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Assessing three methods for identification of desirable genotypes in white cabbage (*Brassica oleracea* L. var. *capitata*)

J. Davik

Kvithamar Agricultural Research Station, N-7500 Stjørdal, Norway

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Summary. A desirable genotype is a genotype performing well in a chosen set of environments. Three methods for identification of desirable genotypes were assessed in two cabbage data sets: regression analysis, multidimensional scaling of dissimilarity matrices, and biplot of deviation matrices. Using the regression approach is not recommended mainly for two reasons: (1) it is difficult to identify the desirable genotypes since one has to unify three parameters into one decision; (2) the regression method failed to identify the most desirable genotypes in one of the data sets. Multidimensional scaling and the biplot method were in accordance with each other and with the mean tables when different subsets where compared. Consequently, they were considered more adequate for identifying desirable genotypes. In cases where rank 2 approximation of the analysed matrix was justified, the biplot revealed more information in one display and was, therefore, considered particularly useful in plant breeding for larger target areas.

Key words: Desirable genotypes – Genotype-environment interactions – Multidimensional scaling – Biplot – Regression analysis

Introduction

Breeding of varieties for wide adaptation is made difficult by the existence of genotype-by-environment interaction (hereafter denoted GXE interaction). Stability parameters are often derived from statistical methods used for analysis of this interaction. These methods were reviewed by Westcott (1986), and the commonly used regression technique of Finlay and Wilkinson (1963) was criticized. This 'approach to analysing genotype-environment interaction cannot be regarded as trustworthy', Westcott wrote. The conclusion was based on several grounds: the deviation from linearity was regarded as an important stability measure by Eberhart and Russel (1966). This deviation depends, however, on the slope of the regression line (Hardwick and Wood 1972). The parameters estimated for a genotype are influenced by the other entries or by a few extreme environments. Finally, the technique may simply fail to identify stable or unstable genotypes. Despite the criticism, however, the regression method is still widely used in the classical Finlay/Wilkinson form, probably because of the attractive concept as such.

Analysing the GXE interaction by a multiplicative model was suggested by Mandel (1971). This method identifies entries (hereafter called genotypes or rows, referring to a two-way table) contributing substantially to the total GXE sum of squares. Especially if the variation of the residual matrix (a two-way table where row and column effects are eliminated) is accounted for by one or two principal components, these entries are readily identified. In cases where deviations from regression on an environmental index are significant, Hardwick and Wood (1972) suggested multiplicative modelling of the residual matrix as an alternative approach. The interpretation of the multiplicative components are not, however, always straightforward.

Implicit in the traditional methods for analysing GXE interaction and stability in plant breeding lies the assumption that a stable genotype contributes little to the GXE sum of squares. A genotype with a small contribution to this sum of squares, but a low mean, is of little interest in practical breeding. Therefore, the level of performance has to be taken into account. For the plant breeder who tests his material in a wide range of environments, a genotype's contribution to the GXE sum of

squares is of marginal interest. When breeding for wide adaptation, the entries of interest to the breeder are those performing above average in the chosen set of environments. These are the stable entries as defined by Westcott (1987). Much of the same philosophy was advocated by Haldane (1947), who pointed out that GXE interactions are important only if genotypes change in rank from one environment to another. We have adopted Westcott's concept, but to avoid confusion on the stability-term, we instead use the term desirable genotypes. We have reserved the term stability for use in connection with a genotype's contribution to the GXE sum of squares.

The objective of this study was to compare three statistical methods for identifying desirable genotypes. In some cases, however, the stability was also considered. The methods assessed were classical multidimensional scaling (MDS), the Eberhart and Russel (1966) regression analysis, and the biplot method (Gabriel 1971).

Materials and methods

Plant material

Two data sets were analysed: one set obtained from growing cabbage seedlings in differing greenhouse environments, and the other set from a cabbage variety trial.

1 Variety trial data set. Nine commercial F_1 hybrids (Table 1) were assessed at 11 locations (labeled 'Loc' accompanied by a figure) in southern Norway, each with three replications. The plots were harvested when subjectively evaluated as fit for storage. The heads were weighed and classified as marketable or not. A head was considered marketable if the weight was 0.6–2.5 kg, and if no deficiencies could otherwise be detected. Here, the mean head weight of the marketable fraction was analysed.

2 Greenhouse data set. The experimental material consisted of the F_1 hybrid 'Pedrillo' (Bejo) and 24 full-sib (FS) families which constitute 4 half-sib (HS) groups. These families were obtained from crosses within a breeding population adapted to marginal areas in northern Norway. Except for the F_1 hybrid 'Pedrillo' (Bejo) with entry number 113, the first two digits in the entry number denote the maternal parent, while the remaining two denote the paternal parent of the FS families (Table 2).

Six randomly chosen individuals from each entry were planted in perforated buckets in each of eight greenhouse environments. Within each environment, the 150 individuals were randomized weekly. The eight environmental conditions were created by four different temperatures (9°, 12°, 15°, and 18 °C), and within each temperature-regime two photoperiods were applied (14 h and 20 h). Light was provided by high-pressure metal halide lamps (HPI) giving 13,000–15,000 mW/m^2. Fertilizer was applied through a sub-irrigation system. The analysed trait, seedling height, was recorded 65 days after sowing.

