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# GENOTYPE ENVIRONMENT ANALYSES of COTTON CULTIVAR TRIALS

by

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Technical Report

to

COTTON RESEARCH COUNCIL

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**CONTENTS**

## PREFACE

This report follows on from that of Williams and van Ewijk.

We have followed the same format to that of Williams and van Ewijk in the naming of years, locations, and cultivars, except where indicated.

Data for 1984/85 and 1985/86 are included in our analysis making a total of 12 years data.

# 1. DESCRIPTION of PROJECT

## 1.1 Outline

The purpose of this project is the same as that of Williams and van Ewijk, namely

> to conduct a critical examination of the ACCT data from 1974/75 to 1985/86 and to learn more about the relative behaviour of cultivars over the testing sites and the effectiveness of locations to evaluate cultivar differences.

We have concentrated on the numerical classification approach to analysis of the data (Byth, Eisemann and DeLacy, 1976).

## 1.2 Cultivars

The 108 cultivars tested in the 12 years of trial are listed in Table 1.2.1. We have allocated a "2-symbol" abbreviation to facilitate the labelling of graphs.

Unlike ideal genotype x location x year studies where the genotypes remain the same over the course of the study, the data for this study are taken from a practical breeding program where a large number of the genotypes under test were replaced from year to year. Only 52 cultivars were tested in two years or more (Table 1.2.2) and of those only 36 were tested in three years or more.

The data used for this analysis can be divided into two basic groups to facilitate interpretation. In the six years 74/75 to 79/80 most of the genotypes were of USA origin and not particularly well adapted to the Australian environment. Whereas, in the six years 80/81 to 85/86 most of the genotypes were advanced selections from the CSIRO breeding program and better adapted to the Australian environment.

In the trials conducted during 80/81 to 84/85, many of the genotypes being tested were of Deltapine origin (dpl6, dp41, dp55, dp61, sicotl, sicotlf, sicot2, n40-1h, n40-39h, n40-286f, n40-439g, n40-439h). This is significant because trial data from the USA (reference) shows that Deltapine genotypes are more generally adapted to a wider range of environments than other cotton genotypes.

**Table 1.2.1 List of cultivars**

| abbreviation | name | no |
|---|---|---|
| 16 | dp16 | deltapine 16 | 1 |
| sm | dpsm | deltapine sm | 2 |
| 13 | dp13 | deltapine sm seln 13 | 3 |
| ki | kimdell | kimdell 11 | 4 |
| ho | hopi | hopicala | 5 |
| g6 | gl06 | gl06 | 6 |
| ms | m8 sok | m8 superokra | 7 |
| dc | delcott | delcott 277 | 8 |
| ta | st7A | stoneville 7A | 9 |
| tn | st7AN | stoneville 7A N | 10 |
| by | bayou | bayou sm 1 | 11 |
| ac | acala70 | acala 70/185 | 12 |
| na | namcala | namcala | 13 |
| r9 | cr79 | cr 79 | 14 |
| r4 | cr74 | cr 74 | 15 |
| rx | rex | rex smoothleaf | 16 |
| h6 | h62 | h62-8 | 17 |
| ha | hancock | hancock | 18 |
| ml | mcnl032 | macnair 1032 | 19 |
| t7 | st702 | stoneville 702 | 20 |
| bl | ls/obG | ls/ob G090 | 21 |
| b2 | ls/ob | ss/ob s081 | 22 |
| b3 | ls/obs | ls/ob field bulk | 23 |
| rp | rivp | riverina poplar | 24 |
| rg | rivg | riverina gold | 25 |
| 61 | dp61 | deltapine 61 | 26 |
| 37 | tamsp37 | tamcott sp37 | 27 |
| c4 | c4104 | coker 4104 | 28 |
| m8 | m8 | m8 | 29 |
| g2 | g245 | g245-2-11 | 30 |
| c0 | c310 | coker 310 | 31 |
| mv | mv81 | mv081 | 32 |
| 70 | 70-081 | 70-081-20-12-19-4 | 33 |
| r2 | cr142 | cr 142-45 | 34 |
| gn | st gN | stoneville gl N | 35 |
| gf | dp gf | deltapine gl fr | 36 |
| r8 | cr128 | cr128-5 | 37 |
| c2 | c312 | coker 312 | 38 |
| ds | des024 | des 024 | 39 |
| m2 | mcn220 | macnair 220 | 40 |
| s2 | sicot2 | sicot 2 | 41 |
| 4g | 40 286f | n40 286 fr | 42 |
| sl | sicotl | sicot 1 | 43 |
| 4f | 40 286 | n40 286 h | 44 |
| 4d | 40 39h | n40 39 h | 45 |
| 7x | 70 28-1 | n70 28/1 | 46 |
| 7y | 70 28-3 | n70 28/3 | 47 |
| 55 | dp55 | deltapine 55 | 48 |
| mo | mo63-277 | mo63-277 br | 49 |
| c6 | c600 | coker br-600 | 50 |
| 80 | dp80 | deltapine 80 | 51 |
| c5 | c315 | coker 315 | 52 |
| cl | c511 | coker sm 511 | 53 |
| 4k | 41 572N | n41 57-2n | 54 |
| 6i | dp61ipr | deltapine 61-ipr | 55 |
| 41 | dp41 | deltapine 41 | 56 |

| abbreviation | name | no |
|---|---|---|
| 71 | dp7146N | deltapine 714 6N | 57 |
| 4a | 40 1h | n40 1h | 58 |
| sf | sicot1f | sicot 1f | 59 |
| s3 | sicot3 | sicot 3 | 60 |
| 4j | 40 439g | n40 439 g | 61 |
| 4h | 40 439h | n40 439 h | 62 |
| mo | mo63-277 | mo63 277j | 63 |
| 3a | 39 10-4 | n39 10/4 | 64 |
| 3b | 39 42-8 | n39 42/8 | 65 |
| 7z | 70 37-10 | n70 37/10 | 66 |
| 8a | 85 33-8 | n85 33/8 | 67 |
| 07 | 75007 | 75007-3 | 68 |
| 23 | 76023 | 76023-1 | 69 |
| 7b | 74 630 | n74 630 | 70 |
| 4c | 40 39f | n40 39 hf | 71 |
| 4i | 40 439ds | n40 439ds | 72 |
| nb | 91 4-109 | n91 4/109 | 73 |
| nc | 91 7-111 | n91 7/111 | 74 |
| nd | 91 8-30 | n91 8/30 | 75 |
| ne | 91 9-111 | n91 9/111 | 76 |
| si | siokra | siokra | 77 |
| 7c | 74 480 | n74 480 | 78 |
| 61 | dp61 | deltapine 61-77 | 79 |
| 90 | dp90 | deltapine 90 | 80 |
| 7d | 74 69 | n74 69 | 81 |
| 7e | 74 250 | n74 250 | 82 |
| 9a | 98 283 | n98 283 | 83 |
| 9b | 98 247 | n98 247 | 84 |
| 9c | 98 249 | n98 249 | 85 |
| 9d | 98 251 | n98 251 | 86 |
| 9e | 98 308 | n98 308 | 87 |
| 9f | 98 320 | n98 320 | 88 |
| 9g | 98 329 | n98 329 | 89 |
| 9h | 98 331 | n98 331 | 90 |
| 9i | 98 335 | n98 335 | 91 |
| 9j | 98 336 | n98 336 | 92 |
| 50 | dp50 | deltapine 50 | 93 |
| 7f | 74 355 | n74 355 | 94 |
| 7g | 74 720 | n74 720 | 95 |
| 7h | 74 666 | n74 666 | 96 |
| 7i | 74 108 | n74 666-108 | 97 |
| 4b | 40 1h565 | 1h 565 | 98 |
| 4c | 40 1h570 | 1h 570 | 99 |
| 2a | sic2374 | sicot 2-374 | 100 |
| 2b | sic2411 | sicot 2-411 | 101 |
| 2c | sic2418 | sicot 2-418 | 102 |
| 2d | sic2436 | sicot 2-436 | 103 |
| sn | siokra N | siokra N | 104 |
| sb | siokra s | siokra bulk seln | 105 |
| ss | siok Ns | siokra N bulk | 106 |
| 7j | 74 720s | n74 720 seln | 107 |
| 7k | 74 355s | n74 355 seln | 108 |

Table 1.2.2 Distribution of cultivars over years for those cultivars tested in two years or more.

| No. | Abbrev. | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | dp16 | x | x | x | x | x | x | x | x | x | x | x | x | x |
| 2 | dpsm | x | x | x | x | | | | | | | | | |
| 3 | dp13 | x | x | x | x | | | | | | | | | |
| 4 | kimdell | x | x | x | x | | | | | | | | | |
| 5 | hopi | x | x | x | x | | | | | | | | | |
| 6 | g106 | x | x | x | x | x | x | x | | | | | | |
| 7 | m8sok | x | x | x | x | x | x | x | | | | | | |
| 8 | delcott | x | x | x | x | | | | | | | | | |
| 9 | st7A | x | x | x | x | x | x | x | | | | | | |
| 10 | st7AN | x | x | x | x | x | x | x | | | | | | |
| 11 | bayou | x | x | x | x | | | | | | | | | |
| 12 | acala70 | x | x | x | x | | | | | | | | | |
| 13 | namcala | x | x | x | x | x | x | x | x | x | x | x | x | x |
| 14 | cr79 | x | x | x | x | | | | | | | | | |
| 15 | cr74 | x | x | x | x | | | | | | | | | |
| 16 | rex | x | x | x | x | | x | x | | | | | | |
| 17 | h62 | x | x | x | x | | | | | | | | | |
| 18 | hancock | x | x | x | x | | | | | | | | | |
| 19 | mcn1032 | | x | x | x | x | x | | | | | | | |
| 25 | rivg | | x | x | x | | | | | | | | | |
| 26 | dp61 | | | x | x | x | x | x | x | x | x | x | x | x |
| 27 | tamsp37 | | | x | x | x | | | | | | | | |
| 29 | m8 | | | x | x | x | x | | | | | | | |
| 31 | c310 | | | | x | x | x | x | x | | | | | |
| 32 | mv81 | | | | x | x | | | | | | | | |
| 35 | st gf | | | | | x | x | | | | | | | |
| 36 | dp gf | | | | | x | x | | | | | | | |
| 38 | c312 | | | | | | x | x | | | | | | |
| 40 | mcn220 | | | | | | | x | x | x | x | x | | |
| 41 | sicot2 | | | | | | | x | x | x | x | x | x | |
| 42 | 40 286f | | | | | | | x | x | | | | | |
| 43 | sicot1 | | | | | | | x | x | x | x | x | | |
| 45 | 40 39h | | | | | | | x | | x | | | | |
| 48 | dp55 | | | | | | | x | x | x | x | x | | |
| 52 | c315 | | | | | | | x | x | x | x | x | x | |
| 56 | dp41 | | | | | | | | x | x | x | x | | |
| 58 | 40 1h | | | | | | | | x | x | | x | | |
| 59 | sicot 1f | | | | | | | | x | x | | | | |
| 61 | 40 439g | | | | | | | | x | x | | | | |
| 62 | 40 439h | | | | | | | | x | x | x | x | | |
| 68 | 75007 | | | | | | | | x | x | | | | |
| 75 | 91 8-30 | | | | | | | | | x | x | x | | |
| 77 | siokra | | | | | | | | | x | x | x | x | x |
| 80 | dp90 | | | | | | | | | | x | x | x | x |
| 81 | 74 69 | | | | | | | | | | x | x | | |
| 82 | 74 250 | | | | | | | | | | x | x | | |
| 84 | 98 247 | | | | | | | | | | x | x | | |
| 86 | 98 251 | | | | | | | | | | x | x | | |
| 87 | 98 308 | | | | | | | | | | x | x | x | |
| 94 | 74 355 | | | | | | | | | | | x | x | |
| 95 | 74 720 | | | | | | | | | | | x | x | |
| 103 | sic2-436 | | | | | | | | | | | x | x | |
| 104 | siokra N | | | | | | | | | | | | x | x |
| 105 | siokra s | | | | | | | | | | | | x | x |
| 106 | siokra Ns | | | | | | | | | | | | x | x |
| 107 | 74 720s | | | | | | | | | | | | x | x |

## 1.3 Locations

We have used "single-letter" abbreviations for location names (Table 1.3.1) to facilitate the labelling of graphs.

**Table 1.2.1 List of Locations**

| abbreviation | location |
|---|---|
| e | Emerald |
| b | Biloela |
| t | Theodore |
| d | Darling Downs |
| s | St George |
| g | Boggabilla |
| c | Moomin Creek |
| m | Moree |
| v | Myall Vale |
| n | West Namoi |
| z | Breeza |
| w | Warren |
| k | Bourke |

The unsprayed locations and Lockyer (see Table 1.2.4 in Williams and van Ewijk) were excluded from our analyses giving a reduced year x location table of 132 cells of which 100 are filled (Table 1.3.2).

This data can be divided into two basic groups to facilitate its interpretation. In the six years 74/75 to 79/80 only eight locations were used for testing giving a year x location table of 48 cells of which 41 are filled. However, eleven locations were used for testing in the years 80/81 to 85/86 giving a year x location table of 66 cells of which 57 are filled. This grouping of the data corresponds to the same grouping of years as determined on genetic origin of cultivars (section 1.2).

**Table 1.3.2 Distribution of locations over years**

| year | location | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | e | b | t | d | s | g | c | m | v | n | z | w | k |
| 74/75 | | 1 | 1 | 1 | 1 | | | | 1 | 1 | | 1 | |
| 75/76 | | 1 | 1 | | 1 | | | | 1 | 1 | | 1 | |
| 76/77 | | 1 | 1 | 1 | 1 | | | | 1 | 1 | | 1 | |
| 77/78 | 1 | 1 | 1 | 1 | 1 | | | | 1 | 1 | | 1 | |
| 78/79 | 1 | 1 | 1 | 1 | 1 | | | | | 1 | | 1 | |
| 79/80 | 1 | 1 | 1 | 1 | 1 | | | | 1 | 1 | | 1 | |
| 80/81 | 1 | | 1 | 1 | 1 | | 1 | 1 | 1 | 1 | | 1 | |
| 81/82 | | 1 | 1 | 1 | 1 | | | 1 | 1 | 1 | | 1 | |
| 82/83 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | |
| 83/84 | | 1 | | 1 | | 1 | 1 | 1 | 1 | 1 | | 1 | |
| 84/85 | 1 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | |
| 85/86 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | | 1 | |
| 86/87 | 1 | 1 | | 1 | 1 | 1 | | 1 | 1 | | 1 | 1 | 1 |

## 1.4 Variates

So far only lint yield has been considered in our analyses because this is the variate of most interest to the cotton breeder when genotype-environment interactions are being considered.

## 1.5 Data

We used the adjusted genotype x location values calculated by Williams and van Ewijk as the starting point of our analyses.

## 1.6 Sets of data

We derived a number of cultivar x location x year data sets (Table 1.6.1) by combining data over years where cultivars were common (see Table 1.2.2).

**Table 1.6.1 Sets of data used in analysis**

| year | matrix size g * e | year | matrix size g * e |
|---|---|---|---|
| 74 | 18 x 7 | 74-77 | 18 x 28 |
| 75 | 25 x 6 | 74-80 | 6 x 80 |
| 76 | 25 x 7 | 80-84 | 8 x 46 |
| 77 | 25 x 8 | 80-85 | 5 x 57 |
| 78 | 16 x 6 | 82-85 | 6 x 40 |
| 79 | 16 x 7 | 83-85 | 8 x 29 |
| 80 | 25 x 9 | 85-86 | 9 x 21 |
| 81 | 25 x 8 | | |
| 82 | 25 x 11 | | |
| 83 | 25 x 8 | | |
| 84 | 30 x 10 | | |
| 85 | 16 x 11 | | |
| 86 | 16 x 10 | | |

# 2. METHODS of ANALYSES

## 2.1 Linear regression analyses

The proportion of genotype-environment information (sum of squares) accounted for by the linear regression coefficients (Finlay and Wilkinson, 1963) is on average 20% (Table 2.1.1) which was too low to help the cotton breeder gain a better understanding of genotype response over environments.

