

**BUREAU OF SUGAR EXPERIMENT STATIONS  
QUEENSLAND, AUSTRALIA**

**Final Report  
SRDC Project BSES  
Genotype X Environment Interaction for Clones  
and Crosses planted in Southern Queensland  
and northern New South Wales  
by Dr J K Bull  
SD97018**

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## **SUMMARY**

The main aims of this project were to assess whether original seedling families produced for south Queensland would be suitable for the New South Wales sugar industry and to determine whether clones selected at the Bundaberg Sugar Experiment Station would perform similarly under northern New South Wales cropping conditions.

### **Families**

In general families produced by the NSW program displayed no advantage over families produced in south Queensland by BSES. Given that the NSW families involved parents that were adapted to NSW conditions and a two-year cropping cycle and that the BSES families involved parents adapted to Queensland conditions and a one-year cropping cycle, this is an excellent result for the BSES program in NSW.

Based on the way in which environments discriminated among families there did not appear to be clear and repeatable differences among environments from Queensland and NSW. Therefore, families can be selected for NSW either based on their performance in NSW or in Bundaberg, Queensland. Based on results from simulated selection, the Bundaberg program could be altered to better service both south Queensland and NSW by evaluating more families at one well-resourced central location.

### **Clones**

A large percentage of clones selected at Bundaberg performed better than the best NSW standard (average 28%) for all one-year crops. For the two-year crops, this advantage was smaller (average 10%) but still indicated that substantial improvement could be made rapidly from the BSES selection system. The gain in sugar yield for the BSES clones, similarly, indicated massive improvement under a one-year cropping system (average 45%) and substantial improvement under a two-year cropping regime (15%).

While there were consistent differences among environments from Queensland and NSW, based on the way in which they discriminated among clones, these differences did not mitigate against making substantial gains in NSW using selection based in Queensland. The results from simulated selection indicate that the Queensland and NSW programs should be more fully integrated, that the number of clones evaluated be increased and that this increase be offset by a proportionate reduction in the number of years and locations used in advanced trials in south Queensland and NSW.

## **BACKGROUND**

The New South Wales (NSW) sugar industry has historically bred its own varieties and directly imported cultivars from overseas. CSR Pty Ltd provided seed and breeding related advice to the NSW Sugar Milling Co-operative (NSWSMC) on a contract basis, and the NSWSMC conducted a small routine selection program to produce one and two year cultivars specifically suited to the local conditions.

This meant that the NSW industry relied heavily on cultivars that had been imported directly from overseas. Given quarantine restrictions on the number of imports per year and exchange protocols which meant many countries only exchanged proven cultivars (rather than elite clones), many of the foreign cultivars used commercially in NSW were originally released in their country of origin many years (decades) earlier. Consequently, many of the foreign cultivars had often been superseded in their home country of origin some time ago.

Over the same period the Queensland industry has become markedly less reliant on directly released foreign cultivars. The Queensland trend coincided with BSES substantially increasing its expenditure on sugarcane breeding and selection and using more scientifically based breeding and selection methods (eg, objective yield assessments, family selection, regional testing, photoperiod facilities for planned cross production, etc).

The NSW industry did not have open access to the superior cultivars released by BSES and, therefore, could not avail themselves of the substantial genetic gains being made by the Queensland-based breeding programs.

Additionally, the NSW breeding and selection program only received part time supervision, operated on a proportionally much smaller budget, and was not well placed to adopt the advances in breeding and selection methodology being made in Queensland. Given this background and the urgent need for improved sugarcane cultivars in NSW, it was decided that a trial to test the relative performance of BSES families and clones in NSW was required. If substantial benefits were demonstrated by the BSES germplasm, a contractual arrangement could be made and the improved BSES germplasm supplied to NSW.

## **OBJECTIVES**

The objectives of this project were as follows:

- 1) compare the performance of families and clones produced by BSES for south Queensland with those routinely used in the NSW breeding program, under NSW growing conditions - *in order to assess the need for a separate breeding and selection program for NSW*
- 2) assess the similarities between locations used in this trial based on their discrimination among families or clones, respectively - *in order to evaluate options for improving selection efficiency (cost/benefit)*
- 3) monitor environmental parameters so that key environmental factors leading to differences in the discrimination among families and clones at the different locations may be identified
- 4) assess the potential of families and clones selected for 12-month cropping in Queensland to produce 24-month crops in NSW
- 5) compare the frost tolerance of advanced clones in south Queensland and New South Wales
- 6) select families with outstanding performance in NSW for further testing in larger populations and identify elite clones for use as parents in subsequent families

## **1.0 INTRODUCTION**



Sugarcane breeding is a lengthy and expensive process. In Australia the BSES program involves making bi-parental crosses to generate seed at a central crossing facility, located at Meringa, Cairns, and subsequently testing this germplasm over a large and geographically, managerially, and environmentally diverse area.

Genotype x environment interaction (GxE) for yield has been found to be large enough to complicate selection in most commercially important crop species (DeLacy *et al*, 1990). This is also the case in sugarcane where both family x environment interaction (FxE) and clone x environment interaction (CxE) may be as large as the main effect of family or clone, respectively (Jackson *et al*, 1991; Bull *et al*, 1992a; Mirzawan *et al*, 1993). As a result of the influence of GxE on genotypic performance, plant breeding trials are usually conducted across a representative sample of environments (Byth *et al*, 1976; DeLacy *et al*, 1990). Such multi-environment testing is time consuming and costly but is critical to identifying specifically and broadly adapted genotypes.

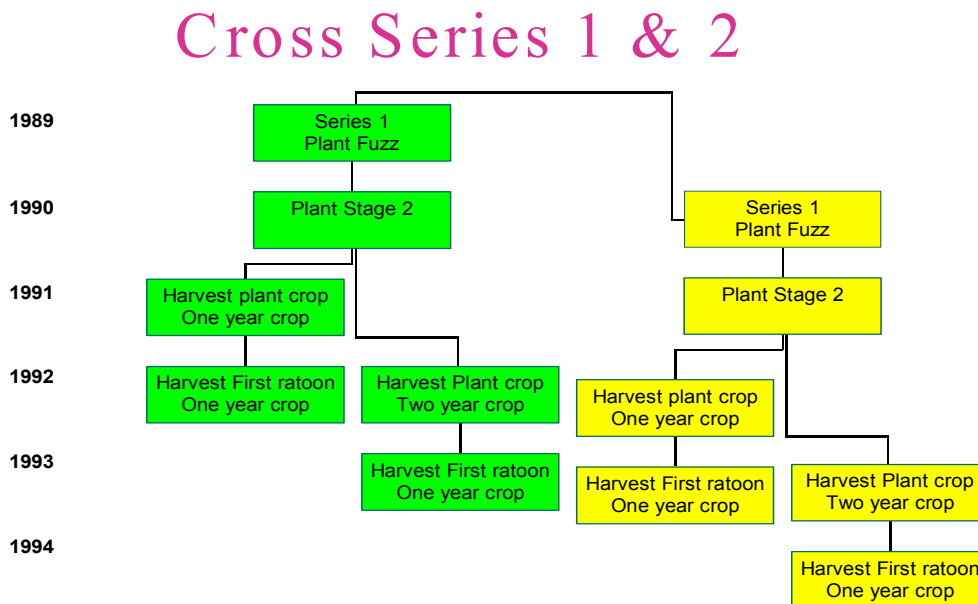
Consequently the definition of a sufficient number of test environments and/or mega-environments to determine optimal multi-environment testing regimes is of crucial importance (Brennan *et al*, 1981; Gauch and Zobel, 1989, 1997). The success or otherwise of a multi-environment testing regime depends on how well the sample of environments relates to the range of production environments in the target population (Comstock, 1977; Cooper *et al*, 1993b; Cooper and DeLacy, 1994).

In sugarcane breeding, this has led BSES to adopt five discrete breeding programs to provide locally adapted cultivars suited to the different areas or regions within Queensland. Given the possibility of BSES providing a selection program to service the NSW industry it was important to identify whether or not the interaction between family and region or clone and region is sufficiently large to justify using another discrete breeding and selection program for NSW. The possibility of linking certain selection stages in NSW with those in the southern Queensland program was of particular interest, as economies of scale could be sought, yielding greater gains per dollar expended. Before such a rationalisation can be implemented, it is necessary to establish the extent of similarity of family and clone performance across NSW and Queensland.

This project was designed to compare the performance of an appropriate number of families and unselected clones across environments within both Queensland and NSW over several years. To sample both family x region and clone x region interaction as well as family x environment within region and clone x environment within region interaction the experiment was repeated using a largely independent set of families and clones planted one year later. The benefits for NSW in obtaining germplasm (families and clones) from BSES were identified and assessed. The information obtained in this project was also used to assess options to maximise the gain from selection on a per dollar basis by optimising the number of clones, regions, locations, years and replicates that are used in the southern Queensland and NSW programs.

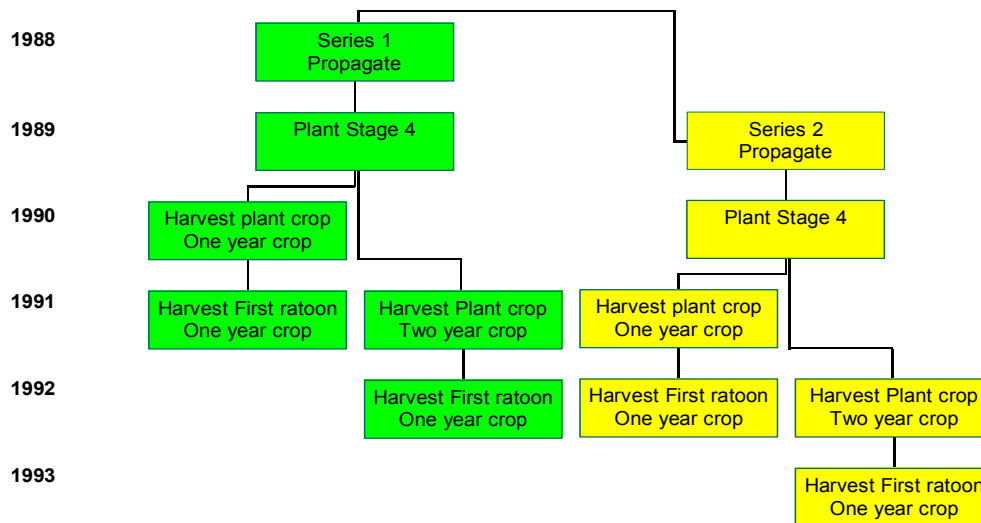
## **2.0 EXPERIMENTAL DETAILS**

A number of trials was planted throughout the cane growing areas of NSW and southern Queensland to determine whether BSES families and clones were superior to the NSW families and clones. To obtain sufficient confidence in the results the entire set of trials was repeated one year later (giving rise to two series of trials). So two series of trials were conducted for the families component in Queensland and NSW (Figure 1) and, similarly, two series of trials were conducted for the clonal component in Queensland and NSW (Figure 2).



**Figure 1. Diagram of the sequence of events for the two series of families grown in Queensland and NSW.**

## Clonal Series 1 & 2



**Figure 2. Diagram of the sequence of events for the two series of clones grown in Queensland and NSW.**

### 2.1 Families

In 1989 the series 1 families trial was established at three locations in NSW (Condong, Broadwater and Harwood) and one in Queensland, the Sugar Experiment Station at Bundaberg (Appendix 1). In order to compare the two sources of families available to the NSW plant breeding program, ‘fuzz’ from 20 families from both the CSR and BSES breeding programs was used to establish family plots at the NSW locations. Fuzz from the BSES families was planted at Bundaberg. The performance of CSR families at this location was not relevant to an assessment of the similarities between the NSW locations and Bundaberg, which may be exploited by BSES germplasm.

At each location 40 randomly chosen clones were planted from each of the 40 families (20 from BSES and 20 from CSR). Four blocks were used at each location and 10 clones from each family were planted as family plots in each block. There was one row with ten 2 m plots per ‘family plot’.

The series 2 trial was established in 1991 and was similar in design to the series 1 (Appendix 1). Nine families were kept in common between the two series.

In each series the trials at Bundaberg and Condong were assessed after one-year’s growth in both plant and first ratoon. However, to simulate grower practice at Harwood and Broadwater, families were harvested after two-year’s growth in the plant crop. To limit the duration of the experiment, families were harvested after one-year’s growth at all environments in the first ratoon.

## 2.2 Clones

The first series of trials was established in 1988. It involved 97 clones which were split into two trial series, 1a (54 clones) and 1b (43 clones), being evaluated for sugar yield (t/ha) at seven locations; of which four were in south-eastern Queensland (Queensland) and three in north-eastern NSW (Appendix 1). The four Queensland locations were the Bundaberg Experiment Station, Bingera sub-station, Fritz sub-station and Maryborough sub-station; and the three NSW locations were Condong, Broadwater and Harwood. The 54 clones in series 1a were comprised of 37 clones selected from a Stage 3 at Bundaberg for superior yield performance and 17 randomly chosen clones. Likewise, the 43 clones in series 1b were comprised of 29 selected clones and 14 randomly chosen clones from the same Bundaberg Stage 3. A randomised complete block design of two replicates was used to evaluate the clones at each location. Each clone was planted in a single row 10m plot in each replicate.

Clones were machine harvested after one-year's growth at the four Queensland locations and at Condong in NSW. Clones at the other two NSW locations were sample harvested after one-year's growth, machine harvested after two-year's growth in the plant crop and machine harvested after one-year's growth in the first ratoon crop. For the sample harvests the weight of cane in each plot (tonnes of cane per hectare, TCH) was estimated by weighing ten randomly chosen stalks and multiplying this weight by the total number of stalks. For the machine harvested trials the whole was weighed using a mobile weighing truck.

In each trial a sample of three or four stalks was taken from each plot to determine commercial cane sugar (CCS), which provides an estimate of the percentage recoverable sucrose in millable cane. Sugar yield per hectare was calculated from the product of CCS and TCH divided by 100.

The second series of trials was initiated in 1989 and involved 69 relatively unselected clones being evaluated for sugar yield (t/ha) at eight locations; of which five were in south-eastern Queensland (Queensland) and three in north-eastern New South Wales (NSW) (Appendix 1). The five Queensland locations were the Bundaberg Experiment Station, Bingera sub-station, Ferguson sub-station, ISIS sub-station, Maryborough sub-station and the Nambour sub-station; and the three NSW locations were Condong, Broadwater and Harwood. The 69 clones in series 2 were comprised of 47 selected clones and 22 randomly chosen clones from a Bundaberg Stage 3. A randomised complete block design of two replicates was used to evaluate the clones at each location and each clone was planted to a single row 10m plot.

All trials in the second series were machine harvested. Clones at the five Queensland locations and Condong in NSW were machine harvested after one-year's growth in both the plant and first ratoon crops. Clones at the other two NSW locations were machine harvested after two-year's growth in the plant crop and machine harvested after one-year's growth in the first ratoon crop. Sample weights and CCS were estimated as for the first series.

### 2.3 Environmental Monitoring and Frost Tolerance

To quantify broad environmental similarities between Queensland and NSW, ambient environmental conditions were monitored using weather stations located at one site at Bundaberg (1991-1996), Broadwater (1993-1994) and Harwood (1990-1994).

Frost tolerance was assessed opportunistically by planting clonal trials within the frost prone regions of both Broadwater and Harwood and assessing frost damage after a frost event. However, over the duration of the experiment frosting only affected one trial (in Broadwater) and was so severe that (useful) clonal differences could not be detected (data not reported).

### 2.4 Analytical methods

#### 2.4.1 Analysis of Variance (ANOVA)

Completely random models were used so that inference from these analyses could be drawn to wider applications. Apart from the grand mean, each effect was assumed to be normally distributed with a mean of zero and a particular constant variance. For simplicity, the linear model equations used are not presented.

#### 2.4.2 Classification

For each series of clones the blocks were considered to be different environments and were grouped using cluster analysis (Bull *et al*, 1994). An hierarchical agglomerative clustering procedure with Ward's method (Ward, 1963) as the fusion strategy and unstandardised squared Euclidean distance as the dissimilarity measure (Wishart, 1969; Burr, 1970) was used for all classifications. The data were transformed before classification. The raw data from each block were first scaled (standardised) by dividing by the block's phenotypic standard deviation, then centred by removing the block effect. This transformation leads to the same squared Euclidean distance values that would be calculated using the standardised data procedure of Fox and Rosielle (1982). Standardising the phenotypic variability of each block and removing the main effect of block, allows blocks to be grouped according to the way in which they discriminate among the clones, without their overall means or magnitudes of variance contributing to the classification. This data transformation was chosen as it has been shown to relate classification methodology to selection theory in plant breeding (Cooper and DeLacy, 1994).

If the variability due to genotype  $\times$  block within environment interaction ((GxB)/E) and experimental error within an environment was small, relative to that due to genotype  $\times$  environment (GxE) interaction, then block-groups each consisting of the two blocks from a particular environment would be an appropriate summary of the data.

For families the mean over replicates was found for each location and a similar procedure used.

### 2.4.3 Principal Component Analysis (PCA)

For clones, blocks were again considered to be different environments, and a PCA of blocks was performed for each series. The PCA was used to provide a graphic illustration (Chatfield and Collins, 1980) of the relationships among blocks, based on their discrimination among clones. The data were transformed before ordination using the same procedure as detailed for classification.

If the variability due to (GxB)/E interaction and experimental error within an environment was small, relative to that due to GxE interaction, then the two blocks from each environment may be placed in close proximity while blocks from different environments may be placed more distantly.

