Analysis of line × environment interactions for yield in navy beans. 3. Pattern analysis of environments over years

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Abstract.   Yield trials of navy bean (*Phaseolus vulgaris* L.) lines were grown over a diverse range of locations for 7 years in Queensland, with changes in entries and locations in each year. The yield data were analysed over years using 3 recently developed pattern analysis techniques for the integration of historical, severely unbalanced data from plant breeding programs to derive relationships among environments in the way they discriminate among the entries grown in them. These techniques have been named as cumulative analysis, sequential analysis, and status analysis. The relationships among the locations for testing navy bean lines, although sensitive to the addition of new locations, quickly stabilised. These relationships were related to management (irrigation and row width) and latitude (north *v*. central *v*. Kingaroy *v*. southern Queensland).

Additional keywords: *Phaseolus vulgaris*, yield, retrospective analysis, cumulative analysis, sequential analysis, status analysis.

Introduction

The genotype × environment (G × E) information from yield multi-environment trials (METs) grown over diverse environments can be studied with pattern analyses (Byth *et al.* 1976; Kempton 1984; Zobell *et al.* 1988; Gauch and Zobell 1990; Cooper *et al.* 1993; Cooper and DeLacy 1994; DeLacy *et al*. 1996*a*, 1996*c*; McLaren 1996) to identify genotypes with similar responses across environments, and to identify those environments which produce similar discriminations among the genotypes growing in them. Pattern analysis is the joint use of classification (clustering) and ordination (low dimensional representation) techniques to study pattern in any data set (Johnson 1977; Basford *et al.*1993). Cluster analysis summarises the complexity in the data with retention of substantial information, by enabling responses to be described with relatively few genotype groups or relatively few environmental groups or both (Mungomery *et al.* 1974; Shorter *et al.* 1977; Brennan *et al.* 1981; Imrie *et al.* 1981; Hayward *et al.* 1982; Ivory *et al.* 1991). Ordination summarises the data by representing the patterns in the data in a small number of dimensions. This enables a substantial pro-portion of the relationships to be displayed graphically in 2 or 3 dimensions.

Pattern analysis methods have been extended for the analysis of historical data accumulated by plant breeding METs conducted over many years (DeLacy and Lawrence 1988; Peterson and Pfeiffer 1989; Lawrence and DeLacy 1993). These methods handle the unbalance which occurs because of change of entries over time and the differing locations (environments) used in years by averaging over years the appropriate proximity (similarity or dissimilarity) matrix from each year. The theoretical basis of these retrospective analyses has been recently developed (DeLacy *et al.* 1996*b*) and a number of applications have appeared (Peterson 1992; DeLacy *et al.* 1994; Ouyang *et al.* 1995; Abdalla *et al.* 1996; DeLacy *et al.* 1996*d*). These studies show that, as data from more years are included in the analysis, the emphasis of the study changes from the response of entries to genetic gain and the relation-ship among the environments in the way they discriminate among the entries grown in them (DeLacy *et al.* 1996*c*). They also showed that sensible relationships among locations in the way they discriminate among genotypes can be determined.

Mirzawan *et al.* (1994) reported 2 variations of retrospective analyses. In the first, the relative relationships among environments is built up over time by adding data from each year's MET one at a time to the analysis. This produces a long-term average relationship among the environments in the way they discriminate among the genotypes grown in them. In the second, should the first provide a stable configuration, the relationships among the discrimination provided by the current year's locations can be compared with their long-term discrimination. Mirzawan *et al.* (1994) were able to demonstrate, using their sugarcane data, that a stable discrimination space did occur and that the ordination of current data, when superimposed on the long-term relationship, gave useful information on the discrimination provided in the current year. Sheppard *et al.* (1996) have reported another case in wheat.

Butler *et al.* (2000) described the entries (their table 1) and locations (their table 2) used in the navy bean METs, analysed in this paper. They reported on sources of variation derived from a REML analysis of variance across years. Redden *et al.* (2000) reported on pattern analyses of the data conducted within years and interpreted over years. This paper reports on the pattern analysis of the data conducted over years and interpreted in the manner of Mirzawan *et al.* (1994).

Methods

Navy bean yield METs were grown in Queensland for 7 years, 1983–1989. The choice of 21 lines and descriptions of 16 growing seasons by management and climatic variables for each year were given in previous papers (Butler *et al.* 2000; Redden *et al.* 2000). The study is based on grain yield data, and relevant agronomic and disease reactions for the entries were measured (Table 1). There were 8–14 lines per year grown at all the locations utilised in any one year (Table 2). Both lines and locations partially changed between years. Only the subset of regional trial entries which were grown in at least 2 years was used in the current study. The trial period spanned the initiation of a plant breeding program (Redden *et al.* 1985) through to the evaluation of the first cycle of derived selections.