**Table 2.1.1 Proportion of ge accounted for by regression**

| year | $R^2$ | year | $R^2$ |
|---|---|---|---|
| 74 | 27 | 74-77 | 8 |
| 75 | 28 | 74-80 | 13 |
| 76 | 15 | 80-84 | 6 |
| 77 | 23 | 80-85 | 6 |
| 78 | 38 | 82-85 | 8 |
| 79 | 13 | 83-85 | 10 |
| 80 | 26 | | |
| 81 | 9 | | |
| 82 | 12 | | |
| 83 | 11 | | |
| 84 | 21 | | |
| 85 | 3 | | |
| average | 19 | | 8 |

## 2.2 Pattern analysis

A numerical classification was employed to derive groupings of genotypes and environments following the approach of Byth, Eisemann and DeLacy (1976). This analysis was refined in two ways. Firstly, environments were classified using ge interaction effects as data (DeLacy, 1981). Since differences in environmental mean yield are often large relative to genotypic differences within environments, this ensured that the grouping of environments was sensitive to differential patterns of genotypic performance within environments by removing any overwhelming influence of environmental mean yields. Secondly, objective determination of the number of genotype and environment groups employed in summarizing the data was made using two criteria. These were the size of the final array of genotype and environment groups to be examined, and the amount of variation, particularly that due to ge interactions, which was retained among groups for this array (DeLacy, 1981).

Classification were obtained using an agglomerative, hierarchical numerical classificatory procedure with incremental sum of squares as the clustering strategy and unstandardized squared Euclidean distance as the measure of dissimilarity (Byth et al, 1976). Several supplementary computer programs (Appendix L) were employed to further summarize the results.

## 2.3 Single year data sets

The number of environments per year ranged from 6 to 11, which was considered small enough not to require truncation of environments but to retain them all as single member environment groups.

Genotypes were classified for each data set and the number of genotype groups truncated at a level whereby the reduced arrays accounted for 55% (or as close as possible) of the ge interaction sum of squares in the original matrices.

The 16 to 30 genotypes in the original data sets were reduced to 3 to 7 genotypes groups (Table 2.3.1). This was an average reduction of 78% in the size of the original matrix, whilst still retaining on average, 84% of the genotype sum of squares and 55% of the ge interaction sum of squares.

**Table 2.3.1 Summary of reduced matrices**

| years | matrix size gen x env | reduced matrix | % reduction matrix | % G SS retained | % GE SS retained |
|---|---|---|---|---|---|
| 74 | 18 x 7 | 4 x 7 | 78 | 74 | 57 |
| 75 | 25 x 6 | 5 x 6 | 80 | 88 | 57 |
| 76 | 25 x 7 | 5 x 7 | 80 | 84 | 56 |
| 77 | 25 x 8 | 6 x 8 | 76 | 90 | 51 |
| 78 | 16 x 6 | 4 x 6 | 75 | 88 | 63 |
| 79 | 16 x 7 | 5 x 7 | 69 | 85 | 59 |
| 80 | 25 x 9 | 6 x 9 | 76 | 92 | 54 |
| 81 | 25 x 8 | 5 x 8 | 80 | 79 | 52 |
| 82 | 25 x 11 | 7 x 11 | 72 | 88 | 54 |
| 83 | 25 x 8 | 4 x 8 | 84 | 85 | 55 |
| 84 | 30 x 10 | 5 x 10 | 87 | 75 | 57 |
| 85 | 16 x 11 | 3 x 11 | 81 | 75 | 55 |
| average | | | 78 | 84 | 55 |
| 74-77 | 18 x 28 | 11 x 8 | 83 | 95 | 55 |
| 74-80 | 6 x 50 | 6 x 5 | 90 | 100 | 58 |
| 80-84 | 8 x 46 | 8 x 5 | 89 | 100 | 53 |
| 80-85 | 5 x 57 | 5 x 4 | 93 | 100 | 55 |
| 82-85 | 6 x 40 | 6 x 5 | 88 | 100 | 61 |
| 83-85 | 8 x 29 | 8 x 4 | 86 | 100 | 52 |
| average | | | 88 | | 55 |

## 2.4 Combined year data sets

Except for the 74-77 data set, the other arrays contained 5 to 8 genotypes which was considered small enough not to require truncation of genotypes but to retain them all as single member genotype groups.

Environments were classified for each data set and the number of environmental groups truncated at a level whereby the reduced arrays accounted for 55% (or as close as possible) of the ge interaction sum of squares in the original matrices.

The 29 to 57 environments in the original data sets were reduced to 4 to 5 environment groups in the reduced arrays (Table 2.3.1). This was an average reduction of 88% in the size of the original array whilst still retaining an average of 55% of the ge interaction sum of squares.

For the 74-77 data set, separate classifications of genotypes and environments were super-imposed to give a two-way reduction of the original 18 x 28 matrix. Two criteria were used to decide the size of the reduced matrix, firstly retaining 55% of the ge interaction sum of squares, and secondly, obtaining the maximum reduction in the size of the original array. The 11 x 8 reduced array was a reduction of 83% in array size, whilst still retaining 95% of the genotype sum of squares and 55% of the ge interaction sum of squares.

## 3. GENOTYPE RESPONSE to ENVIRONMENTS - SINGLE YEARS

For each single year data set the genotype response to environments was considered by examining:

(i) the dendogram illustrating the classification of genotype groups (all dendogram figures in Section 3) and the genotype composition of each of those groups (Appendix C).

(ii) the graph illustrating all the genotype group responses over environments. The overall contribution of genotype main effects and ge interaction effects (Shorter and DeLacy, 1981) is given for the separation of these genotype groups.

(iii) the graphs illustrating the contrasting responses to environments of the two genotype groups at each fusion level (Appendix J). The contribution of genotype main effects and ge interaction effects is given for each fusion level.

(iv) the contributions of ge effects to the classification of genotypes at each fusion level (Appendix I).

(v) the two-way analysis of variance (Appendix A).

### 3.1 74/75 genotypes

group 23 - CSIRO bred selections from the Riverina
- two member group which is low yielding at all environments.

group 7 - "m8 superokra" has variable response across environments, highest yielding genotype at Biloela and lowest yielding genotype at Warren and St George.

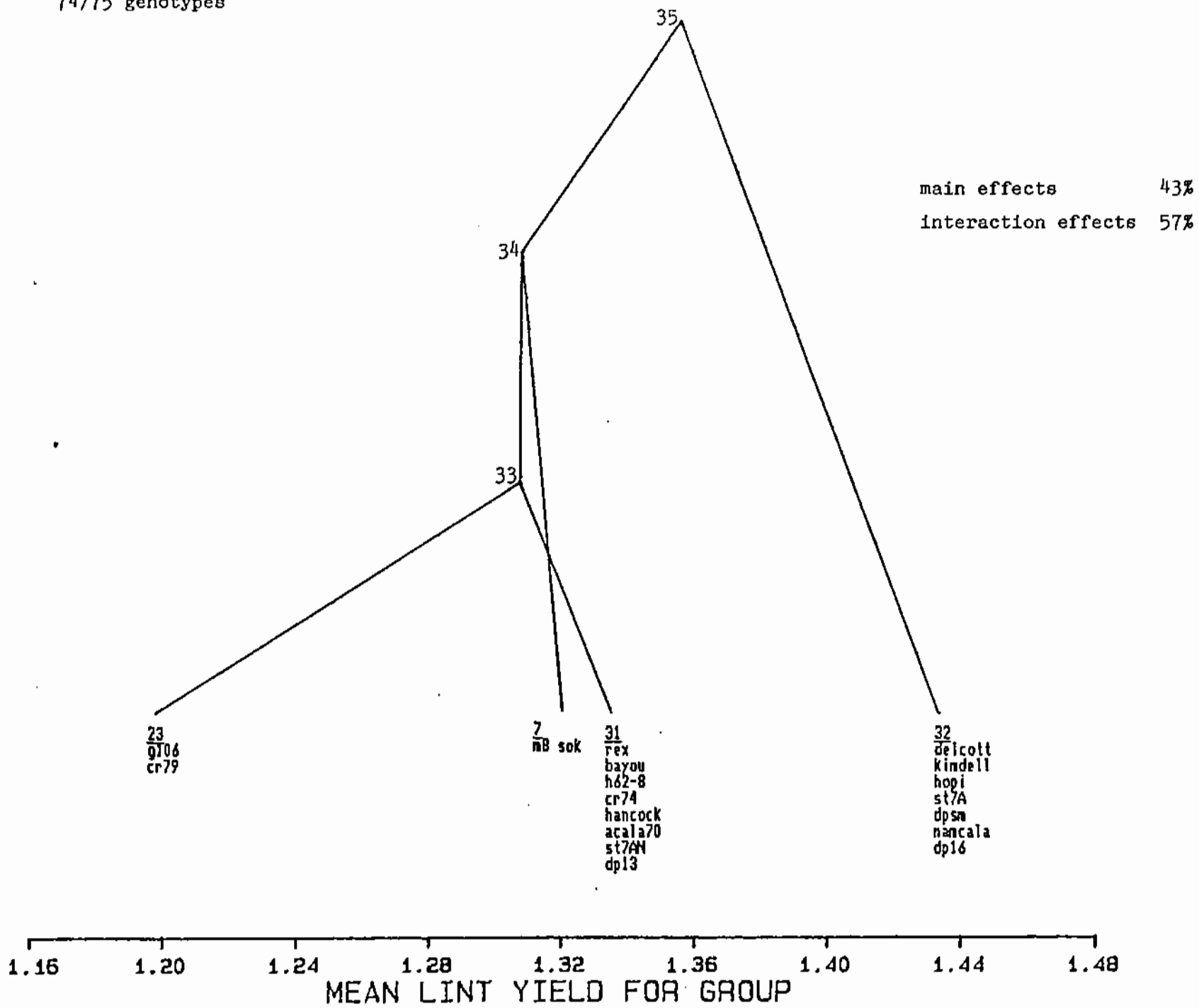
group 31 - miscellaneous group of genotypes
- average yield at all environments.

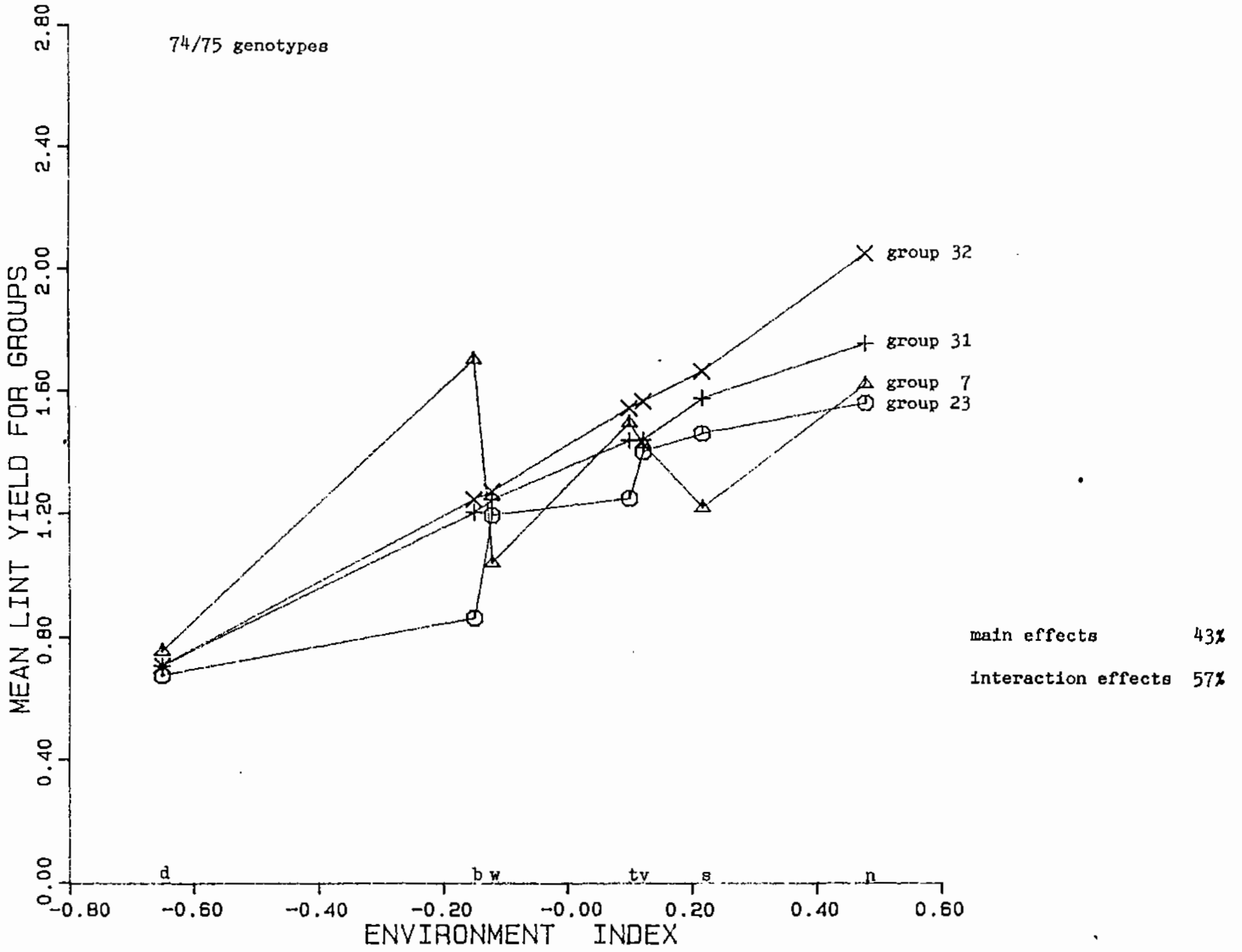
group 32 - mostly Deltapine related genotypes
- high yielding genotypes at all locations, except Biloela.

Genotype-environment effects (57%) are a major component in separating genotype groups. The main environments contributing to the separation of genotype groups are

n separates higher yielding adapted genotypes (group 32) from other genotypes.

b separates other genotypes into three groups, unadapted (group 23), specifically adapted to biloela (m8sok) and generally adapted (group 31).


74/75 genotypes
35
34
33
main effects 43%
interaction effects 57%
23
gl06
cr79
7
mB sok
31
rex
bayou
h62-8
cr74
hancock
acala70
st7AN
dp13
32
delcott
kindell
hopi
st7A
dpsm
nancala
dp16
1.16
1.20
1.24
1.28
1.32
1.36
1.40
1.44
1.48
MEAN LINT YIELD FOR GROUP


74/75 genotypes
MEAN LINT YIELD FOR GROUPS
2.80
2.40
2.00
1.60
1.20
0.80
0.40
0.00
group 32
group 31
group 7
group 23
main effects 43%
interaction effects 57%
d
b w
tv
s
n
-0.80
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
ENVIRONMENT INDEX

### 3.2 75/76 genotypes

group 45 - CSIRO bred selections from the riverina
- low yielding at all sites.

group 43 - USA developed selections
- low to average yields at all locations except Warren where it is low yielding.

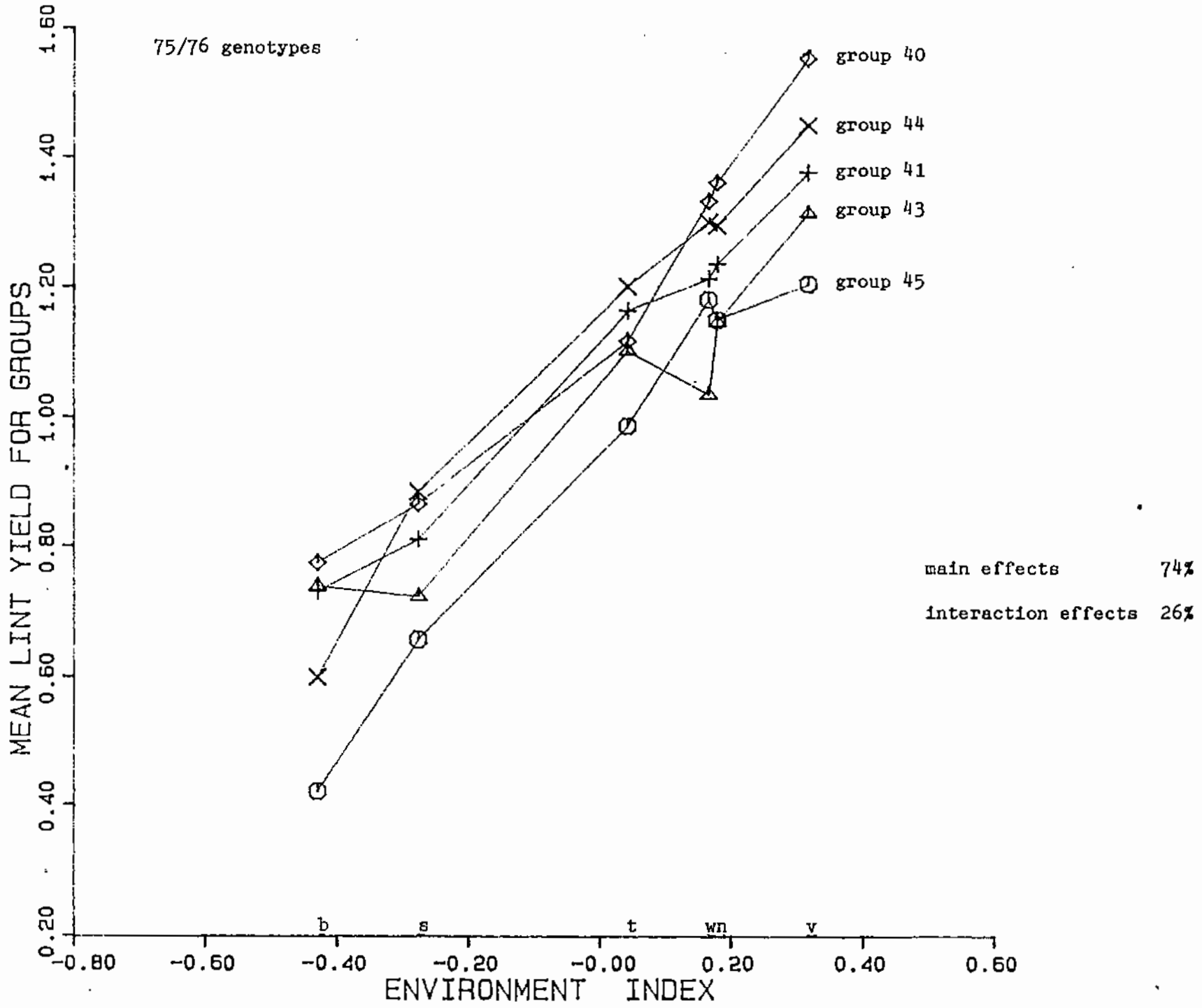
group 41 - stoneville related genotypes
- average yields at all locations.