Statistical methods

1 The regression approach. In the classical analysis of GXE interaction, i.e., the regression analysis, the measure of stability is derived from the model which, when omitting the replication term, is

$$Y_{ijk} = \mu + \alpha_i + \psi_j + \gamma_{ij} + \varepsilon_{ijk}, \quad (1)$$

Table 1. Commercial F_1 hybrid (and their labels) used in the varietal trial data

Cultivar		Owner
Marathon	(1)	Sluis and Groot
Froggy	(2)	Kees Broersen
Lennox	(3)	Bejo
Manrico	(4)	Bejo
Polinius	(5)	Bejo
Slawdena	(6)	Bejo
Apex	(7)	Nickerson-Zwaan
Horizon	(8)	Royal Sluis
SG648	(9)	Sluis and Groot

Table 2. Mean plant height (cm), coefficients of regression (b_i), and deviation mean squares (S^2_{di}) estimated for plant height of 25 entries grown in eight greenhouse environments

Entry	b_i	S^2_{di}	Mean
113	0.42***	0.11	6.3
2103	1.35*	0.75	17.4
2113	1.39	1.51	18.9
2122	1.09	1.22	21.2
2128	1.35	1.28	20.6
2143	0.85	0.49	18.7
2145	0.94	0.28	16.6
3003	0.86	0.96	15.4
3027	0.62*	0.43	16.1
3034	0.77	0.35	17.0
3035	1.02	0.74	17.1
3051	0.77	0.29	15.9
3056	0.73*	1.05	12.3
5507	0.94	0.35	18.2
5519	0.97	0.35	16.0
5523	0.85	0.93	14.7
5530	0.83	0.31	15.9
5546	1.24	1.07	17.0
5552	0.95	2.45*	17.1
6405	1.04	0.96	17.1
6408	1.36	1.15	19.7
6415	1.04	1.37	19.0
6418	1.11	2.61*	17.6
6443	0.96	4.16***	17.8
6455	1.56*	1.37	19.2

*, **, *** Significance level of 5%, 1%, and 0.1%, respectively

where μ stands for the general mean, α_i is the effect of the row (or genotype), ψ_j the effect of the column (or environment), γ_{ij} the GXE interaction, and ε_{ijk} the unexplained component of the variation. The interaction term may also be written as

$$\gamma_{ij} = \beta_i I_j + \delta_{ij}, \quad (2)$$

were I_j is the deviation of the jth environment from the grand mean, β_i is the regression coefficient, and δ_{ij} is the deviation from linearity. In addition to the coefficient of regression, the deviation mean squares (S^2_{di}) describe the contribution of genotype i to the GXE interaction (Eberhart and Russel 1966). Both statistics are used to assess the reaction of the genotypes to varying environments. The coefficient of regression characterizes the specific response of genotypes to environmental conditions and is the predictable part of a genotype's variability over environments. The S^2_{di} is related to the unpredictable part of the variability.

The definition of a stable genotype may vary, depending on how one wishes to look at the problem. Our main objective was to identify desirable genotypes, i.e., genotypes performing well in all environments. Consequently, we were looking for the genotypes with high means. The use of the estimated coefficients of regression is, in this connection, questionable. A genotype may have a low or a high coefficient of regression and still perform above the average in the chosen environment. Thus, these coefficients should be regarded as additional information on the average response of a genotype to a set of environmental conditions. The deviation mean squares should, however, be low (Becker and Léon 1988). Consequently, when trying to identify the desirable genotypes by means of the regression approach, one is left with the three parameters: the regression coefficients, the means, and the deviation mean squares. The two latter are the most important.

2 Multidimensional scaling (MDS). Westcott (1987) proposed a method for identifying stable genotypes based on Gower's (1966) principal coordinate analysis of a carefully defined similarity matrix. In a particular environment, the largest and smallest performing genotypes are denoted by L and S, respectively. The similarity between genotype performances x_i and x_j is given by

$$s(x_i, x_j) = \frac{L - \frac{x_i + x_j}{2}}{L - S} \qquad (3)$$

if $i \langle\rangle j$, and $s(x_i, x_j) = 1$ if $i = j$.

Smaller values of $s(x_i, x_j)$, appearing when performances of genotypes i and j are high, indicate greater proximity to L (greater dissimilarity to S); higher values indicate greater proximity to S. When more than one environment is considered, the similarity between i and j is the mean of the similarities between i and j across environments.

Gower (1966) suggested using a similarity matrix, but the result will be identical if a dissimilarity matrix is analysed by classical multidimensional scaling (Chatfield and Collins 1980). Here the latter technique was used.

Our dissimilarity, or distance matrix D, was defined by

$$d_{ij} = 1 - s(x_i, x_j) \quad \text{if} \quad i \langle\rangle j \quad \text{and} \quad d_{ij} = 0 \quad \text{if} \quad i = j. \qquad (4)$$

Using the distance matrix the smaller values of d_{ij}, appearing with low performances of i and j, indicate closer proximity to S and greater dissimilarity to L. Higher values of d_{ij} indicate closer proximity to L and greater dissimilarity to S. For the pair (L, H) within an environment, the distance is 0.5.

The measure of dissimilarity between any pair of genotypes compares its average mean with the worst performer in a given environment. MDS constructs a configuration of points in Euclidean space using information about the distances, or in this case the dissimilarities. The measure of dissimilarity allows the best performing genotypes to be represented by points located further away from genotypes that perform below the average. Entries that consistently appear further away from the centre of the scatter plot are the best performers and the desirable ones.

