*2.43*	0.143	0.010	1.52	0.06
	G/GxE		0.18		0.55		0.14	
Model 2	Gen	40	31.66	*9.54*	0.135	0.037	0.49	0.18
	Gen.Reg	200	30.41	*5.30*	0.089	0.016	0.92	0.15
	Gen.Reg.Env	333400	163.17	*3.07*	0.227	0.010	3.19	0.08
Model 3	Gen	40	32.34	*9.71*	0.136	0.037	0.48	0.18
	Gen.Reg	200	25.11	*5.11*	0.072	0.015	0.75	0.14
	Gen.Reg.Loc	146200	64.45	*3.51*	0.096	0.010	1.45	0.08
	Gen.Reg.Loc.Cclass	438600	101.87	*2.55*	0.145	0.010	1.66	0.06
Model 4	Gen	40	30.84	*9.43*	0.131	0.036	0.45	0.18
	Gen.Reg	200	21.30	*4.53*	0.062	0.014	0.69	0.14
	Gen.Pyear	480	11.37	*2.53*	0.020	0.006	0.30	0.06
	Gen.Reg.Loc	146200	58.78	*3.57*	0.082	0.010	1.16	0.07
	Gen.Reg.Loc.Cclass	438600	101.79	*2.54*	0.144	0.010	0.95	0.04
	G/GxE		0.16		0.42		0.15	
	Variance	7866	9.90		0.600		2.23	

Table 13-4 Summary of genotype and genotype by environment variance components in four sets of experiments: 1. MegaGxE, 2. BS5S (re-analysis of Cox 1995: 1 location in each of 3 regions), 3. BSES-FAT (variances analysed within region, averaged across regions) and 4. BSES-Across (variances from FAT trials across regions using 12 years of data).

Source	1. MegaGxE		2. BS5S report		3. BSES-FAT		4. BSES-Across (model 1)	
	tch	ccs	tch	ccs	tch	ccs	tch	ccs
Gen	156	0.87	66	0.97	62	0.52	30	0.15
GxE	124	0.49	43	0.22	71	0.25	182	0.25
G/GxE	1.26	1.76	1.54	4.45	0.87	2.1	0.18	0.55
G/(G+GxE)	0.56	0.64	0.61	0.82	0.47	0.68	0.14	0.38







Appendix 14 List of important folders and files in CTA028 report

Note that the direct shortcuts may not work from this document. In this case, please open the files from Explorer

BS5S Mike Cox SRDC report	Folder of files relating to re-analysis of BS5S
BSES Across FATS analysis 1991-2002	Folder of files for analysis of Across Regions FATs analysis for 1991-2002
BSES FATs analysis 2000-2001	Folder of files relating to within region (multi-regions) FATs analysis 2000-2001
BSES Mac Hogarth - prior GxE studies	Folder of results of prior GxE studies reported in milestone 4 and Appendix 1 of final report
dman	Folder of BSES data extraction tool
doc\Guidelines to MegaGxE matrices.doc	Document about climate and soil databases and data files
doc\SugarTrialAudit.xls	Audit data for REMS information databases
markers\markers summary.xls	Summary of results of marker verification tests of lines
doc\Workshop June 2004	Folder of .ppt files from final workshop
envdef\splus\cc028 envdef splus.zip	Folder and files containing analyses of environment indices output from SugCalc. Includes SugCalc source code etc. as described in Appendix 2.
megagxe\Analysis methods.doc	Description of analysis methods for row/col and spatial analyses using SAMM or ASREML
megagxe\alldat140205.csv	MASTER harvest data file produced from a 'mgxeall' sheet in 'harvest data Feb 05.xls'. Used as input to first S-Plus analysis file ..\megagxe\SAMM\CTA028 Met 01 Data prep.ssc
megagxe\Clone list.xls	List of clones and parentage
megagxe\Env covariables.xls	Sheets for all planting & harvest dates and

	environment covariables (weather, soil chem., soil path etc) used in the spreadsheets covar*.csv. NOTE: all environmental data is stored in REMS database (see below)
megagxe\harvest data Feb 2005.xls	MASTER harvest data file. Used to produce alldat140205.csv which is used in the S-Plus processing files
megagxe\soil pathology data.xls	Raw and processed soil pathology data - summarised in 'Env covariables.xls'
megagxe\Soil textures all sites.xls	Estimates of soil textures
megagxe\iat.asd	Abbreviated version of datafile from 1st processing
megagxe\ASREML	Folder of various ASREML analyses in several folders
megagxe\DataAudit\SugarTrialAudit.xls	Tracks auditing of environmental data for entry into REMS database
megagxe\DataCollation\Soil	Folder of files related to accumulating soil data together for REMS
megagxe\DataCollation\MetData	Folder of weather data for the actual trial sites, collated from BOM sites
megagxe\DataCollation\MetData\sugcalc\MetFiles.zip	Raw data from SILO BOM
megagxe\DataCollation\MetData\Instructions PPD Met Data.doc	How the weather data was processed
megagxe\DataCollation\4Scott\Documents\Guidelines to MegaGxE matrices.doc	Same file as above in DOC directory. Explains access to climate and weather and REMS data
..\megagxe\Genstat\	Folder of Genstat files for environment covariable analysis
..\megagxe\Pedigrees\GxEPARENTS.xls	Additional info on pedigrees of clones used in CTA028 experiments
..\megagxe\R	Folder of R code for automation of single trial analysis
..\megagxe\Raw data	Folder of raw data files (zipped with path names)
..\megagxe\REMS\REMS.exe	REMS database of all trial environment information.