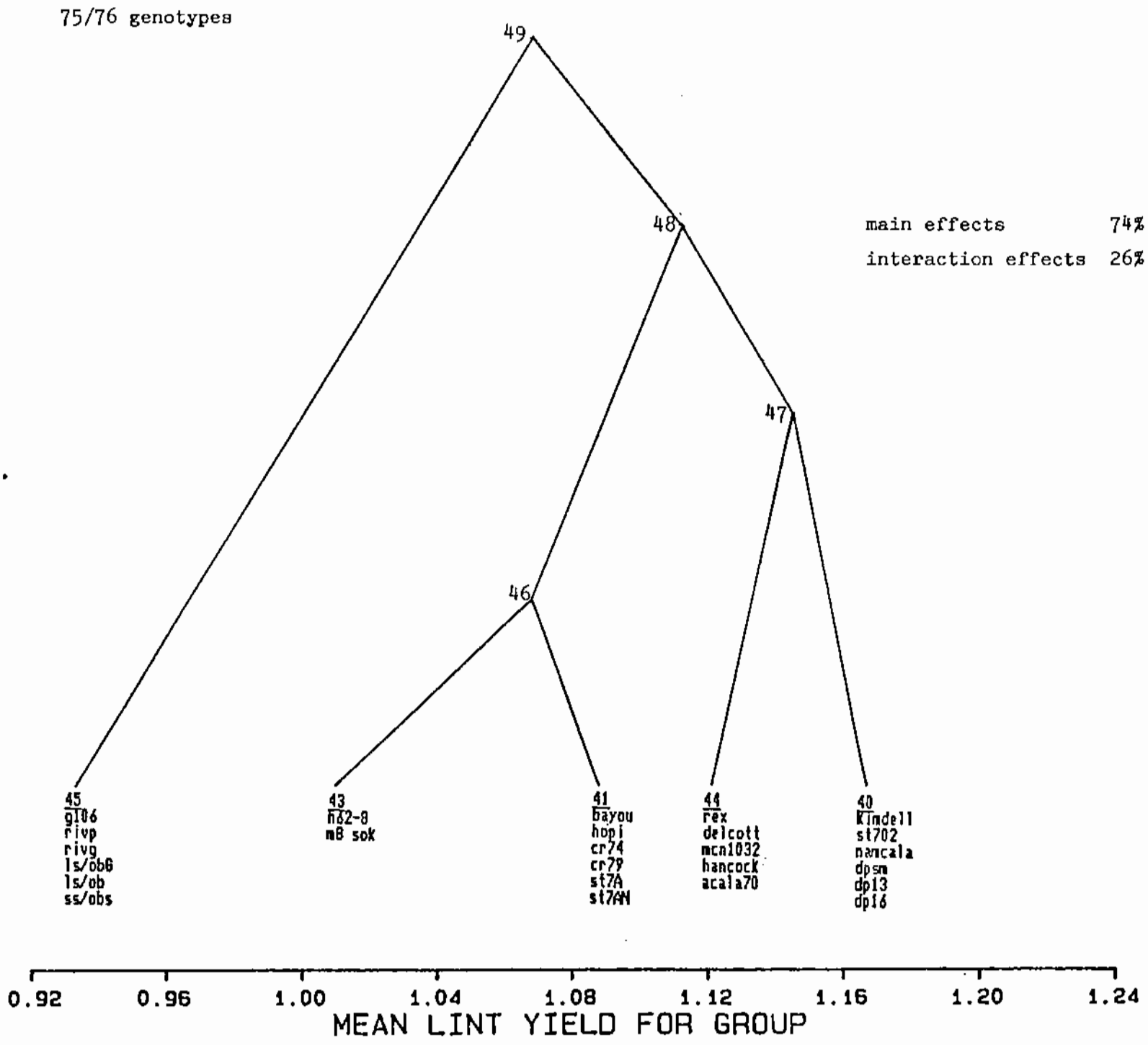
group 44 - mostly USA developed genotypes
- high yielding group at most sites.

group 40 - recently developed varieties of USA origin
- highest yielding group at all sites except Theodore.

Genotype groups are mostly separated by genotype main effects (74%) and not ge interaction effects. The main environments contributing to the separation of genotype groups are

b,v main locations for separating genotype groups


75/76 genotypes
group 40
group 44
group 41
group 43
group 45
main effects 74%
interaction effects 26%
MEAN LINT YIELD FOR GROUPS
ENVIRONMENT INDEX
0.20
0.40
0.60
0.80
1.00
1.20
1.40
1.60
-0.80
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
b
s
t
wn
v


75/76 genotypes
49
48
47
46
main effects 74%
interaction effects 26%
45
gl06
rivp
rivg
ls/ob6
ls/ob
ss/obs
43
n82-8
n8 sok
41
bayou
hopi
cr74
cr79
st7A
st7AN
44
rex
delcott
mcn1032
hancock
acala70
40
Kindell
st702
namcala
dpsm
dp13
dp16
0.92
0.96
1.00
1.04
1.08
1.12
1.16
1.20
1.24
MEAN LINT YIELD FOR GROUP

### 3.3 76/77 genotypes

group 37 - CSIRO bred selections from the Riverina
- group of two genotypes with low yields at all sites.

group 40 - USA developed genotypes
- low to average yielding group.

group 45 - miscellaneous group ofgenotypes
- average yielding group with low yields at high yielding environments.

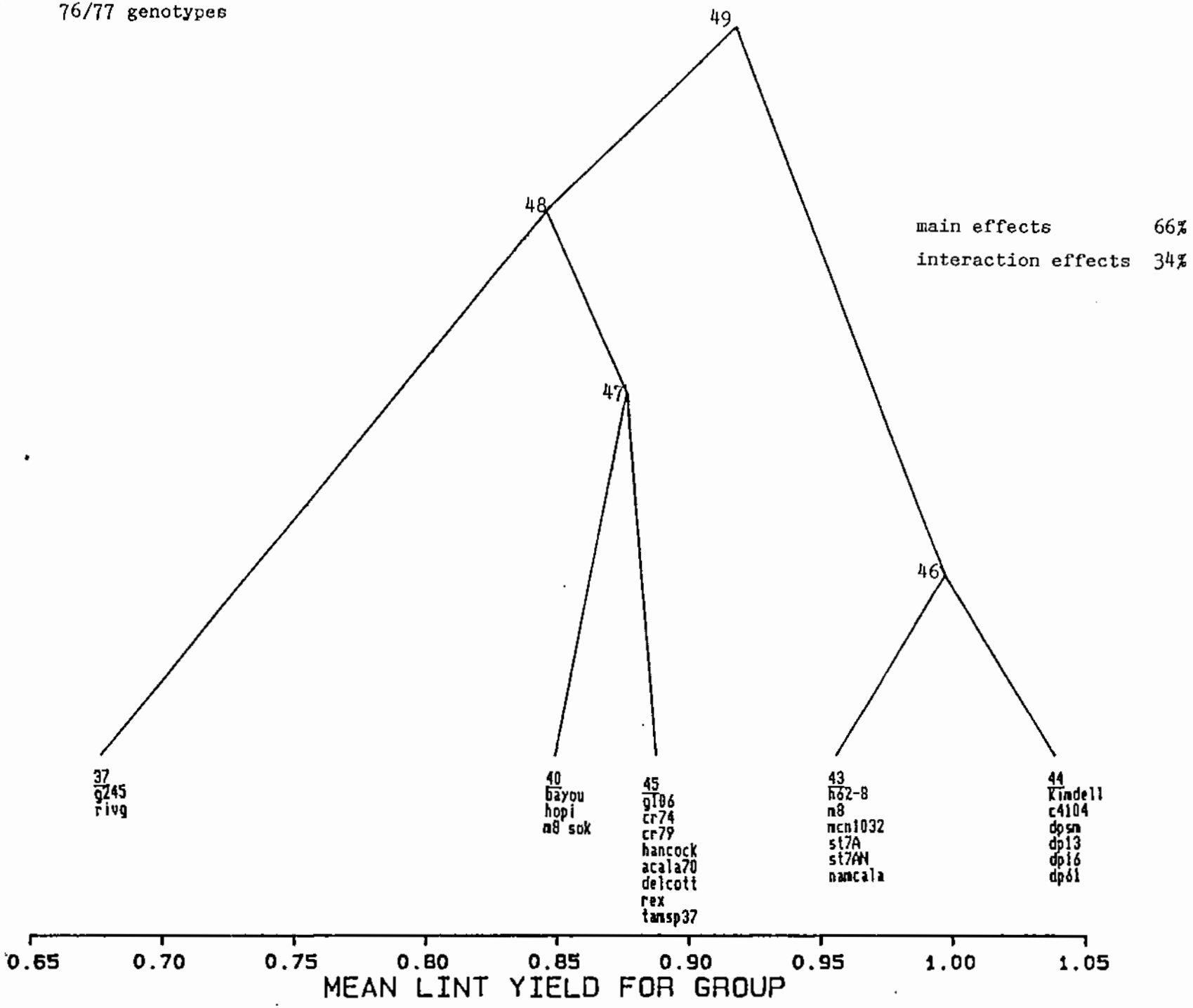
group 43 - mostly Stoneville related genotypes
- high to average yields at all locations except Darling Downs which is low yielding.

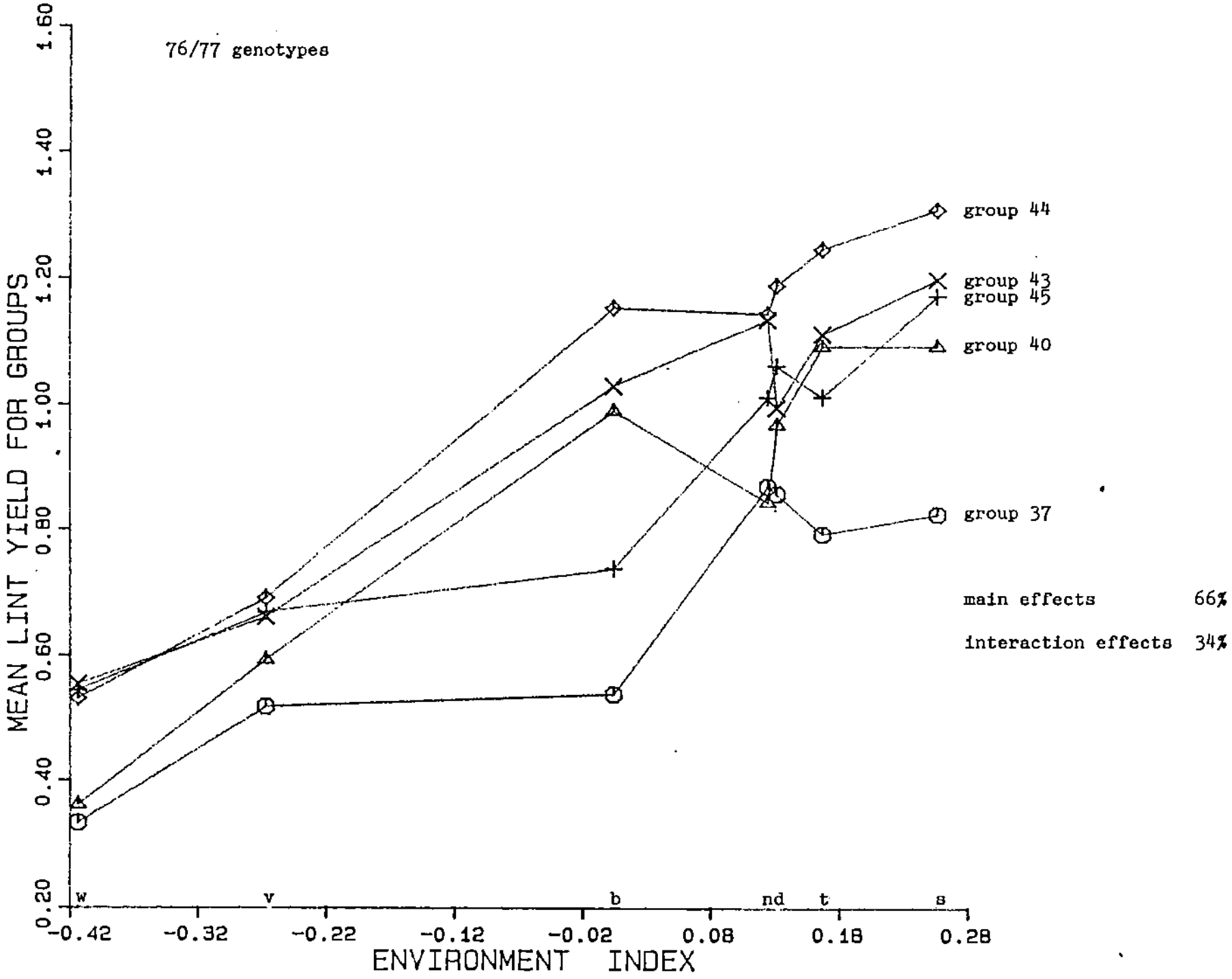
group 44 - deltapine related genotypes
- high yielding at all environments.

Genotype groups are separated by both genotype main effects (64%) and ge interaction effects (34%). The main environments contributing to the separation of genotype groups are

b main environment for separating genotypes into five groups

w contrasting environment to biloela for separating groups 40 and 45.


76/77 genotypes
49
48
47
46
main effects 66%
interaction effects 34%
37
gZ45
rivg
40
bayou
hopi
m8 sok
45
gl06
cr74
cr79
hancock
acala70
delcott
rex
tamsp37
43
h62-8
m8
mcn1032
st7A
st7AN
namcala
44
Kimdell
c4104
dpsn
dp13
dpl6
dp61
0.65
0.70
0.75
0.80
0.85
0.90
0.95
1.00
1.05
MEAN LINT YIELD FOR GROUP


76/77 genotypes
MEAN LINT YIELD FOR GROUPS
1.60
1.40
1.20
1.00
0.80
0.60
0.40
0.20
group 44
group 43
group 45
group 40
group 37
main effects 66%
interaction effects 34%
w
v
b
nd
t
s
-0.42
-0.32
-0.22
-0.12
-0.02
0.08
0.18
0.28
ENVIRONMENT INDEX

### 3.4 77/78 genotypes

group 43 - CSIRO developed selections from Riverina
- low yielding at all sites.

group 44 - USA developed genotypes which are low to average yielding at all locations.

group 36 - acala related genotypes.
- average yield at most locations but relative high yielding at Darling Downs and low yielding at Biloela.

group 41 - mixed group of genotypes.
- average yield at all locations.

group 39 - stoneville relative genotypes.
- average yield at most locations, but high yielding at Biloela and West Namoi and relatively low yielding at Warren and Theodore.