For families a PCA was conducted on the mean data over replicates within each location.

### 2.4.4 Efficiency of Selection

The efficiency of selection was calculated using standard genetic formulae (Falconer, 1989), as follows:

$$\text{Efficiency}_{(x/y)} = r_{gxy}h_y/h_x$$

where:

$r_{gxy}$  = genetic correlation among environments  $x$  and  $y$

$h_y$  = heritability, on a genotype mean basis, in environment  $y$

$h_x$  = heritability, on a genotype mean basis, in environment  $x$

(Note: It was taken that the same selection intensity would be used in both environments and that accordingly this term cancels out.)

Put simply, efficiency is the estimated gain from indirect selection divided by the estimated gain from direct selection.

To simplify the comparisons among possible options the estimated efficiency between each pair of environments was averaged over the series involved. These data were then averaged over environment pairs involved in the selection scenarios of most interest.

### 2.4.5 Simulated Selection

The gains from simulated selection based on various numbers of genotypes, replicates within locations, locations, and years were calculated using standard genetic formulae as follows:

$$\text{Gain} = i\sigma_g h$$

where,

$$i = 0.8 + 0.41 * \ln(1/P_s - 1)$$

$P_s$  = proportion selected

$\sigma_g$  = square root of the estimated variance component for genotypes

$h$  = the square root of heritability, on a genotype mean basis.

For each estimated variance component used in this formula, the @Risk<sup>®</sup> simulation program was used to randomly sample an estimate based on a normal distribution with mean equal to the estimated variance component and variance equal to its associated standard error. These new variance component estimates were then averaged over trial series and genetic gain was calculated. This process was repeated 1,000 times for each scenario.

The predicted gain (and its associated standard error) for each scenario was calculated and was expressed as a percentage gain over the current evaluation system.

The predicted gains associated with increased numbers of genotypes are based on selecting the same number of genotypes (ie a higher selection intensity).

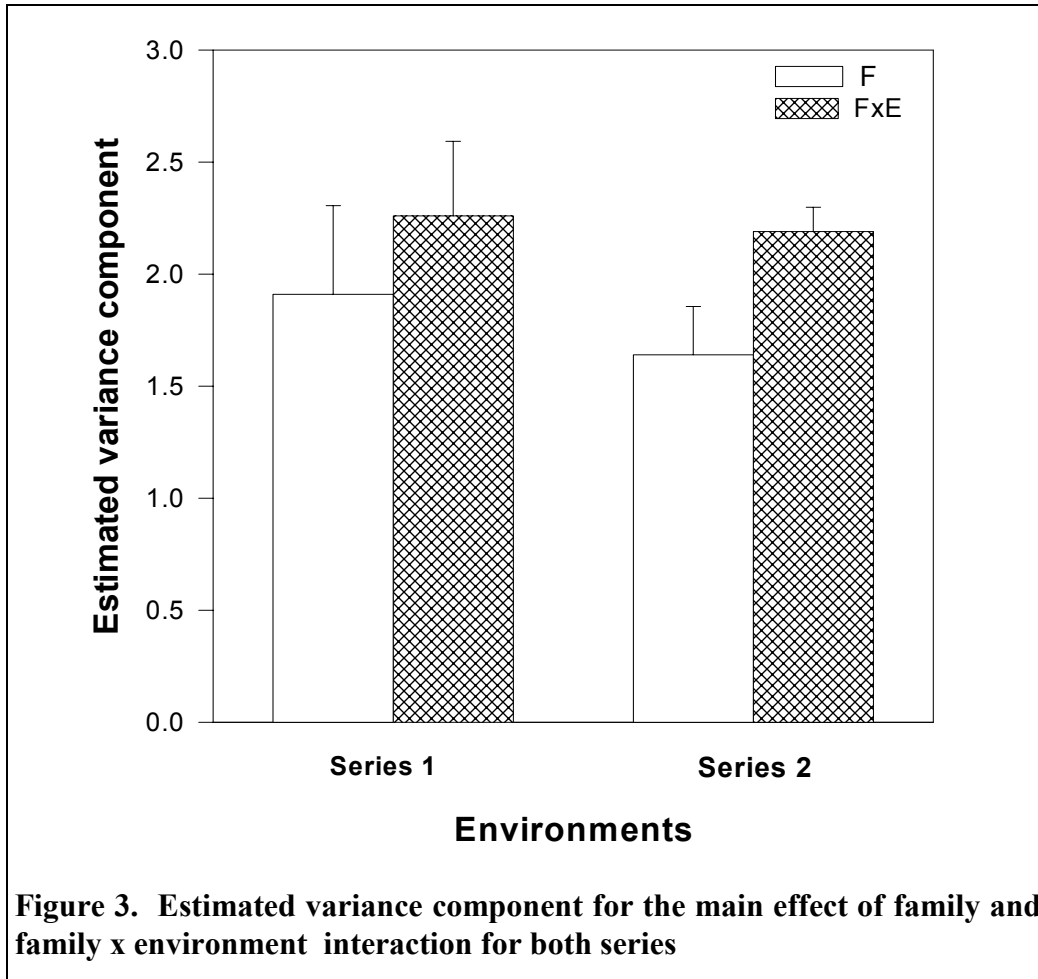
### **3.0 RESULTS AND DISCUSSION**

#### **3.1 Families**

##### **3.1.1 ANOVA**

Coefficients of variation (CV) for the individual analyses of sugar yield for each environment in the two series (12 analyses in total) were less than 35% (Appendix 2). The majority of these trials had an acceptable level of experimental error for Stage 2 family yield evaluation trials. It is worth noting that the experimental error term for this stage of selection is inflated because some genetic differences are included in the error term as individual clones are not replicated across experimental units.

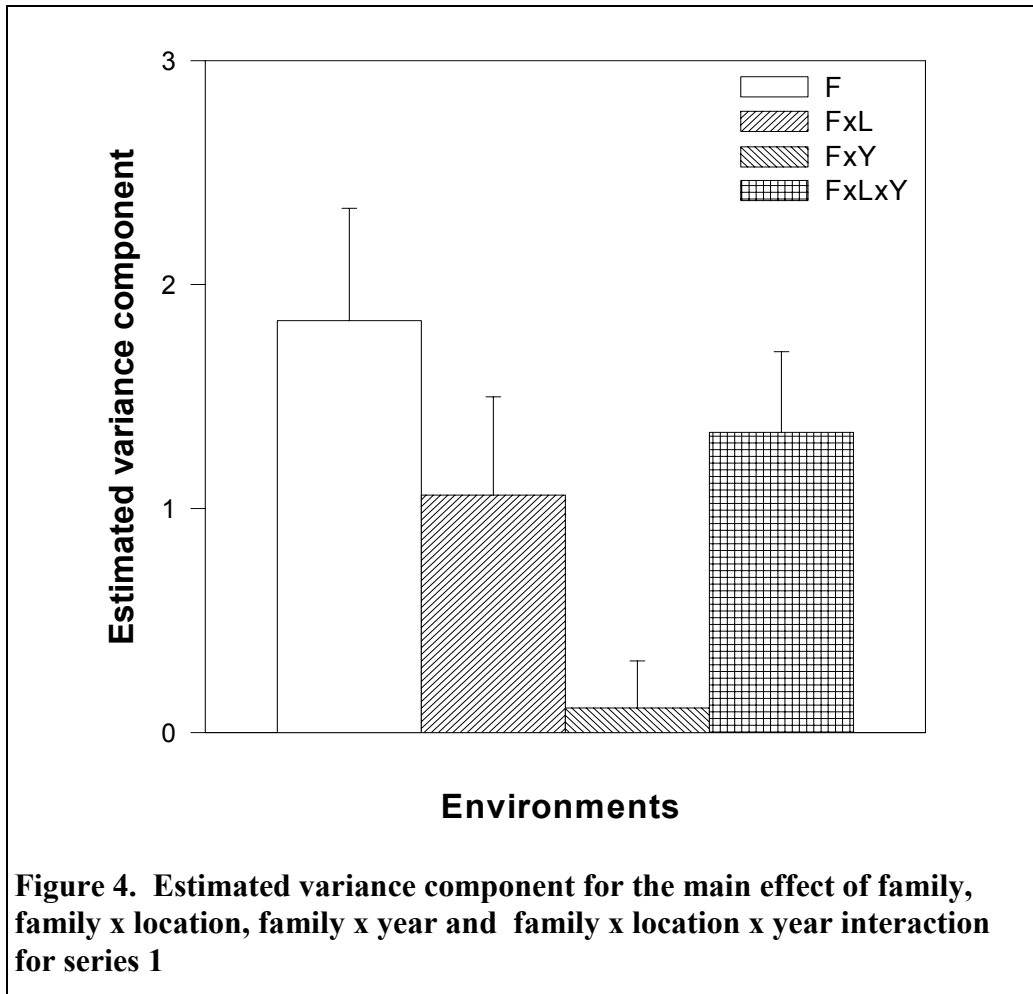
Across all trial environments, family and family  $\times$  environment interaction (FxE) were highly significant ( $P < 0.01$ ) for each of the two series. Estimated variance components for family and FxE across all trials for each series and are given in Figure 3. The relative ratios of the amount of variation associated with FxE to that associated with the main effect of family for series 1 and 2, were 119% and 138%, respectively. These ratios suggest that the interaction effect was as important as the main effect of family.



For the nine families that were common to both series both family and FxE were highly significant. The variation associated with FxE was 143% of the main effect of family for these data.

For series 1 the estimated variance components for family, family x location interaction (F<sub>x</sub>L), family x year interaction (F<sub>x</sub>Y) and family x location x year interaction (F<sub>x</sub>L<sub>x</sub>Y) interactions were estimated (Figure 4). To obtain a balanced data set the Broadwater two-year plant crop was omitted as subsequent ratoon crop was not harvested. The 'year' term in this analysis was not 'cleanly' estimated and represents a confounding of year, crop-age and crop-class. Due to the lack of first ratoon crops in three of the four locations used in series 2 no estimates were made.





From this analysis the second order interaction and the FxL were large relative to the main effect of family. Without additional information, the second order interaction may be taken as representing unpredictable interaction, whereas the FxL interaction may be taken as predictable interaction generated from differential family performance at these locations.

### 3.1.2 Performance

The sugar yield performance of the BSES and NSW families was compared for each harvest of each series (Table 1)

**Table 1. Performance of BSES and NSW families for both series 1 and 2 in NSW.**

| Location       | Series | Crop class <sup>a</sup> | Crop age          | Number of BSES families |            | Sugar yield gain (%)             |  |
|----------------|--------|-------------------------|-------------------|-------------------------|------------|----------------------------------|--|
|                |        |                         |                   | Top 10                  | Bottom 10  | for best BSES cross <sup>b</sup> | for the best 10 BSES families over the best 10 NSW families <sup>c</sup> |
| Condong        | 1      | P                       | 1-yr              | 9                       | 1          | 15.1                             | 22.5   |
|                |        | 1R                      | 1-yr              | 7                       | 3          | 11.2                             | 10.4   |
|                | 2      | P                       | 1-yr              | 2                       | 7          | 2.4                              | -11.7  |
| Broadwater     | 1      | P                       | 2-yr              | 4                       | 4          | -9.5                             | -7.3   |
|                | 2      | P                       | 1-yr              | 4                       | 4          | 3.3                              | -4.5   |
| Harwood        | 1      | P                       | 2-yr              | 9                       | 4          | 8.3                              | 18.5   |
|                |        | 1R                      | 1-yr              | 6                       | 4          | -2.1                             | 2.5  |
|                | 2      | P                       | 2-yr              | 4                       | 4          | -8.3                             | -8.1   |
|                |        | 1R                      | 1-yr              | 2                       | 7          | -24.9                            | -15.5  |
| <b>Average</b> |        |                         | <b>1-yr</b>       | <b>5.0</b>              | <b>4.3</b> | <b>0.8</b>                       | <b>0.6</b>   |
|                |        |                         | <b>2-yr</b>       | <b>5.7</b>              | <b>4.0</b> | <b>-3.2</b>                      | <b>1.0</b>   |
|                |        |                         | <b>1&amp;2-yr</b> | <b>5.2</b>              | <b>4.2</b> | <b>-0.5</b>                      | <b>0.8</b>   |

<sup>a</sup>P = plant crop, 1R= First ratoon

<sup>b</sup>(Yield of best BSES family - Yield of best NSW family)/(Yield of best NSW family)

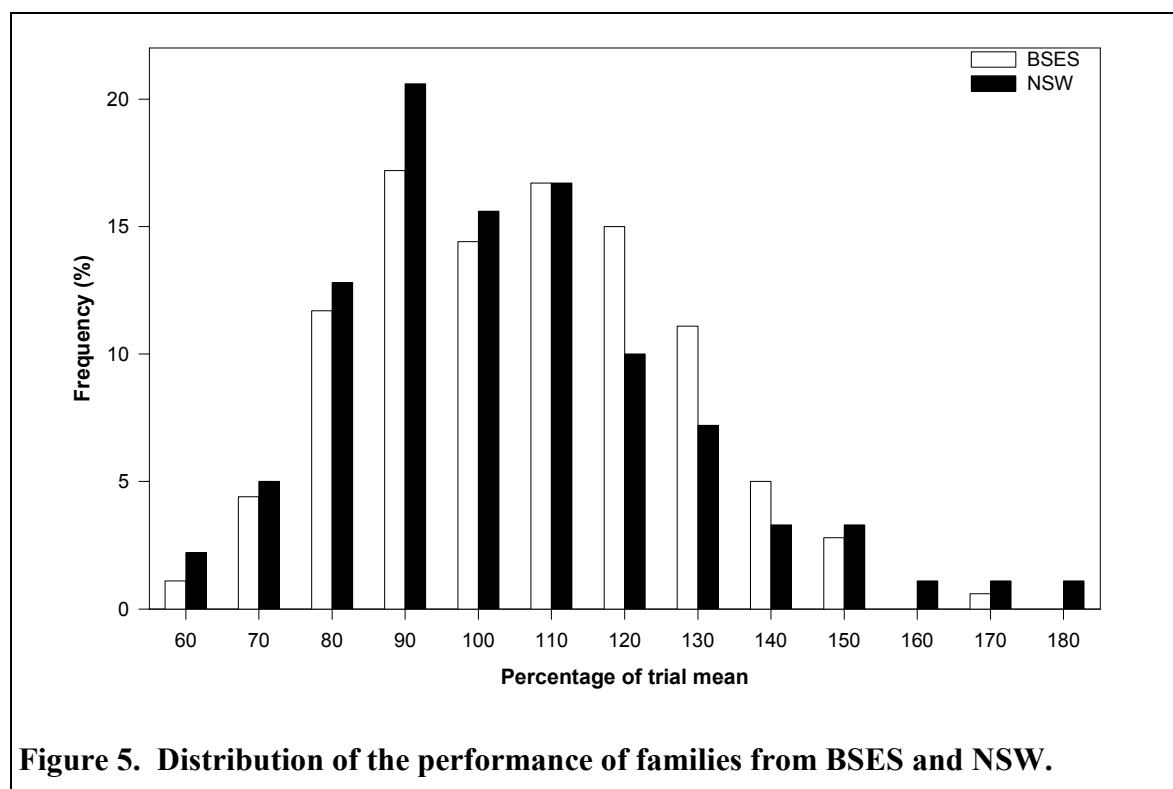
<sup>c</sup>(Yield of best 10 BSES families - Yield of best 10 NSW families)/(Yield of best 10 NSW families)

The number of families in the top ten from BSES and NSW over all trials was, on average, marginally in favour of BSES. However, this advantage did not translate into substantial yield gains, with less than a one percentage point differential between the two sources of material. However, at Condong there were generally more positive gains from using BSES families.

By conducting an ANOVA of the performance of families based on their respective sources (BSES or NSW) over all of the NSW trials significant differences were identified ( $P < 0.001$ ). For the first series the BSES families were on average significantly superior

by 10%, but for the second series the NSW families were on average significantly superior by 14%.