3 Biplot method. This method gives an idea not only of relationships within the set of entries and within the set of environments, but also of the interrelationships. Thus, the prefix 'bi' in 'biplot' does not refer to the resulting plot being two-dimensional, but indicates a joint display of rows and columns of the matrix X. Given a matrix, X, of rank 2, the biplot is obtained by writing the matrix as a product of two other matrices, $X = GH'$, where the rows of G are assigned to the rows of X, and the columns of H′ are assigned to the columns of X. They are frequently called row-markers and column-markers.

A two-dimensional approximation to a column-centred matrix of rank greater than 2 can be obtained from least squares fit to the matrix in two dimensions (Gabriel 1971). This is done by singular value decompositon of the matrix. Thus, a graphical display of a matrix by the biplot method leans heavily on rank 2 approximations, and the adequacy of this approximation may be measured by the proportion of the sum of squared singular values which is due to the first two values.

The variance of the kth column (environment), is given by the length of the kth column-marker in the plot. The correlation between two columns is given by the cosine of the angle between the corresponding pair of markers. Further, the differences between the row-markers (entries) are shown by the positions of the points (Gordon 1981). Ranking of the entries within a specific environment can be done, if the deviation matrix is analysed, by projecting the row-markers (i.e., the entries) in question onto the appropriate column-marker, and the overall ranking is found by projecting the row-markers onto the abscissa (Kempton 1984).

Since one of our objectives here was to identify entries performing above average, i.e., the desirable entries, the X-matrix used in the biplot analysis was the column-centred matrix of entry by environment performances (hereafter called the deviation matrix). the biplot method may, however, also be applied to the residual matrix and thus provide a tool for a closer examination of the GXE interaction. In such cases the distance from origo to a row-marker corresponds to the point's contribution to the GXE sum of squares. This is analogous to writing the interaction term in (1) as

$$\gamma_{ij} = \sum_{i=1}^{J} \theta_m u_{mi} v_{mj}, \qquad (5)$$

where the v-vectors relate to the column contributions; the u-vectors relate to the row contributions; the θ's are the eigenvalues, and m is the number of components retained (Mandel 1971).

Results

The greenhouse data set

1 Regression approach. Table 2 gives the entry means over all environments, the estimated coefficients of regression, and the deviation mean squares. Note that the observations were taken on individuals and not on plot means. This leads to large sampling errors and, thus, significant deviations from unity are difficult to obtain. In Fig. 1, the height observations from two entries, the F_1 hybrid, 'Pedrillo', and the FS family 6455 (FS6455), are plotted against the environmental deviations. The plot shows the apparent difference between the two entries in the deviation from the regression line. Provided the F_1 hyrbid's parental lines were highly inbred, the variation within this entry was expected to be only intra-environmental variation. The FS families exhibit, in addition to this variation, genetic variation within families. An apparent feature of the estimated coefficients of regression (Table 2) was the low b_i-value of the F_1 hybrid as compared to the FS families. Thus, the hybrid had a more uniform performance over varying environmental conditions than the FS families with which it was compared.

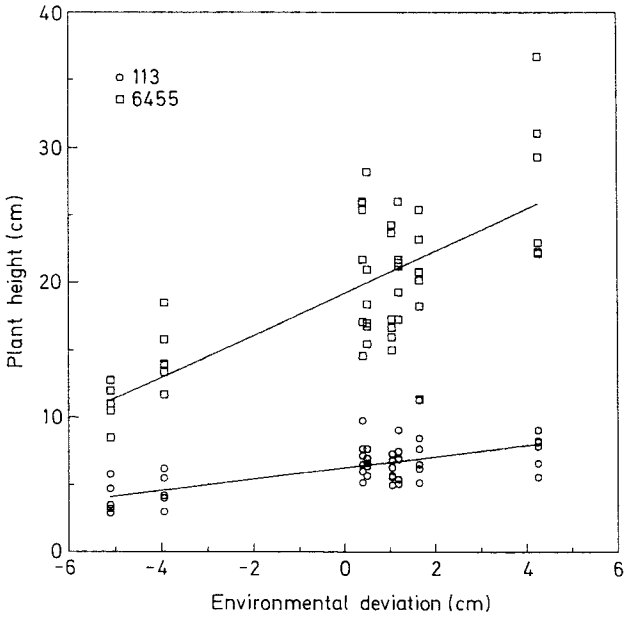

Fig. 1. Regression lines for plant height of the F_1 hybrid 'Pedrillo' (entry 113) and the FS family 6455 on the environmental deviations using the complete greenhouse data set

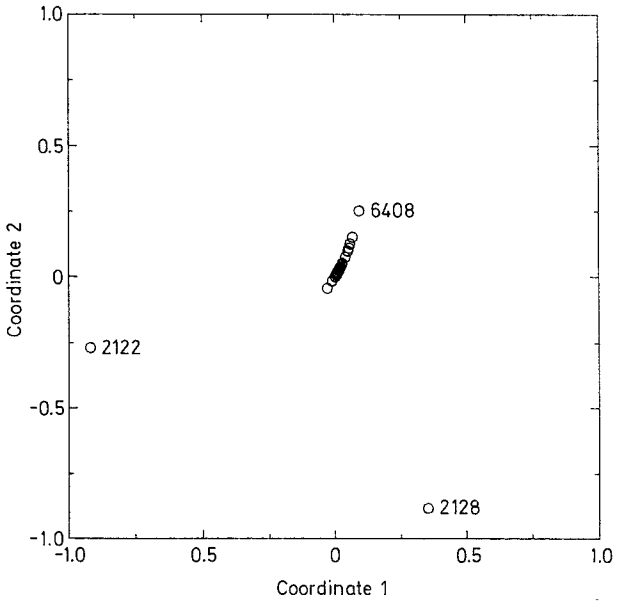

Fig. 2. Plot of the two first coordinates from multidimensional scaling (MDS) of the averaged dissimilarity matrix using the complete greenhouse data set. See text for dissimilarity measure