Analytic procedures

The data were analysed by the types of retrospective analysis introduced by Mirzawan *et al.* (1994) for a study of sugarcane (MET) data. Pattern analysis was conducted using the weighted environment standardised squared Euclidean distance (esSED) method, equation (36), given by DeLacy *et al.* (1996*b*). Empty cells occurred and locations were eliminated using rule 1 (DeLacy *et al.* 1966*b*).

For the first analysis the data were arranged on a year basis. The initial data set (1983 harvesting year) was analysed first. The 1984 data set was then added and a second analysis conducted on the average esSED matrix over the 2 sets. Data sets from the subsequent years were sequentially accumulated in this way, so that all the data from the 7 available sets were included in the retrospective analyses. A separate pattern analysis of the environments was done on those 7 data sets as they were generated. These cumulative analyses enable investigation of the interactions among lines and locations by observation of any changes over time of the environmental groupings from the cluster analysis and/or spatial arrangement in the ordination scatter or proximity plot due to the addition of the new data sets. In this process any 2 sites which have no comparison between them, i.e. both have not been used in the same year in the total set of data, will have an empty cell in the proximity matrix and one or the other or both will be eliminated from the analysis.

Changes in the association among the environments across harvesting years identified by the principal coordinate analysis (PCO) were portrayed by proximity plots, whereas those identified by classification were portrayed by dendrograms. Each new proximity plot, showing the

Table 1. Lines entered in the regional navy bean yield trials in the seven years 1983–1989
Numbers in cells refer to the number of sites harvested in each year

Line	1983	1984	1085	1986	1987	1988	1989
Gallaroy	4	6	4	5	10	8	8
Kerman	4	6	4	5	10	9	8
Actolac	4	6	4	5	10	9	8
Banker	4	6	4	5	10		
Campbell 11	4	6	4		10	9	8
Revenue	4	6	4	5	10	9	8
Bac 125				5	10	9	8
Bac 134				5	10		
Nep 2				5	10		
CH14-8D					10	9	
CH14-11D					10		
CH14-27D					10		
CH14-28D					10	9	8
CH9-4D					10	9	8
2GA	4	6	4				
W1401	4	6	4			9	8
Campbell 16	4	6	4				
Actosan	4	6	4				
Sel 46	4	6					
W1885	4						
Campbell 15	4						

Table 2. **Abbreviations, irrigation, row widths, region, year in which used, and number of entries grown for the environments used in the seven years of navy bean regional yield variety trials**

I, irrigation; RF, rainfed; NR, narrow rows; WR, wide rows. CQ, central Queensland; SQ, southern Queensland; SWQ, south-western Queensland; NQ, northern Queensland; KI, Kingaroy region

Environment	Abbrev.	Irrigation	Row width	Region	No. of entries grown in the environment each year						
					1983	1984	1985	1986	1987	1988	1989
Biloela	bi	I	WR	CQ		11	10		14	10	9
Clifton	cl	RF	WR	SQ	13	11					
Gatton	ga	I	WR	SQ	13						
Hermitage	he	RF	WR	SQ	13	11	10	8	14	10	9
Hermitage	hn	RF	NR	SQ				8	13	10	9
Inglewood	in	IF	WR	CWQ	13	11			14		
Kairi	ka	I	WR	NQ			10	8	14	10	9
Kingaroy	ki	RF	WR	KI						10	
Kumbia	ku	RF	WR	KI							9
Mareeba	mb	I	WR	NQ		11					9
Mt Wooroolin	mw	RF	WR	KI					14	10	
Redvale	rv	RF	WR	KI		11	10	8	14	10	
Redvale	rn	RF	NR	KI					12		
Rocklea	rl	RF	WR	SQ				8	13		
Teakle	te		WR								9
Wallaville	wa	I	WR	CQ					14	10	

cumulative relationship among locations, was superimposed on the plot derived from the cumulative analysis up to the previous year's data. In a similar manner, each new dendrogram from the grouping of the locations on each sequential data set depicted the cumulative relationships among locations in another way. Both give a graphical display of how the relationships among the locations, for their ability to discriminate among the entries, changed over time as more data were accumulated. Mirzawan *et al.* (1994) called this procedure a 'cumulative analysis', but we have renamed this type of retrospective analysis a 'sequential analysis' to distinguish it from a 'cumulative analysis', which we restrict to a single analysis of all accumulated data up to a particular year. The space, modelled by the first few PCOs, is referred to as a 'discrimination space', as it places the environments in a Euclidian space, the proximity plot, according to the way they differ in producing discrimination among the genotypes grown in them.