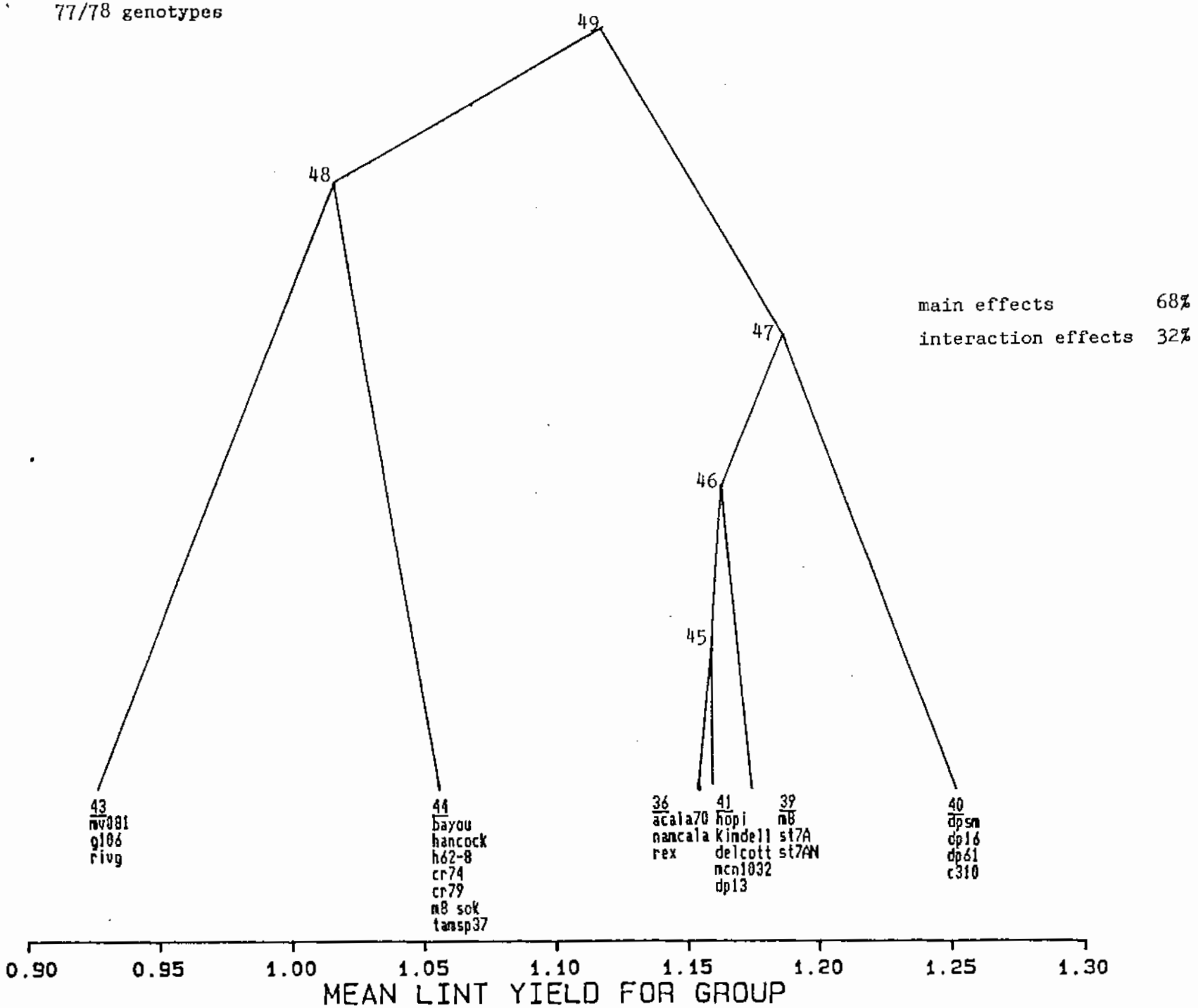
group 40 - recently developed varieties of USA origin.
- high yielding at all locations except st george.

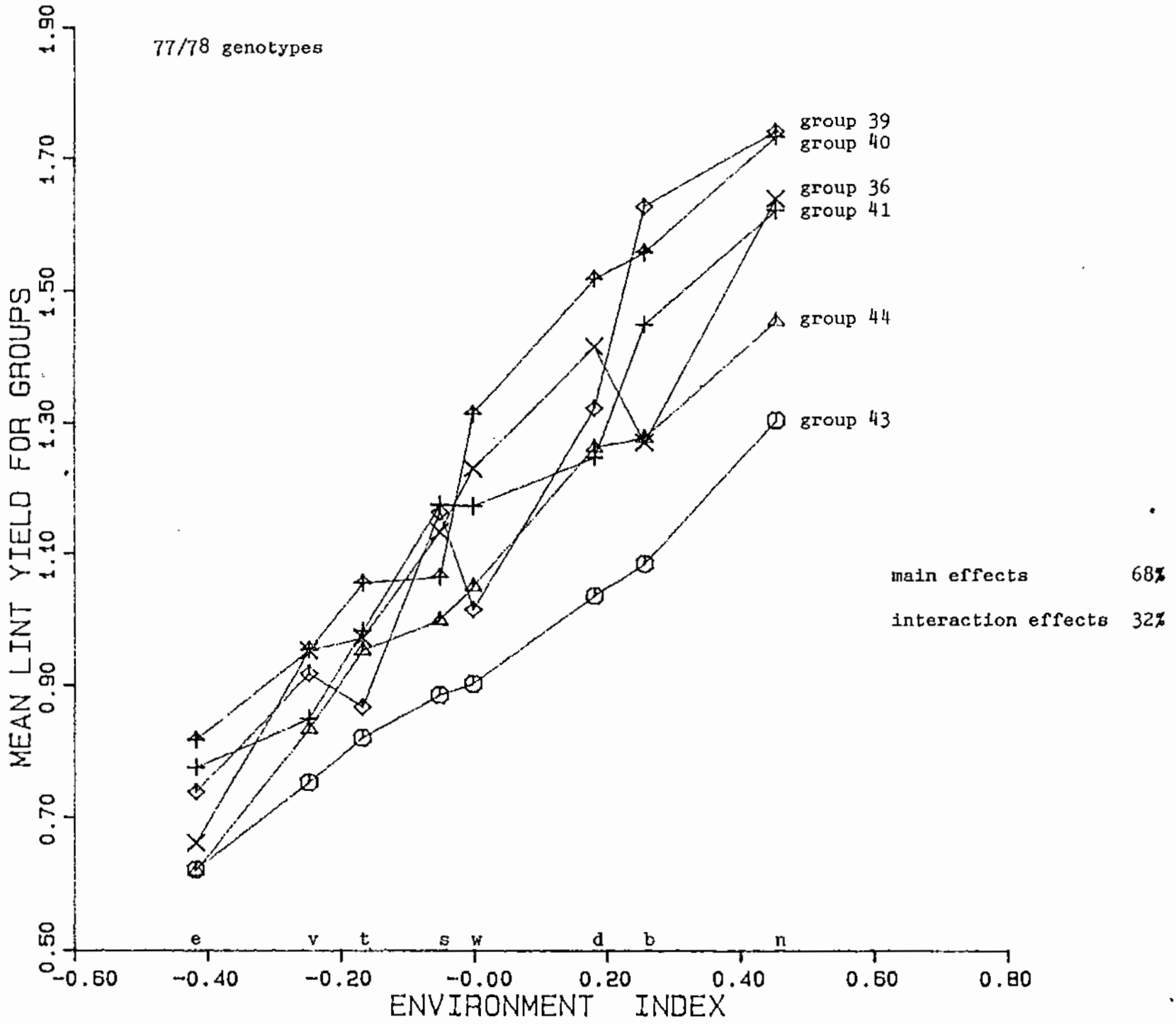
Groups 36, 39 and 41 have the same average yields but they differ in their response over environments.

Both genotype main effects (68%) and ge interaction effects (32%) contribute to the separation of these genotype groups. The main environments contributing to the separation of genotype groups are

b,n,d,w — four main locations for separating genotypes into four groups, unadapted (group 43), low to medium yield (group 44), medium to high yield (group 46), and high yield (group 40).

b — contrasting environment to either warren or darling downs for separating three groups, acala related genotypes (group 36), stoneville related genotypes (group 39), and group 41 (mixed group of genotypes).


77/78 genotypes
49
48
47
46
45
main effects 68%
interaction effects 32%
43
nv081
g106
rivg
44
bayou
hancock
h62-8
cr74
cr79
m8 sok
tamsp37
36
acala70
nancala
rex
41
hopi
kindell
delcott
mcn1032
dp13
39
m8
st7A
st7AN
40
dpsm
dp16
dp61
c310
0.90
0.95
1.00
1.05
1.10
1.15
1.20
1.25
1.30
MEAN LINT YIELD FOR GROUP


77/78 genotypes
group 39
group 40
group 36
group 41
group 44
group 43
main effects 68%
interaction effects 32%
MEAN LINT YIELD FOR GROUPS
0.50
0.70
0.90
1.10
1.30
1.50
1.70
1.90
e
v
t
s
w
d
b
n
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
0.80
ENVIRONMENT INDEX

### 3.5 78/79 genotypes

group 28 - mostly CSIRO selections developed for the Riverina
- low yielding at all locations.

group 25 - stoneville related genotypes
- average yield at all locations.

group 16 - "deltapine glabrous frego" has variable yield response over environments, highest yielding genotype at some sites and lowest yielding genotype at other sites.

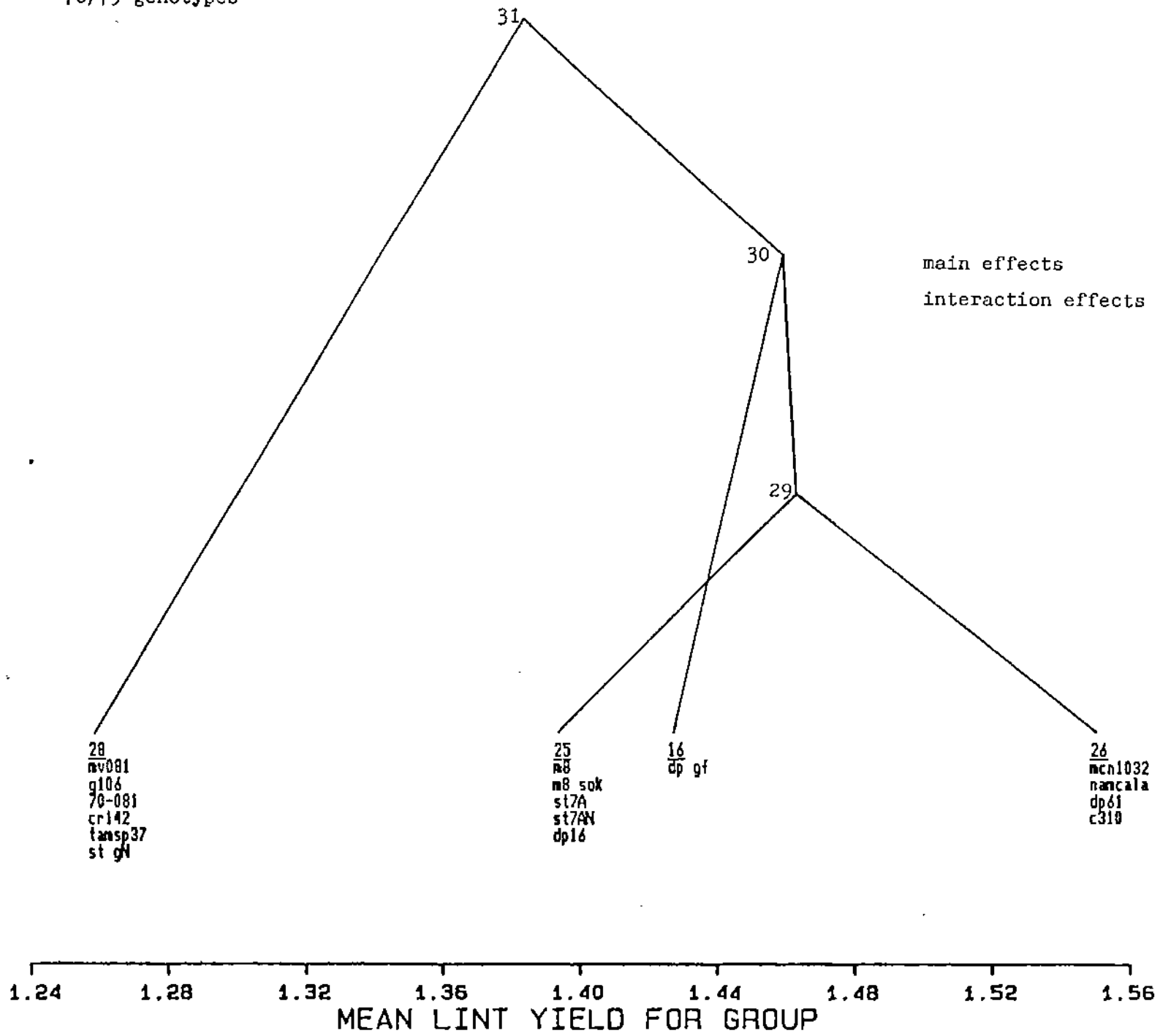
group 26 - recently developed varieties of USA origin.
- high yielding at all locations, except emerald.

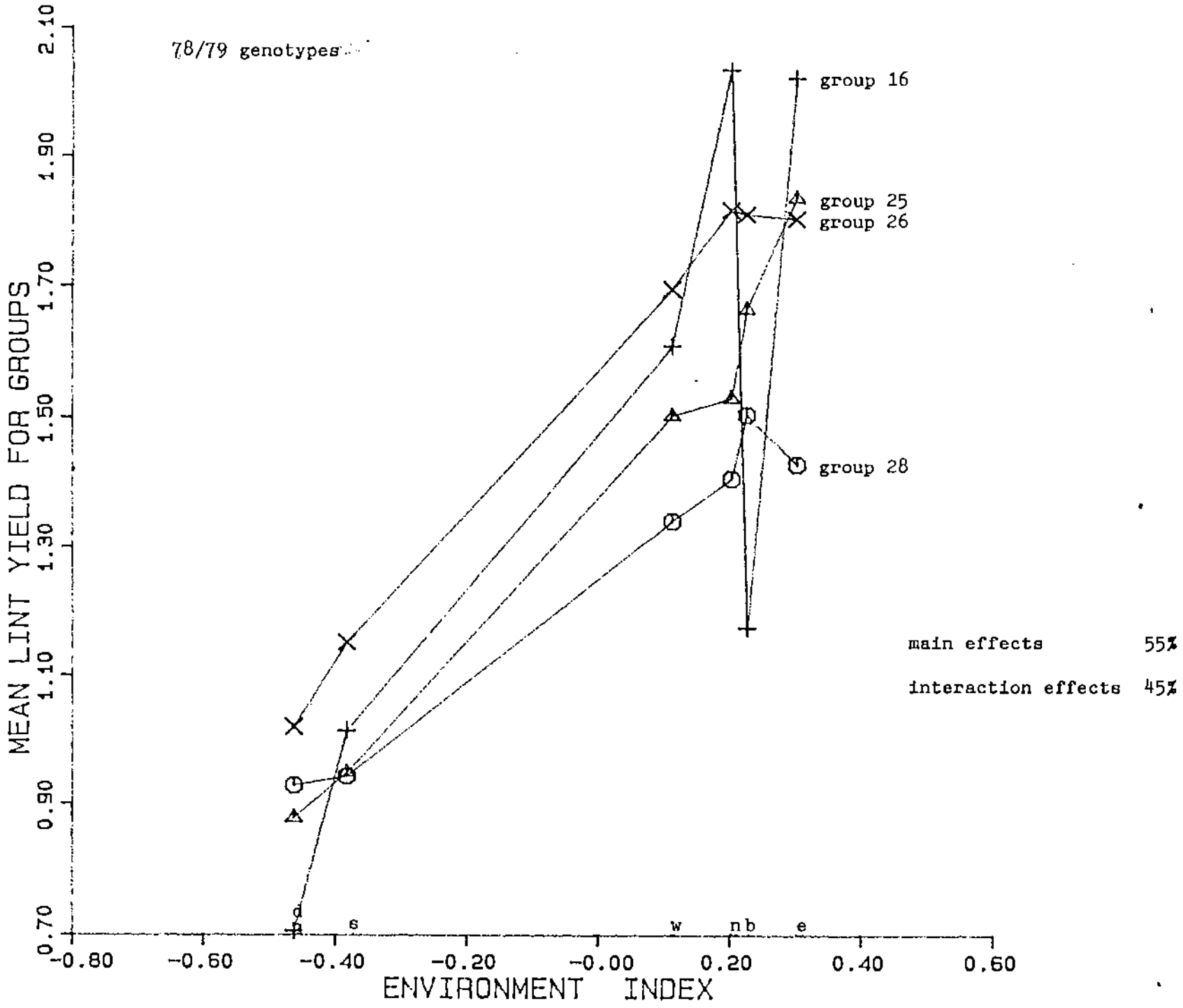
Both genotype main effects (55%) and ge interaction effects (45%) contribute to the separation of genotype groups. The main environments contributing to the separation of genotype groups are

e separates unadapted genotypes (group 28) from the rest

n separates Stoneville related genotypes (group 25) from recently developed USA cultivars (group 26)

b separates "deltapine gl fr" from other genotypes


78/79 genotypes
31
30
29
main effects 55%
interaction effects 45%
28
nv081
g106
70-081
cr142
tamsp37
st gN
25
m8
m8 sok
st7A
st7AN
dp16
16
dp gf
26
mcn1032
nancala
dp61
c319
1.24
1.28
1.32
1.36
1.40
1.44
1.48
1.52
1.56
MEAN LINT YIELD FOR GROUP


78/79 genotypes
group 16
group 25
group 26
group 28
main effects 55%
interaction effects 45%
MEAN LINT YIELD FOR GROUPS
ENVIRONMENT INDEX
0.70
0.90
1.10
1.30
1.50
1.70
1.90
2.10
-0.80
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
d
s
w
n b
e

### 3.6 79/80 genotypes

group 2 - "gl06" is CSIRO selection from Riverina
- low yielding at all sites.

group 14 - "crl26" is CSIRO selection from Riverina
- low to average yield
- variable response over environments, similar "dp gf".

group 27 - stoneville related genotypes.
- average yield at all sites.

group 13 - "dp gf" has variable yield response over environments, highest yielding genotype at some sites and lowest yielding genotype at other sites.

group 26 - recently developed varieties of deltapine and coker origin.
- high yields at all environments.