Extensive studies in *Nicotiana* ssp. have shown that additive and dominance gene actions and the different kinds of non-allelic interactions usually have different environmental sensitivities (Mather and Jinks 1982). In our case, it seemed that the heterozygote, i.e., the F_1 hybrid, interacted less with the environment than did the homozygotes represented at least partially by the FS families.

Similar patterns were observed by Bucio Alanis and Hill (1966), and Becker and Léon (1988) referred to several studies with similar results. This pattern is, however, not general. If the sampled environments were divided into low- and high-performing ones, Jinks and Pooni (1988) found that an F_1 hybrid was less sensitive to environmental changes as compared with their homozygous parental lines in the low-performing environments. In the high-performing environments the F_1 hybrid was, however, considerably more sensitive to environmental changes than the parental lines.

Assuming that above average performance over environments was desired, FS2122 was an obvious choice (Table 2). Its coefficient of regression was relatively close to unity and its mean was the highest in the sample. Another candidate for selection would be FS6415. Families like 2128, 6408, and 6455 all performed well by their means and had, like FS2122, non-significant deviation sum of squares. Their coefficients of regression were, however, high. A closer examination of the data showed that these entries rank high in most environments. However, 6408 performed only about average in environments 1 and 3 (E1 and E3), while 6455 performed poor in E1. This was the reason for the high regression estimates. It was only FS6455, however, that had a regression line intersecting the overall regression line. So this FS family performed poorly only in the low-performing environments, in particular in E1, and it might be a candidate for discarding. There was no reason to discard FS2128 and FS6408.

2 Multidimensional scaling. Of the 25 entries in the full data set, the 5 best overall performing FS families were 2122, 2128, 6408, 6455, and 6415 (Table 2). They all come from two HS groups, HS21 and HS64. Neither the FS families belonging to HS30 and HS55, nor the F_1 hybrid (entry 113), appeared outside the centre cluster, due to their low mean performances. The MDS plot corresponds well with the ranking based on overall means (Table 2 and Fig. 2). Taking the third coordinate into account, 6415 and 6455 appeared as distinct points on the plot. The desirability of the latter FS family was questioned when analysed by the regression method, and there was a possible disagreement between the two methods.

3 Biplot approach. When the deviation matrix was used in the biplot analysis, 88% of the matrix's variation was accounted for by the first two dimensions. Therefore, the use of the biplot method seemed justified. It should, however, be noted that in cases where not all the variation is accounted for by the first two dimensions, information is lost by this two-dimensional visualization of the matrix. Graphically, this means that the points in the plot have non-zero coordinates in the dimensions higher than two. The more the first two dimensions account for, the closer

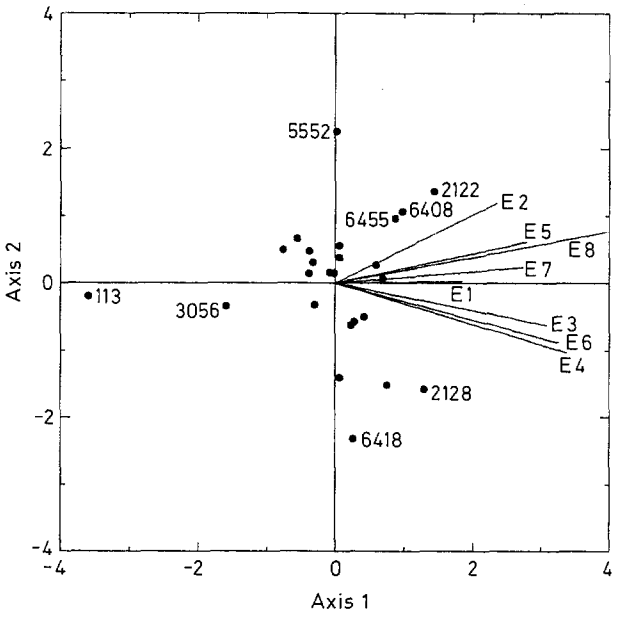

Fig. 3. Biplot of the deviation matrix from the complete greenhouse data set

to zero are these coordinates, and the better is the fit of the matrix to the plane or the rank 2 approximation.

The first axis of Fig. 3 ranks the entries approximately according to the overall mean performances given in Table 2. Ranking of the entries within a specific environment can be done by projecting the row-markers in question onto the appropriate column-marker. Thus, some of the entries rank different in the two most dissimilar environments E2 and E4. For example; 2128 performed well in E3, E4, and E6, and poor in E2, while 5552 performed well in E2, but inferior in E3, E4, and E6. Entries 113 and 3056 were inferior in all environments.

The biplot method identified the same entries as the MDS method. The biplot method apparently didn't give such a distinct display, but provided a more differentiated picture, concealing no information as the MDS plot tended to do (Figs. 2 and 3).