In addition, the final year's data set (1989) was analysed separately and the proximity plot for these data was superimposed on the proximity plot from the cumulative analysis of all previous data (1983–1988). This procedure allows an assessment of how the line discrimination at the locations sampled in a particular year relates to that observed at those locations in the historical database. We call this procedure a 'status analysis'.

Results

Sequential analysis

The sequential pattern analysis (Figs 1–3) showed a marked change in the discrimination provided by the locations when the 1984 data and the 1987 data were added to the sequential analysis. These were the result of adding 3 central and northern Queensland locations to the southern Queensland locations in the 1984 season and adding a further 5 locations in the 1987 season.

In 1983, the first year included in this analysis, all locations were from southern Queensland. The 2 irrigated sites, Inglewood and Gatton, provided similar discrimination, but

the 2 rainfed sites differed from each other and from the irrigated sites. This was in spite of the fact that Hermitage, the research station site, and Clifton, a farmer site, are close together and have similar soils.

In 1984, a site (Redvale) from the Kingaroy region, an irrigated site (Biloela) from central Queensland, and an irrigated site (Mareeba) from the Atherton Tableland in northern Queensland were added and Gatton was dropped from the analysis. This substantially changed the relationships among the locations. Two of the irrigated sites, Biloela and Inglewood, grouped with Hermitage on the same side of the major division with Clifton in contrast to Redvale and Mareeba. When first added, Biloela was more similar to Hermitage than Inglewood, another irrigated site. This arrangement persisted until more locations were added in the 1987 season, except that Biloela first grouped with Inglewood rather than with Hermitage. Although Biloela and Hermitage are close in the proximity plots for the 1983–85 and 1983–86 seasons (Fig. 2) they are separated in the classification. This indicates the advantage of examining both the classification and the ordination together. Because the first 2 vectors of the ordination do not account for all of the variation (43% of the total sum of squares for vector 1 and 27% for vector 2 in 1983–85 cumulative analysis), distortions in the representation of similarity can occur. The 2 locations will be separated on the third or later vectors. In contrast, the dendrogram represents relationships using all the information. A similar case occurs with Kairi, which is separated from the other locations on the third axis (Figs 4–5), from the 1983–87 seasons on.