	REMS is a database tool developed by APSRU (www.apsru.gov.au) with input from Scott Chapman. Execute REMS.exe and open 'MegaGxERems.mdb'. This provides easy access to all environment and management information for every trial.
..\megagxe\SAMM	Folder of major work area for analysis. The analysis programs are written in code for S-Plus (2000 or v. 6) and are numbered in order of execution. Almost all of the Appendix 4 results come from graphs and tables produced from these files or in the associated spreadsheets. The files are not documented further here.
..\megagxe\stats	Folder of files used in earlier analyses of harvest data results

Appendix 15 Summary of results from series of variance models applied to TCH or CCS

SUMMARY
- see notes below. Has GxE, GxLxY, GxR, GxR (with loc, cclass, locXcclass within) & GxR new regions
- also, VC ratios do not change much at all if we consider checks as fixed (they just all decrease a bit)

TCH

- with current regions (B C H N S W O) G.R.E = GxE within regions

$G.E:

	gamma	component	std.error	z.ratio	constraint
Gen	183.84207	183.84207	29.120574	6.313133	Positive
Gen:Env	88.20326	88.20326	4.834443	18.244763	Positive

$G.L.Y:

source	gamma	component	std.error	z.ratio	constraint
Gen	161.45865	161.45865	27.906590	5.785682	Positive
Gen:Loc	73.75432	73.75432	5.253861	14.038120	Positive
Gen:Cclass	14.99516	14.99516	2.845271	5.270204	Positive
Gen:Loc:Cclass	12.42047	12.42047	3.073665	4.040932	Positive

$G.R:

	gamma	**component**	**std.error**	**z.ratio**	**constraint**
Gen	**171.62537**	**171.62537**	**29.008517**	**5.916379**	**Positive**
Gen:Reg	**28.69922**	**28.69922**	**4.869738**	**5.893381**	**Positive**
Gen:Reg:Env	**70.41857**	**70.41857**	**4.502623**	**15.639455**	**Positive**

$G.R2:

	gamma	component	std.error	z.ratio	constraint
Gen	165.047751	165.047751	28.211767	5.850316	Positive
Gen:Reg	5.803288	5.803288	4.689936	1.237392	Positive
Gen:Reg:Loc	67.871084	67.871084	5.502210	12.335242	Positive
Gen:Reg:Cclass	21.141325	21.141325	3.021474	6.997024	Positive
Gen:Reg:Env	4.769869	4.769869	3.253243	1.466189	Positive

- aggregated N + H, B + N3 + N6, C + S + W, O

$G.newReg:

	gamma	component	std.error	z.ratio	constraint
Gen	**164.80302**	**164.80302**	**28.677322**	**5.746806**	**Positive**
Gen:RegAgg2	**28.05730**	**28.05730**	**6.047062**	**4.639824**	**Positive**
Gen:RegAgg2:Env	**78.23943**	**78.23943**	**4.586706**	**17.057868**	**Positive**

i.e. Important conclusion is that aggregating regions does not change either the GxR or GxE within R

CCS

- with current regions (B C H N S W O) G.R.E = GxE within regions

$G.E:

	gamma	component	std.error	z.ratio	constraint
Gen	0.8682854	0.8682854	0.13376188	6.491277	Positive
Gen:Env	0.3562497	0.3562497	0.02010235	17.721796	Positive

$G.L.Y:

	gamma	component	std.error	z.ratio	constraint
Gen	8.230632e-001	8.230632e-001	0.13089093	6.288160	Positive
Gen:Loc	2.211193e-001	2.211193e-001	0.02075884	10.651811	Positive
Gen:Cclass	2.950242e-007	2.950242e-007	NA	NA	Boundary
Gen:Loc:Cclass	1.680184e-001	1.680184e-001	0.01747339	9.615676	Positive

$G.R:

	gamma	component	std.error	z.ratio	constraint
Gen	**0.7883758**	**0.7883758**	**0.12908377**	**6.107474**	**Positive**
Gen:Reg	**0.1192034**	**0.1192034**	**0.01966181**	**6.062687**	**Positive**
Gen:Reg:Env	**0.2815653**	**0.2815653**	**0.01872265**	**15.038747**	**Positive**

$G.R2:

	gamma	component	std.error	z.ratio	constraint
Gen	7.885941e-001	7.885941e-001	0.12906144	6.110223	Positive
Gen:Reg	7.096833e-002	7.096833e-002	0.01893220	3.748551	Positive
Gen:Reg:Loc	1.670373e-001	1.670373e-001	0.02068127	8.076745	Positive
Gen:Reg:Cclass	8.442665e-007	8.442665e-007	NA	NA	Boundary
Gen:Reg:Env	1.677405e-001	1.677405e-001	0.01746197	9.606051	Positive

- aggregated N + H, B + N3 + N6, C + S + W, O

$G.newReg:

	gamma	**component**	**std.error**	**z.ratio**	**constraint**
Gen	**0.7877074**	**0.7877074**	**0.13045719**	**6.038053**	**Positive**
Gen:RegAgg2	**0.1039964**	**0.1039964**	**0.02373853**	**4.380914**	**Positive**
Gen:RegAgg2:Env	**0.3133375**	**0.3133375**	**0.01920043**	**16.319295**	**Positive**

i.e. Again, important conclusion is that aggregating regions does not change either the GxR or GxE within R