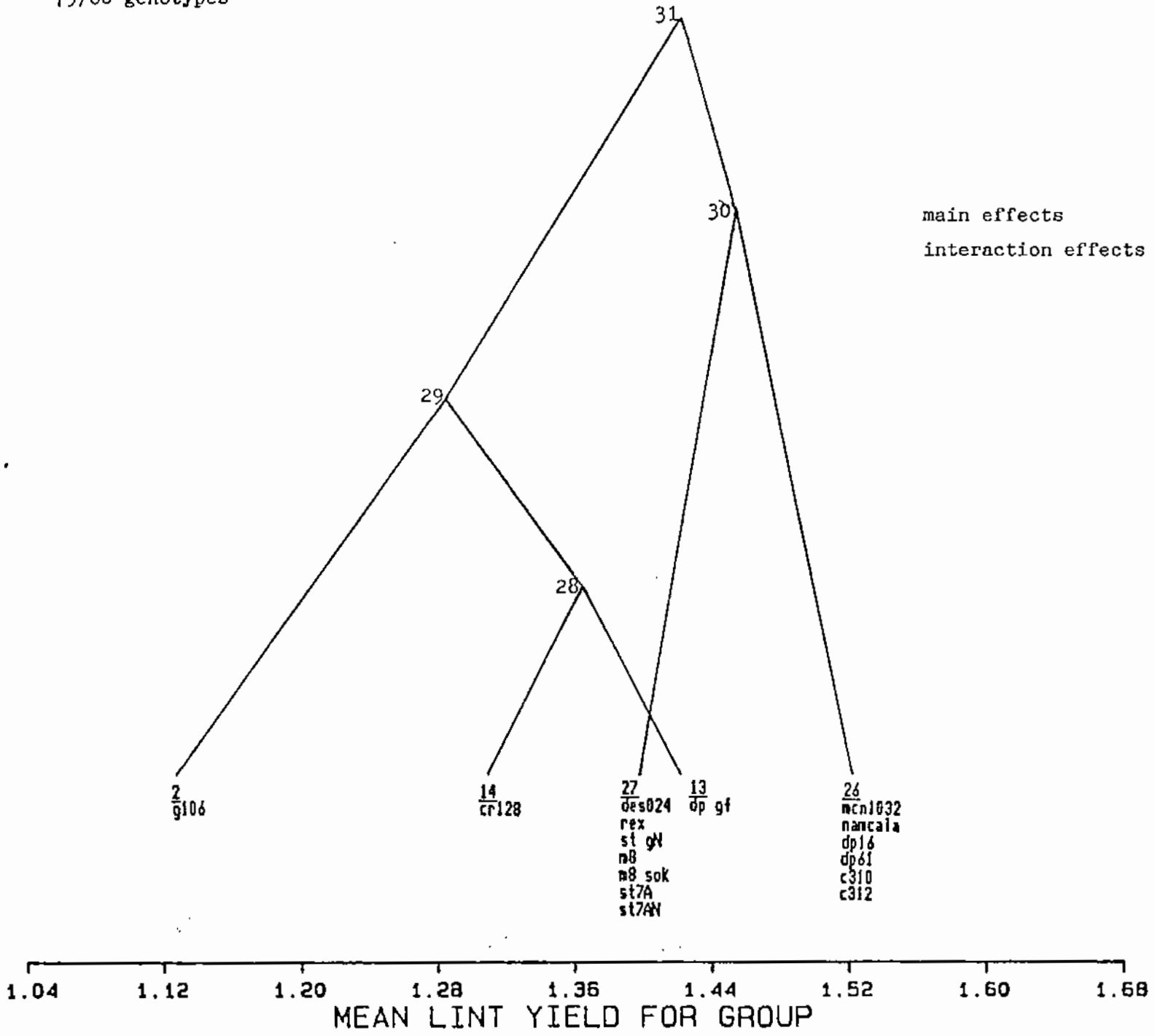
Three genotypes, the single member groups 2, 13, 14, make the largest contribution to ge interaction.

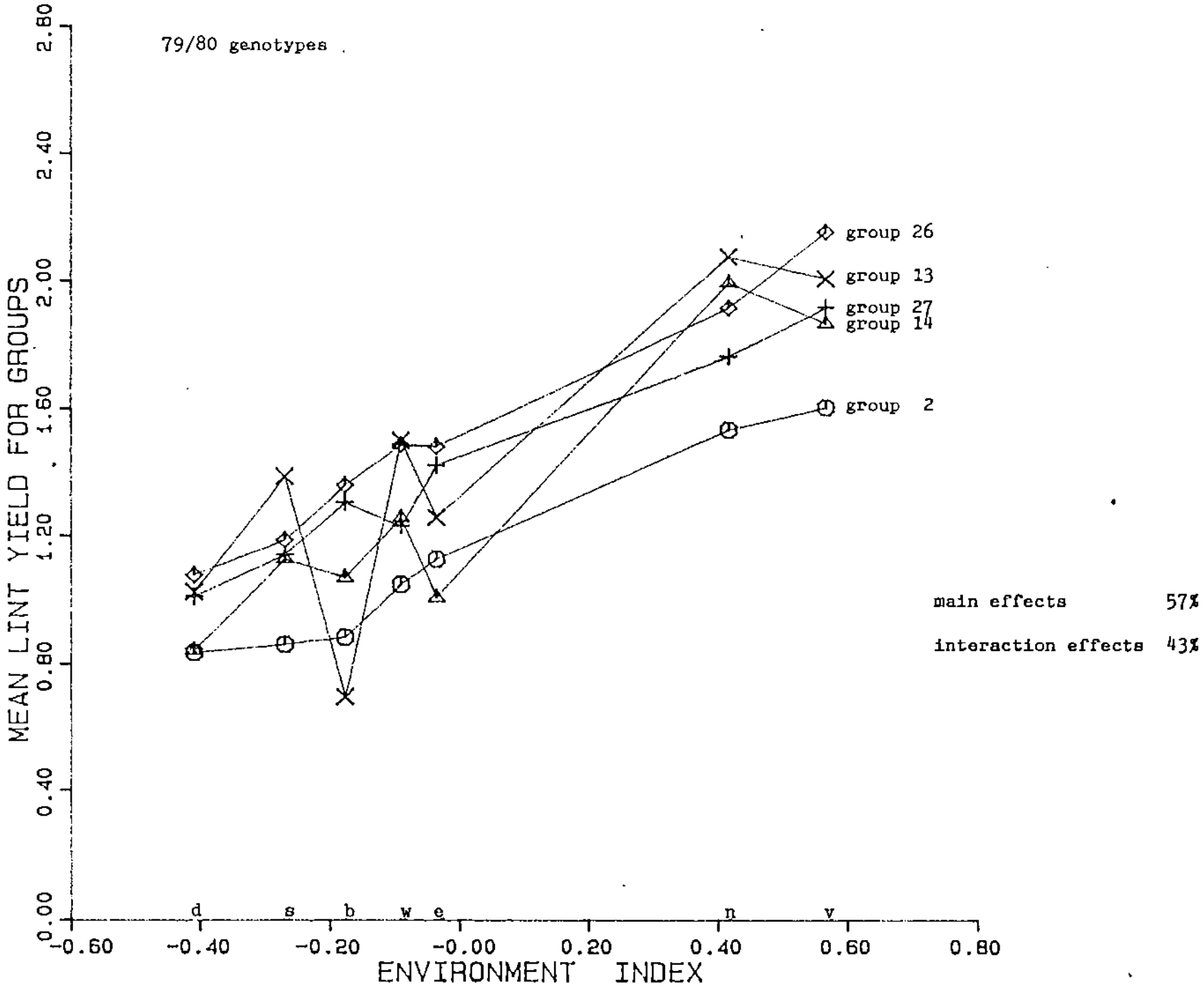
Both genotype main effects (57%) and ge interaction effects (43%) contribute to the separation of genotype groups. The main environments contributing to the separation of genotype groups are

w,v separates stoneville related genotypes (group 27) from deltapines and cokers (group 26)

b separates "deltapine gl fr" from other genotypes

79/80 genotypes




79/80 genotypes
MEAN LINT YIELD FOR GROUPS
0.00
0.40
0.80
1.20
1.60
2.00
2.40
2.80
group 26
group 13
group 27
group 14
group 2
main effects 57%
interaction effects 43%
d
s
b
w
e
n
v
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
0.80
ENVIRONMENT INDEX

### 3.7 80/81 genotypes

group 2 - "gl06" is CSIRO selection from Riverina
- lowest yielding genotype at all sites.

group 30 - two member group of USA origin.
- second lowest yielding group at all environments.

group 43 - coker varieties.
- average yielding at all sites except high yielding at theodore and low yielding at warren.

group 44 - mixed group of genotypes of earlier maturity.
- average yield at all environments.

group 37 - stoneville related genotypes.
- average yield at all locations except high yield at Moree.

group 42 - deltapine related genotypes.
- highest yielding at all locations, except theodore.

Group 43 (coker varieties), group 44 (early maturity), and group 37 (stoneville related genotypes) have similar mean yields but differ in their response over environments.

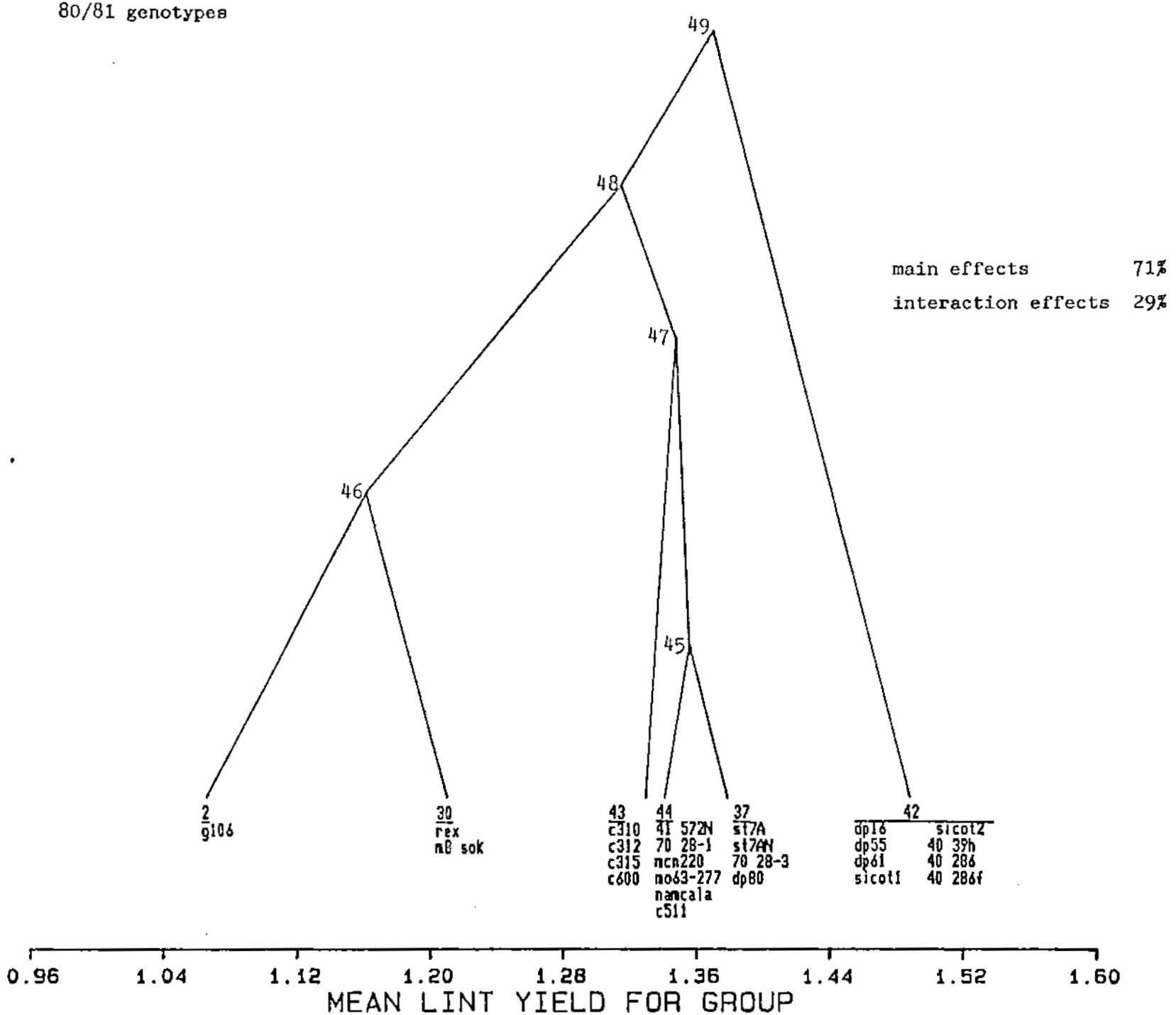
Genotype groups are mostly separated by genotype main effects (71%) and not ge effects. The main environments contributing to the separation of genotype groups are