The greenhouse sub dataset

Excluding the hybrid (entry no. 113) and environment 8 did not influence the ranking of the entry means. The highest performing FS families are still found within HS21 and HS64 (Tables 2 and 3). The significant difference among the coefficients of regression when analysing the complete set ($P = 0.006$) disappeared when the subset was analysed. Estimates of regression coefficients which deviated significantly from unity (Table 2) now appeared non-significant (Table 3), and shifts in the magnitude of the regression estimates were very pronounced in cases

Table 3. Mean plant height (cm), coefficients of regression (b_i), and deviation mean squares (S^2_{di}) estimated for plant height of 24 entries grown in 7 greenhouse environments

Entry	b_i	S^2_{di}	Mean
2103	1.22	0.73	16.4
2113	1.45	1.67	18.2
2122	0.99	1.41	20.4
2128	1.41	1.39	19.9
2143	0.76	0.51	18.1
2145	0.87	0.30	16.0
3003	0.90	1.13	14.9
3027	0.48***	0.28	15.5
3034	0.75	0.42	16.5
3035	1.04	0.88	16.6
3051	0.77	0.35	15.4
3056	0.85	1.03	12.0
5507	0.98	0.37	17.7
5519	0.98	0.41	15.4
5523	0.73	1.02	14.1
5530	0.89	0.29	15.5
5546	1.38	0.92	16.4
5552	0.71	2.35	16.2
6405	0.85	0.78	16.2
6408	1.15	0.90	18.6
6415	0.99	1.65	18.3
6418	1.42	1.51	17.4
6443	1.07	4.77***	17.4
6455	1.35	1.27	18.0

*** Significance level of 0.1%

where loss of significant deviation mean squares appeared.

FS5552 performed above average in E2, E7, and E8, and was well below average in the other environments. In the subset analysis, the estimated coefficient of regression dropped from $b_i = 0.95$ to 0.71 in the case of FS5552. FS6418, on the other hand, performed relatively poorly in E8, resulting in a substantial increase in the estimated coefficient of regression ($b_i = 1.11$ to 1.42) and a corresponding reduction in the deviation mean square (Table 3). All these changes in the estimates were also observed when only environment E8 was excluded, demonstrating the impact of this particular environment.

The most desirable entries were 2122, 2143, and 6415. All have relatively low regression coefficients and high means. In addition to the entries displayed by the MDS plot when the complete set was assessed (Fig. 2), 6415 appeared as a desirable entry in the MDS plot of the subset. This was actually no contradiction, since this FS family in the full-set analysis had a high score on the third coordinate. Again, there were no contradictions towards the regression results (Table 3).

The biplot of the subset deviation matrix was very similar to the corresponding full-set biplot (Fig. 4). The ranking along the first axis corresponded well to the overall mean ranking (Table 3). Comparing Figs. 3

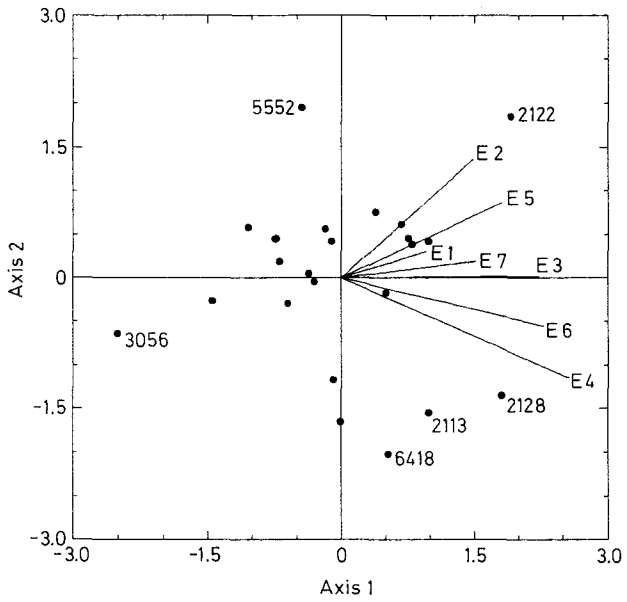

Fig. 4. Biplot of the deviation matrix from the greenhouse subdata set

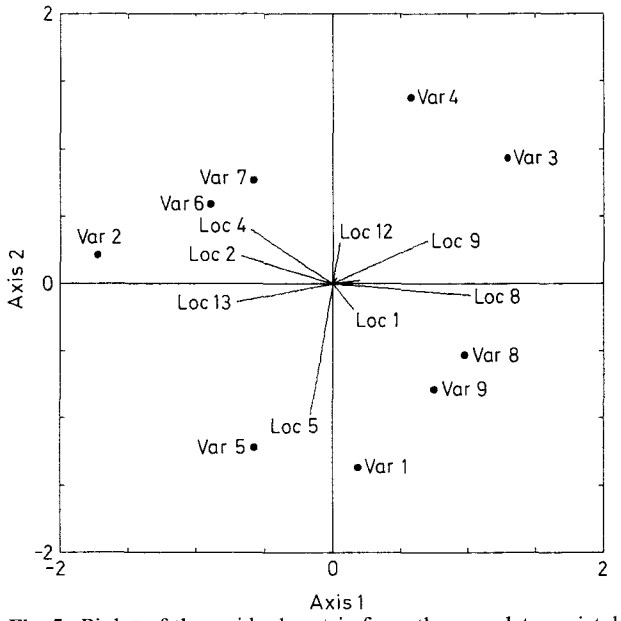

Fig. 5. Biplot of the residual matrix from the complete varietal testing data set

and 4, it seems that the correlation between environments decreases as judged from the angles between the environmental vectors. In fact, since the two dimensions in Figs. 3 and 4 accounted for 88% and 57% of the variation, respectively, the angle increment was probably larger than it appears on the plots. The main effect was caused by exclusion of the hybrid (entry 113), since this entry performed almost equally in the different environments and by its presence increased the correlation between the environments (Fig. 1).

