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Relationships between genotype × environment interactions and rank orders for a set of genotypes tested in different environments

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Abstract. Multilocation trials in plant breeding lead to cross-classified data sets with rows = genotypes and columns = environments, where the breeder is particularly interested in the rank orders of the genotypes in the different environments. Non-identical rank orders are the result of genotype × environment interactions. Not every interaction, however, causes rank changes among the genotypes (rank-interaction). From a breeder's point of view, interaction is tolerable only as long as it does not affect the rank orders. Therefore, the question arises of under which circumstances does interaction become rank-interaction. This paper contributes to our understanding of this topic. In our study we emphasized the detection of relationships between the similarity of the rank orders (measured by Kendall's coefficient of concordance W) and the functions of the diverse variance components (genotypes, environments, interaction, error). On the basis of extensive data sets on different agricultural crops (faba bean, fodder beet, sugar beet, oats, winter rape) obtained from registration trials (1985–1989) carried out in the Federal Republic of Germany, we obtained the following as main result: $W \cong \sigma_g^2/(\sigma_g^2 + \sigma_v^2)$ where σ_g^2 = genotypic variance and $\sigma_v^2 = \sigma_{ge}^2 + \sigma_o^2/L$ with σ_{ge}^2 = interaction variance, σ_o^2 = error variance and L = number of replications.

Key words: Two-way classification – Rank orders – Genotype × environment interaction – Coefficient of concordance – Variance components – Agricultural crops

Introduction

Multilocation trials play an important role in breeding programmes in the testing of the environmental adaptability of new varieties. Such trials lead to cross-classified datasets with K rows (genotypes), N columns (environments) and L replicates. The ideal situation for the plant breeder is that the rank orders of genotypes are constant across environments, so that the best genotype in one of the environments is also the best in all other environments. In real applications, however, this is generally not the case. Any deviation from the ideal situation of identical rank orders is the result of genotype-environment interactions. If the interaction is so large that it causes a rank change among the genotypes, one can speak of rank-interaction. Obviously, not every interaction is rank-interaction. This will depend greatly on the relative size of both the genotypic effect and the interaction effect in the datasets.

For a precise description of these relationships some authors have introduced the terms qualitative interactions (crossover interactions) and quantitative interactions (noncrossover interactions). In noncrossover interactions the true treatment differences vary in magnitude but not in direction, whereas in crossover interactions, the direction of true treatment differences varies. Although these concepts have been developed in the field of medicine, they can be applied to questions concerning genotype-environment interactions in crop improvement.

Some interesting statistical test procedures have been published by Azzalini and Cox (1984), Berger (1984), Gail and Simon (1985) and Zelterman (1990). For applications to agricultural crops see, for example, Baker (1988) and Virk and Mangat (1991). An attractive non-parametric approach for computing and

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testing rank-interactions has been proposed by de Kroon and van der Laan (1981) and van der Laan (1987).

From a breeder's point of view, interaction is tolerable as long as it does not affect the rank orders. So the question that arises is under which circumstances does interaction become rank-interaction.

Problem

For datasets with more than two genotypes and more than two environments, genotype-environment interactions are commonly calculated by an analysis of variance techniques that leads to an estimated variance component for genotype-environment interactions. For a two-way table with K genotypes (rows), N environments (columns) and L replications, the relationships between the numerical value of the variance component of genotype-environment interactions and the rank changes of the genotypes in the different environments are of particular practical interest.

With respect to these problems, many prominent statements have been published, for example: "Procedure for estimation of genotype × environment interaction variances has been outlined and numerous estimates have actually been obtained and reported. In general, however, these have been interpreted with reference to genotype-environment interaction as a source of nongenetic variance among selection units of one kind or another. In contrast, quantitative genetics has not shown how such estimates can logically be employed in decisions concerning target populations of environments. For example, I do not know how large a component of genotype-environment interaction variances can be, as a fraction or multiple of genetic variance, when there is no variation among environments in the rank order values of genotypes (or family groups of genotypes) nor am I aware that this has been discussed in the literature" (Comstock 1977).