Again, the relationships among the locations were substantially changed when 5 more locations were added and
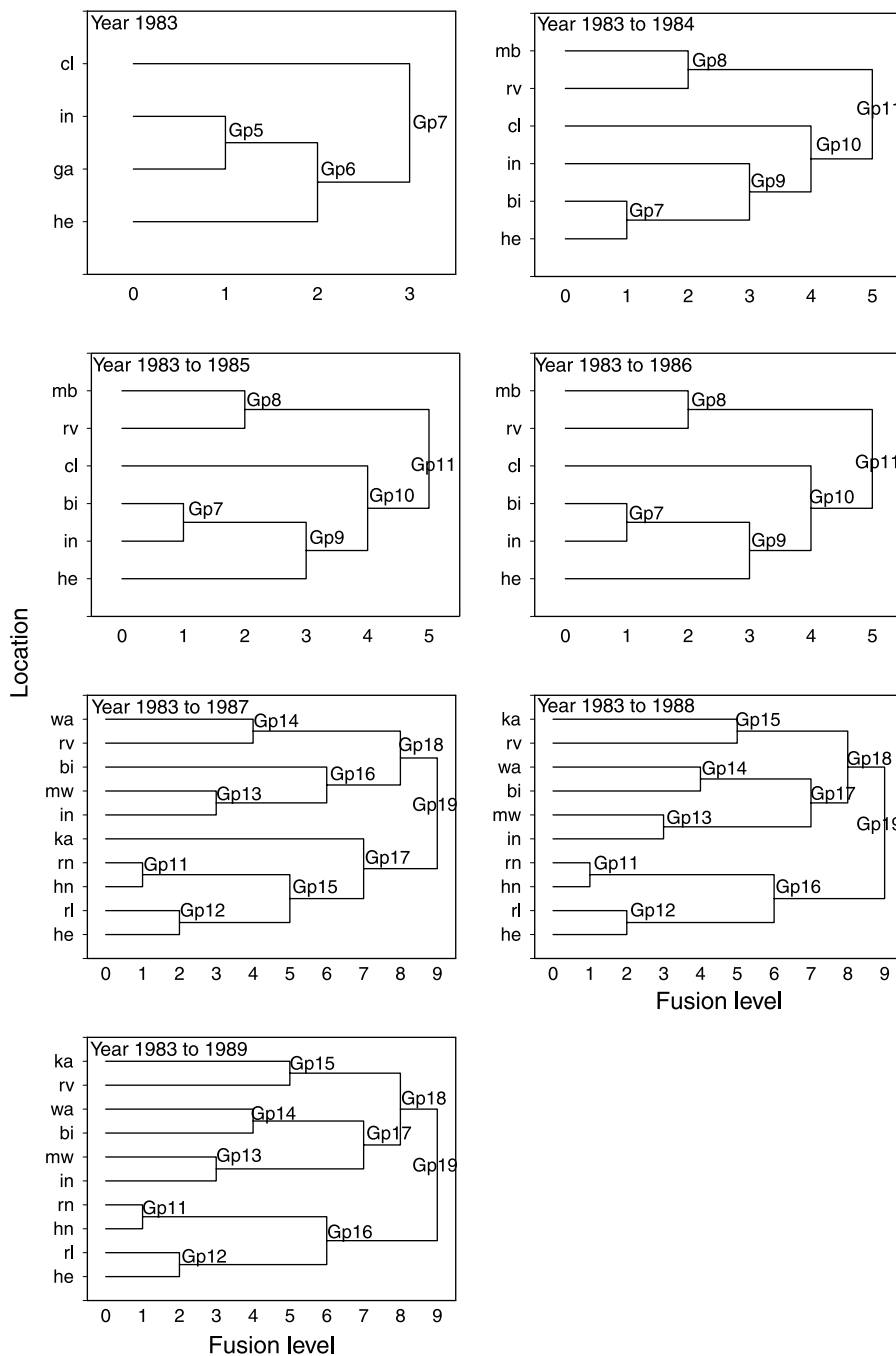
Fig. 1. Dendrograms for the sequential classifications of environments based on standardised grain yield of navy bean lines sown in the 1983–1989 seasons. See Table 2 for the list of abbreviations for the environments.