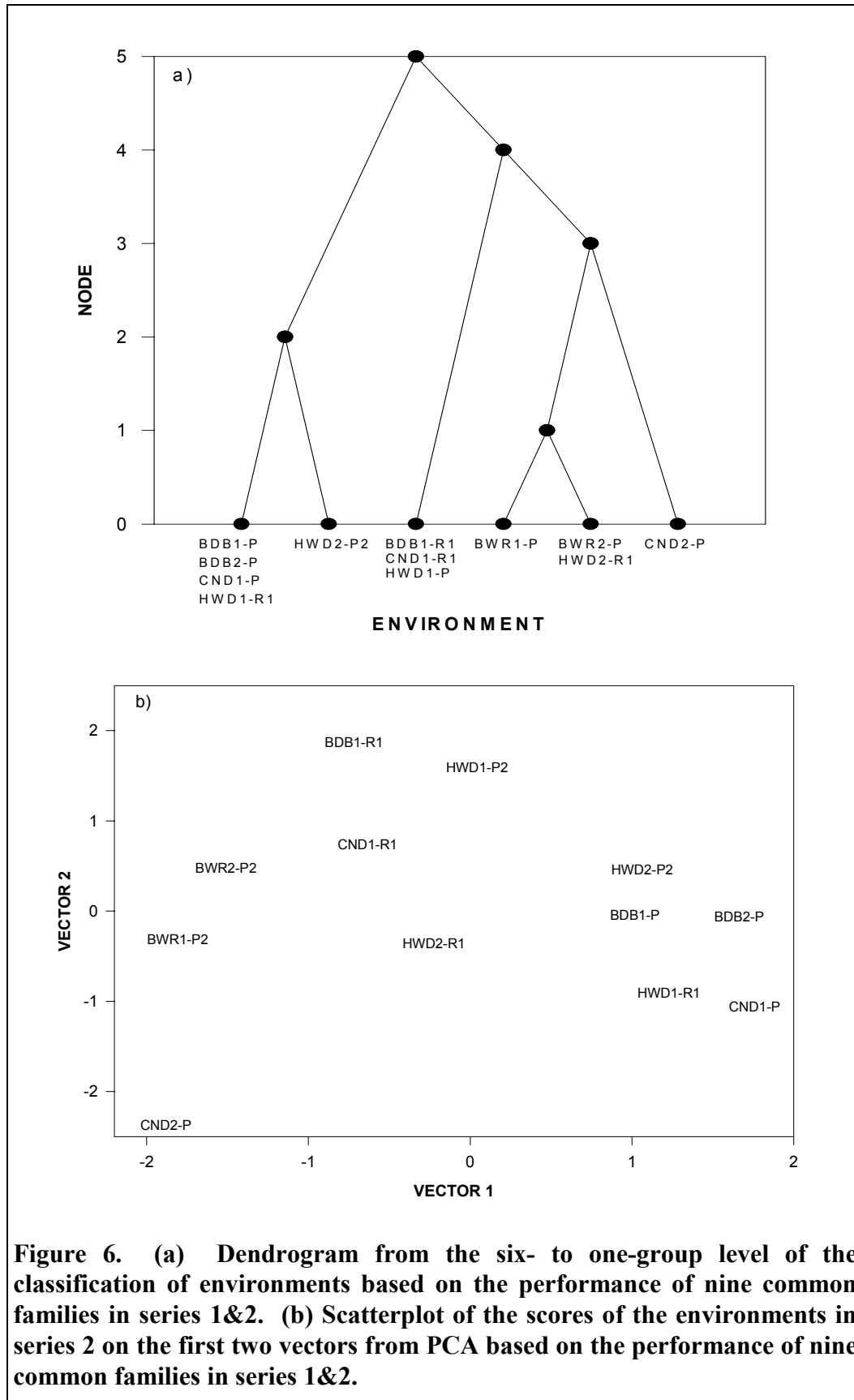
To examine the distribution in sugar yield performance of families from the two sources within the NSW trials, family performance was determined as a percentage of the trial mean and all of the data combined (Figure 5). The frequency of superior families from NSW were higher beyond 150% better than the trial mean but were lower from 110% to 140% of the trial mean. Since the differences were not dramatic either of these two source of families would be acceptable.



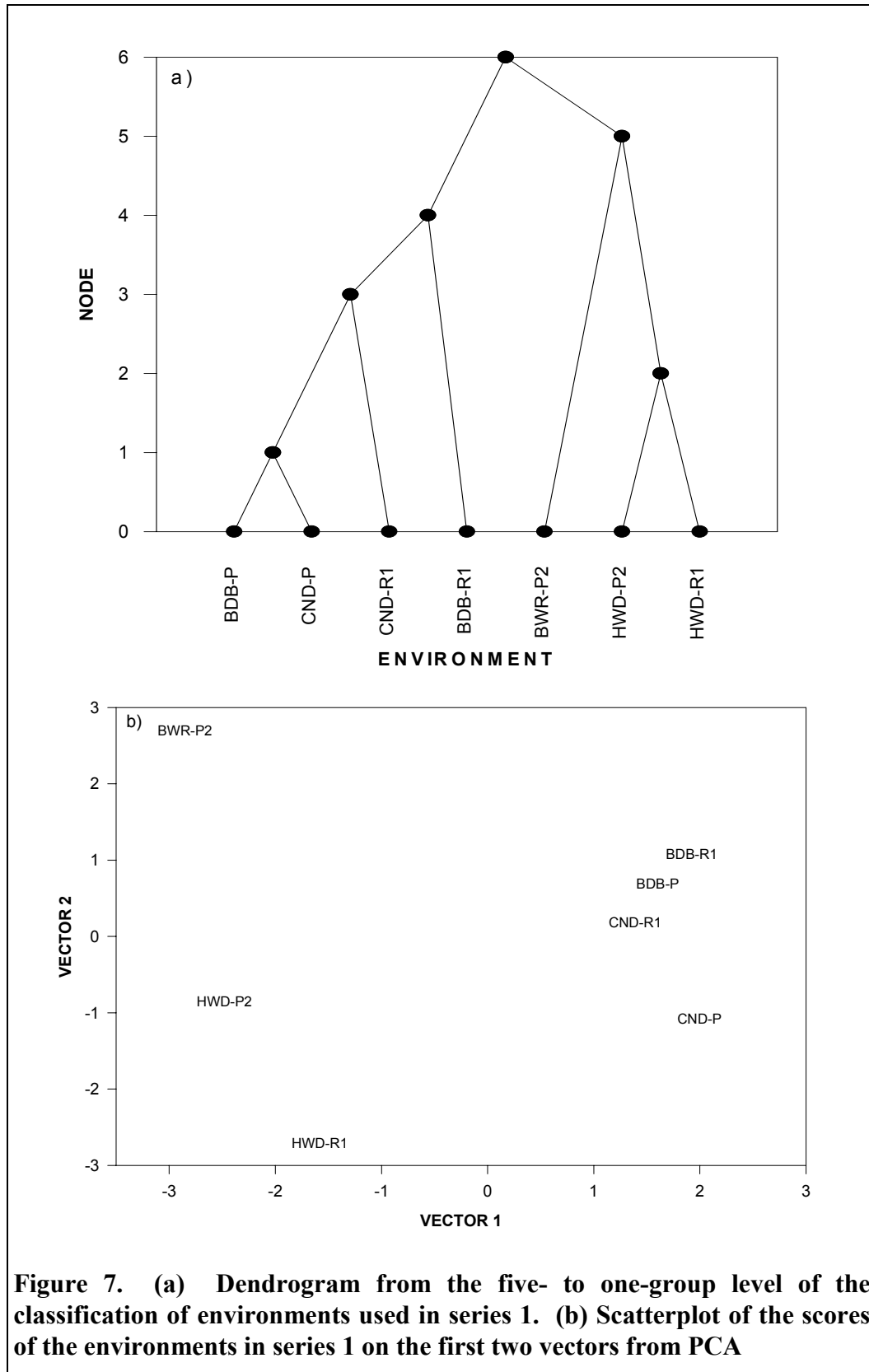
### 3.1.3 Similarity among environments

From a pattern analysis of the performance of the nine families that were common to the two series there was no clear differentiation between the Queensland and NSW trials (Figure 6). This indicates that the Queensland and NSW trial environments elicited responses that were not markedly different from the families.

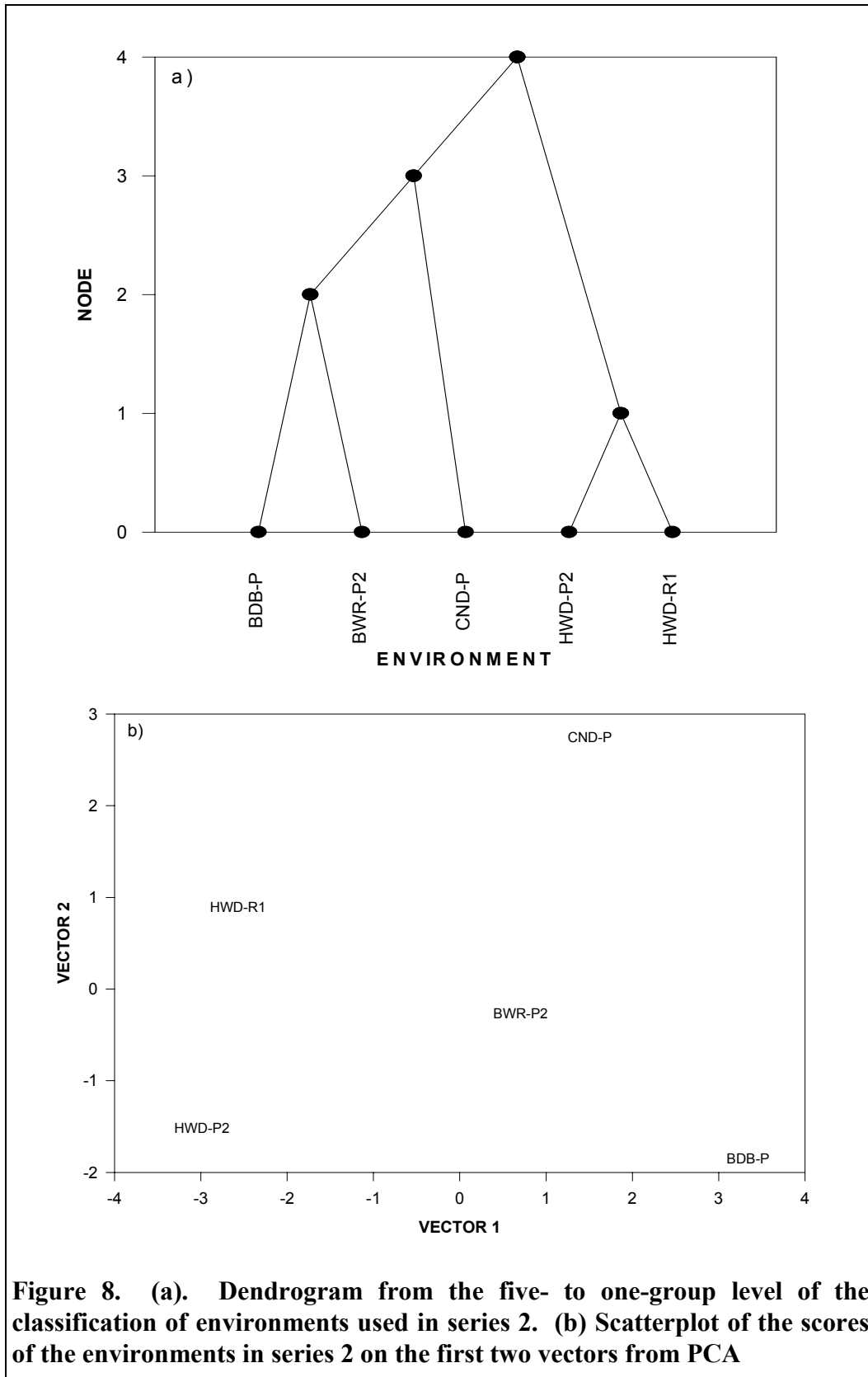
Using pattern analysis the similarity among environments based on the way in which they discriminated among for 20 families for series 1 and 18 families for series 2, was determined (Figure 7, Figure 8). For series 1 there was some separation among the one year trials from Bundaberg and Condong and trials from the more southerly Broadwater and Harwood sites. This separation was not evident for the series 2 trials.



**Figure 6. (a) Dendrogram from the six- to one-group level of the classification of environments based on the performance of nine common families in series 1&2. (b) Scatterplot of the scores of the environments in series 2 on the first two vectors from PCA based on the performance of nine common families in series 1&2.**

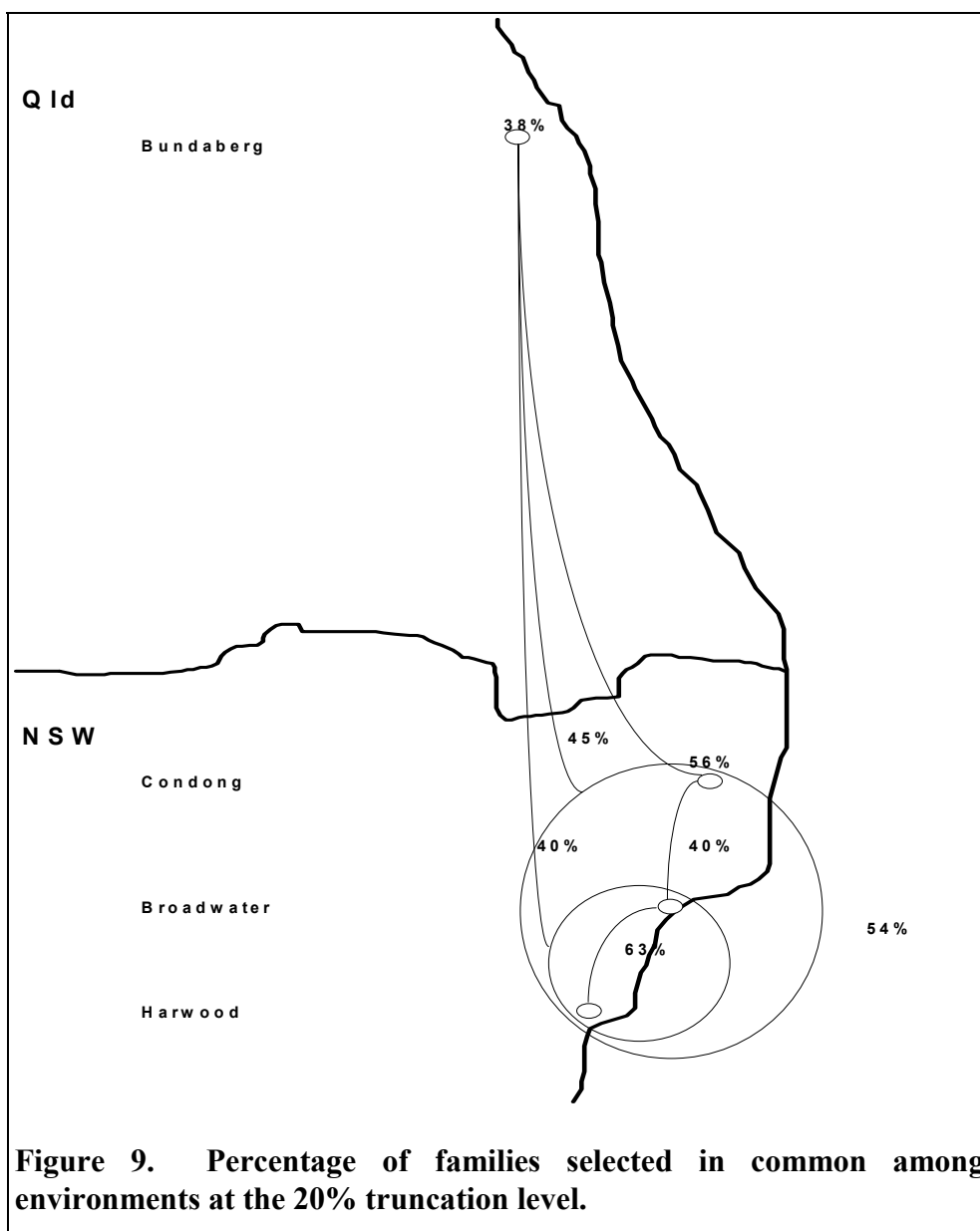


**Figure 7. (a) Dendrogram from the five- to one-group level of the classification of environments used in series 1. (b) Scatterplot of the scores of the environments in series 1 on the first two vectors from PCA**



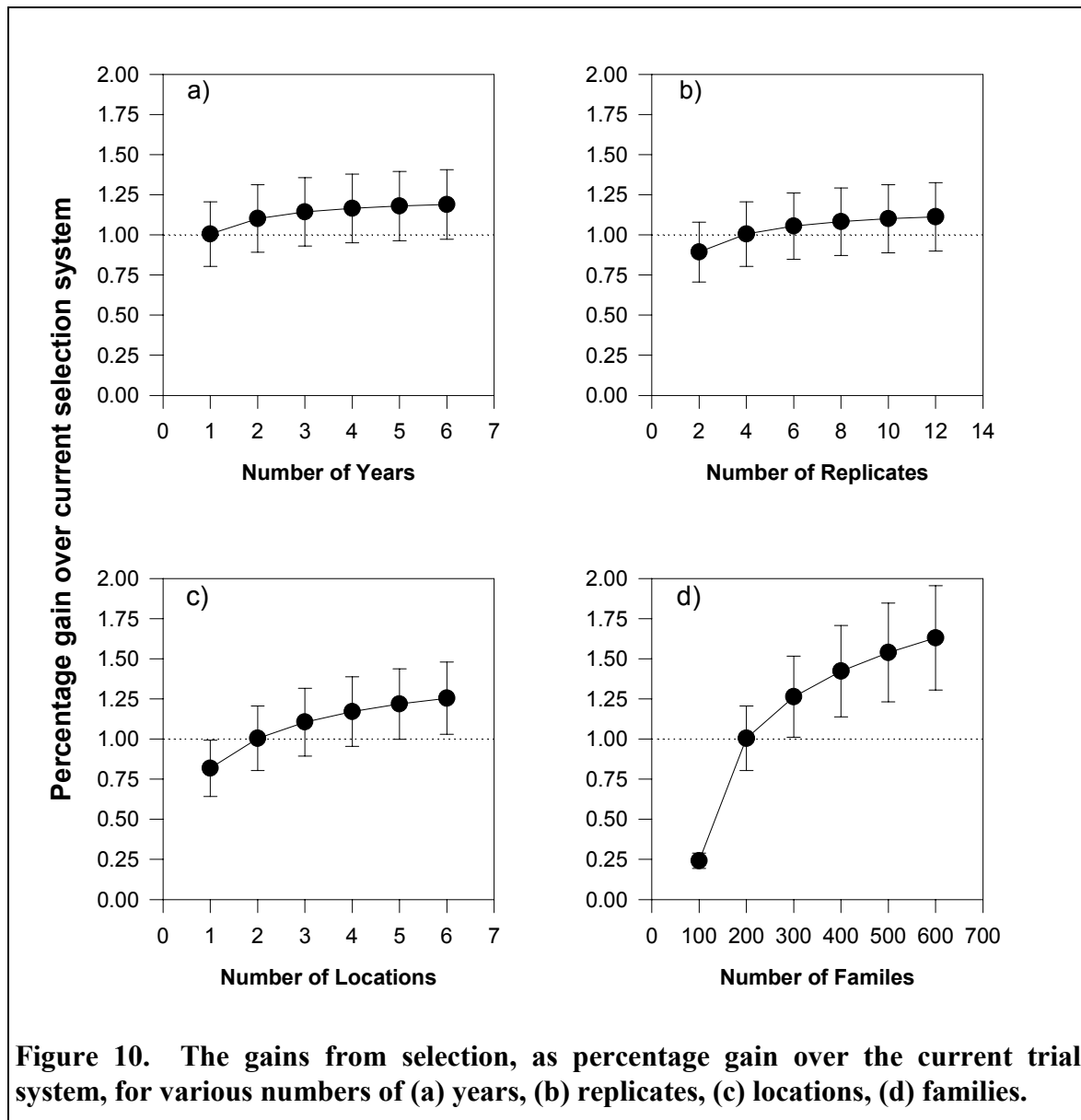
### 3.1.4 Efficiency of selection

To further examine whether there was any advantage in considering the Queensland environments to be different from the NSW environments in terms of selecting adapted families, the number of families selected (at the 20% truncation point) in common among test environments was assessed (Figure 9). This analysis indicated that the benefit for selecting for NSW in NSW (54%) over selecting for NSW using Queensland (45%) trials was only marginal, particularly given that using Queensland may be markedly less expensive. In fact using the Bundaberg station as the sole predictor of performance in NSW (45%) was more effective than using Bundaberg in one year to predict performance in Bundaberg the next year (38%).