The purpose of our paper is to present some contributions to this topic. In it, we concentrate on possible relationships between parametric approaches (variance components) and nonparametric approaches (rank orders).

The central question of the following investigations can be stated as follows: at the parametric side, the $K \times N \times L$ dataset can be characterized by the variance components, i.e. genotypic, environmental, interaction, and error variances. At the nonparametric side, the same dataset can be described by the similarity respective dissimilarity of the rank orders of the genotypes in the different environments.

We are mainly interested in possible relationships between the similarity of the rank orders and these variance components or functions of them. Furthermore, these investigations can help to clarify the nature of rank-interaction.

Theory

The data can be arranged in a two-way layout with K rows and N columns, having L replicates in each cell. The following linear model is used to analyse the data:

$$y_{ijr} = \mu + g_i + e_j + (ge)_{ij} + \varepsilon_{ijr} \qquad (1)$$

where

y_{ijr} = observed phenotypic value of the r-th replicate ($r = 1, \ldots, L$) of the i-th genotype ($i = 1, \ldots, K$) in the j-th environment ($j = 1, \ldots, N$),
μ = overall mean,
g_i = effect of the i-th genotype,
e_j = effect of the j-th environment,
$(ge)_{ij}$ = interaction effect of genotype i in environment j and
ε_{ijr} = error of the r-th replicate of the i-th genotype in the j-th environment.

The variance components σ_g^2 (genotypes), σ_e^2 (environments), σ_{ge}^2 (interaction) and σ_o^2 (error) can be estimated using the linear model in Eq. 1 by applying elementary statistical theory. In the field of practical applications, however, most stability analyses are carried out for datasets consisting of the means of genotypes in different environments.

Turning to the cell means, model 1 becomes

$$y_{ij} = \mu + g_i + e_j + v_{ij} \qquad (2)$$

where

$v_{ij} = (ge)_{ij} + \bar{\varepsilon}_{ij}$,
y_{ij} = mean of the i-th genotype in the j-th environment and
$\bar{\varepsilon}_{ij}$ = mean error of genotype i in the environment j.

The variance components for this two-way classification of the cell means are σ_g^2, σ_e^2 and σ_v^2 with $\sigma_v^2 = \sigma_{ge}^2 + \sigma_o^2/L$ (interaction plus mean error variance).

The aforementioned functions of these variance components are ratios of the following form:

$$R = \frac{c_1\sigma_g^2 + c_2\sigma_e^2 + c_3\sigma_{ge}^2 + c_4\sigma_o^2}{c_5\sigma_g^2 + c_6\sigma_e^2 + c_7\sigma_{ge}^2 + c_8\sigma_o^2}$$

for model 1 (with replications) (3)

$$T = \frac{k_1\sigma_g^2 + k_2\sigma_e^2 + k_3\sigma_v^2}{k_4\sigma_g^2 + k_5\sigma_e^2 + k_6\sigma_v^2}$$

for model 2 (without repliations) (4)

Each coefficient $c_i, i = 1, 2, \ldots, 8$, and also each coefficient $k_i, i = 1, 2, \ldots 6$, takes the value zero or one.

After ranking the cell means of genotypes within environments, the table entries r_{ij} denote the rank of the i-th genotype ($i = 1, \dots, K$) in the j-th environment ($j = 1, \dots, N$). Each column is a permutation of the numbers $1, 2, \dots, K$. Maximum concordance occurs when the rankings of genotypes are identical in all environments. If this is so, the row totals will be some permutation of the numbers $1N, 2N, \dots, KN$. The sums of squares of row totals ($SSRT$) for maximum concordance can be shown to be $SSRT_{\max} = N^2K(K^2 - 1)/12$.

To have a measure of concordance, i.e. a measure of similarity of rankings, one can put the actual $SSRT$ in relation to the maximum $SSRT$. The corresponding ratio is Kendall's coefficient of concordance $W = SSRT_{\mathrm{act}}/SSRT_{\max}$. This can be written as (Gibbons 1985):

$$W = \frac{12S}{N^2K(K^2-1)} \tag{5}$$

where $S = N^2\sum_i \{\bar{r}_{i\cdot} - (K+1)/2\}^2$ with $\bar{r}_{i\cdot} = \sum_j r_{ij}/N$.