TCH

```
> tch.VC
$simple:
                          gamma  component  std.error  z.ratio constraint
at(Env, B1-0-0):Gen  303.24813  303.24813 129.834182 2.335657   Positive
at(Env, B1-1-1):Gen  282.63401  282.63401 129.511352 2.182311   Positive
at(Env, B1-2-2):Gen  168.05970  168.05970  76.864147 2.186451   Positive
at(Env, B2-0-0):Gen  508.42569  508.42569 141.126910 3.602613   Positive
at(Env, B2-1-1):Gen  273.98260  273.98260  71.266712 3.844468   Positive
at(Env, B3-0-2):Gen  138.42112  138.42112  98.703631 1.402391   Positive
at(Env, B3-1-3):Gen  172.39107  172.39107  77.925698 2.212249   Positive
at(Env, B3-2-4):Gen  198.67317  198.67317 119.270666 1.665734   Positive
at(Env, B4-0-3):Gen  350.67123  350.67123 152.077699 2.305869   Positive
at(Env, B4-1-4):Gen  156.32280  156.32280  53.859148 2.902437   Positive
at(Env, C1-0-0):Gen  342.07393  342.07393  85.750942 3.989157   Positive
at(Env, C1-1-1):Gen  145.48370  145.48370  41.332979 3.519797   Positive
at(Env, C1-2-2):Gen  153.26540  153.26540  40.250324 3.807805   Positive
at(Env, C2-0-0):Gen  370.52237  370.52237  92.323955 4.013285   Positive
at(Env, C2-1-1):Gen  308.80091  308.80091  73.485595 4.202196   Positive
at(Env, C3-0-1):Gen  150.40394  150.40394  60.862770 2.471198   Positive
at(Env, C3-1-2):Gen  174.19299  174.19299  65.280690 2.668369   Positive
at(Env, C3-2-3):Gen  200.41916  200.41916  51.417127 3.897907   Positive
at(Env, C4-0-1):Gen  159.02759  159.02759  42.398505 3.750783   Positive
at(Env, C4-1-2):Gen   43.75548   43.75548  13.296084 3.290855   Positive
at(Env, C4-2-3):Gen   95.08690   95.08690  22.854093 4.160607   Positive
at(Env, H1-0-0):Gen  262.84836  262.84836  58.048435 4.528087   Positive
at(Env, H1-1-1):Gen  202.70359  202.70359  53.255820 3.806224   Positive
at(Env, H2-0-0):Gen  235.62266  235.62266  58.044466 4.059347   Positive
at(Env, H2-1-1):Gen  492.28889  492.28889 103.206362 4.769947   Positive
at(Env, H2-2-2):Gen  341.55437  341.55437  78.147895 4.370615   Positive
at(Env, H3-0-1):Gen  204.29273  204.29273  58.893042 3.468877   Positive
at(Env, H3-1-2):Gen  150.13193  150.13193  35.684273 4.207230   Positive
at(Env, H3-2-3):Gen   32.69837   32.69837   7.999607 4.087498   Positive
at(Env, H4-0-1):Gen  225.06534  225.06534  57.810210 3.893176   Positive
at(Env, H4-1-2):Gen  160.00114  160.00114  52.662476 3.038238   Positive
at(Env, H4-2-3):Gen  259.13431  259.13431  64.565703 4.013498   Positive
at(Env, N1-0-2):Gen  406.99721  406.99721 104.037752 3.912015   Positive
at(Env, N1-1-3):Gen  336.67580  336.67580  76.394762 4.407053   Positive
at(Env, N2-0-1):Gen  146.20074  146.20074  54.995834 2.658397   Positive
at(Env, N2-1-2):Gen  685.25835  685.25835 169.144559 4.051318   Positive
at(Env, N2-2-3):Gen  321.34427  321.34427  84.422686 3.806373   Positive
at(Env, N3-0-1):Gen  331.28055  331.28055  96.754335 3.423935   Positive
at(Env, N3-1-2):Gen  384.05816  384.05816 123.203201 3.117274   Positive
at(Env, N4-0-2):Gen  146.44014  146.44014  40.162954 3.646150   Positive
```

```
at(Env, N4-1-3):Gen  277.53286  277.53286  67.058402 4.138674   Positive
at(Env, N5-0-2):Gen  271.86821  271.86821  73.657767 3.690965   Positive
at(Env, N5-1-3):Gen  533.65064  533.65064 131.229598 4.066542   Positive
at(Env, N6-0-1):Gen  162.99753  162.99753  44.030509 3.701922   Positive
at(Env, N6-1-2):Gen  346.73761  346.73761  83.888722 4.133304   Positive
at(Env, O1-0-2):Gen  488.82534  488.82534 139.450708 3.505363   Positive
at(Env, O1-1-3):Gen  547.59573  547.59573 150.143384 3.647152   Positive
at(Env, S1-0-0):Gen  211.39646  211.39646  61.856402 3.417536   Positive
at(Env, S1-1-1):Gen  254.42633  254.42633  78.985048 3.221196   Positive
at(Env, S1-2-2):Gen  258.64479  258.64479  69.868525 3.701878   Positive
at(Env, S3-0-1):Gen  175.44584  175.44584  50.613345 3.466395   Positive
at(Env, S3-1-2):Gen  187.73761  187.73761  53.698724 3.496128   Positive
at(Env, S3-2-3):Gen  257.01934  257.01934  71.543507 3.592490   Positive
at(Env, S4-0-3):Gen  435.38558  435.38558 128.824025 3.379692   Positive
at(Env, S4-1-4):Gen  168.32636  168.32636  46.279853 3.637141   Positive
at(Env, W1-0-0):Gen  226.72977  226.72977  72.465836 3.128782   Positive
at(Env, W1-1-1):Gen  344.78251  344.78251  85.504701 4.032322   Positive
at(Env, W2-0-1):Gen 1051.27006 1051.27006 306.109108 3.434299   Positive
at(Env, W2-1-2):Gen  898.79433  898.79433 249.161242 3.607280   Positive

$G.E:
            gamma component std.error   z.ratio constraint
    Gen 183.84207 183.84207 29.120574  6.313133   Positive
Gen:Env  88.20326  88.20326  4.834443 18.244763   Positive

$G.L.Y:
                  gamma component std.error   z.ratio constraint
           Gen 161.45865 161.45865 27.906590  5.785682   Positive
       Gen:Loc  73.75432  73.75432  5.253861 14.038120   Positive
    Gen:Cclass  14.99516  14.99516  2.845271  5.270204   Positive
Gen:Loc:Cclass  12.42047  12.42047  3.073665  4.040932   Positive

$G.L.Y2samm:
                  gamma component std.error   z.ratio constraint
       Gen:Loc  78.95028  78.95028  5.527332 14.283615   Positive
    Gen:Cclass 137.19567 137.19567 15.022949  9.132406   Positive
Gen:Loc:Cclass  11.11732  11.11732  3.057133  3.636519   Positive

$G.R:
                gamma component std.error   z.ratio constraint
         Gen 171.62537 171.62537 29.008517  5.916379   Positive
    Gen:Reg  28.69922  28.69922  4.869738  5.893381   Positive
Gen:Reg:Env  70.41857  70.41857  4.502623 15.639455   Positive
```