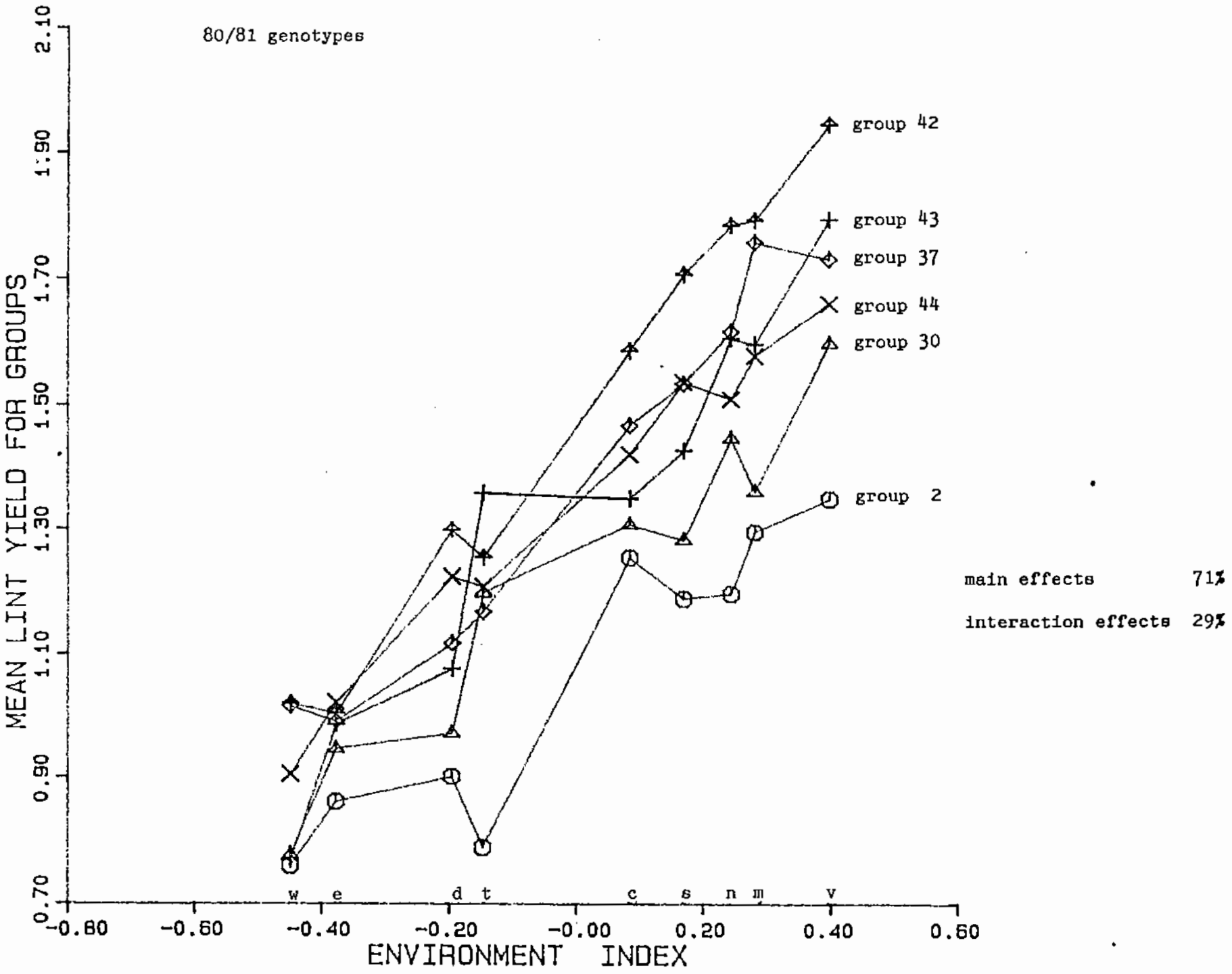
v,n,s — separates Deltapines (group 42) from other genotypes

m — separates low yielders (gl06, rex, m8) from Coker and Stoneville related genotypes (group 47)

t — separates Cokers (group 43) from other genotypes

m/d — two contrasting locations for separating stoneville genotypes (group 37) from McNair, Namcala, and Coker genotypes (group 44)


80/81 genotypes
49
48
47
46
45
main effects 71%
interaction effects 29%
2
g106
30
rex
n8 sok
43
c310
c312
c315
c600
44
41 572N
70 28-1
ncn220
no63-277
namcala
c511
37
st7A
st7AN
70 28-3
dp80
42
dp16
dp55
dp61
sicotI
sicot2
40 39h
40 286
40 286f
0.96
1.04
1.12
1.20
1.28
1.36
1.44
1.52
1.60
MEAN LINT YIELD FOR GROUP


80/81 genotypes
MEAN LINT YIELD FOR GROUPS
2.10
1.90
1.70
1.50
1.30
1.10
0.90
0.70
-0.80
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
ENVIRONMENT INDEX
w e d t c s n m v
group 42
group 43
group 37
group 44
group 30
group 2
main effects 71%
interaction effects 29%

### 3.8 81/82 genotypes

group 42 - namcala related genotypes.
- low yielding at all sites except Darling Downs.

group 43 - early maturity genotypes.
- low to average yield at all sites except darling downs.

group 45 - deltapine related genotypes plus other CSIRO selections.
- average yield at all locations except low at darling downs.

group 40 - deltapine related genotypes plus coker 315.
- average yield at all locations except high at warren.

group 44 - deltapine related genotypes.
- high yielding at all locations except darling downs.

The Deltapine related genotypes (groups 40, 44, 45) fuse to form group 48 which is different from the non-Deltapine related genotypes (groups 42, 43) which fuse to form group 46.

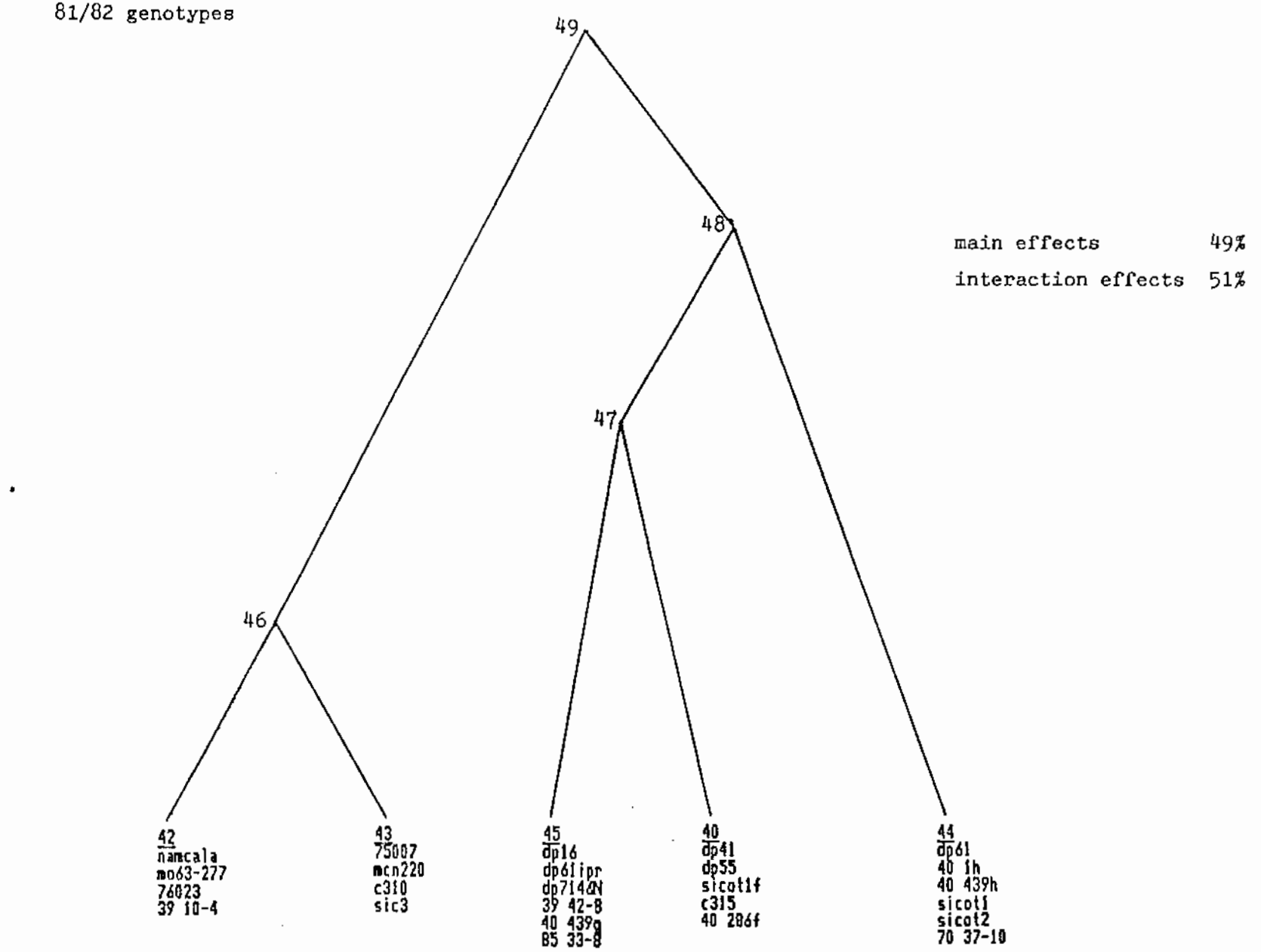
Genotype-environment interaction effects (51%) are a major component in the separation of genotype groups. The main environments contributing to the separation of genotype groups are

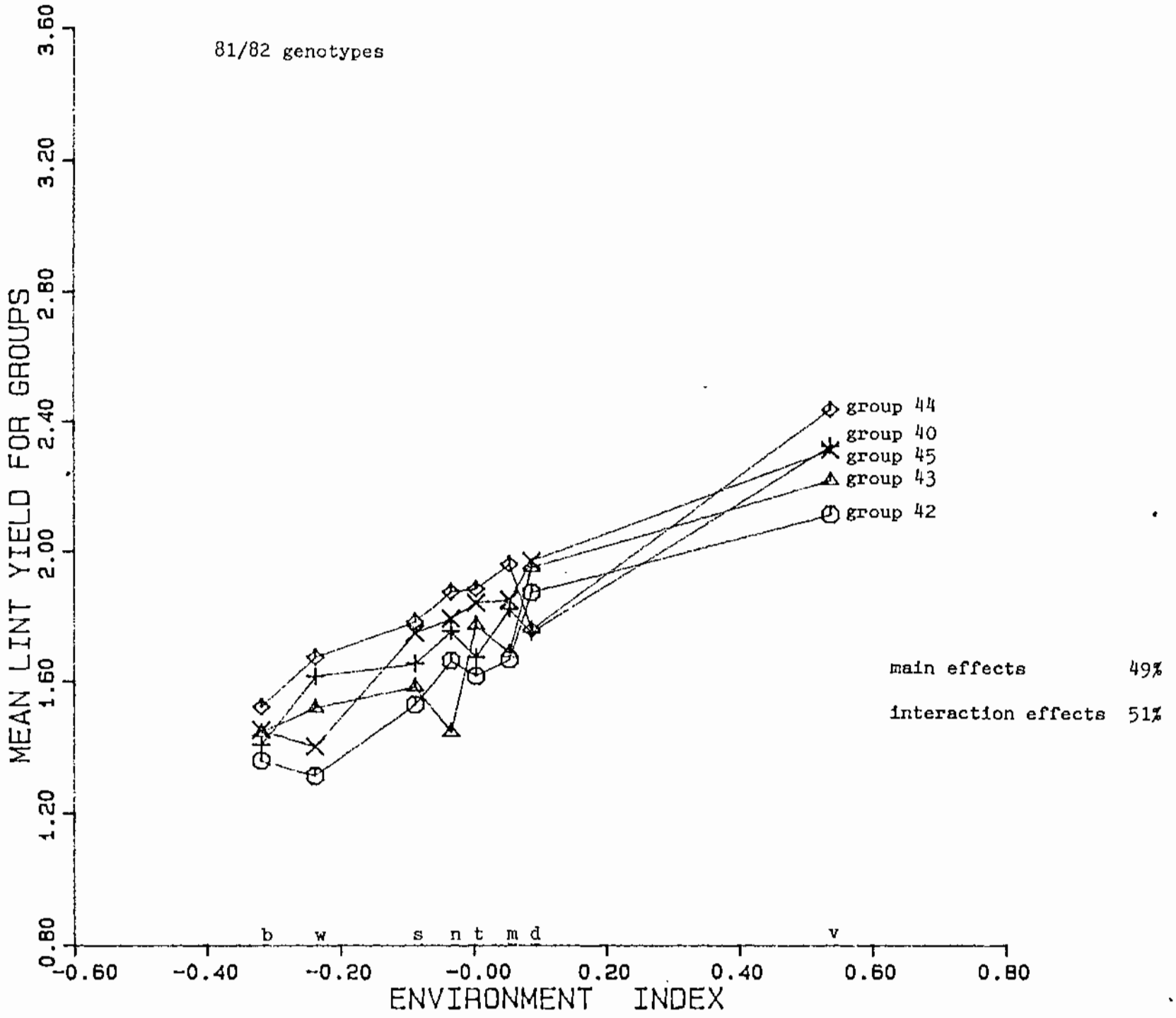
n,m,v/d — separates deltapine related genotypes (group 48) from short season genotypes (group 46)

w/d — two contrasting locations for separating deltapine genotypes into three response groups (group 40,44,45)

Myall vale has a higher yield than all other locations.

81/82 genotypes




81/82 genotypes
MEAN LINT YIELD FOR GROUPS
3.60
3.20
2.80
2.40
2.00
1.60
1.20
0.80
group 44
group 40
group 45
group 43
group 42
main effects 49%
interaction effects 51%
b w s n t m d v
-0.60 -0.40 -0.20 -0.00 0.20 0.40 0.60 0.80
ENVIRONMENT INDEX

### 3.9 82/83 genotypes

group 43 - early maturity genotypes.
- lowest yielding group at all locations except darling downs.

group 42 - mixed group of genotypes which are low yielding at most locations.

group 41 - mostly Deltapine related genotypes of average yield.

group 38 - genotypes which are low yielding in southern Queensland.

group 36 - deltapine related genotypes of above average yield.

group 9 - "coker 315" is high yielding at Queensland locations and average at NSW locations.

group 14 - "n40 439h" is highest yielding at most sites except darling downs, biloela and theodore.

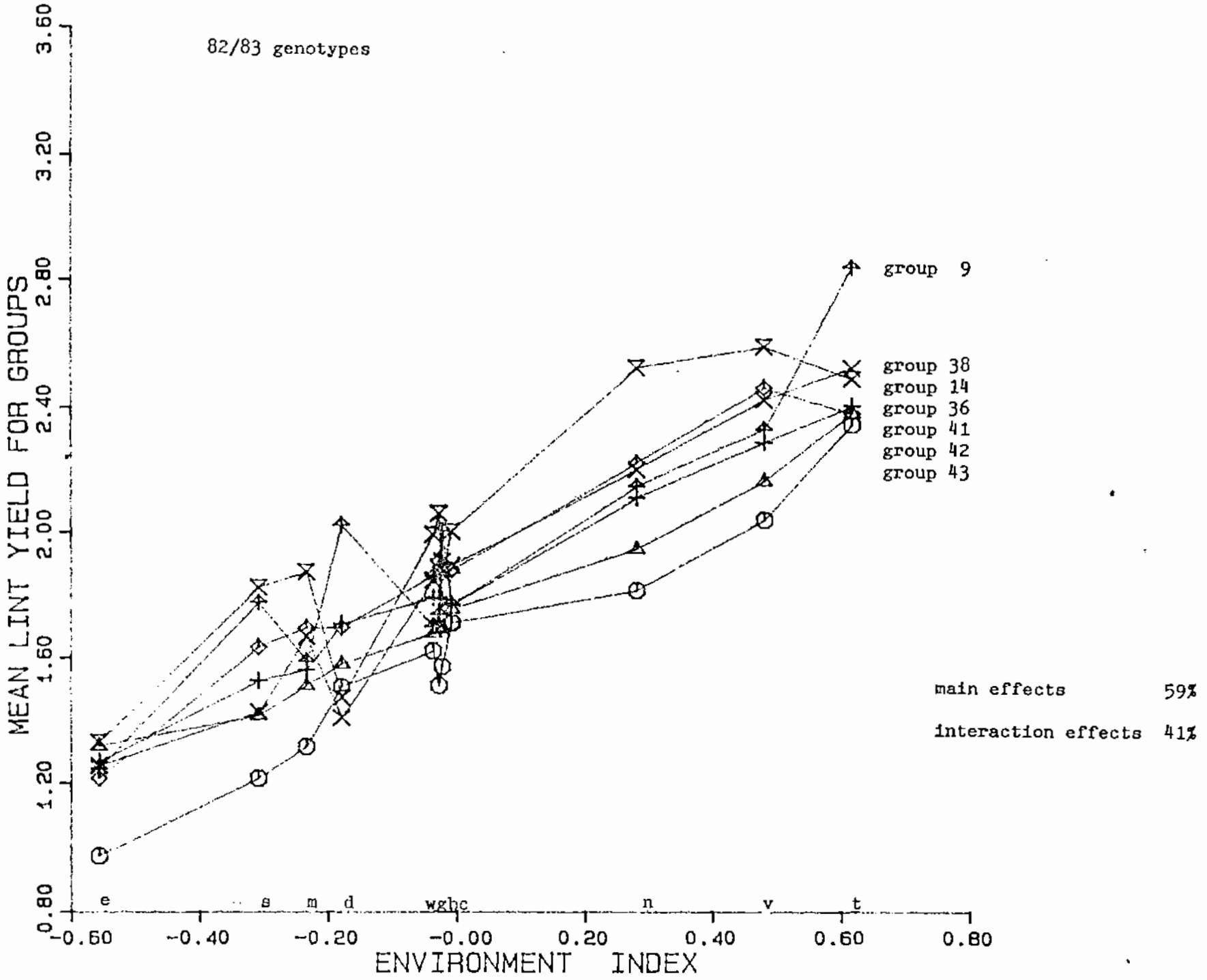
Both genotype main effects (58%) and ge interaction effects (41%) contribute to the separation of genotype groups. The main environments contributing to the separation of genotype groups are

n,v separates deltapine related genotypes (group 48) from other genotypes (group 47)