The large shifts in the parameter estimates when comparing subsets of the data have been used as an argument against the regression method (Crossa 1988). The influence of the analysed material is, however, not a characteristic of the regression method. The basic cause for this lies in the nature of the GXE interaction. An interaction can only arise from a comparison between at least two genotypes and thus it refers to a specific set of observations. Thus, this problem has to be acknowledged in most other methods as well.

For the greenhouse data set we conclude that the three methods assessed gave practically identical results. The same desirable genotypes were identified. We do, however, question the regression approach when the objective is merely to identify the desirable genotypes. The main reason for this is the difficulties in unifying the three estimated parameters into one decision. Both the multivariate methods, on the other hand, gave clear and unambiguous displays, which are relatively easy to interpret. Problems may arise, however, in the MDS approach when more than two dimensions are required to rank the entries, and in the biplot method when rank 2 approximation is not appropriate.

The variety trial data set

1 Analysing the residual matrix. ANOVA showed significant GXE interaction ($P = 0.03$), but it was not possible to assign this interaction to differences among regression coefficients (Table 4). Some of the deviation mean squares were, however, highly significant. Modelling the residual matrix in multiplicative terms showed that the two first components described 42% and 21% of the variation, respectively. In spite of the small fraction of the variation accounted for, the biplot method was applied (Fig. 5). Keeping in mind the previously mentioned precautions regarding loss of information in cases with bad fit to rank 2 approximation, we imply the following: Loc5 and Loc8 had a large impact on the variation of the residual matrix (i.e., the GXE interaction), while Loc3, Loc7, and Loc11 (not labelled on the plot) contributed insignificantly. The varieties all contributed to the GXE sum of squares as indicated by their distance from the centre of the plot; variety 2 especially seemed to contribute much. This variety contributed to the GXE sum of squares by scoring high in Loc2, Loc4, and Loc13, and by the low score in Loc8 and Loc9. This variety was also identified by the regression method by having a large deviation mean square (Table 4). The other varieties contributed more or less equally to the sum of squares. Variety 3, however, having a large deviation mean square, was not particularly remotely located on the plot.

2 Analysing the deviation matrix. Judged from the mean performances and the estimated coefficients of regression, variety 2 is the obvious choice (Table 4, full set). Its deviation mean square was, however, disturbing and it should be discarded. Such a decision may be founded on

Table 4. Mean head weight (kg), coefficients of regression (b_i), and deviation mean squares (S^2_{di}) estimated from two subsets from cabbage variety trials

Variety	Eleven sites			Six sites		
	b_i	S^2_{di}	Mean	b_i	S^2_{di}	Mean
1	1.12	1.29	1.06	1.48	1.64	1.13
2	0.97	3.28***	1.45	0.73	6.92***	1.50
3	0.95	2.38*	1.26	0.37	4.20**	1.31
4	0.95	1.89	1.17	0.62	3.32*	1.22
5	1.21	1.59	1.20	2.03*	1.43	1.27
6	0.97	1.41	1.06	1.08	1.78	1.08
7	0.97	0.94	1.25	0.54	0.59	1.30
8	1.08	1.89	1.11	1.24	2.85*	1.15
9	0.77	1.53	1.03	0.91	1.78	1.08

*, **, *** Significance level of 5%, 1%, and 0.1%, respectively

loose grounds. It is a possibility that a genotype has a large deviation mean square simply because it reacts differently to environments when compared with the average genotype tested. In fact, this was the case for variety 2, both in this analysis and in the following subset analysis (Fig. 6) Nevertheless, the breeder has to make his decision from the parameters given by the regression analysis. Thus, one may argue that variety 7 is a better choice.

Eighty-seven percent of the variation in the deviation matrix was explained by the two first components, so the rank 2 approximation is fairly close to the original matrix. Equally, 86% of the variation in the dissimilarity matrix used in the MDS approach was accounted for by the two first components. MDS and biplot of the deviation matrix both identified varieties 2, 3, 5, and 7 as the most desirable. The former method gave an easily interpretable plot (not shown), but the ranking among the second-best varieties was not straightforward. This was easier using the biplot method. Clearly, the overall ranking is 2, 7, 3, and 5 (Fig. 7). This ranking is practically identical to the ranking of the means in Table 4. For clarity of the plot, variety 7 is not labeled, but it is located in the middle of the swarm of column-markers. In contrast, varieties 2 and 3 were discarded in the regression approach due to the large deviation mean squares.