### 3.1.5 Simulated selection

A mathematical model was constructed using the variance component estimates so that the amount of genetic gain made from differing allocations of resources could be calculated. From this model the effect of altering the number of families, replicates per location and years on predicted extent of genetic gain was assessed. The gains from selection were expressed as percentage gain over the current trial system (Figure 10).



Increasing the number of replicates and years to more than one resulted in very marginal increases in effectiveness. Increasing the number of locations to more than two also resulted in only minor gains in efficiency. Increasing the total number of families to be tested and still selecting the same absolute number of families (ie raising the selection intensity) markedly increased the expected gains from selection.



Using this mathematical model more efficient and effective allocations of resources were determined (Table 2). From this Table, assessing 800 families in one location in one year with two replicates would be of substantial benefit to both the Queensland and NSW programs and avoids the cost and resource duplication associated with raising seedlings at two different locations.

**Table 2. Percentage gain over that from the current allocation of resources for various numbers of families, locations, replicates and years.**

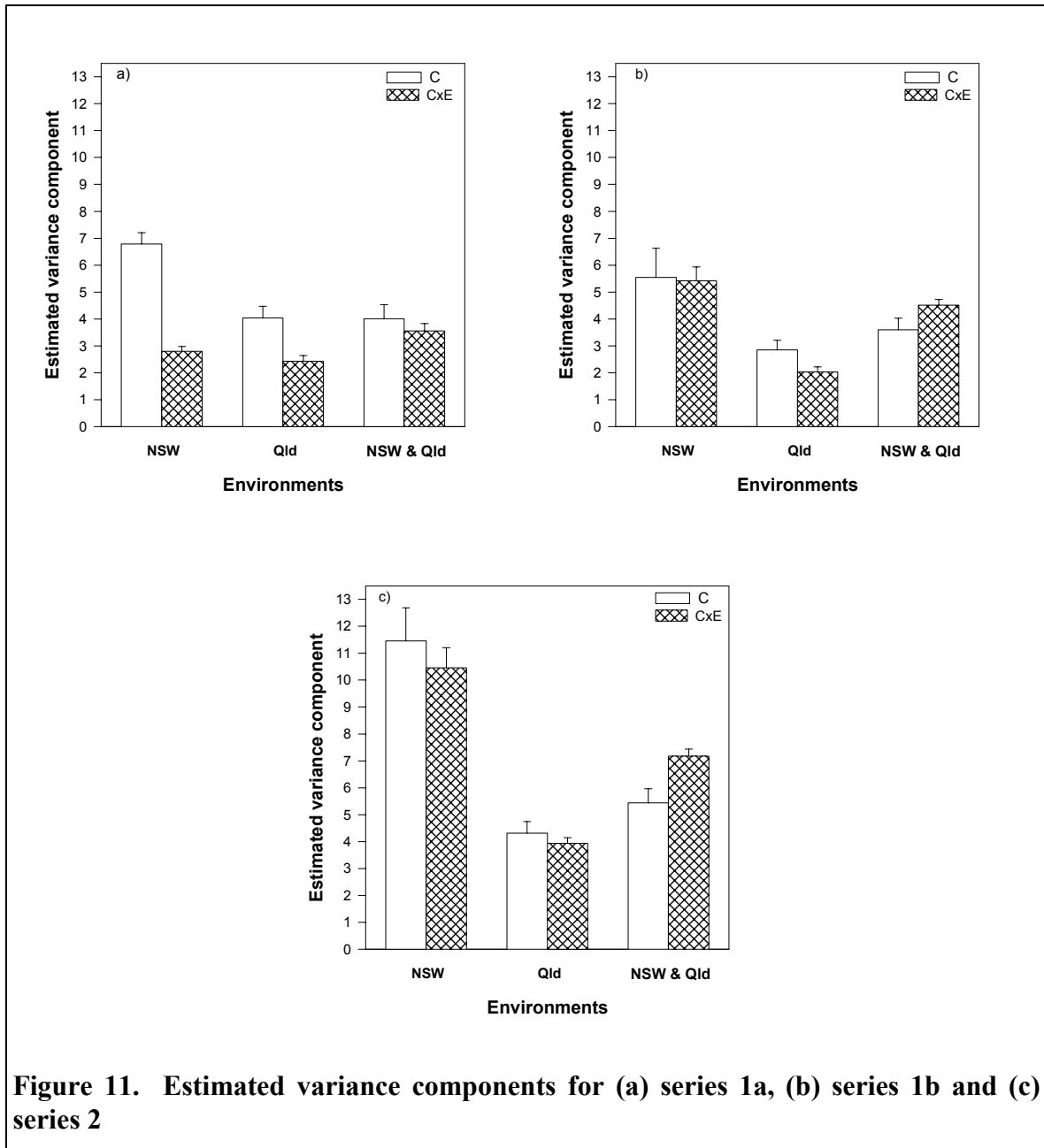
| Plots       | Number   |           |            |       | Gain (%)   |
|-------------|----------|-----------|------------|-------|------------|
|             | Families | Locations | Replicates | Years |            |
| <b>1600</b> | 200      | 2         | 4          | 1     | <b>100</b> |
| <b>1600</b> | 400      | 1         | 4          | 1     | <b>116</b> |
| <b>1600</b> | 400      | 2         | 2          | 1     | <b>126</b> |
| <b>1599</b> | 533      | 1         | 3          | 1     | <b>121</b> |
| <b>1600</b> | 800      | 1         | 2          | 1     | <b>124</b> |

### 3.2 Clones

#### 3.2.1 ANOVA

Coefficients of variation (CV) for the individual analyses of sugar yield for each environment in the three trial series (51 analyses in total) were less than 32% for all trials (see Appendix 2). These trials, therefore, had typical levels of experimental error for sugarcane yield evaluations using single-row plots.

Across all trial environments, clone and clone  $\times$  environment interaction (CxE) were highly significant ( $P < 0.01$ ) for each of the three trial series. Estimated variance components for clone and CxE across all NSW trials, all Queensland trials and all trials for each series were determined (Figure 11). The relative ratios of the amount of variation associated with CxE to that associated with the main effect of clone for trial series 1a, 1b and 2, was 89%, 125% and 132%, respectively. The magnitude of these percentages suggests that the interaction effect was generally as important as the main effect of clone.



**Figure 11. Estimated variance components for (a) series 1a, (b) series 1b and (c) series 2**

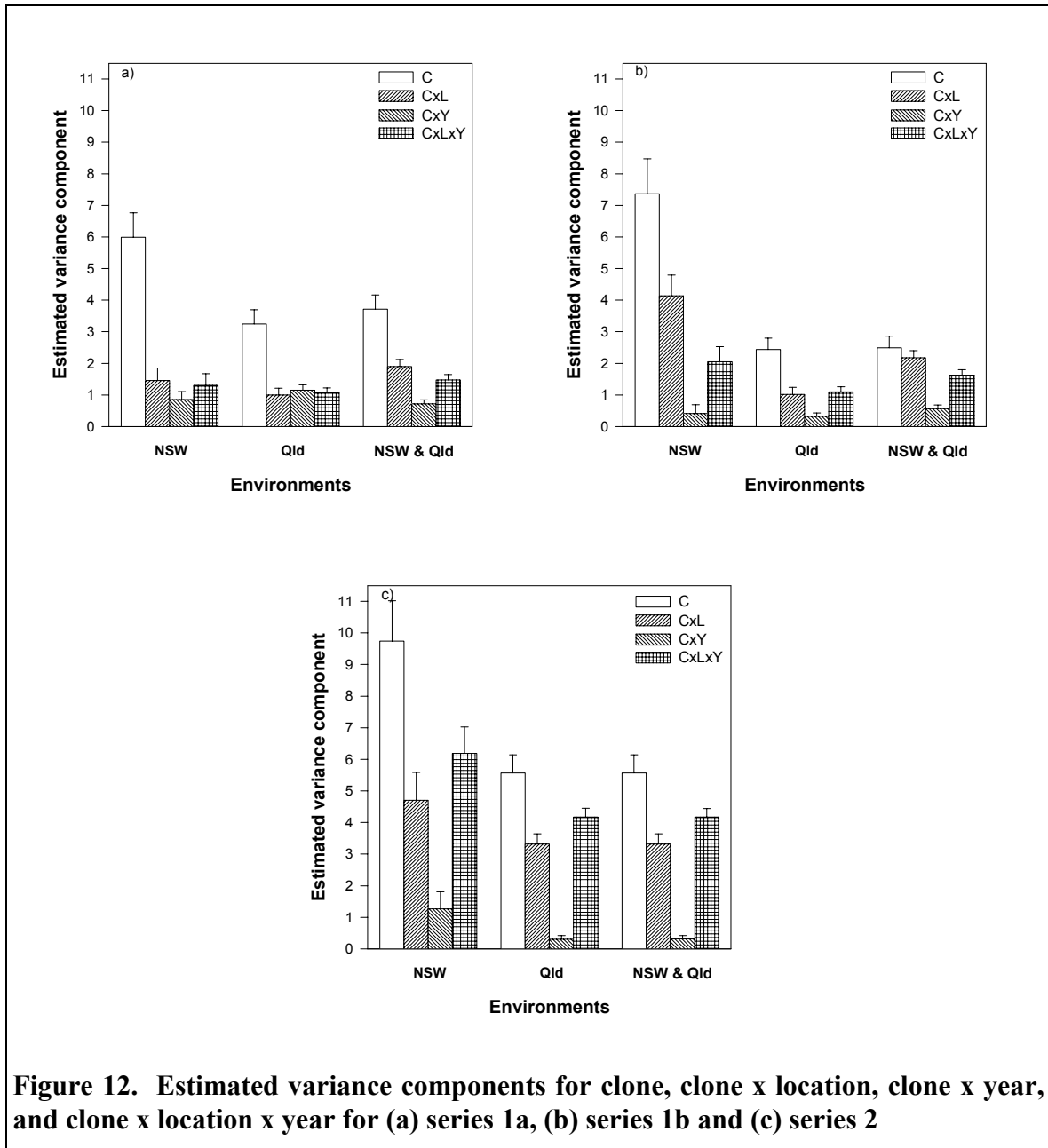
Considering only the Queensland based trials, the effects of clone and CxE were also highly significant ( $P < 0.01$ ) for each of the three series (Figure 11). However, the ratio of CxE variance to clone variance for the Queensland trials was generally much lower than when all environments were considered and for series 1a, 1b and 2, being 60%, 71% and 91%, respectively.

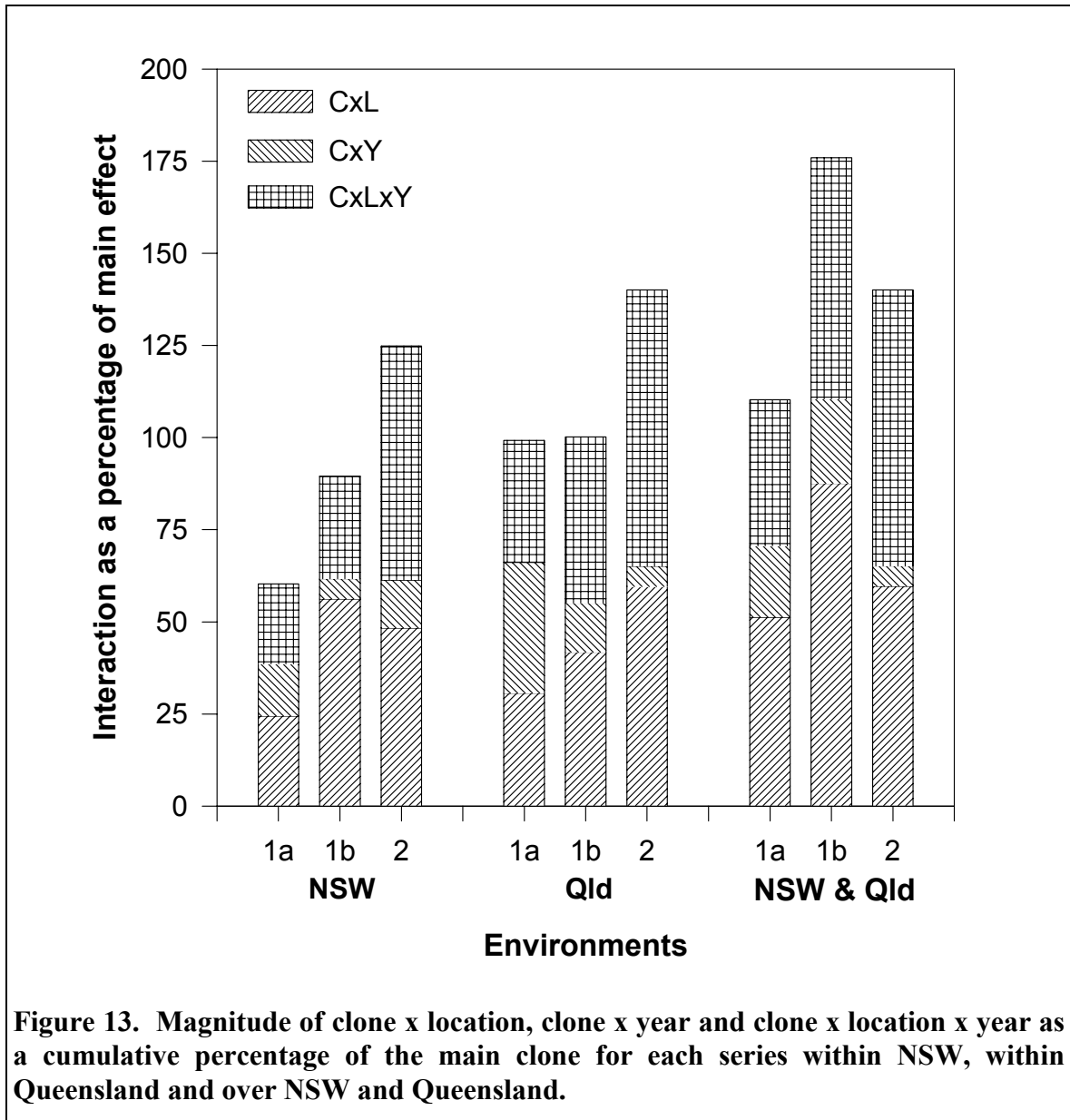
For the NSW based trials only, the effects of clone and CxE were also highly significant ( $P < 0.01$ ) for each of the three series (Figure 11). Again the ratio of CxE to clone was lower than when all environments were considered with the ratio for each series 1a, 1b and 2, being 41%, 97% and 91%, respectively.

These results show that there is less interaction within both Queensland and NSW than there is between Queensland and NSW.

Similarly, for each series, the estimates of the variance components for clone, clone x location interaction (CxL), clone x year interaction (CxY) and clone x location x year (CxLxY) interactions were calculated from trials within NSW, within Queensland and overall (Figure 12). For NSW, for series 1a and 1b, the sample harvested one-year Broadwater and one-year Harwood trials were omitted, as was the second ratoon Condong trial. Also, the Maryborough plant crop was omitted for Queensland in series 2 as the subsequent ratoon crop failed. Accordingly the 'year' term is not cleanly estimated and in Queensland represents a confounding of year and crop-class and for NSW represents a confounding of year, crop-age and crop-class.

From these analyses the second order interaction and the CxL was large for all trials relative to the main effect of clone. By expressing these estimates as percentages of the main effect of clone (Figure 13), it is clear that, by combining the data across NSW and Queensland, more interaction was generated and that this increase was principally due to increases in the CxL term and to a lesser extent the CxLxY.