$G.R2:

	gamma	component	std.error	z.ratio	constraint
Gen	165.047751	165.047751	28.211767	5.850316	Positive
Gen:Reg	5.803288	5.803288	4.689936	1.237392	Positive
Gen:Reg:Loc	67.871084	67.871084	5.502210	12.335242	Positive
Gen:Reg:Cclass	21.141325	21.141325	3.021474	6.997024	Positive
Gen:Reg:Env	4.769869	4.769869	3.253243	1.466189	Positive

$atReg.G.E:

	gamma	component	std.error	z.ratio	constraint
at(Reg, B):Gen	209.27381	209.27381	40.914047	5.114962	Positive
at(Reg, C):Gen	106.04398	106.04398	23.992256	4.419926	Positive
at(Reg, H):Gen	161.81128	161.81128	32.059540	5.047211	Positive
at(Reg, N):Gen	184.75823	184.75823	40.417308	4.571265	Positive
at(Reg, O):Gen	390.32350	390.32350	122.928167	3.175216	Positive
at(Reg, S):Gen	200.62375	200.62375	45.456591	4.413524	Positive
at(Reg, W):Gen	345.18794	345.18794	83.246491	4.146577	Positive
at(Reg, B):Gen:Loc:Cclass	53.28394	53.28394	18.228460	2.923118	Positive
at(Reg, C):Gen:Loc:Cclass	59.10494	59.10494	8.178179	7.227151	Positive
at(Reg, H):Gen:Loc:Cclass	60.08033	60.08033	7.420732	8.096282	Positive
at(Reg, N):Gen:Loc:Cclass	107.50016	107.50016	12.195036	8.815075	Positive
at(Reg, O):Gen:Loc:Cclass	126.73109	126.73109	46.956274	2.698917	Positive
at(Reg, S):Gen:Loc:Cclass	40.09594	40.09594	9.863340	4.065148	Positive
at(Reg, W):Gen:Loc:Cclass	69.40292	69.40292	30.640095	2.265101	Positive

$atReg.G.L.Y:

	gamma	component	std.error	z.ratio	constraint
at(Reg, B):Gen	1.772124e+002	1.772124e+002	40.742570	4.3495635	Positive
at(Reg, C):Gen	1.002320e+002	1.002320e+002	26.063440	3.8456933	Positive
at(Reg, H):Gen	1.493324e+002	1.493324e+002	31.500107	4.7406939	Positive
at(Reg, N):Gen	1.687992e+002	1.687992e+002	41.082776	4.1087589	Positive
at(Reg, O):Gen	3.162333e+002	3.162333e+002	122.928217	2.5725035	Positive
at(Reg, S):Gen	1.615686e+002	1.615686e+002	43.482522	3.7157139	Positive
at(Reg, W):Gen	3.540864e+002	3.540864e+002	99.867151	3.5455745	Positive
at(Reg, B):Gen:Loc	6.943479e+001	6.943479e+001	18.627841	3.7274742	Positive
at(Reg, C):Gen:Loc	5.084834e+001	5.084834e+001	8.798507	5.7792006	Positive
at(Reg, H):Gen:Loc	2.452575e+001	2.452575e+001	7.009109	3.4991256	Positive
at(Reg, N):Gen:Loc	1.008341e+002	1.008341e+002	13.015034	7.7475090	Positive
at(Reg, O):Gen:Loc	7.409026e+001	7.409026e+001	NA	NA	Singular
at(Reg, S):Gen:Loc	6.911560e+001	6.911560e+001	15.148988	4.5623903	Positive
at(Reg, W):Gen:Loc	1.074226e+002	1.074226e+002	51.322045	2.0931092	Positive
at(Reg, B):Gen:Cclass	1.407278e+001	1.407278e+001	12.884519	1.0922237	Positive
at(Reg, C):Gen:Cclass	2.300613e+001	2.300613e+001	5.329200	4.3169940	Positive
at(Reg, H):Gen:Cclass	1.279540e+001	1.279540e+001	5.515432	2.3199267	Positive

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    at(Reg, N):Gen:Cclass 2.359085e+001 2.359085e+001   6.754738 3.4924899   Positive
    at(Reg, O):Gen:Cclass 5.264086e+001 5.264086e+001  46.956300 1.1210606   Positive
    at(Reg, S):Gen:Cclass 1.306950e+001 1.306950e+001   5.594007 2.3363396   Positive
    at(Reg, W):Gen:Cclass 2.498102e+001 2.498102e+001  34.125408 0.7320359   Positive
at(Reg, B):Gen:Loc:Cclass 3.642413e-007 3.642413e-007         NA        NA   Boundary
at(Reg, C):Gen:Loc:Cclass 1.628325e-007 1.628325e-007         NA        NA   Boundary
at(Reg, H):Gen:Loc:Cclass 2.952015e+001 2.952015e+001   7.931880 3.7217087   Positive
at(Reg, N):Gen:Loc:Cclass 2.488227e-007 2.488227e-007         NA        NA   Boundary
at(Reg, O):Gen:Loc:Cclass 7.409026e+001 7.409026e+001         NA        NA   Singular
at(Reg, S):Gen:Loc:Cclass 1.141593e-007 1.141593e-007         NA        NA   Boundary
at(Reg, W):Gen:Loc:Cclass 2.193469e+001 2.193469e+001  40.186027 0.5458288   Positive