one dropped in the 1987 season. Kairi, on the Atherton Tableland proper, was substituted for Mareeba. Another Kingaroy site (Mt Wooroolin), a southern Queensland site (Rocklea), and 2 sites with a different management, narrow rows (Hermitage and Redvale), were added. As before, the new relationships among the locations quickly stabilised. Again it is instructive to compare the classification and the ordination (Figs 1–3). The first vector separates the narrow row locations (Hermitage narrow and Redvale narrow) from the southern Queensland (Hermitage and Rocklea), from Kairi, from the Kingaroy (Redvale and Mt Wooroolin), from the irrigated sites (Wallaville, Biloela, and Inglewood). Note that, although Kairi is close to Rocklea on the proximity plot using the first 2 vectors, it is separated in the classification.
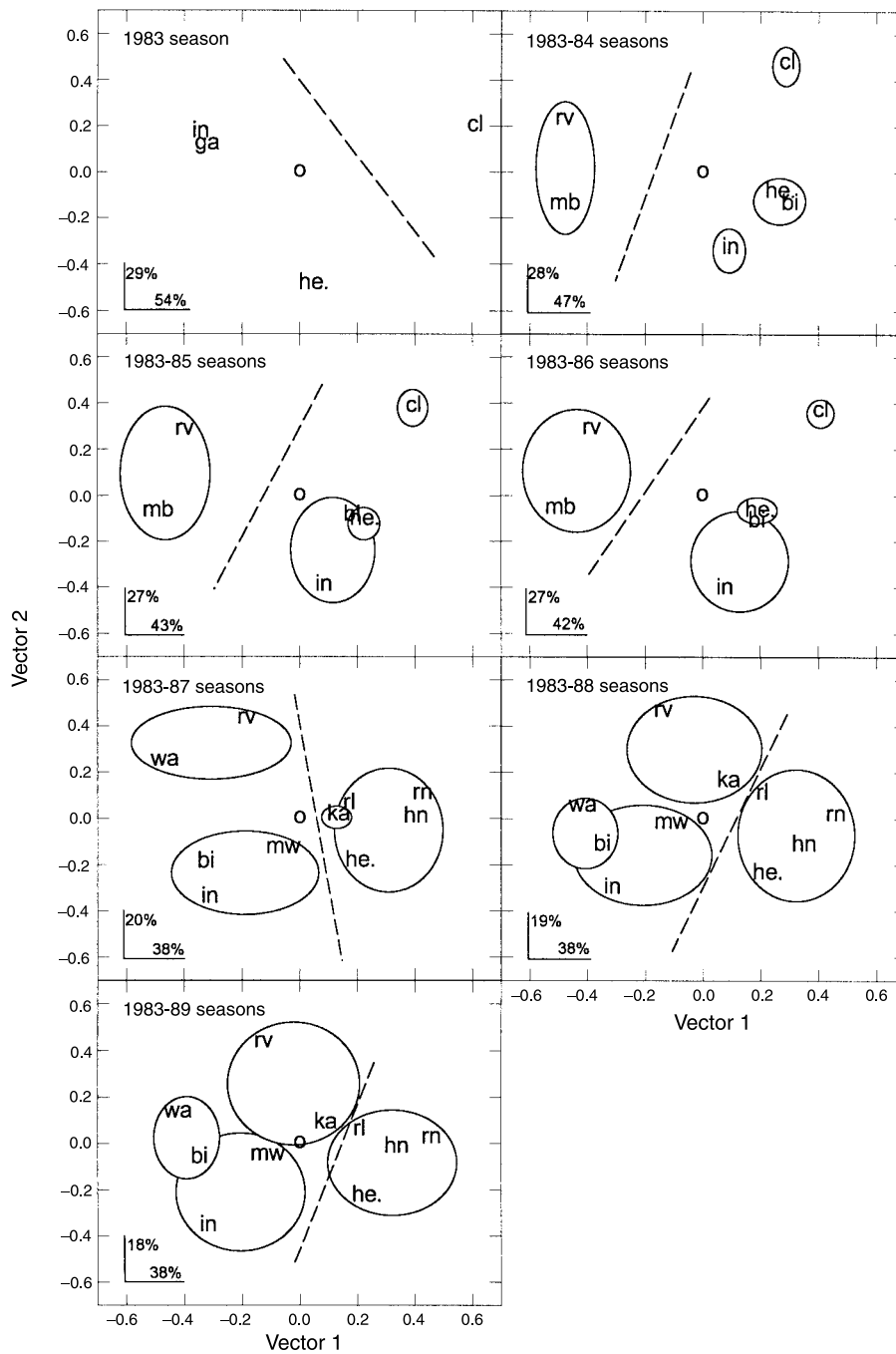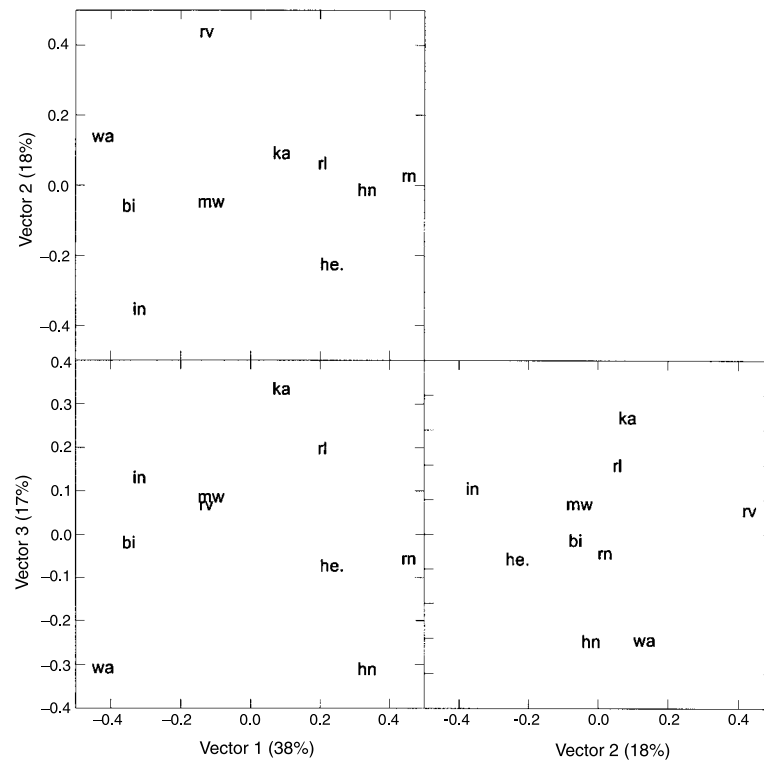
Fig. 2. Proximity plots of the first 2 vectors from the sequential principal coordinate analysis of environments based on standardised grain yield of navy bean lines sown in the 1983–1989 seasons. The percentage of the total sum of squares accounted for by each vector is indicated in the bottom left hand corner of each proximity plot. The dotted line delineates the environments which are members of the same group at the 2 group level and the boundaries those which are members of the same group at the 4 group level as determined by the classification.