### 3.2.2 Performance

The sugar yield performance of the BSES clones and NSW standards was compared for each harvest of each series (Table 3) and also summarised over locations and crop ages (Table 4).

**Table 3. Performance of BSES and NSW clones for both series 1 and 2 in NSW.**

| Location   | Series | Crop class <sup>a</sup> | Trial  | Crop age | Percentage of BSES clones better than best NSW standard for sugar yield | Sugar yield gain (%) <sup>b</sup> |
|------------|--------|-------------------------|--------|----------|---|-----------------------------------|
| Condong    | 1      | P                       | a      | 1-year   | 67.2  | 89.1                              |
|            |        |                         | b      |          | 38.0  | 50.1                              |
|            | 2      | 1R                      | a      | 1-year   | 12.1  | 18.8                              |
|            |        |                         | b      |          | 14.0  | 29.6                              |
|            |        | 2R                      | a      | 1-year   | 24.1  | 30.3                              |
|            |        |                         | b      |          | 8.0   | 18.3                              |
|            |        | P                       | 1-year | 43.0     | 49.2  |                                   |
| 1R         | 1-year | 48.1                    | 82.2   |          |   |                                   |
| Broadwater | 1      | P                       | a      | 1-year   | 35.1  | 29.6                              |
|            |        |                         | b      |          | 38.2  | 46.0                              |
|            |        | P                       | a      | 2-year   | 10.7  | 18.2                              |
|            |        |                         | b      |          | 14.6  | 16.4                              |
|            | 2      | 1R                      | a      | 1-year   | 7.0   | 19.7                              |
|            |        |                         | b      |          | 47.9  | 67.2                              |
|            |        | P                       | a      | 2-year   | 0.0   | -3.1                              |
|            |        |                         | b      |          | 3.8   | 1.4                               |
| Harwood    | 1      | P                       | a      | 1-year   | 51.8  | 68.0                              |
|            |        |                         | b      |          | 40.9  | 36.3                              |
|            |        | P                       | a      | 2-year   | 7.1   | 11.0                              |
|            |        |                         | b      |          | 15.9  | 22.2                              |
|            | 2      | 1R                      | a      | 1-year   | 7.1   | 15.6                              |
|            |        |                         | b      |          | 26.1  | 47.3                              |
|            |        | P                       | a      | 2-year   | 12.8  | 27.5                              |
|            |        |                         | b      |          | 1.3   | 14.4                              |

<sup>a</sup>P = plant crop, 1R= First ratoon, 2R = Second ratoon

<sup>b</sup>Gain = (yield of best clone - yield of best standard)/(yield of best standard)

**Table 4. Summary of the performance of BSES and NSW clones for both series 1 and 2 in NSW.**

| <b>Location</b> | <b>Crop age</b>     | <b>Percentage of BSES clones better than best NSW standard for sugar yield</b> | <b>Sugar yield gain (%)<sup>b</sup></b> |
|-----------------|---------------------|--|---|
| Condong         | 1-year              | 31.8   | 67.1                                    |
| Broadwater      | 1-year              | 26.4   | 32.9                                    |
|                 | 2-year              | 8.4  | 10.5                                    |
|                 | 1&2-year            | 19.7   | 24.4                                    |
| Harwood         | 1-year              | 25.4   | 36.3                                    |
|                 | 2-year              | 11.9   | 20.2                                    |
|                 | 1&2-year            | 20.4   | 30.3                                    |
| <b>Average</b>  | <b>1-year</b>       | <b>27.9</b>  | <b>45.4</b>                             |
|                 | <b>2-year</b>       | <b>10.2</b>  | <b>15.4</b>                             |
|                 | <b>1&amp;2-year</b> | <b>24.0</b>  | <b>40.6</b>                             |

The percentage of clones better than the best NSW standard was large (average 28%) for all one-year crops. For the two-year crops this percentage was smaller (average 10%) but still indicated that substantial improvement could be made rapidly from the BSES selection system. The gain in sugar yield for the BSES clones, similarly, indicated massive improvement under a one-year cropping system (average 45%) and substantial improvement under a two-year cropping regime (15%).

### 3.2.3 Similarity among environments

The genetic correlations among locations were averaged over trial series and a pattern analysis performed on the resultant matrix (Figure 14). For this classification there was a clear separation between the Queensland and NSW trial environments. Similarly for the PCA there was a clear separation of the Queensland and NSW trial environments on vector 1. Together these results show that the Queensland and NSW trial environments elicited different responses from the clones.

Considering each series separately the similarity among environments based on the way in which they discriminated among clones for series 1a was determined (Figure 15). The majority of the Queensland and NSW environments were separated but the Condong trial environments were grouped with the Queensland environments.

For series 1b the Queensland and NSW environments were not grouped discretely (Figure 16). Rather, at the two group level the Bingera and Fritz environments were grouped separately from all remaining environments. This indicated that most Queensland and

NSW environments were not dramatically different in the way they discriminated among the clones but rather some Queensland environments elicited clonal responses that were more similar to those elicited from NSW environments than from some Queensland environments.

Similarly, results from series 2 reflect the findings from trial series 1b (Figure 17), in that some of the Queensland environments differed more from other Queensland environments than from the NSW environments in the way they discriminated among clones. Again for this series there was no clear separation of the NSW environments from the Queensland environments up to the five-group level.



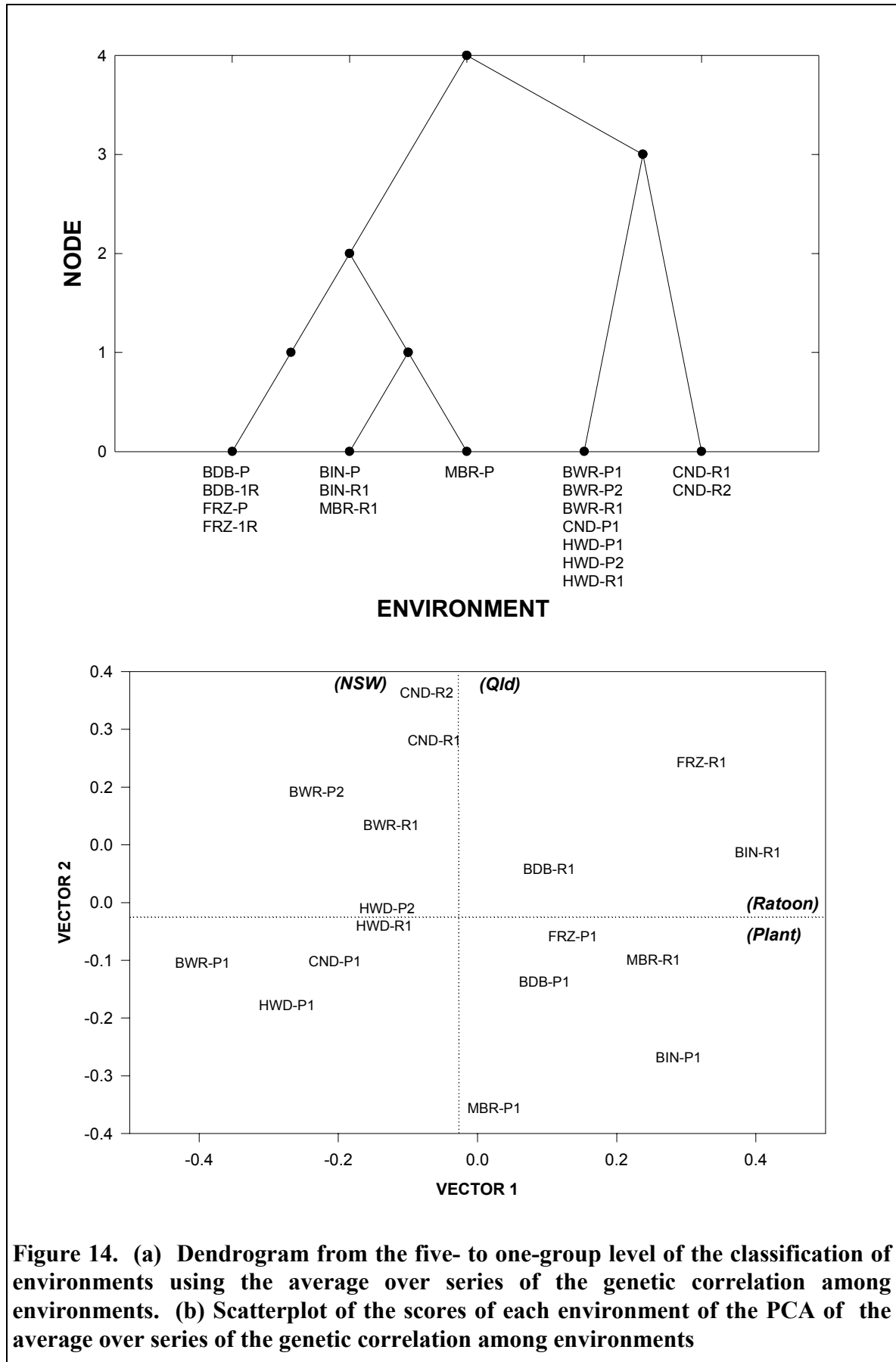
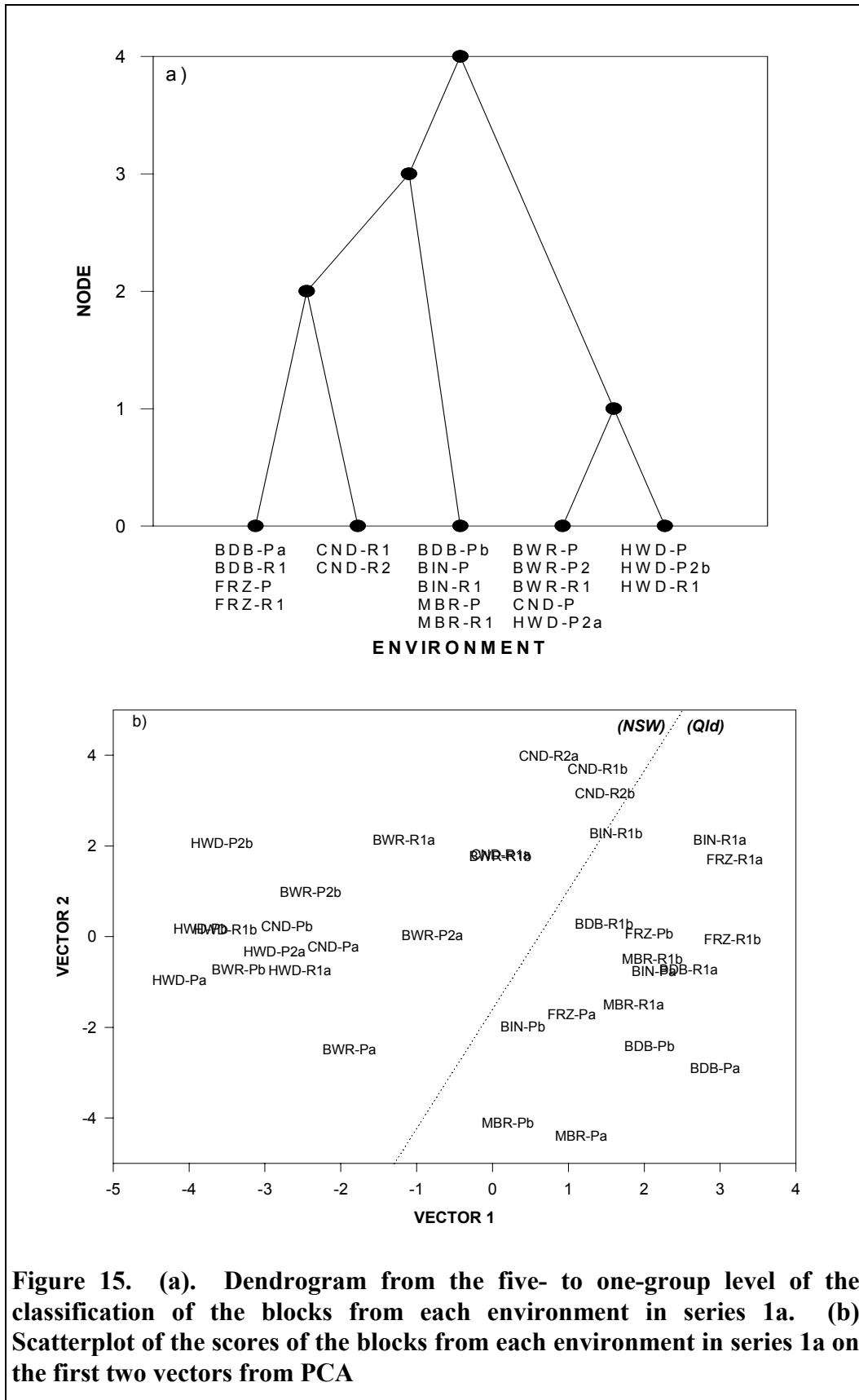
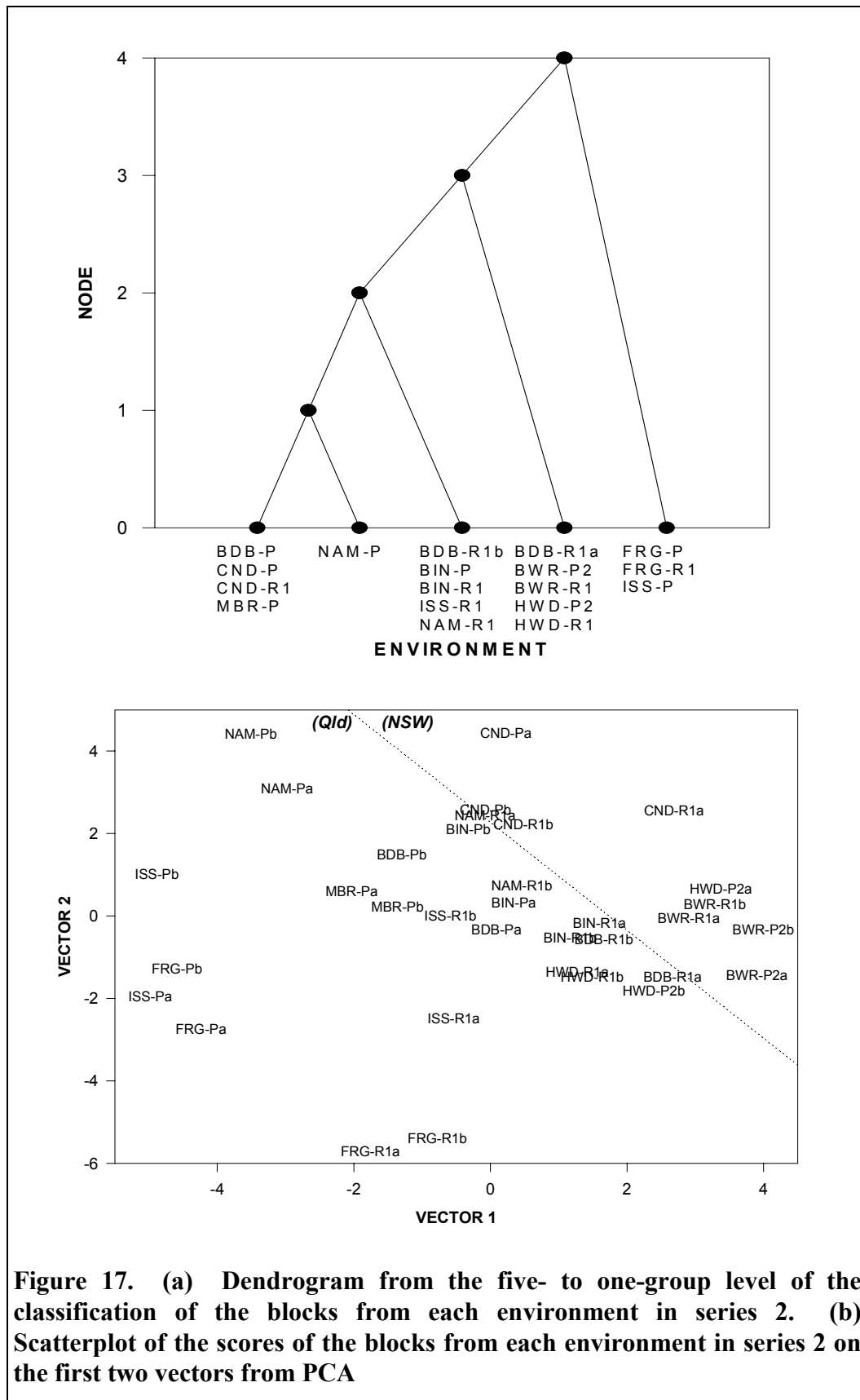


Figure 14. (a) Dendrogram from the five- to one-group level of the classification of environments using the average over series of the genetic correlation among environments. (b) Scatterplot of the scores of each environment of the PCA of the average over series of the genetic correlation among environments



**Figure 15. (a). Dendrogram from the five- to one-group level of the classification of the blocks from each environment in series 1a. (b) Scatterplot of the scores of the blocks from each environment in series 1a on the first two vectors from PCA**





**Figure 17. (a) Dendrogram from the five- to one-group level of the classification of the blocks from each environment in series 2. (b) Scatterplot of the scores of the blocks from each environment in series 2 on the first two vectors from PCA**

### 3.2.4 Efficiency of selection

The efficiency of indirect selection to direct selection was calculated for each pairwise combination of environments. These estimates were averaged over trial series and over the various selection scenarios of interest (Figure 18). From this Figure the average efficiency of selecting within Queensland was 56% and for within NSW it was 62%.