$atReg.G.E.R:
                     gamma component  std.error  z.ratio constraint
    at(Reg, B):Gen 209.27381 209.27381  40.914047 5.114962   Positive
    at(Reg, C):Gen 106.04398 106.04398  23.992256 4.419926   Positive
    at(Reg, H):Gen 161.81128 161.81128  32.059540 5.047211   Positive
    at(Reg, N):Gen 184.75823 184.75823  40.417308 4.571265   Positive
    at(Reg, O):Gen 390.32350 390.32350 122.928167 3.175216   Positive
    at(Reg, S):Gen 200.62375 200.62375  45.456591 4.413524   Positive
    at(Reg, W):Gen 345.18794 345.18794  83.246491 4.146577   Positive
at(Reg, B):Gen:Env  53.28394  53.28394  18.228460 2.923118   Positive
at(Reg, C):Gen:Env  59.10494  59.10494   8.178179 7.227151   Positive
at(Reg, H):Gen:Env  60.08033  60.08033   7.420732 8.096282   Positive
at(Reg, N):Gen:Env 107.50016 107.50016  12.195036 8.815075   Positive
at(Reg, O):Gen:Env 126.73109 126.73109  46.956274 2.698917   Positive
at(Reg, S):Gen:Env  40.09594  40.09594   9.863340 4.065148   Positive
at(Reg, W):Gen:Env  69.40292  69.40292  30.640095 2.265101   Positive

$G.newReg: aggregated N + H, B + N3 + N6, C + S + W, O
                   gamma component std.error   z.ratio constraint
            Gen 164.80302 164.80302 28.677322  5.746806   Positive
    Gen:RegAgg2  28.05730  28.05730  6.047062  4.639824   Positive
Gen:RegAgg2:Env  78.23943  78.23943  4.586706 17.057868   Positive

$atG.newReg:
                               gamma component  std.error   z.ratio constraint
      at(RegAgg2, Btype):Gen 192.18397 192.18397  36.821388  5.219357   Positive
     at(RegAgg2, CStype):Gen 155.26374 155.26374  30.899502  5.024797   Positive
     at(RegAgg2, NHtype):Gen 174.64517 174.64517  33.189399  5.262077   Positive
    at(RegAgg2, Ordtype):Gen 390.32350 390.32350 122.928167  3.175216   Positive
  at(RegAgg2, Btype):Gen:Env  95.26911  95.26911  14.995259  6.353282   Positive
 at(RegAgg2, CStype):Gen:Env  68.56265  68.56265   6.554730 10.460028   Positive
 at(RegAgg2, NHtype):Gen:Env  76.55544  76.55544   6.752846 11.336767   Positive
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at(RegAgg2, Ordtype):Gen:Env 126.73109 126.73109  46.956274  2.698917   Positive

$G.RTable:
                 gamma component std.error   z.ratio constraint
          Gen 166.07109 166.07109 28.734557  5.779490   Positive
    Gen:Reg2  41.24701  41.24701  5.720431  7.210472   Positive
Gen:Reg2:Env  64.32440  64.32440  4.308846 14.928449   Positive