Indeed it is grouped on the other side of the first division. It is clear that Kairi is separated on the third axis (Figs 4–5). Redvale is separated on the second axis. At the 4-group level, the 2 irrigated central Queensland sites (Biloela and Wallaville) are grouped, as are the 2 narrow row locations and the 2 southern Queensland (Hermitage and Rocklea) locations. Kairi is grouped with one of the Kingaroy locations (Redvale, both are research stations), and Inglewood is grouped with the other Kingaroy site, Mt Wooroolin. Note that Clifton was eliminated from the analysis after 1987, and
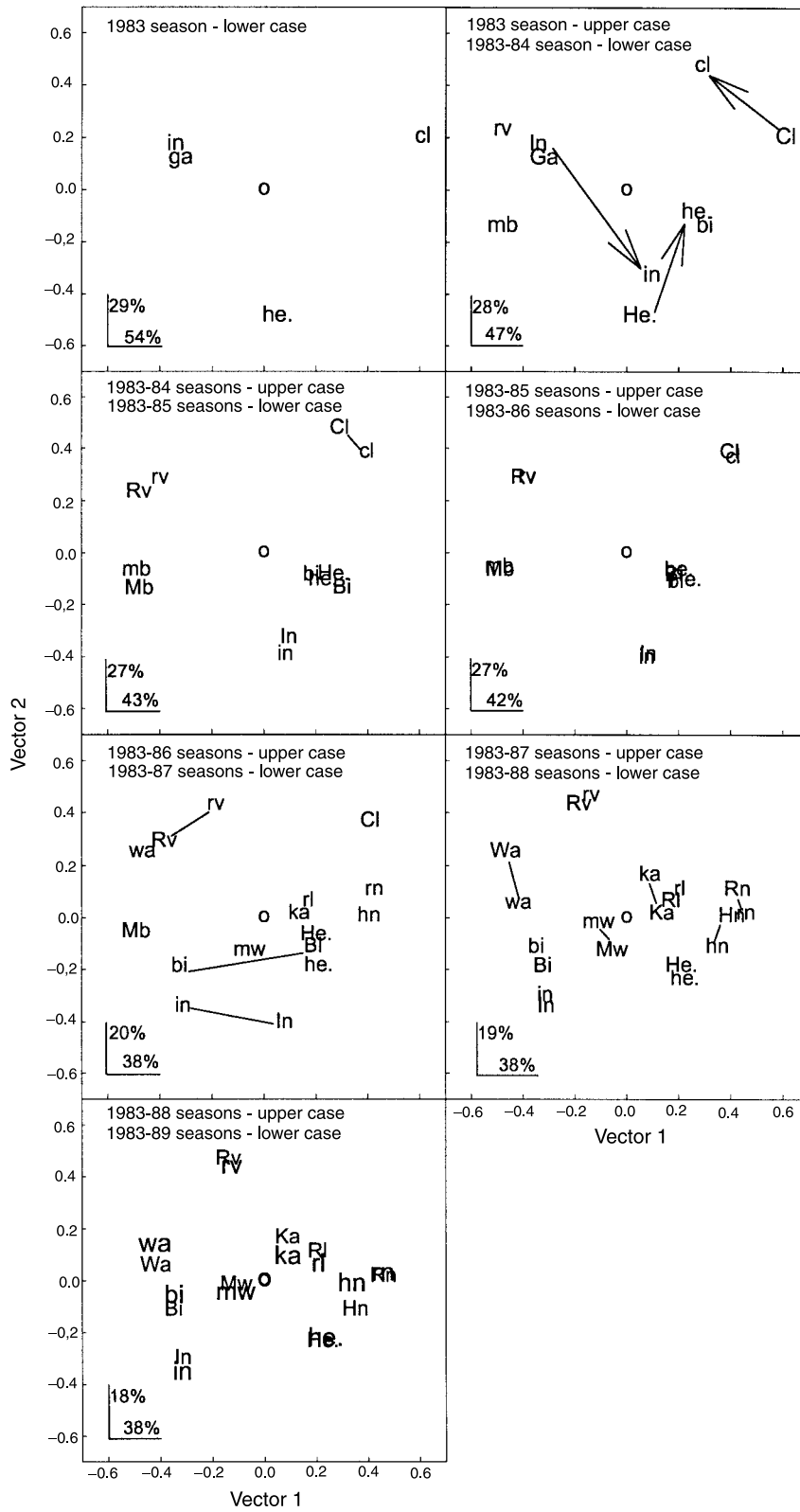
Fig. 3. Proximity plots of the first 2 vectors from the sequential principal coordinate analysis (PCO) of environments based on standardised grain yield (t/ha) of navy bean lines sown in the 1983–1989 seasons. The percentage of the total sum of squares accounted for by each vector is indicated in the bottom left hand corner of each proximity plot. Arrows indicate changes of the PCO scores of environments when extra information was added.