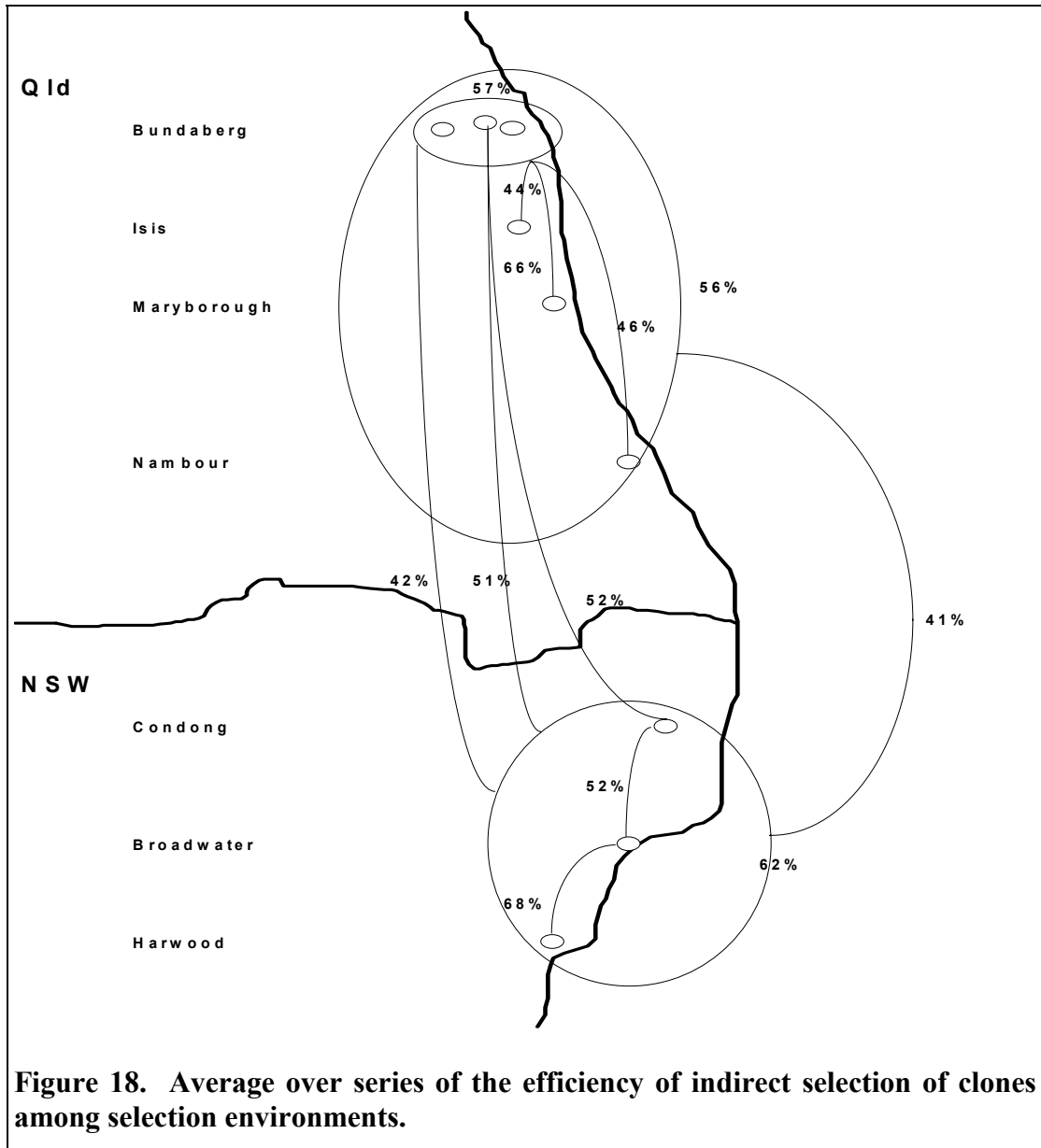
These analyses indicated that the benefit of selecting for NSW in NSW (62%) over selecting for NSW using Queensland environments (41%) was somewhat marginal. In fact using the Bundaberg station as the sole predictor of performance in NSW was quite efficient (51% versus 62%).

In order to examine the effect that these options had on selection, the number of selected clones in common, at the 20% truncation level, among all combinations of environments was calculated. These estimates were averaged over trial series and over the various selection scenarios of interest (Figure 19)<sup>1</sup>. From this Figure there were on average some 40% of selected clones selected in common among pairs of Queensland environments and some 39% of selected clones selected in common among pairs of NSW environments.

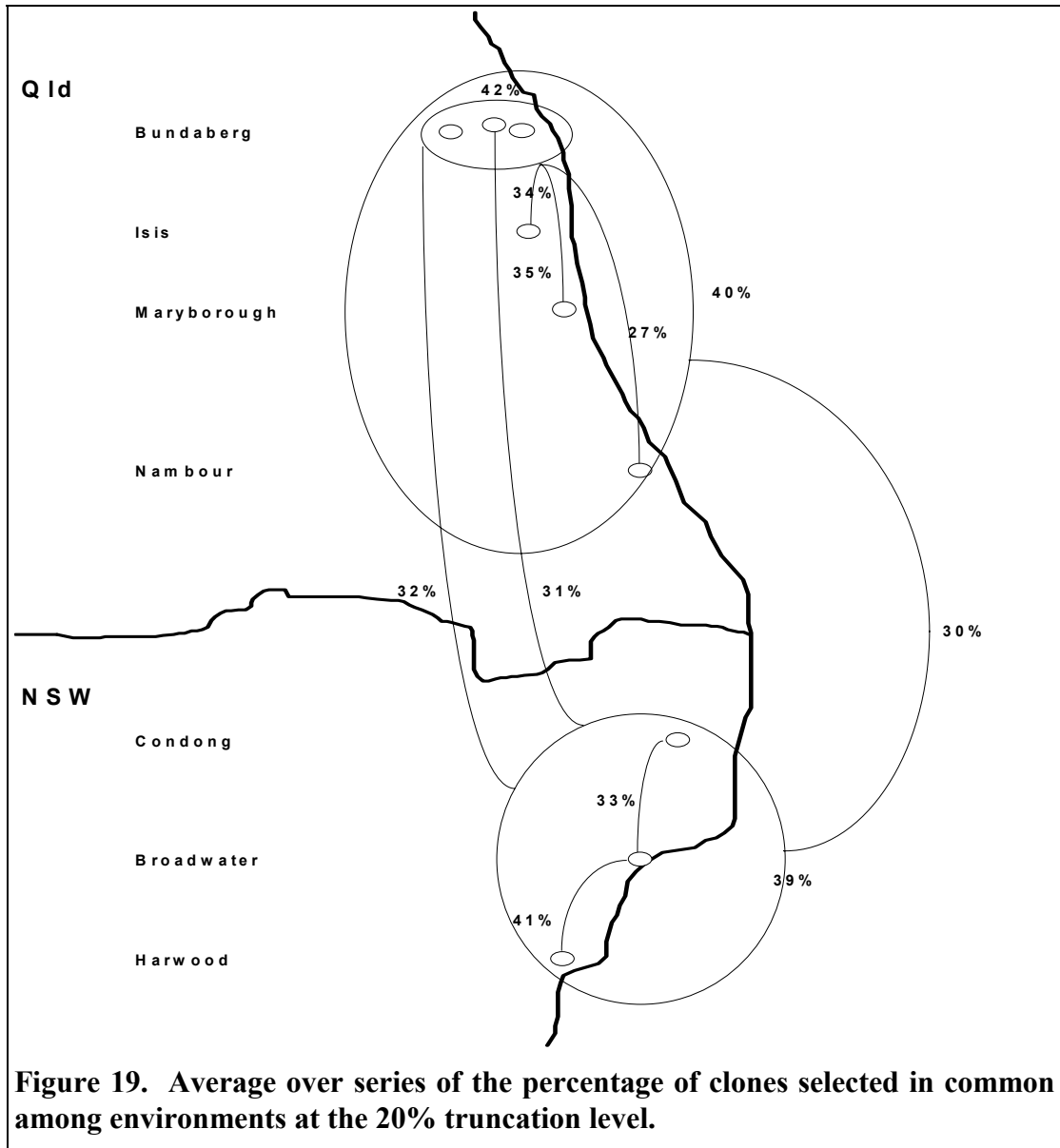
The percentage of clones selected in common by selecting for NSW in NSW (39%) compared with selecting for NSW using Queensland environments (30%) was quite marginal. In fact just using the Bundaberg station meant that 31% of the clones that would be selected in NSW were selected.

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<sup>1</sup> This procedure avoids comparing indirect selection with an artificially high (100%) direct selection estimate by using the average across combinations of environments within the same category only and ignoring the relationship to self.

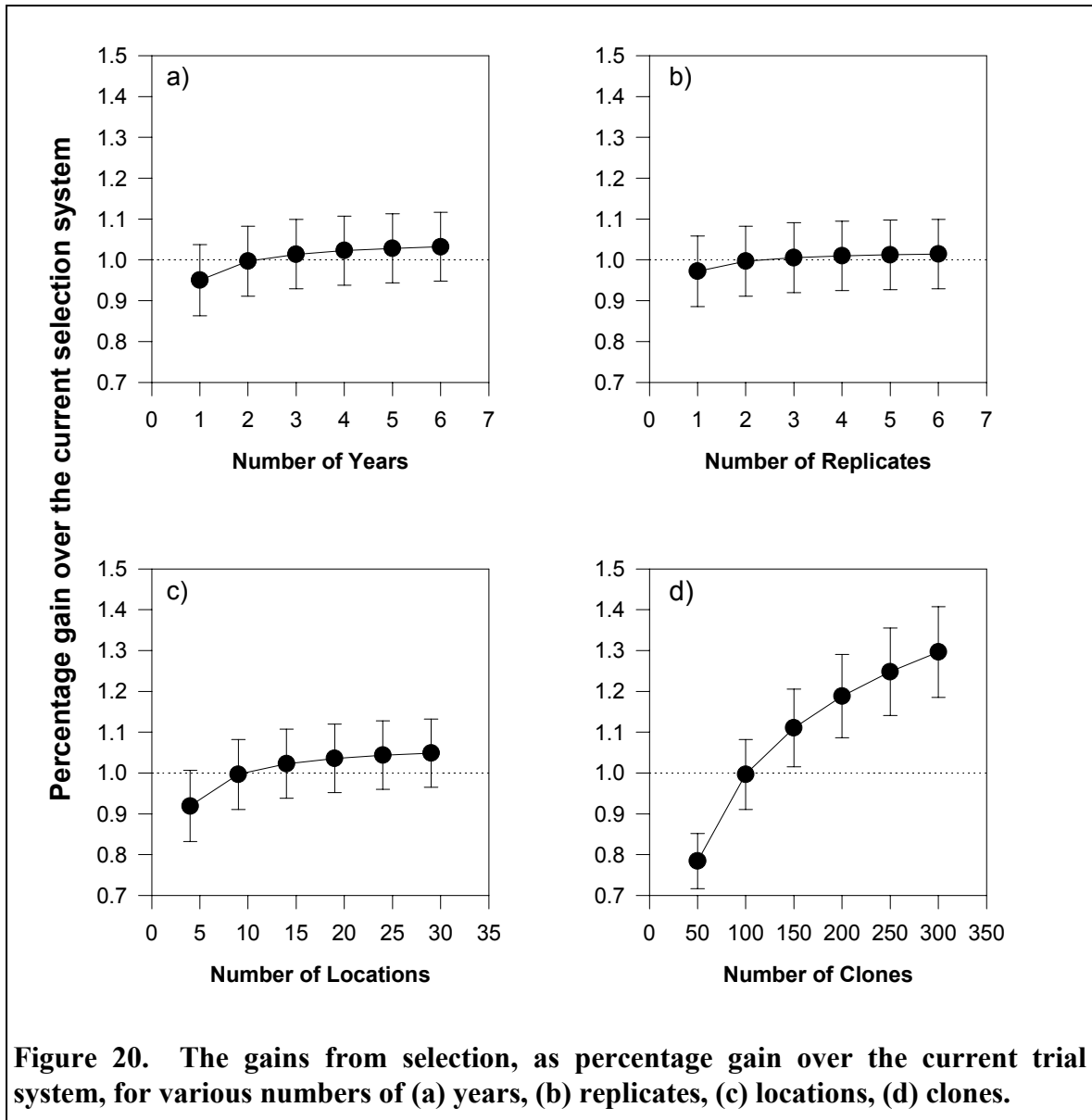


**Figure 18. Average over series of the efficiency of indirect selection of clones among selection environments.**



### 3.2.5 Simulated selection

Using the variance component estimates a mathematical model was constructed so that the amount of genetic gain made from differing allocations of resources could be calculated. From this model the effect of altering the number of clones, replicates per location, locations, and years on the extent of genetic gain achieved was assessed. The gains from selection were expressed as percentage gain over the current trial system (Figs 16a,b,c&d).



Increasing the number of replicates and years to more than one resulted in very marginal increases in effectiveness. Increasing the number of locations to more than five also resulted in minor gains in efficiency. Increasing the total number of clones to be tested and selecting the same number of clones (ie a higher intensity of selection) markedly increased the expected gains from selection.

By using this resource allocation model a number of more efficient and effective options were determined (Table 5). From this analysis the evaluation of a large number of clones (720) over only five locations in one year using one replicate would give substantially greater gains from selection than the current system.



**Table 5. Percentage gain over that from the current allocation of resources for various numbers of clones, locations and replicates in one year.**

| Plots | Number |           |            |       | Gain (%)   |
|-------|--------|-----------|------------|-------|------------|
|       | Clones | Locations | Replicates | Years |            |
| 3600  | 100    | 9         | 2          | 2     | <b>100</b> |
| 3600  | 360    | 5         | 2          | 1     | <b>120</b> |
| 3600  | 450    | 4         | 2          | 1     | <b>121</b> |
| 3600  | 600    | 3         | 2          | 1     | <b>121</b> |
| 3600  | 720    | 5         | 1          | 1     | <b>129</b> |

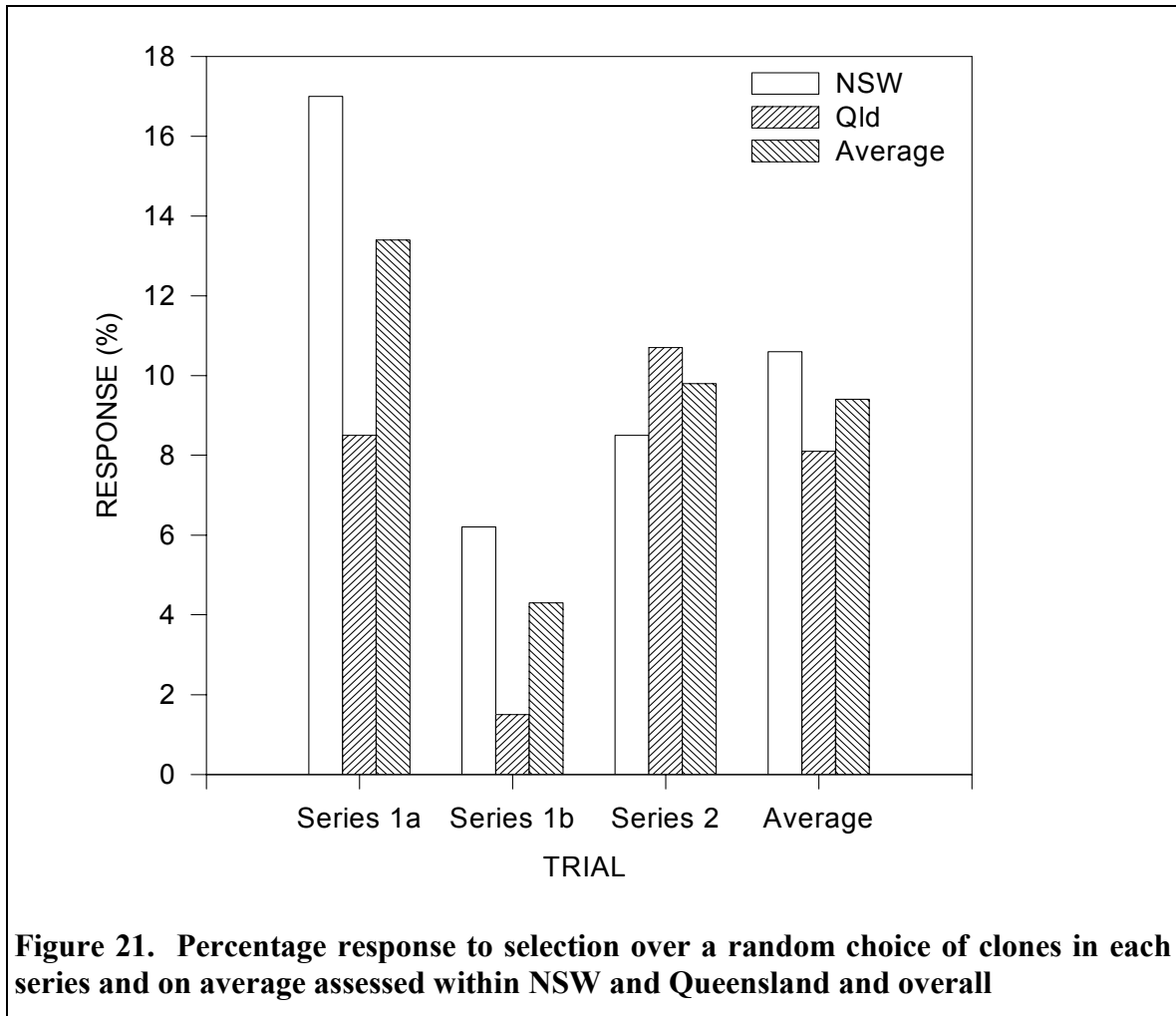
Also estimated was the gain associated with adopting two mega-environments, NSW and Queensland, over selecting for average performance across both states. For each series clone x state interaction (CxS) accounted for 37%, 40% and 30% of the total interaction variance respectively for each of the three series. For each series the extra estimated genetic gain was 8.6%, 8.8% and 2.6%, respectively, and on average was 6.7%. By evaluating and releasing specifically adapted clones within Queensland and NSW extra genetic gain can be made. However, if broad adaptation is desired, clones will need to be evaluated over both Queensland and NSW.