$atG.RTable:
                       gamma component  std.error  z.ratio constraint
    at(Reg2, B):Gen 209.27381 209.27381  40.914046 5.114962   Positive
    at(Reg2, C):Gen 106.04398 106.04398  23.992256 4.419926   Positive
    at(Reg2, H):Gen 161.81128 161.81128  32.059540 5.047211   Positive
    at(Reg2, N):Gen 226.93046 226.93046  49.224260 4.610135   Positive
    at(Reg2, O):Gen 390.32350 390.32350 122.928167 3.175216   Positive
    at(Reg2, S):Gen 200.62375 200.62375  45.456591 4.413524   Positive
    at(Reg2, T):Gen 187.52632 187.52632  48.360827 3.877649   Positive
    at(Reg2, W):Gen 345.18794 345.18794  83.246490 4.146577   Positive
at(Reg2, B):Gen:Env  53.28394  53.28394  18.228460 2.923118   Positive
at(Reg2, C):Gen:Env  59.10494  59.10494   8.178179 7.227151   Positive
at(Reg2, H):Gen:Env  60.08033  60.08033   7.420732 8.096282   Positive
at(Reg2, N):Gen:Env  74.66517  74.66517  11.907825 6.270261   Positive
at(Reg2, O):Gen:Env 126.73109 126.73109  46.956274 2.698917   Positive
at(Reg2, S):Gen:Env  40.09594  40.09594   9.863340 4.065148   Positive
at(Reg2, T):Gen:Env  91.33519  91.33519  23.712684 3.851744   Positive
at(Reg2, W):Gen:Env  69.40292  69.40292  30.640095 2.265101   Positive
```

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> ccs.VC
$simple:
                          gamma component std.error  z.ratio constraint
at(Env, B1-0-0):Gen 3.1481493 3.1481493 0.9177765 3.430192   Positive
at(Env, B1-1-1):Gen 0.8166579 0.8166579 0.2623508 3.112847   Positive
at(Env, B1-2-2):Gen 2.1867911 2.1867911 0.6377327 3.429009   Positive
at(Env, B2-0-0):Gen 2.0736252 2.0736252 0.5024248 4.127235   Positive
at(Env, B2-1-1):Gen 0.8760694 0.8760694 0.2732930 3.205605   Positive
at(Env, B3-0-2):Gen 2.1985513 2.1985513 0.5899635 3.726589   Positive
at(Env, B3-1-3):Gen 4.3185542 4.3185542 1.2371979 3.490593   Positive
at(Env, B3-2-4):Gen 2.9475539 2.9475539 0.9045563 3.258563   Positive
at(Env, B4-0-3):Gen 0.5056955 0.5056955 0.3664055 1.380153   Positive
at(Env, B4-1-4):Gen 0.5082553 0.5082553 0.1337235 3.800792   Positive
at(Env, C1-0-0):Gen 2.4480204 2.4480204 0.5595598 4.374904   Positive
at(Env, C1-1-1):Gen 0.8070035 0.8070035 0.1998201 4.038650   Positive
at(Env, C1-2-2):Gen 1.6018868 1.6018868 0.3621683 4.423045   Positive
at(Env, C2-0-0):Gen 1.1858731 1.1858731 0.3053812 3.883255   Positive
at(Env, C2-1-1):Gen 0.8972366 0.8972366 0.2036840 4.405042   Positive
at(Env, C3-0-1):Gen 1.1501854 1.1501854 0.2786314 4.127982   Positive
at(Env, C3-1-2):Gen 1.4540576 1.4540576 0.3415035 4.257812   Positive
at(Env, C3-2-3):Gen 2.1064852 2.1064852 0.5160685 4.081794   Positive
at(Env, C4-0-1):Gen 0.5370163 0.5370163 0.1723821 3.115267   Positive
at(Env, C4-1-2):Gen 1.7305913 1.7305913 0.3760569 4.601940   Positive
at(Env, C4-2-3):Gen 1.3522112 1.3522112 0.3068143 4.407263   Positive
at(Env, H1-0-0):Gen 0.9687985 0.9687985 0.2246737 4.312024   Positive
at(Env, H1-1-1):Gen 1.1280892 1.1280892 0.2562232 4.402759   Positive
                          gamma component std.error  z.ratio constraint
at(Env, H2-0-0):Gen 1.6610265 1.6610265 0.3627899 4.578480   Positive
at(Env, H2-1-1):Gen 1.8352740 1.8352740 0.4245799 4.322564   Positive
at(Env, H2-2-2):Gen 0.9588301 0.9588301 0.3192787 3.003113   Positive
at(Env, H3-0-1):Gen 1.9269463 1.9269463 0.4077837 4.725413   Positive
at(Env, H3-1-2):Gen 1.9779487 1.9779487 0.4985955 3.967041   Positive
at(Env, H3-2-3):Gen 0.8630181 0.8630181 0.2507854 3.441261   Positive
at(Env, H4-0-1):Gen 0.7218871 0.7218871 0.1814788 3.977805   Positive
at(Env, H4-1-2):Gen 0.8605825 0.8605825 0.2181152 3.945540   Positive
at(Env, H4-2-3):Gen 1.0299273 1.0299273 0.2983269 3.452345   Positive
at(Env, N1-0-2):Gen 1.5037956 1.5037956 0.3689780 4.075570   Positive
at(Env, N1-1-3):Gen 3.2343673 3.2343673 0.7754105 4.171168   Positive
at(Env, N2-0-1):Gen 1.1130157 1.1130157 0.2981971 3.732483   Positive
at(Env, N2-1-2):Gen 1.0060533 1.0060533 0.4536221 2.217822   Positive
at(Env, N2-2-3):Gen 1.3975117 1.3975117 0.3836845 3.642346   Positive
at(Env, N3-0-1):Gen 1.2738691 1.2738691 0.3347205 3.805769   Positive
at(Env, N3-1-2):Gen 1.6661985 1.6661985 0.4974997 3.349145   Positive
at(Env, N4-0-2):Gen 2.5757388 2.5757388 0.6840315 3.765526   Positive
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at(Env, N4-1-3):Gen 2.2742383 2.2742383 0.5300153 4.290892   Positive
at(Env, N5-0-2):Gen 1.4244282 1.4244282 0.3974351 3.584052   Positive
at(Env, N5-1-3):Gen 1.9170091 1.9170091 0.4620881 4.148579   Positive
at(Env, N6-0-1):Gen 1.5056090 1.5056090 0.4070806 3.698553   Positive
at(Env, N6-1-2):Gen 1.0322385 1.0322385 0.2738646 3.769156   Positive
at(Env, O1-0-2):Gen 1.4760750 1.4760750 0.6997587 2.109406   Positive
                        gamma component std.error  z.ratio constraint
at(Env, O1-1-3):Gen 1.6164468 1.6164468 0.5727727 2.822144   Positive
at(Env, S1-0-0):Gen 1.7296157 1.7296157 0.3966420 4.360647   Positive
at(Env, S1-1-1):Gen 1.2415815 1.2415815 0.2987371 4.156100   Positive
at(Env, S1-2-2):Gen 0.9697903 0.9697903 0.2766548 3.505416   Positive
at(Env, S3-0-1):Gen 1.1232839 1.1232839 0.2930512 3.833063   Positive
at(Env, S3-1-2):Gen 1.1503063 1.1503063 0.2932941 3.922023   Positive
at(Env, S3-2-3):Gen 1.1721879 1.1721879 0.3031388 3.866836   Positive
at(Env, S4-0-3):Gen 1.6453393 1.6453393 0.4160750 3.954430   Positive
at(Env, S4-1-4):Gen 1.1225124 1.1225124 0.3003122 3.737818   Positive
at(Env, W1-0-0):Gen 2.3994496 2.3994496 0.5620401 4.269179   Positive
at(Env, W1-1-1):Gen 0.8029267 0.8029267 0.2023816 3.967390   Positive
at(Env, W2-0-1):Gen 0.7330653 0.7330653 0.1933633 3.791130   Positive
at(Env, W2-1-2):Gen 1.0940637 1.0940637 0.2924296 3.741289   Positive

$G.E:
            gamma component  std.error   z.ratio constraint
    Gen 0.8682854 0.8682854 0.13376188  6.491277   Positive
Gen:Env 0.3562497 0.3562497 0.02010235 17.721796   Positive

$G.L.Y:
                        gamma     component  std.error   z.ratio constraint
           Gen 8.230632e-001 8.230632e-001 0.13089093  6.288160   Positive
       Gen:Loc 2.211193e-001 2.211193e-001 0.02075884 10.651811   Positive
    Gen:Cclass 2.950242e-007 2.950242e-007         NA        NA   Boundary
Gen:Loc:Cclass 1.680184e-001 1.680184e-001 0.01747339  9.615676   Positive

$G.L.Y2samm:
                    gamma component  std.error   z.ratio constraint
       Gen:Loc 0.2348359 0.2348359 0.02177624 10.784045   Positive
    Gen:Cclass 0.8190378 0.8190378 0.08549502  9.579948   Positive
Gen:Loc:Cclass 0.1711590 0.1711590 0.01835303  9.325927   Positive

$G.R:
                gamma component  std.error   z.ratio constraint
        Gen 0.7883758 0.7883758 0.12908377  6.107474   Positive
    Gen:Reg 0.1192034 0.1192034 0.01966181  6.062687   Positive
Gen:Reg:Env 0.2815653 0.2815653 0.01872265 15.038747   Positive
```