Fig. 4. The three 2-dimensional proximity plots for the first three vectors from the cumulative principal coordinate analysis of environments based on standardised grain yield of navy bean lines sown in the 1983–1989 seasons.

its place in the discrimination space was not occupied by another location, whereas, while Mareeba was also eliminated, its position was occupied by other locations.
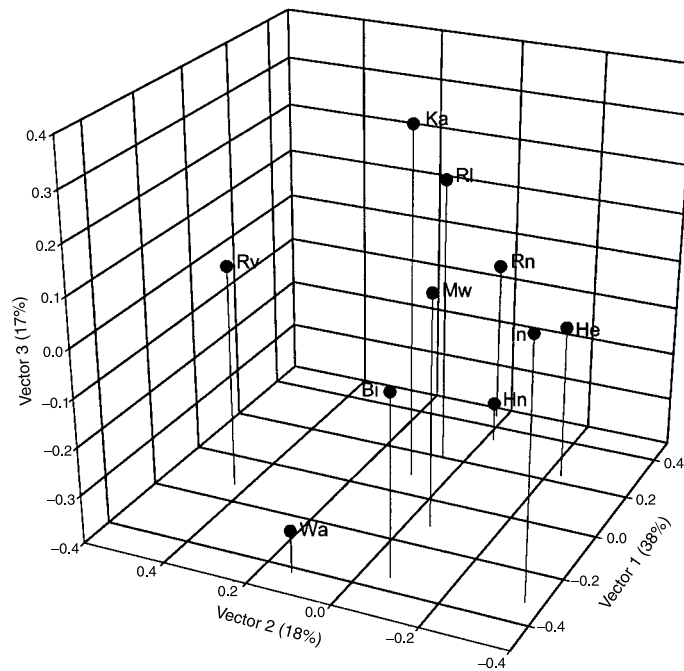
Status analysis

The pattern analysis for the 1989 data and that for the cumulative analysis for the 1983–88 seasons are compared in the status analysis (Fig. 6). The proximity plots from the 2 ordinations are superimposed. Of the 4 locations which were common, the 2 Hermitage sites and Biloela remained in the same place, indicating that they produced similar discrimination to their long-term average. However, Redvale changed to be similar to the Inglewood–Mt Wooroolin–Biloela type discrimination. The Kingaroy and Teakle Farm sites also mimicked this type of discrimination, whereas Kumbia, another Kingaroy site, was similar to the usual Redvale discrimination. Mareeba occupied a position close to Kairi, another northern Queensland site. It is clear that the locations used in the 1989 season occupied much of the discrimination space; locations were spread over the whole proximity plot derived from the full sequence of testing. Hence, the status analysis enables an objective comparison of the discrimination achieved in a year's testing compared with the long-term trends.

Discussion

It is clear that the management regimes have a major influence on the type of discrimination produced, as the irrigated and narrow row environments occupied opposite extremes on the first vector. Geographical position is also important as the northern, central, Kingaroy, and southern Queensland environments occupied characteristic positions in the discrimination space. It is also interesting that the discrimination provided by Clifton has not been replaced by other locations.

In this study, the relationships among the environments in the discrimination space, while sensitive to major changes in the environments used in the METs, quickly stabilised. There is evidence that the position occupied in the long-term discrimination space by the current year's environments gives sensible information on the type of discrimination produced by these environments in relation to long-term average. This reinforces a similar conclusion reached by Mirzawan *et al.* (1994), and enables breeders to make more sensible interpretations of the results of their selection trials. This is of importance, because the type of discrimination produced by the set of environments used in any one year varies widely, as demonstrated in the second paper in this series (Redden *et al.* 2000) as well as other studies. It is important to investi-