### 3.2.6 Actual response to selection

The pooled analysis over all environments and series was constructed to test whether selection in Bundaberg was effective. The *type* (selected and randomly chosen) term was highly significant over all series and the type x state (Queensland and NSW) interaction was also significant. This was also the case for series 1a. For series 1b the type effect was significant and for series 2 the type effect was highly significant, but for both series the type x state interaction was non-significant.

The response to selection, expressed as a percentage gain over a random choice of clones, was assessed for each series over Queensland, NSW and on average (Figure 21).

The percentage gain on average was about 9.5% and the difference in response between Queensland and NSW, while significant, was not substantial.



### 3.3 Key Environmental Factors

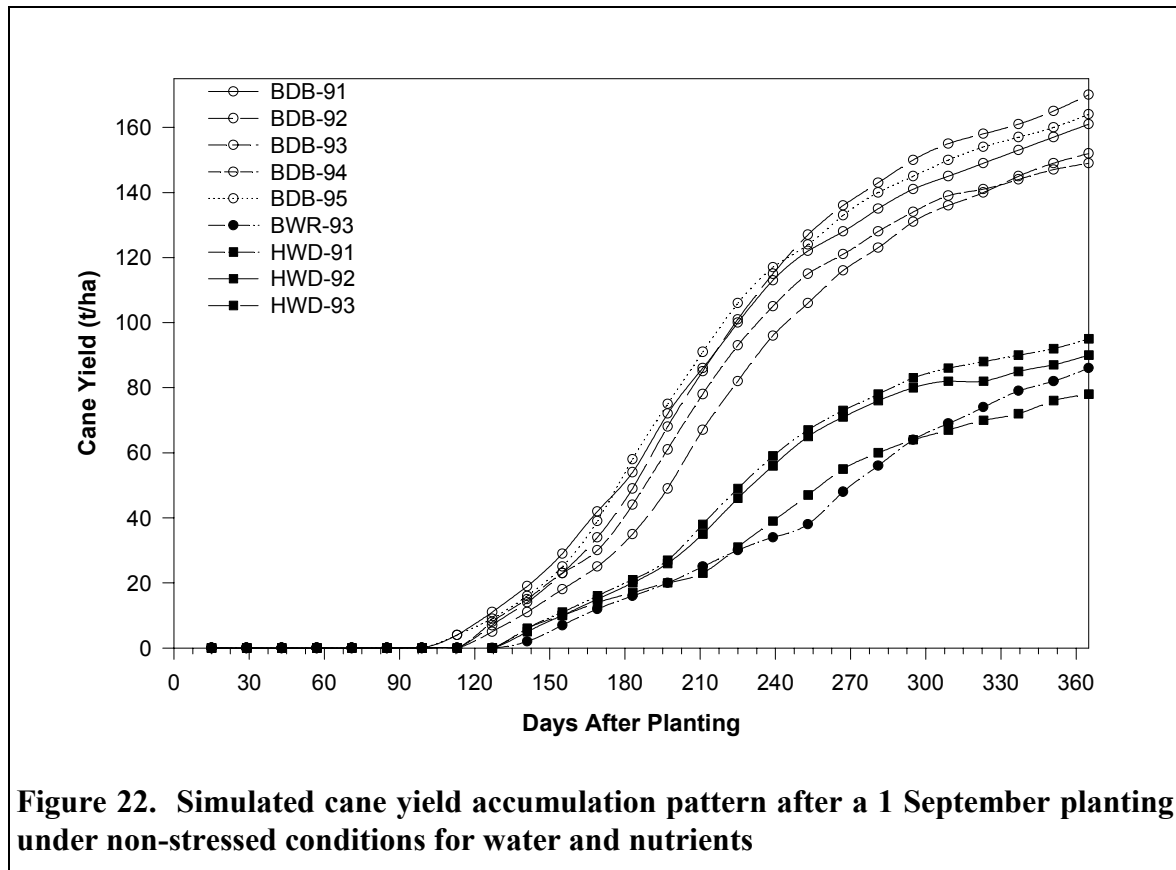
The key environmental factors of temperature, rainfall and solar radiation were monitored at the Bundaberg Experiment Station, Broadwater Mill Farm and the Harwood Mill Farm using weather stations over varying periods during the years 1990 to 1996.

The mean monthly maximum and minimum temperatures were calculated for each of these stations over this time period (Appendix 3). From the overlapping regions of these figures Bundaberg maintained higher mean monthly minima throughout the year, while the mean monthly maxima were comparable throughout much of the year.

Total rainfall (Appendix 3), however, was characterised by its variability for each of these three environments. Given the extent of this variability each of the three locations received similar rainfall in at least one year to one or both of the other locations.

Solar radiation (Appendix 3) was, as expected, much less variable than the other characters measured. Bundaberg on average received higher annual levels of solar radiation in each year than the other more southerly locations.

In order to integrate these environmental measures (temperature, rainfall and radiation) from these three locations into a single measure more related to plant growth, the QCane crop simulation was used. Using solar radiation and temperature data recorded at Bundaberg from 1991 to 1995, Broadwater in 1993 and Harwood from 1991 to 1993, cane yield accumulation was simulated using QCane (Figure 22). For this simulation non-stress conditions for nutrients and water were imposed and 'potential' yield was estimated on a daily time step.



In each of the years the potential yield for the NSW environments was estimated to be lower than for the Queensland environment. The shape of the curve indicates that both emergence and subsequent crop growth are delayed by the cooler temperatures in NSW compared with Queensland. Maximal growth rates are also higher for Queensland than NSW. The extent of the difference in crop growth is quite marked and final one-year cane yields varied between NSW and Queensland by around 80 t/ha.

#### 4.0 FULFILMENT OF OBJECTIVES AND OUTCOMES DELIVERED

| Objective   | Extent of Achievement | Process  | Outcomes   |
|---|-----------------------|--|--|
| 1) Compare the performance of families and clones produced by BSES for south Queensland with those routinely planted in the NSW breeding program, under NSW growing conditions              | <b>Full</b>           | Two series of both families and clones were evaluated in Queensland and NSW                          | <ul style="list-style-type: none"> <li>• <b>The BSES breeding and selection program for NSW was established based on the promising results of this project</b></li> <li>• <b>Selections have been taken from superior BSES and NSW families and used in the core selection program</b></li> <li>• <b>Commercial cultivars have been released from the clonal series</b></li> </ul>   |
| 2) Assess the similarities between location used in this trial based on their discrimination among families or clones, respectively   | <b>Full</b>           | ANOVA, pattern analyses and simulated selection was performed for both series of families and clones | <ul style="list-style-type: none"> <li>• <b>Family and clone x environment interaction was identified and found to be as large as the respective main effect</b></li> <li>• <b>There was no clear and consistent separation of the Queensland and NSW environments.</b></li> <li>• <b>Results from simulated selection suggested that fewer selection locations and more stringent clonal selection would increase gains from selection</b></li> </ul> |
| 3) Monitor environmental parameters so that key environmental factors that lead to differences in the discrimination among families and clones at the different locations may be identified | <b>Partial</b>        | Ambient environmental conditions were monitored at Bundaberg, Broadwater and Harwood                 | <ul style="list-style-type: none"> <li>• <b>General assessments of the prevalent environmental conditions during crop growth</b></li> </ul>  |

| Objective   | Extent of Achievement | Process  | Outcomes   |
|---|-----------------------|--|--|
| 4) Assess the potential of families and clones selected for 12-month cropping in Queensland to produce 24-month crops in NSW                                      | <b>Full</b>           | Two series of both families and clones were evaluated in Queensland and NSW  | <ul style="list-style-type: none"> <li>• <b>Selections have been taken from superior BSES and NSW families and used in the core selection program</b></li> <li>• <b>Cultivars have been released from the clonal series</b></li> </ul>   |
| 5) Compare the frost tolerance of advanced clones in south Queensland and New South Wales   | <b>Full</b>           | Frost tolerance was assessed on an opportunistic basis by planting trials in frost prone areas   | <ul style="list-style-type: none"> <li>• <b>Clones that displayed superior yield following severe frosting were identified and selected</b></li> <li>• <b>The practice of planting trials in frost prone areas to assess the ability to yield after frosting has been adopted in the core selection program</b></li> </ul> |
| 6) Select families with outstanding performance for further testing in larger populations and to identify elite clones, for use as parents in subsequent families | <b>Full</b>           | Outstanding families were re-tested in larger populations to identify elite clones. Elite clones were sent to Meringa for use as parents | <ul style="list-style-type: none"> <li>• <b>Several families have been re-tested in larger numbers in the core BSES NSW selection program</b></li> <li>• <b>A range of superior clones (&gt;15) from these trials has been used as parents</b></li> </ul>  |

## 5.0 RECOMMENDATIONS AND CONCLUSIONS

From this project it may be concluded that for families:

- Seed could be supplied by either BSES or NSW as the performance of families in NSW from these two sources was comparable.
- Family performance varied substantially across NSW and Queensland.
- Based on restricted data, just over half of the variability in family performance across environments was unpredictable and associated with location by year differences and about 40% was due to locational differences.
- The difference in family performance in NSW and Queensland was not sufficient to warrant two selection programs.
- One family evaluation site in either NSW or Queensland would be adequate for identifying elite families and could also offer opportunities of scale.
- The use of higher selection intensities (larger populations of families) at one location would give greater genetic gain (by around 20%) than the current two location low selection intensity family evaluation system.

Likewise, it may be concluded for clones that:

- The performance of clones from BSES in NSW was outstanding compared with that of the current NSW cultivars (particularly in one-year cropping scenarios).
- BSES germplasm offers greater potential for the production of superior cultivars for the NSW industry than the NSW program.
- Clonal performance varied substantially both within NSW and Queensland and across NSW and Queensland.
- Over half of the variability in clonal performance across environments was due to locational differences and about 40% was due to unpredictable location by year differences.
- Greater gains (more than 20%) could be made by using fewer selection sites (by around 50%), increasing selection intensity (increased clonal population size by around 360%) and limiting selection to plant crops.
- The benefit of selecting in NSW for NSW over selecting for NSW in Queensland, and *vice versa*, was marginal and is considerably more expensive.
- Despite major differences in crop production environments some clones were broadly adapted to NSW and Queensland.
- From a practical viewpoint the best economic indicator of suitability to frosting is sugar yield after regrowth from a frost event.

The following recommendations arise from this project:

- BSES clones that are adapted to NSW conditions and cropping cycles be recycled as parents and used in crossing.
- BSES clones selected in south Queensland offer substantial potential for the NSW sugar industry, under both a one-year and two-year cropping system. Therefore this source of germplasm should be used in the core selection program.
- The Bundaberg family evaluation stage be increased to evaluate more (eg 800) families

- Stages 1 or 2 be conducted at only one location.
- The southern Queensland and NSW multi-environment selection program be integrated and that the number of clones evaluated be increased.
- This increase in number of clones evaluated be offset by a proportionate reduction in the number of years and locations used in advanced trials in south Queensland and NSW.
- Statistical methods for improving the accuracy of both within and across trial yield estimation be adopted.
- That routine multi-environment analyses of variety trials and statistical methods to enhance data accuracy and interpretability be adopted.
- An assessment of benefit of regionalised selection programs be commenced for all BSES programs and economies of scale sought.
- The merit of broad versus specific adaptation be (re)evaluated for all BSES programs and a product development/delivery policy be enunciated for each major and distinct market (maturity type, management, quality, districts, soil type, major stresses, etc).

## **6.0 INTELLECTUAL PROPERTY ARISING FROM THIS PROJECT**

There are no issues arising from this project that pertain to intellectual property rights.

## **7.0 ACKNOWLEDGMENTS**

The Australian Sugar Research and Development Corporation provided partial financial support for the conduct of these trials. Dr DM Hogarth initiated this project, designed all field trials and managed the project until 1992. The technical assistance of Messrs. JF Reimers, JH Panitz, ER Halili and PB Hansen, for the conduct of trials is gratefully acknowledged. The weather records and simulated yield accumulation data were compiled by Dr DL Liu. I also wish to thank Drs DM Hogarth and TA Bull for their help in improving the presentation and clarity of this report.

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## **APPENDIX 1**

### **Trial Description**

**Table 1-1. Trial description and environment code for the series 1 families experiments**

| <b>Location</b>   | <b>Crop<sup>a</sup></b> | <b>Age (years)</b> | <b>Environment Code</b> |
|-------------------|-------------------------|--------------------|-------------------------|
| <b>Bundaberg</b>  | P                       | 1                  | <b>BDB-P</b>            |
|                   | R1                      | 1                  | <b>BDB-R1</b>           |
| <b>Broadwater</b> | P                       | 2                  | <b>BWR-P2</b>           |
| <b>Condong</b>    | P                       | 1                  | <b>CND-P</b>            |
|                   | R1                      | 1                  | <b>CND-R1</b>           |
| <b>Harwood</b>    | P                       | 2                  | <b>HWD-P2</b>           |
|                   | R1                      | 1                  | <b>HWD-R1</b>           |

**Table 1-2. Trial description and environment code for the series 2 families experiments**

| <b>Location</b>   | <b>Crop<sup>a</sup></b> | <b>Age (years)</b> | <b>Environment Code</b> |
|-------------------|-------------------------|--------------------|-------------------------|
| <b>Bundaberg</b>  | P                       | 1                  | <b>BDB-P</b>            |
| <b>Broadwater</b> | P                       | 2                  | <b>BWR-P2</b>           |
| <b>Condong</b>    | P                       | 1                  | <b>CND-P</b>            |
| <b>Harwood</b>    | P                       | 2                  | <b>HWD-P2</b>           |
|                   | R1                      | 1                  | <b>HWD-R1</b>           |

**Table 1-3. Trial description and environment code for the series 1a and 1b clones experiments**

| <b>Location</b>    | <b>Crop<sup>a</sup></b> | <b>Age (years)</b> | <b>Environment Code</b> |
|--------------------|-------------------------|--------------------|-------------------------|
| <b>Bundaberg</b>   | P                       | 1                  | <b>BDB-P</b>            |
|                    | R1                      | 1                  | <b>BDB-R1</b>           |
| <b>Bingera</b>     | P                       | 1                  | <b>BIN-P</b>            |
|                    | R1                      | 1                  | <b>BIN-R1</b>           |
| <b>Broadwater</b>  | P                       | 1                  | <b>BWR-P1</b>           |
|                    | P                       | 2                  | <b>BWR-P2</b>           |
|                    | R1                      | 1                  | <b>BWR-R1</b>           |
| <b>Condong</b>     | P                       | 1                  | <b>CND-P</b>            |
|                    | R1                      | 1                  | <b>CND-R1</b>           |
|                    | R2                      | 1                  | <b>CND-R2</b>           |
| <b>Fritz</b>       | P                       | 1                  | <b>FRZ-P</b>            |
|                    | R1                      | 1                  | <b>FRZ-R1</b>           |
| <b>Harwood</b>     | P                       | 1                  | <b>HWD-P1</b>           |
|                    | P                       | 2                  | <b>HWD-P2</b>           |
|                    | R1                      | 1                  | <b>HWD-R1</b>           |
| <b>Maryborough</b> | P                       | 1                  | <b>MBR-P</b>            |
|                    | R1                      | 1                  | <b>MBR-R1</b>           |