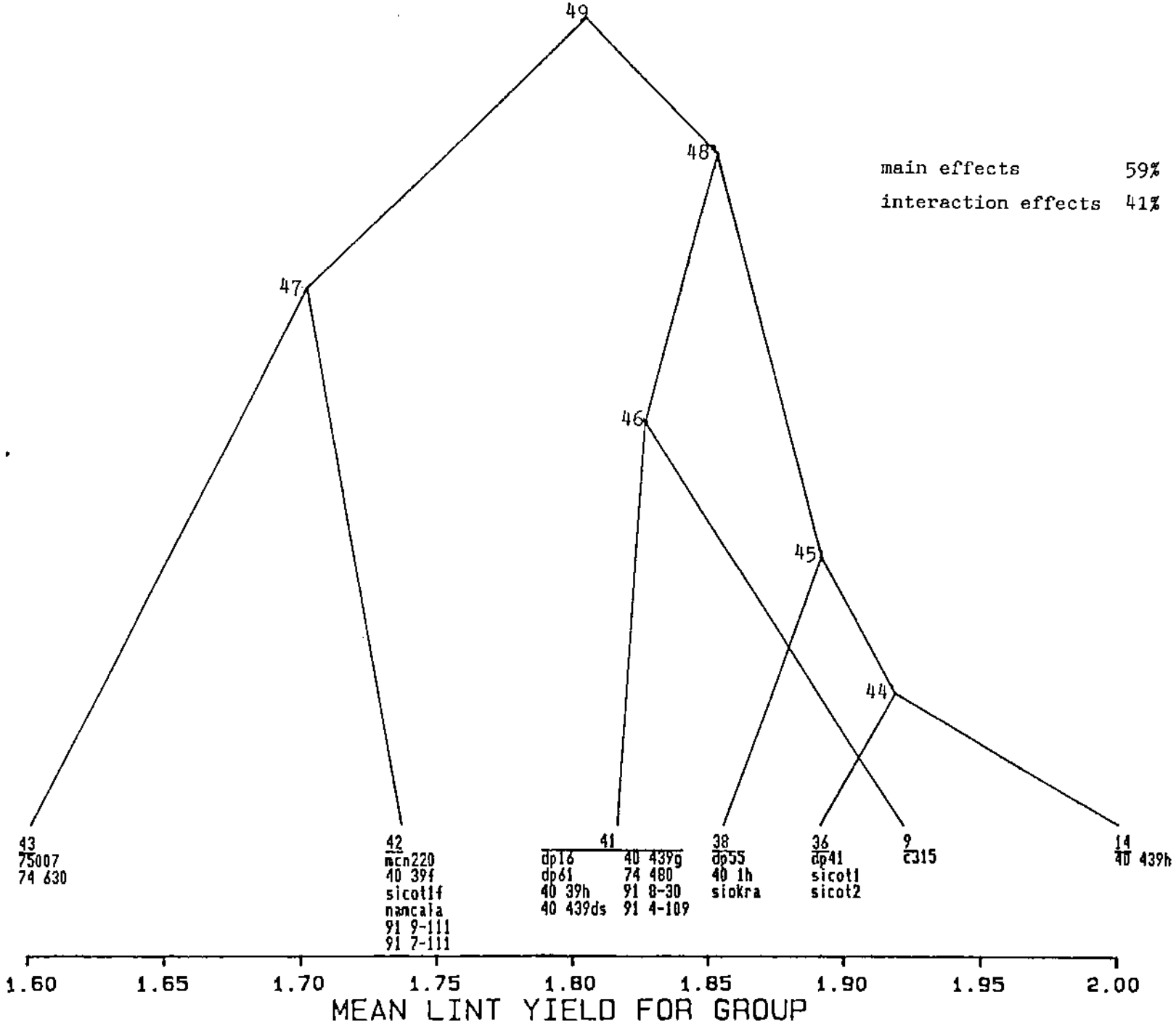
d separates deltapine genotypes into groups which have general adaptation or specific adaptation

t separates Coker (group 9) from other genotypes

e separates short season cultivars (group 43) from other genotypes


82/83 genotypes
MEAN LINT YIELD FOR GROUPS
ENVIRONMENT INDEX
0.80
1.20
1.60
2.00
2.40
2.80
3.20
3.60
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
0.80
e
s
m
d
wghc
n
v
t
group 9
group 38
group 14
group 36
group 41
group 42
group 43
main effects 59%
interaction effects 41%

82/83 genotypes



### 3.10 83/84 genotypes

group 46 - deltapine related genotypes.
- low yielding at all sites except central Queensland.

group 44 - mixed group of genotypes of average yield.

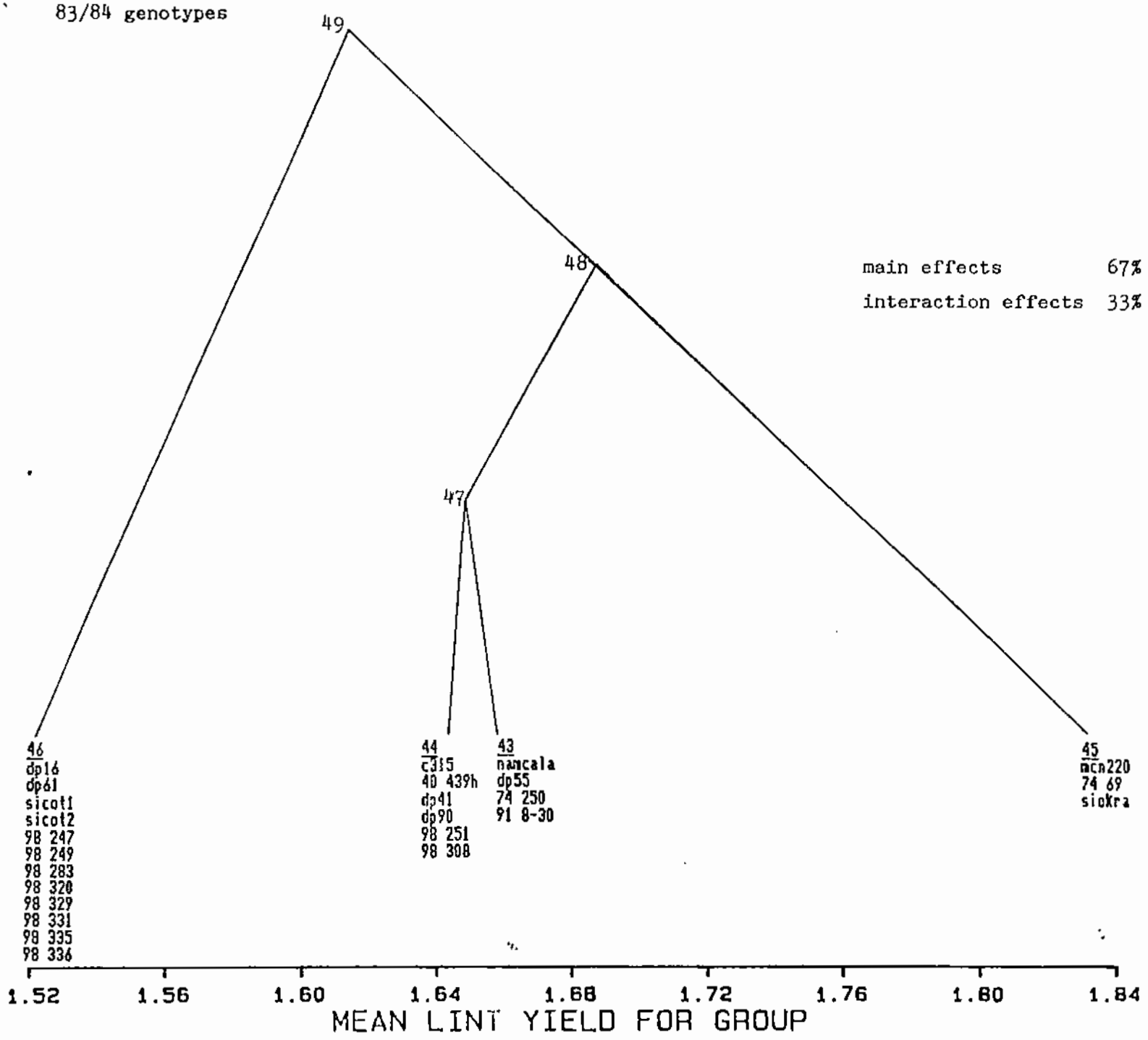
group 43 - namcala related genotypes.
- average yield at all sites except Biloela where it is low.

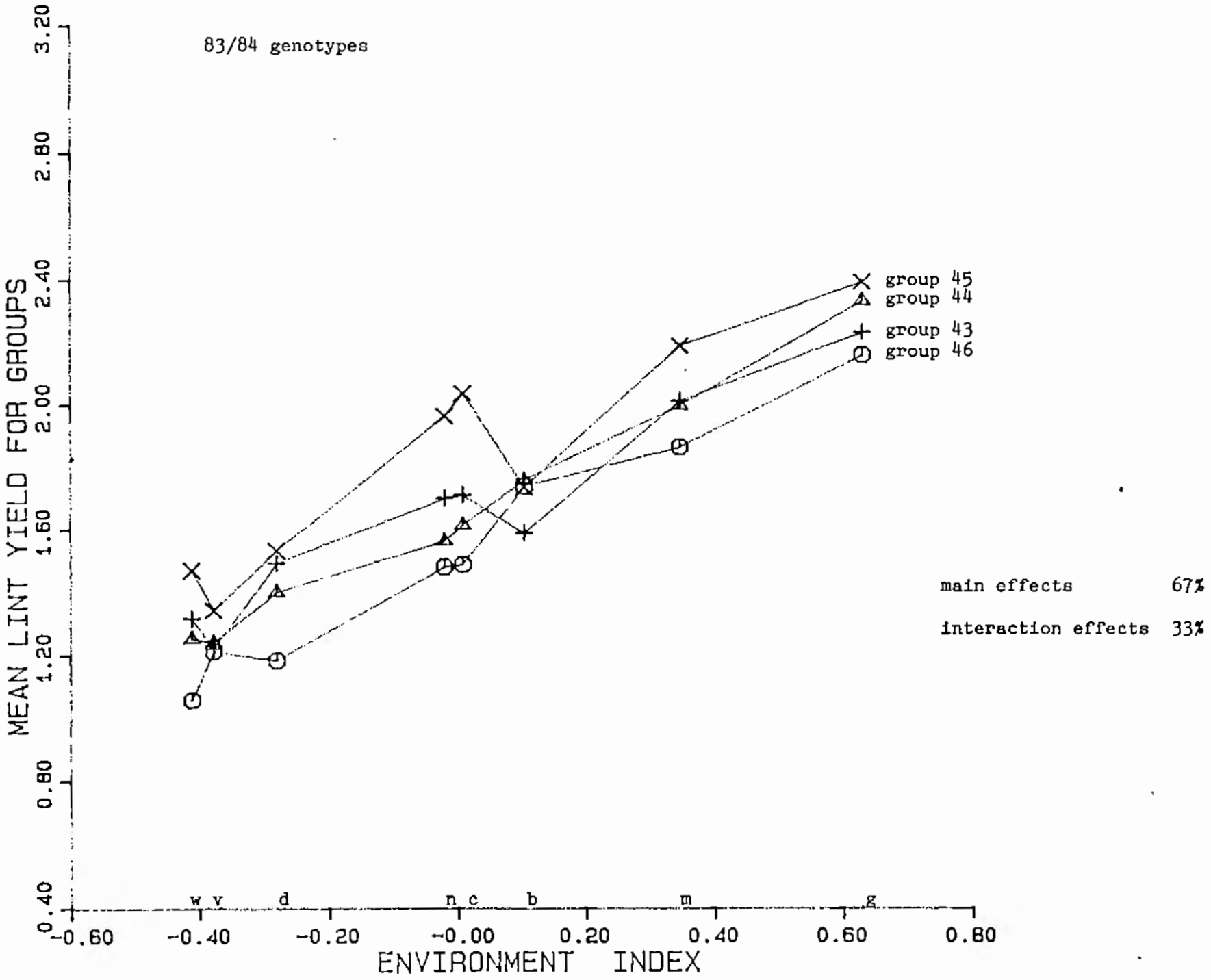
group 45 - early maturity genotypes.
- high yielding at all sites except central Queensland.

Groups 45, 46 and 47 are mostly separated by genotype main effects (67%). Groups 43 and 44 are separated by ge interaction effects, with biloela and west namoi being the two contrasting environments. The main environments contributing to the separation of genotype groups are

d,w,c,n — separates genotypes into three groups, short season genotypes (group 45), n98 and deltapine genotypes (group 46), and Namcala, Coker genotypes (group 47)

b — separates namcala related genotypes (group 43) from other genotypes


83/84 genotypes
49
48
47
main effects 67%
interaction effects 33%
46
dp16
dp61
sicot1
sicot2
98 247
98 249
98 283
98 320
98 329
98 331
98 335
98 336
44
c315
40 439h
dp41
dp90
98 251
98 308
43
namcala
dp55
74 250
91 8-30
45
mcn220
74 69
siokra
1.52
1.56
1.60
1.64
1.68
1.72
1.76
1.80
1.84
MEAN LINT YIELD FOR GROUP


83/84 genotypes
MEAN LINT YIELD FOR GROUPS
3.20
2.80
2.40
2.00
1.60
1.20
0.80
0.40
group 45
group 44
group 43
group 46
main effects 67%
interaction effects 33%
w v d n c b m g
-0.60 -0.40 -0.20 -0.00 0.20 0.40 0.60 0.80
ENVIRONMENT INDEX

### 3.11 84/85 genotypes

group 49 - genotypes which are low yielding at all locations.

group 54 - mostly early maturity genotypes.
- generally low yielding except darling downs.

group 53 - mostly USA developed varieties
- high yielding in central Queensland.

group 55 - mostly deltapine related genotypes.

group 14 - "Deltapine 90" is genetically different from the other deltapine genotypes.
- high yielding at most locations.

Groups 14 and 54 have similar response patterns over environments, but group 14 is higher yielding than group 54.