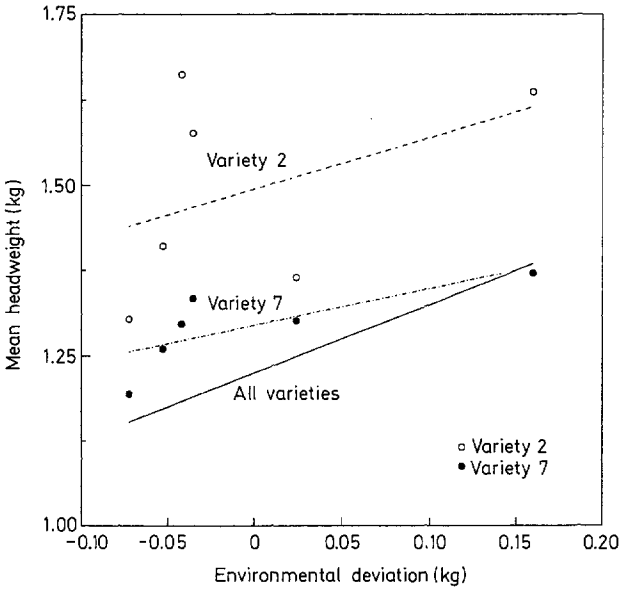

Fig. 6. Regression lines for mean head weight of the F_1 hybrids Froggy (variety 2) and Apex (variety 7)

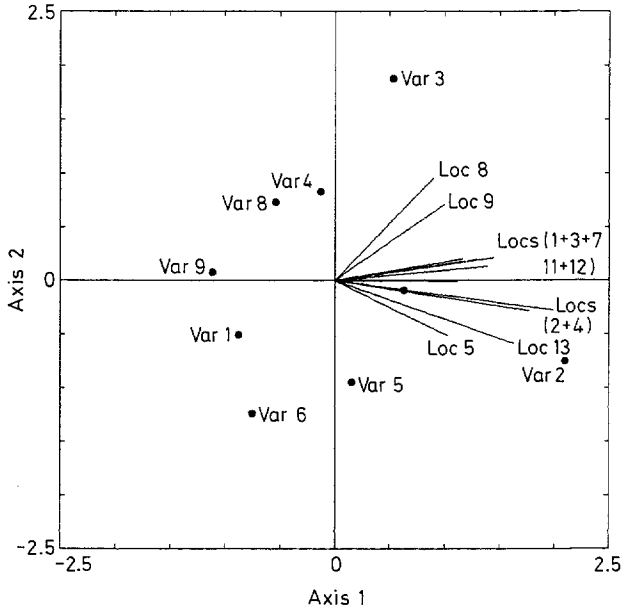

Fig. 7. Biplot of the deviation matrix from the complete varietal testing data set

A subset of the variety trial data

1 Analysing the deviation matrix. The highly correlated testing sites (or collinear columns) gave the same information as far as ranking of the varieties was concerned (Fig. 7), and some of them may therefore be excluded, thus saving resources in the testing procedure. The locations (1+3+7+11+12) and (2+4) appeared in two clusters.

The subset was obtained by retaining the low-collinear environments in addition to one environment from each of the two clusters of collinear environments (Fig. 7). The latter two environments were the ones with the largest variance within the respective cluster, i.e., environments 2 and 12. The resulting biplot described 71% of the deviation matrix's variation (Fig. 8). Comparing this plot with the plot corresponding to the full set's analysis (Fig. 7), the structures were consistent. The relation between varieties and between locations as well as the interrelationships were practically identical.

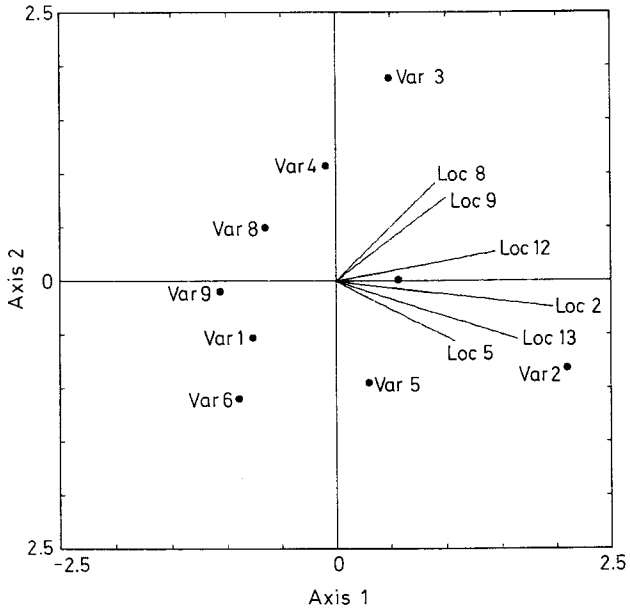

Fig. 8. Biplot of the deviation matrix from varietal testing subset data

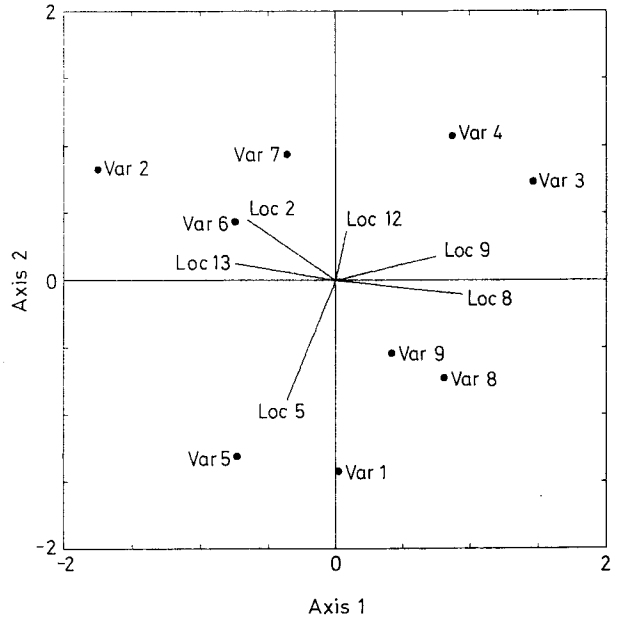

Fig. 9. Biplot of the residual matrix from the varietal testing subset data

There were no large shifts in the ranking by the MDS method. Here the two dimensions described 82% of the variation in the dissimilarity matrix. The only change distinguishing the subset plot from the full set was a slightly better performance of variety 5.