<sup>a</sup> P = plant crop, R1= First ratoon, R2= Second ratoon

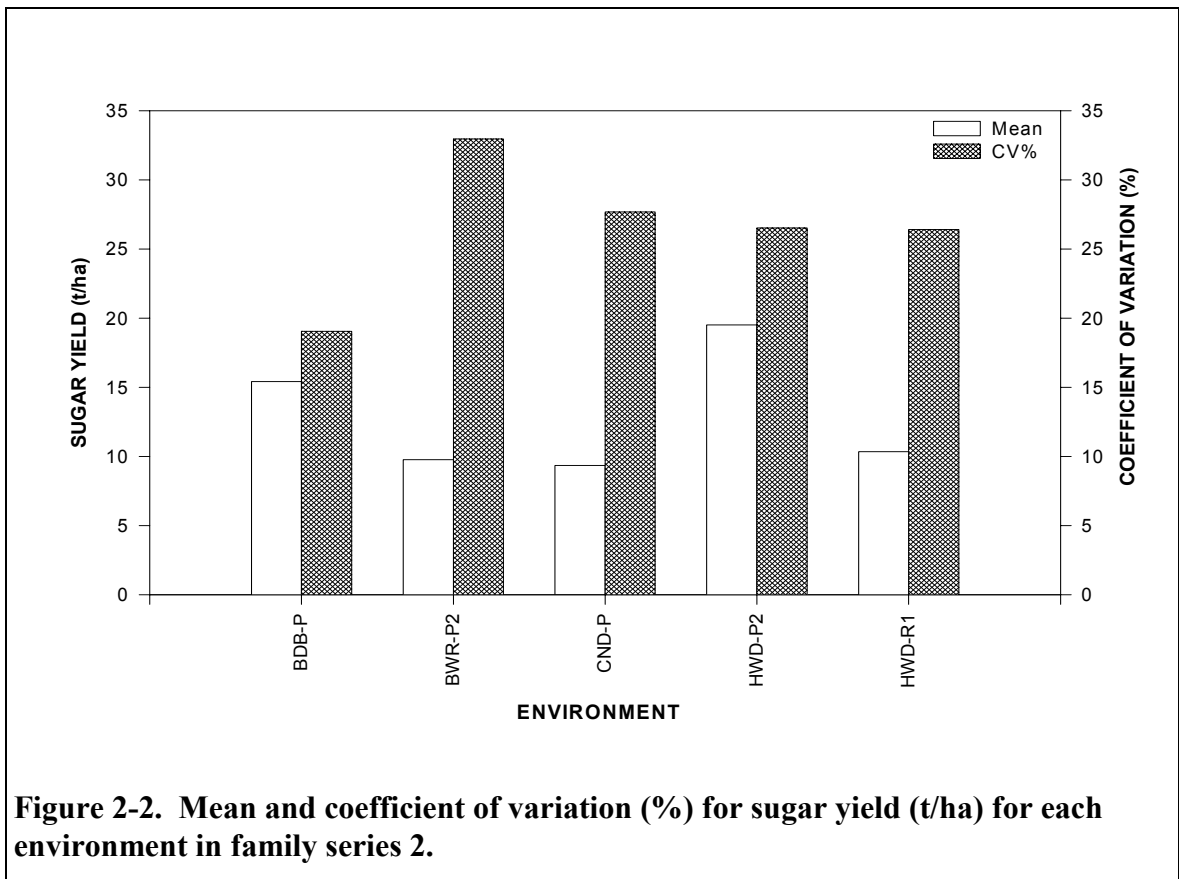
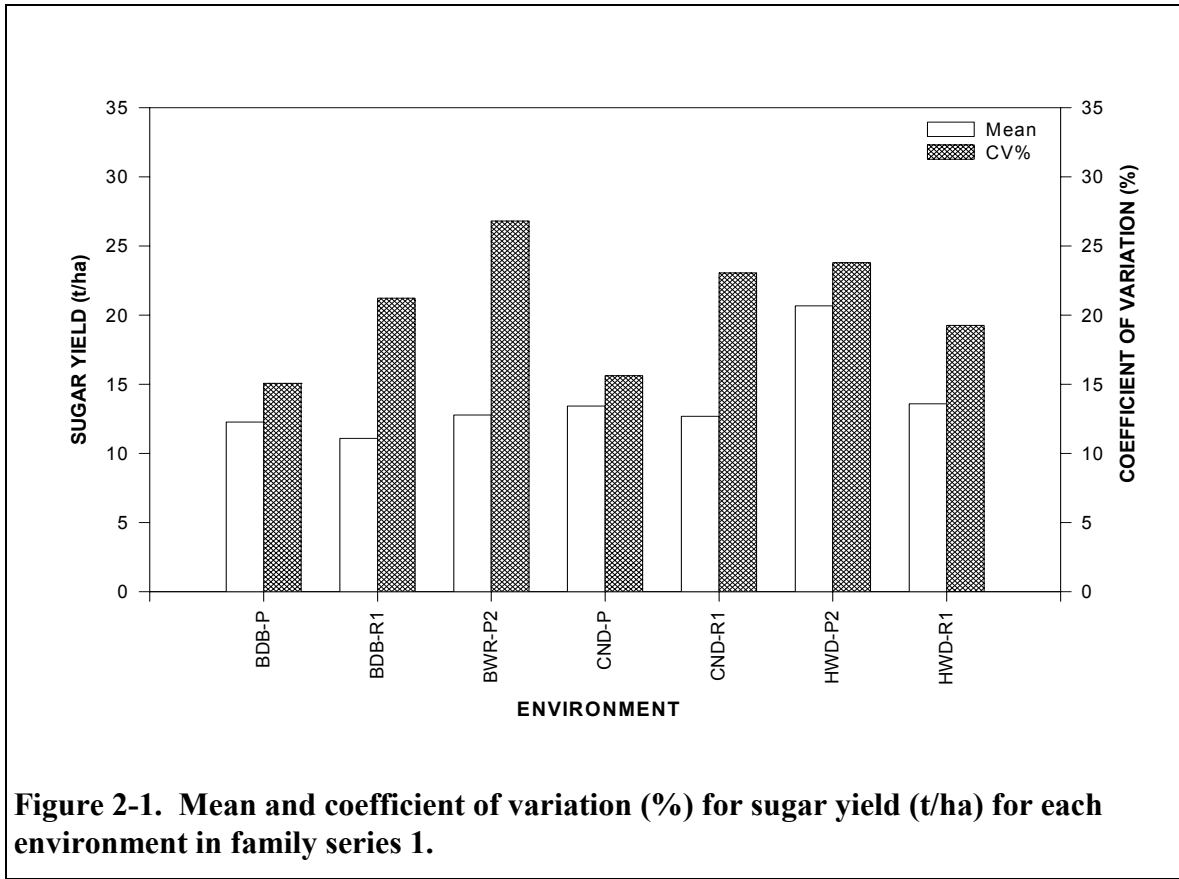
**Table 1-4. Trial description and environment code for the series 2 clones experiments**

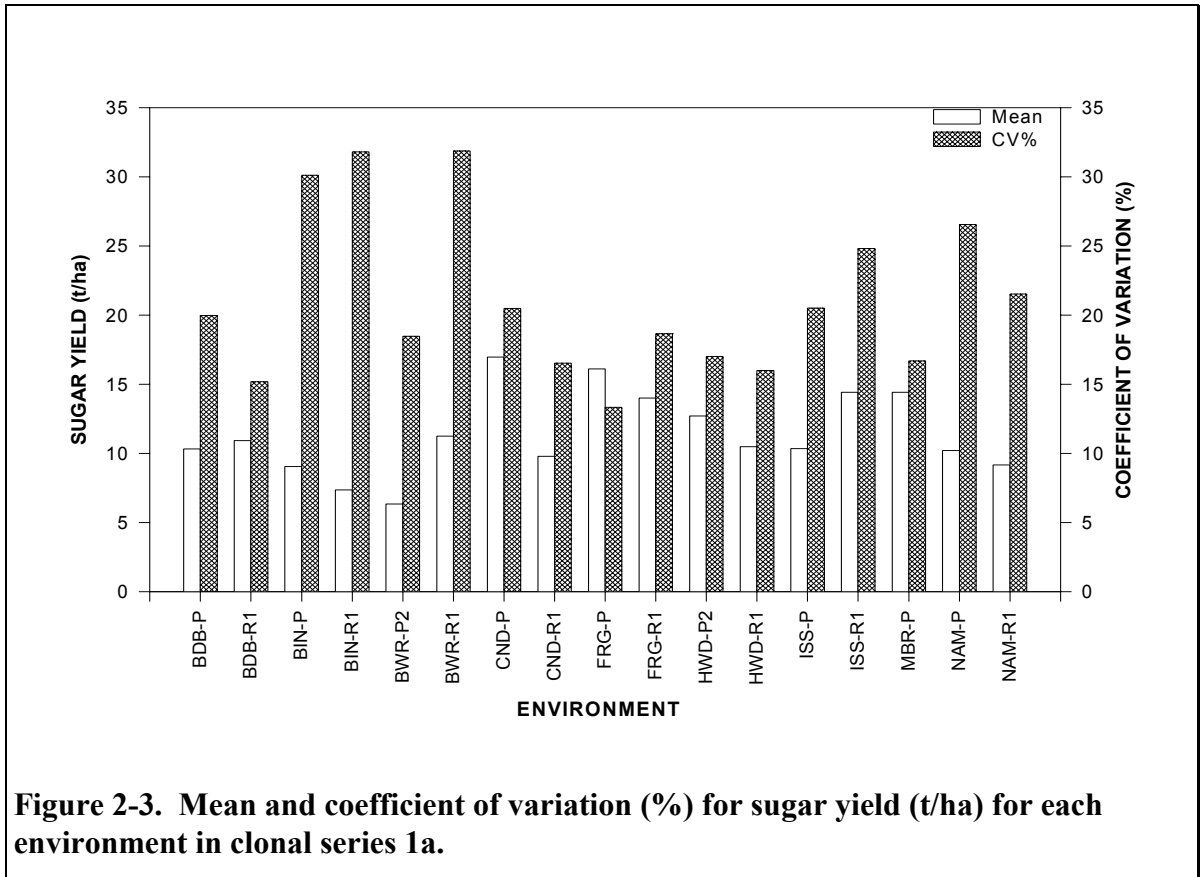
| <b>Location</b>    | <b>Crop<sup>a</sup></b> | <b>Age (years)</b> | <b>Environment Code</b> |
|--------------------|-------------------------|--------------------|-------------------------|
| <b>Bundaberg</b>   | P                       | 1                  | <b>BDB-P</b>            |
|                    | R1                      | 1                  | <b>BDB-R1</b>           |
| <b>Bingera</b>     | P                       | 1                  | <b>BIN-P</b>            |
|                    | R1                      | 1                  | <b>BIN-R1</b>           |
| <b>Broadwater</b>  | P                       | 2                  | <b>BWR-P2</b>           |
|                    | R1                      | 1                  | <b>BWR-R1</b>           |
| <b>Condong</b>     | P                       | 1                  | <b>CND-P</b>            |
|                    | R1                      | 1                  | <b>CND-R1</b>           |
| <b>Fergusson</b>   | P                       | 1                  | <b>FRG-P</b>            |
|                    | R1                      | 1                  | <b>FRG-R1</b>           |
| <b>Harwood</b>     | P                       | 2                  | <b>HWD-P2</b>           |
|                    | R1                      | 1                  | <b>HWD-R1</b>           |
| <b>Isis</b>        | P                       | 1                  | <b>ISS-P</b>            |
|                    | R1                      | 1                  | <b>ISS-R1</b>           |
| <b>Maryborough</b> | P                       | 1                  | <b>MBR-P</b>            |
| <b>Nambour</b>     | P                       | 1                  | <b>NAM-P</b>            |
|                    | R1                      | 1                  | <b>NAM-R1</b>           |

<sup>a</sup> P = plant crop, R1= First ratoon

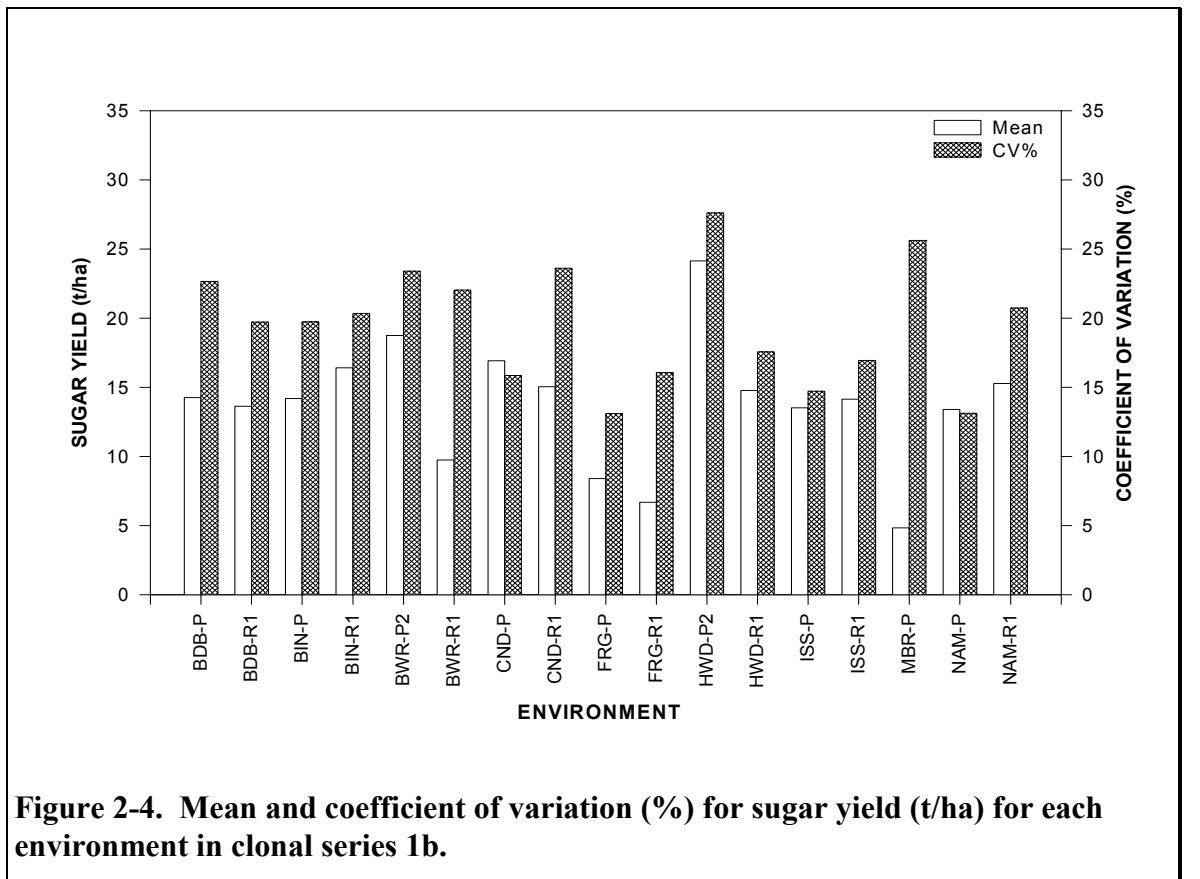
## **APPENDIX 2**

### **Trial Summary**



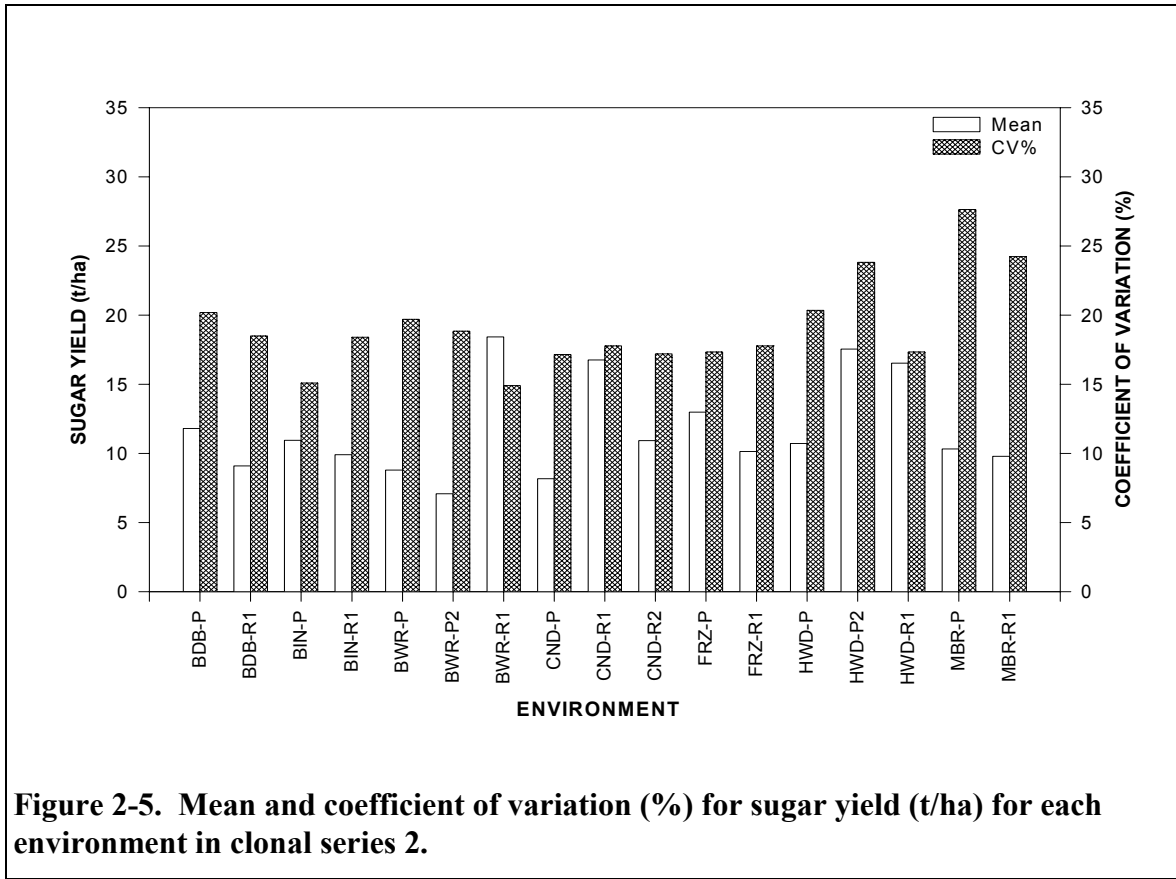


**Figure 2-3. Mean and coefficient of variation (%) for sugar yield (t/ha) for each environment in clonal series 1a.**



**Figure 2-4. Mean and coefficient of variation (%) for sugar yield (t/ha) for each environment in clonal series 1b.**





## **APPENDIX 3**

### **Weather Summary**