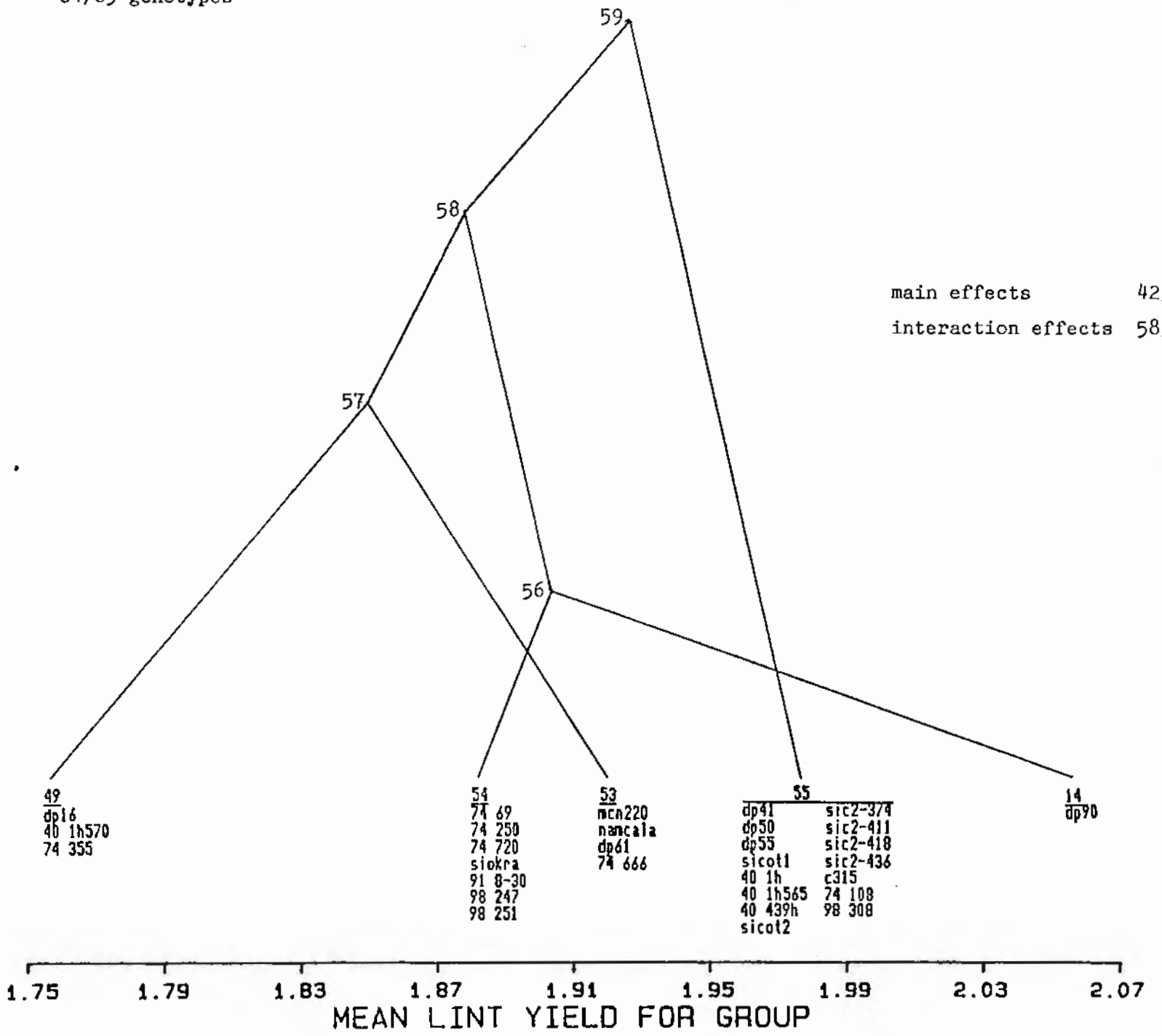
Genotype-environment interaction effects (58%) are a major component in separating genotype groups. The main environments contributing to the separation of genotype groups are

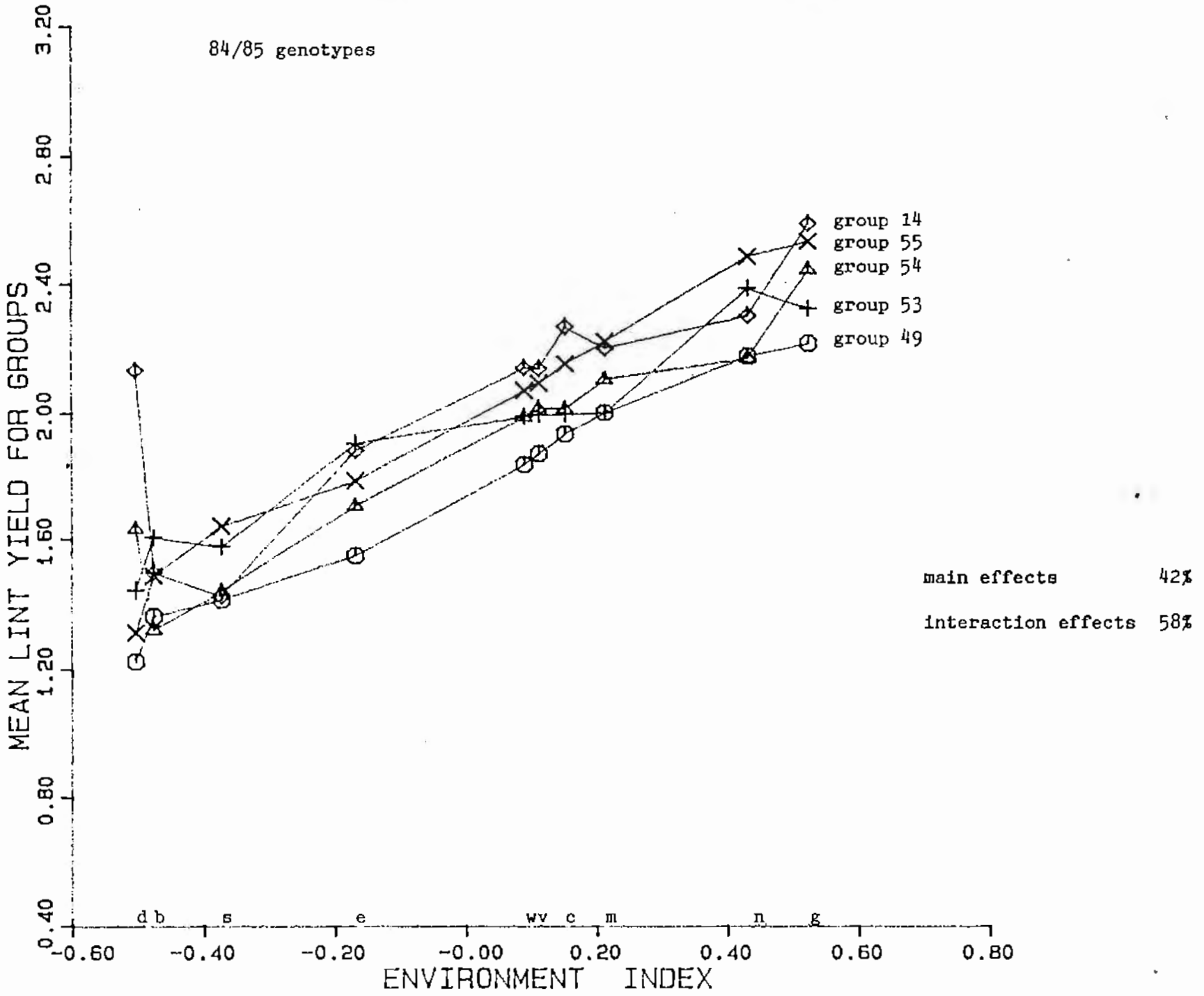
n separates deltapine related genotypes (group 55) from others

d separates Deltapine 90 from other genotypes

e separates low yielding genotypes (group 49) from others

84/85 genotypes




84/85 genotypes
MEAN LINT YIELD FOR GROUPS
3.20
2.80
2.40
2.00
1.60
1.20
0.80
0.40
group 14
group 55
group 54
group 53
group 49
main effects 42%
interaction effects 58%
d b s e wv c m n g
-0.60 -0.40 -0.20 -0.00 0.20 0.40 0.60 0.80
ENVIRONMENT INDEX

### 3.12 85/86 genotypes

group 25 - all recent Siokra selections.
- highest yielding of the 3 groups, especially at Biloela.

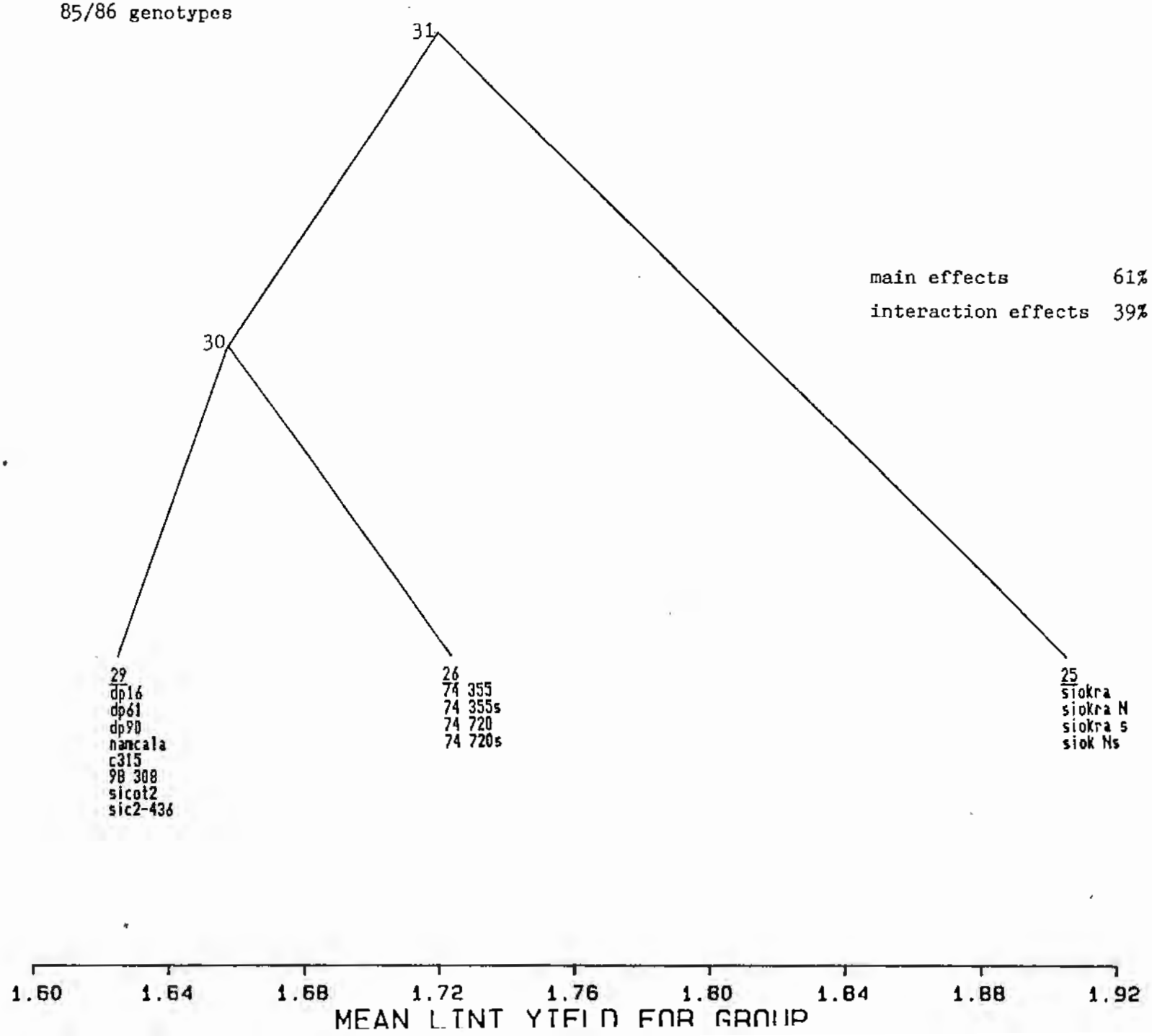
group 26 - all recent selections from cross n74.
- intermediate yield of the 3 groups.

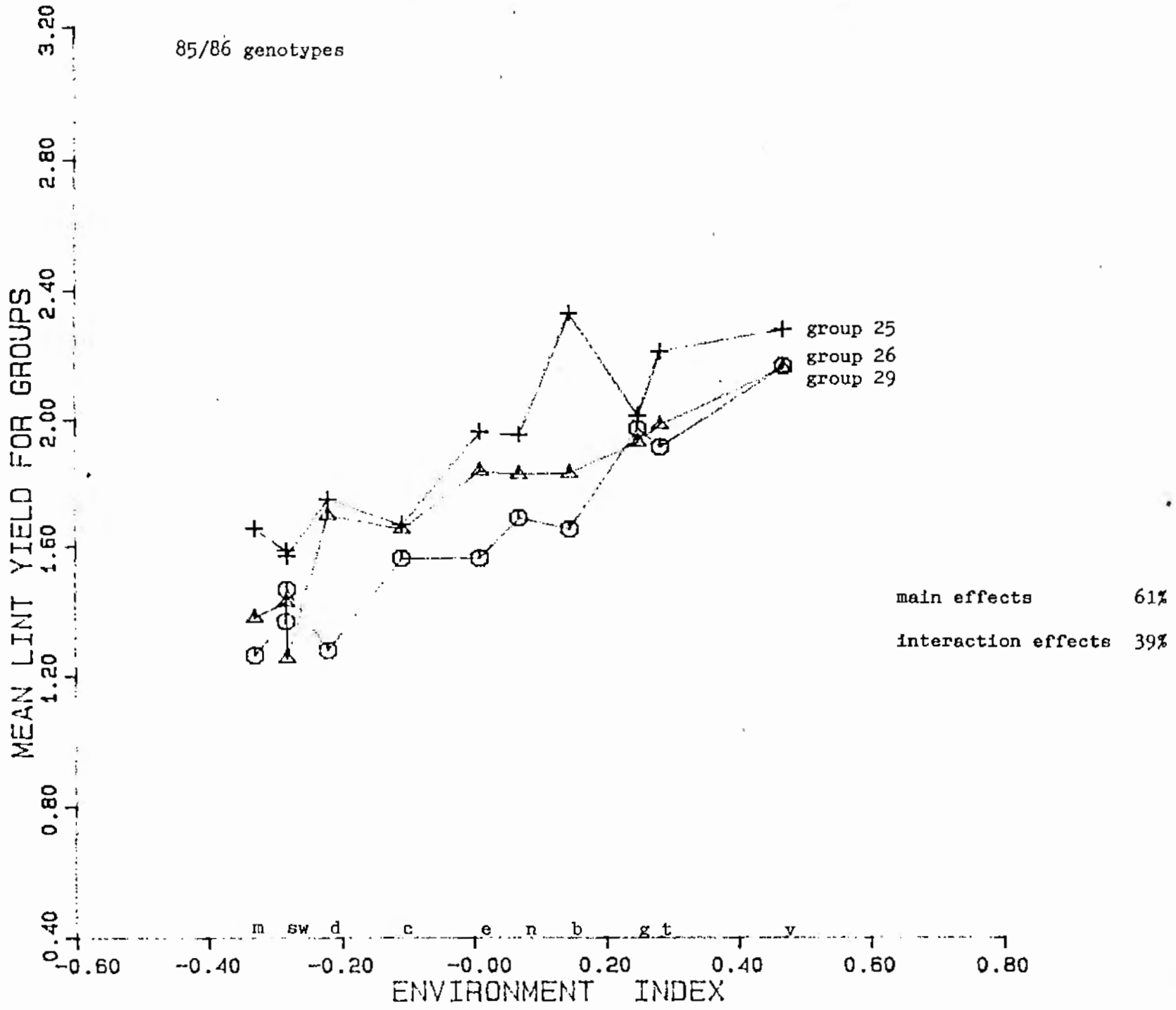
group 29 - remaining genotypes in trial, all older selections.
- lowest yielding of 3 groups, especially at darling downs.

Both genotype main effects (61%) and ge interaction effects (39%) are important in separating genotype groups. The main environments contributing to the separation of genotype groups are

b separates the Siokra selections (group 25) from the other genotypes.

d separates the early maturity genotypes (groups 25 and 26) from the other genotypes.


85/86 genotypes
31
30
main effects 61%
interaction effects 39%
29
dp16
dp61
dp90
nancala
c315
9B 308
sicot2
sic2-436
26
74 355
74 355s
74 720
74 720s
25
siokra
siokra N
siokra s
siok Ns
1.60
1.64
1.68
1.72
1.76
1.80
1.84
1.88
1.92
MEAN LINT YIELD FOR GROUP


85/86 genotypes
MEAN LINT YIELD FOR GROUPS
3.20
2.80
2.40
2.00
1.60
1.20
0.80
0.40
group 25
group 26
group 29
main effects 61%
interaction effects 39%
m sw d c e n b g t y
-0.60
-0.40
-0.20
-0.00
0.20
0.40
0.60
0.80
ENVIRONMENT INDEX

## 3.13 Summary

On average, ge interaction effects contributed 41% and genotype main effects contributed 59% to the classification of genotypes (Table 3.13, Appendix I). This is clear evidence of the importance of genotype-environment interactions in determining groupings of genotype response patterns over environments.

**Table 3.13 Contributions of ge interaction effects (%) to classification of genotypes.**

| year | ge contribution(%) |
|---|---|
| 74 | 57 |
| 75 | 26 |
| 76 | 34 |
| 77 | 32 |
| 78 | 45 |
| 79 | 43 |
| 80 | 29 |
| 81 | 51 |
| 82 | 41 |
| 83 | 33 |
| 84 | 58 |
| 85 | 39 |
| average | 41 |

The within group composition of all genotype groups was examined in relation to the genetical origin of the genotypes. In summary, the results indicate that the classification of genotypes into groups is definitely related to the genetical origin of genotypes.

Therefore, the numerical classification analysis is summarizing the genotype-environment interactions in a manner that can easily be interpreted by a cotton breeder and readily used to make decisions about various aspects of a cotton breeding program.

Generalizing over the 12 data sets, the main contribution of locations to the separation of genotype groups is

| | |
|---|---|
| West namoi | separates high yielding Deltapine related genotypes |
| Myall vale | similar to west namoi but separation not as significant |
| Darling downs | separates early maturity genotypes |
| Biloela | separates some specifically adapted genotypes such as "deltapine gl fr" or namcala related genotypes |
| Warren | contrasting environment in some years |
| Emerald | separates generally unadapted genotypes |
| Theodore | separates Coker related genotypes |