Fig. 5. The 3-dimensional proximity plot for the first three vectors from the cumulative principal coordinate analysis of environments based on standardised grain yield of navy bean lines sown in the 1993–1989 seasons.
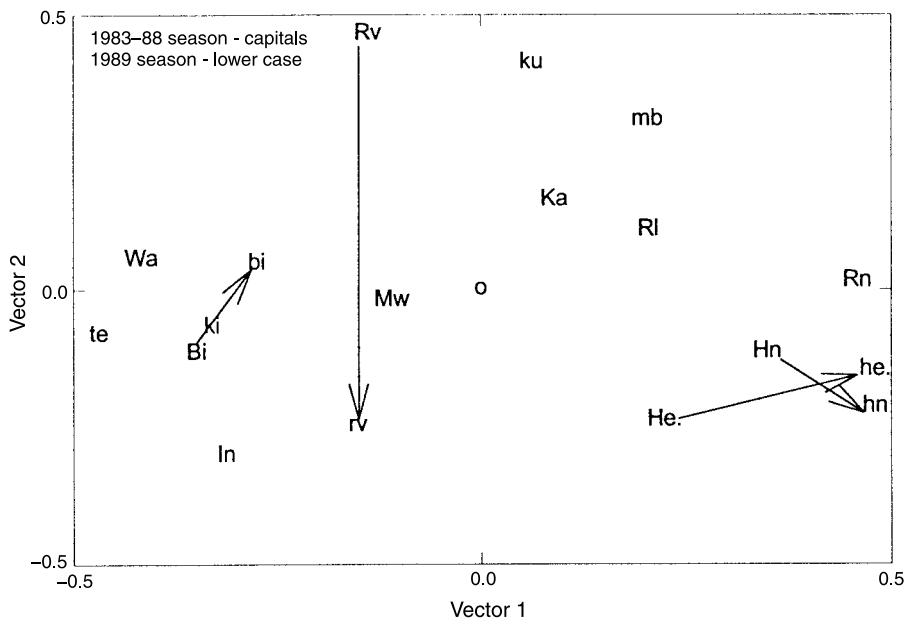
Fig. 6. Status analysis of the environments used in the 1989 season achieved by comparing their classification and principal coordinate analysis with the cumulative analysis of the environments from the 1983 to 1988 seasons. All analyses were based on standardised grain yield of navy bean lines sown in the environments.

gate whether the conclusions reached in this study can be confirmed with further data.

This analysis of environments does not indicate major redundancies which would allow reduction in test sites, since the environments are spread evenly over the discrimination space, at least in the last stages of yield testing. Trials conducted for the final testing of yield for the purposes of release of lines as cultivars are defined as stage 4 trials by Lazenby

et al. (1994). The data for this analysis are from stage 4 trials. There is some evidence that Clifton should be added to the test sites as its position in the discrimination space has not been taken by any other environment since it has been dropped from the test regime as a test site. There is evidence that one environment with narrow rows would be sufficient due to their close proximity in spite of the difference in soils and latitude. As described by Redden *et al.* (2000), changes in plant architecture towards selecting more erect cultivars contributed to the critical sensitivity of row spacing to genotypic discrimination. A minimum set of environments for earlier testing in the program should include a site from each of southern Queensland (rainfed), Kingaroy (rainfed), central Queensland (irrigated), northern Queensland (irrigated), and a site with narrow rows. This recommendation could be tempered with data about the frequency of occurrence of these environments in the target set. The analysis shows that yield testing in one environment (no matter at what stage in the breeding program) is fraught with danger, as the data from any environment in any year could occupy any place in the discrimination space.

The methodology appears robust to the vagaries of data from real breeding programs with the endemic unbalance caused by change in germplasm under test and the variability in the number and set of environments used in different years. This study demonstrates that methodology can be used to make useful interpretations of data from small-sized breeding programs. It is emphasised that these analyses use plant breeding data generated by the programs and do not rely on special experiments. However, the cumulative, sequential, and status analyses described here do waste valuable information when environments are eliminated to provide average similarity matrices without empty cells. Methods for including these data in the retrospective analyses are required.

The 3 types of retrospective analyses described in the 3 papers of this series (Butler *et al.* 2000; Redden *et al.* 2000; this paper) are complementary. The retrospective analysis of variance of the first paper, the individual analyses and collective interpretation of each year's data of the second paper, and the retrospective pattern analysis approaches described here provide different but useful perspectives on the patterns in the data. In particular, each provides different and valuable information about the testing strategies of the breeding program. Especially, it appears that the status analysis is a valuable tool for enhancement of the information gleaned in each years testing program.

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