$G.R2:

	gamma	component	std.error	z.ratio	constraint
Gen	7.885941e-001	7.885941e-001	0.12906144	6.110223	Positive
Gen:Reg	7.096833e-002	7.096833e-002	0.01893220	3.748551	Positive
Gen:Reg:Loc	1.670373e-001	1.670373e-001	0.02068127	8.076745	Positive
Gen:Reg:Cclass	8.442665e-007	8.442665e-007	NA	NA	Boundary
Gen:Reg:Env	1.677405e-001	1.677405e-001	0.01746197	9.606051	Positive

$atReg.G.E:

	gamma	component	std.error	z.ratio	constraint
at(Reg, B):Gen	0.9817160	0.9817160	0.19728922	4.9760245	Positive
at(Reg, C):Gen	1.1023712	1.1023712	0.23457351	4.6994700	Positive
at(Reg, H):Gen	0.9865339	0.9865339	0.19169475	5.1463792	Positive
at(Reg, N):Gen	1.1099729	1.1099729	0.23897624	4.6446999	Positive
at(Reg, O):Gen	1.3539838	1.3539838	0.48926648	2.7673750	Positive
at(Reg, S):Gen	1.0432992	1.0432992	0.22522055	4.6323446	Positive
at(Reg, W):Gen	0.7287691	0.7287691	0.18312453	3.9796365	Positive
at(Reg, B):Gen:Loc:Cclass	0.5026612	0.5026612	0.08964561	5.6072040	Positive
at(Reg, C):Gen:Loc:Cclass	0.1853646	0.1853646	0.02699088	6.8676753	Positive
at(Reg, H):Gen:Loc:Cclass	0.2976865	0.2976865	0.03931583	7.5716715	Positive
at(Reg, N):Gen:Loc:Cclass	0.4518652	0.4518652	0.05762170	7.8419273	Positive
at(Reg, O):Gen:Loc:Cclass	0.1070462	0.1070462	0.29867907	0.3583988	Positive
at(Reg, S):Gen:Loc:Cclass	0.1207939	0.1207939	0.03134550	3.8536294	Positive
at(Reg, W):Gen:Loc:Cclass	0.3821367	0.3821367	0.07987927	4.7839283	Positive

$atReg.G.L.Y:

	gamma	component	std.error	z.ratio	constraint
at(Reg, B):Gen	7.578117e-001	7.578117e-001	0.19500179	3.88617799	Positive
at(Reg, C):Gen	1.096147e+000	1.096147e+000	0.23431204	4.67814861	Positive
at(Reg, H):Gen	9.488429e-001	9.488429e-001	0.19248933	4.92932725	Positive
at(Reg, N):Gen	1.085452e+000	1.085452e+000	0.23958681	4.53051790	Positive
at(Reg, O):Gen	9.451553e-001	9.451553e-001	0.45710002	2.06772098	Positive
at(Reg, S):Gen	1.012524e+000	1.012524e+000	0.22643602	4.47156707	Positive
at(Reg, W):Gen	7.287692e-001	7.287692e-001	0.18312515	3.97962369	Positive
at(Reg, B):Gen:Loc	5.055816e-001	5.055816e-001	0.10674784	4.73622271	Positive
at(Reg, C):Gen:Loc	2.815962e-002	2.815962e-002	0.02110395	1.33432915	Positive
at(Reg, H):Gen:Loc	1.742784e-001	1.742784e-001	0.04176272	4.17306141	Positive
at(Reg, N):Gen:Loc	2.797499e-001	2.797499e-001	0.05738172	4.87524532	Positive
at(Reg, O):Gen:Loc	2.950242e-001	2.950242e-001	NA	NA	Singular
at(Reg, S):Gen:Loc	9.856405e-002	9.856405e-002	0.03688729	2.67203295	Positive
at(Reg, W):Gen:Loc	1.159703e-007	1.159703e-007	NA	NA	Boundary
at(Reg, B):Gen:Cclass	1.557512e-001	1.557512e-001	0.07038324	2.21290210	Positive
at(Reg, C):Gen:Cclass	2.950242e-007	2.950242e-007	NA	NA	Boundary