Large changes were observed in the estimates of the regression parameters when regression analysis was applied to the subset data (Table 4). Practically all of the estimated regression coefficients changed dramatically. The most pronounced change was shown by variety 5, shifting from $b_i = 1.21$ to $b_i = 2.03$. Likewise, the changes in the deviation mean squares were large. Such changes are expected, since the regression coefficients are calculated using an environmental index derived from the entries assessed. The origin of the large deviation mean square of variety 2 is illustrated in Fig. 6. This variety responded differently to environments when compared with the average variety in the data set, resulting in large deviations from regression. The regression line of the variety with the lowest deviation sum of squares, variety 7, is also shown. Another feature of Fig. 6 is that one of the environments deviated quite a bit from the average environment. This means that the statistics of a variety may be unduly influenced and seriously misleading. The desirable genotypes in this subset were, however, again varieties 5 and 7, since varieties 2 and 3 have significant deviation mean squares.

2 Analysing the residual matrix. By modelling the residual matrix in multiplicative terms, 71% of the variation was described in the rank 2 approximation (Fig. 9). Again, there were no discrepancies between this approximation and the approximation of the full-set residual matrix (Fig. 5), indicating that the reduction of the number of testing sites in this variety trial could be justified.

When the residual matrix was analysed, the biplot's advantage was that it specified the combination of genotype and environment which had the largest GXE sum of squares. There was good agreement between the biplot and the regression approach in this case. The variety sample was, however, limited.

The varietal testing data revealed the weakness of the regression approach. While the MDS and biplot methods appeared consistent, identifying the desirable genotypes, the regression method failed to identify the highest performing varieties as desirable ones because of high deviation mean squares. The advantage of the biplot method lies in the overall ranking of all entries as well as the ranking within environments. Further, the use of the biplot in identifying highly correlated environments should be of interest as a means of reducing the number of testing sites in variety testing routines.

Discussion

The major problem with the use of regression analysis for assessing stability is the choice of environmental index. The approach of Finlay and Wilkinson (1963), and extended by Eberhart and Russel (1966), uses the environmental mean performance of all genotypes as a measure of the environment. Therefore, identification of desirable genotypes depends not only on the environments included in the study, but also on the particular set of

genotypes tested. Thus, the relative performance of two genotypes will vary according to the choice of other genotypes to be included and can, therefore, not represent an absolute measure of performance. This was clearly exemplified in the variety trial data set. A closer examination of this data set showed, however, that the highest performing variety, variety 2, only responded atypically compared to the average variety. This leaves us wondering which of the estimated parameters from the regression analysis is of any use in identifying the desirable genotypes. Provided the candidate genotype performs above average in all environments, the regression coefficient does not provide much additional information. This was exemplified in the greenhouse data set (e.g., FS6415 versus FS6455). Similarily, the deviation mean squares may be high and the candidate genotype may still be the most desirable one. Moreover, this parameter was questioned by Hardwick and Wood (1972) on theoretical grounds, since it is not independent of the slope of the regression line.

We find the regression method difficult to apply when identification of desirable genotypes is the objective. The results of the method depend too much on the samples of both genotypes and environments, leading to low reliability and stability of the estimated parameters. Making a decision thus becomes very difficult.

The MDS approach reveals the highest performing genotypes over the given set of environments; it is model-free and can thus be applied without a large set of environments. The choice of dissimilarity measure is, however, critical (Westcott 1986). The dependency problem when a subset of genotypes is analysed is partly overcome. As long as the reference genotypes, i.e., the highest- and the lowest-performing genotypes, are not excluded from the data, the dissimilarities between the remaining entries in a subset will not change. If such an exclusion is done, these dissimilarities changes. This did not, however, cause any difficulties in identifying the desirable entries in our study.

Crossa (1988) compared the MDS method with the modified regression analysis of Verma et al. (1978), and concluded that the former method was the most useful of the two due to its consistency in identifying the desirable entries when subsets were analysed. The shifts in parameter estimates is a feature of most statistical methods used in this connection up to now, but the MDS seems to be a step forward. Ranking of the entries near the centre of the plots is, however, difficult. In a population breeding programme where selection intensity often is low, this ranking might be of importance. In variety trials, however, where the major concern is to identify the few best performing entries, this objection is probably of little relevance.

If the performance in only one single environment is desired, a scaling plot may be obtained from that particular site. Having several sites to consider, a corresponding number of plots has to be made. The biplot approach using the deviation matrix unifies all the scaling plots into one, and this plot is highly reliable provided rank 2 approximation is appropriate. In this case the biplot facilitates identification of the overall best performing entries and, in addition, rank them within testing sites. Due to the method's clear ranking of the second best entries, the biplot approach in plant breeding may prove a useful tool in identifying desirable entries. Further, the collinearity of testing sites is displayed, and this may be used to reduce the number of testing sites in future variety trials.

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