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    at(Reg, H):Gen:Cclass 2.116517e-004 2.116517e-004 0.02090750 0.01012324   Positive
    at(Reg, N):Gen:Cclass 1.412291e-007 1.412291e-007         NA         NA   Boundary
    at(Reg, O):Gen:Cclass 1.627257e-007 1.627257e-007         NA         NA   Boundary
    at(Reg, S):Gen:Cclass 2.950242e-007 2.950242e-007         NA         NA   Boundary
    at(Reg, W):Gen:Cclass 9.028038e-007 9.028038e-007         NA         NA   Boundary
at(Reg, B):Gen:Loc:Cclass 1.436307e-002 1.436307e-002 0.08263290 0.17381785   Positive
at(Reg, C):Gen:Loc:Cclass 1.604330e-001 1.604330e-001 0.02983960 5.37651541   Positive
                                 gamma     component  std.error    z.ratio constraint
at(Reg, H):Gen:Loc:Cclass 1.564904e-001 1.564904e-001 0.04143094 3.77713840   Positive
at(Reg, N):Gen:Loc:Cclass 1.821682e-001 1.821682e-001 0.05479523 3.32452674   Positive
at(Reg, O):Gen:Loc:Cclass 2.950242e-001 2.950242e-001         NA         NA   Singular
at(Reg, S):Gen:Loc:Cclass 7.677440e-002 7.677440e-002 0.02854774 2.68933358   Positive
at(Reg, W):Gen:Loc:Cclass 3.821370e-001 3.821370e-001 0.07987955 4.78391559   Positive

$atReg.G.E.R:
                       gamma component  std.error   z.ratio constraint
    at(Reg, B):Gen 0.9820808 0.9820808 0.19734217 4.9765378   Positive
    at(Reg, C):Gen 1.1032392 1.1032392 0.23467042 4.7012283   Positive
    at(Reg, H):Gen 0.9859229 0.9859229 0.19163709 5.1447393   Positive
    at(Reg, N):Gen 1.1099723 1.1099723 0.23897613 4.6446993   Positive
    at(Reg, O):Gen 1.3528906 1.3528906 0.48912202 2.7659572   Positive
    at(Reg, S):Gen 1.0404270 1.0404270 0.22595088 4.6046602   Positive
    at(Reg, W):Gen 0.7303461 0.7303461 0.18381931 3.9731738   Positive
at(Reg, B):Gen:Env 0.5021353 0.5021353 0.08966764 5.5999617   Positive
at(Reg, C):Gen:Env 0.1553646 0.1553646 0.02676003 5.8058453   Positive
at(Reg, H):Gen:Env 0.2992437 0.2992437 0.03946426 7.5826509   Positive
at(Reg, N):Gen:Env 0.4518656 0.4518656 0.05762186 7.8419128   Positive
at(Reg, O):Gen:Env 0.1084089 0.1084089 0.29950184 0.3619642   Positive
at(Reg, S):Gen:Env 0.1388583 0.1388583 0.03573427 3.8858582   Positive
at(Reg, W):Gen:Env 0.3736907 0.3736907 0.07952554 4.6990024   Positive

$G.newReg:
                     gamma component  std.error   z.ratio constraint
            Gen 0.7877074 0.7877074 0.13045719  6.038053   Positive
    Gen:RegAgg2 0.1039964 0.1039964 0.02373853  4.380914   Positive
Gen:RegAgg2:Env 0.3133375 0.3133375 0.01920043 16.319295   Positive

$atG.newReg:
                                gamma component  std.error    z.ratio constraint
      at(RegAgg2, Btype):Gen 0.8737167 0.8737167 0.16445136  5.3129191   Positive
     at(RegAgg2, CStype):Gen 0.8908765 0.8908765 0.16974059  5.2484588   Positive
     at(RegAgg2, NHtype):Gen 1.0829182 1.0829182 0.20223703  5.3546978   Positive
    at(RegAgg2, Ordtype):Gen 1.3528904 1.3528904 0.48912200  2.7659570   Positive
  at(RegAgg2, Btype):Gen:Env 0.4949017 0.4949017 0.06703615  7.3826086   Positive
```

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 at(RegAgg2, CStype):Gen:Env 0.2385627 0.2385627 0.02225691 10.7185917   Positive
 at(RegAgg2, NHtype):Gen:Env 0.3474620 0.3474620 0.03488873  9.9591492   Positive
at(RegAgg2, Ordtype):Gen:Env 0.1084091 0.1084091 0.29950197  0.3619647   Positive

$G.RTable:
                 gamma component  std.error   z.ratio constraint
         Gen 0.7855673 0.7855673 0.12896813  6.091174   Positive
    Gen:Reg2 0.1369564 0.1369564 0.02042238  6.706193   Positive
Gen:Reg2:Env 0.2683294 0.2683294 0.01835481 14.619027   Positive

$atG.RTable:
                       gamma component  std.error   z.ratio constraint
    at(Reg2, B):Gen 0.9817160 0.9817160 0.19728922 4.9760245   Positive
    at(Reg2, C):Gen 1.1023712 1.1023712 0.23457351 4.6994700   Positive
    at(Reg2, H):Gen 0.9865339 0.9865339 0.19169475 5.1463792   Positive
    at(Reg2, N):Gen 1.2403628 1.2403628 0.27123663 4.5729914   Positive
    at(Reg2, O):Gen 1.3539838 1.3539838 0.48926648 2.7673750   Positive
    at(Reg2, S):Gen 1.0432992 1.0432992 0.22522055 4.6323446   Positive
    at(Reg2, T):Gen 1.0304927 1.0304927 0.24519062 4.2028226   Positive
    at(Reg2, W):Gen 0.7287691 0.7287691 0.18312453 3.9796365   Positive
at(Reg2, B):Gen:Env 0.5026612 0.5026612 0.08964561 5.6072040   Positive
at(Reg2, C):Gen:Env 0.1853646 0.1853646 0.02699088 6.8676753   Positive
at(Reg2, H):Gen:Env 0.2976865 0.2976865 0.03931583 7.5716715   Positive
at(Reg2, N):Gen:Env 0.4466749 0.4466749 0.07196427 6.2068982   Positive
at(Reg2, O):Gen:Env 0.1070462 0.1070462 0.29867907 0.3583988   Positive
at(Reg2, S):Gen:Env 0.1207939 0.1207939 0.03134550 3.8536294   Positive
at(Reg2, T):Gen:Env 0.2197182 0.2197182 0.08651817 2.5395615   Positive
at(Reg2, W):Gen:Env 0.3821367 0.3821367 0.07987927 4.7839283   Positive
```