It is clear from this definition that W must lie between zero and one. The minimum possible value of the sum of squares of row totals is zero, in which case W is also zero. If $SSRT_{\mathrm{act}}$ takes the maximum possible value, then $W = 1$.

W can also be defined and interpreted as an evident generalization of Spearman's rank correlation coefficient $\rho_{jj'}$, which measures the similarity of the rankings of genotypes in two environments j and j'. The similarity of the rank orders in more than two environments can be expressed by W. Apart from a certain standardization, W has the meaning of the mean $\bar{\rho}$ of all Spearman rank correlation coefficients for all possible pairs of environments (Kendall 1962):

$$\left.\begin{aligned} \bar{\rho} &= \frac{2\sum\limits_{j<j'} \rho_{jj'}}{N(N-1)} = \frac{NW-1}{N-1} \\ W &= \frac{1+(N-1)\bar{\rho}}{N} \end{aligned}\right\} \tag{6}$$

From the breeder's point of view, it is desirable to have a maximum association ($W = 1$) between the rankings in different environments. $W = 1$ implies identical rank orders of the genotypes in each environment, which means $\rho_{jj'} = 1$ for each pair j and j' and, therefore, $\bar{\rho} = 1$.

If the ranks of the genotypes are assigned at random within each environment, then all of the individual Spearman coefficients are zero ($\rho_{jj'} = 0$ for each pair j and j' with $\bar{\rho} = 0$). This case corresponds to a W of $1/N$. For an increasing number of environments ($N \to \infty$) this value tends to $W = 0$.

For large W, one might expect a high chance that the ranking will be similar to or even the same as in other environments if this set of genotypes is transferred to another environment (not too different from the ones used for computing W). Such a high predictability can be obscured, of course, by two sources: genotype-environment interaction and experimental error.

For applications, it is of particular interest to know whether the concordance between the rankings significantly differs from one completely due to chance. For a sufficiently large number of genotypes an asymptotic test based on the chi-squared distribution can be applied:

$$\chi^2 = N(K-1)W \tag{7}$$

with $K - 1$ degrees of freedom (Kendall 1962).

If W is significant, there are differences in the genetic effects g_i. Note that $N(K-1)W$ is the statistic of the Friedman-test. If W is significant, the Friedman-test for equality of all genotypic means will also be significant (Gibbons 1985). If W is nonsignificant, this may have two different causes. Either there are no differences in the genetic effects, or the v_{ij} effects, i.e. the experimental error and genotype-environment-interaction, are so large in relation to the genetic effects that differences in the g_i's are obscured. The latter reason is the more probable in practical applications.

Material and methods

Twenty-seven datasets of yield from official registration trials carried out in the Federal Republic of Germany (1985–1989) were used for the calculations. The sizes of the datasets are given in Table 1. (The complete nonorthogonal dataset for oats for 1989 has been partitioned into three orthogonal sub-datasets (a, b and c)).

Since the tested genotypes result from the actual breeding work of a limited number of breeders, these genotypes cannot be considered to be a random sample from a larger universe. Genotypic effects are, therefore, regarded as fixed, while environmental, interaction and error effects are considered as random. The variance components were computed for this mixed-effects model 1 by equating the actual mean squares with the expected mean squares. (For simplicity we denote the term $\sum_i g_i^2/(K-1)$ for fixed genotypic effects by σ_g^2, although it is not a variance component in the general sense.)

For the tests of significance we used error probabilities 5%, 1% and 0.1% denoted by *, **, and ***, respectively. For every dataset, Kendall's coefficient of concordance W was calculated. All possible ratios of the forms (3) and (4) were calculated from estimates of the variance components.

We were mainly looking for possible relationships between the similarity of the rank-orders (measured by W) and specific functions of the variance components (measured by R or T, respectively). It is, therefore, of particular relevance which of the expressions R or T exhibits the strongest dependency on W. For this functional relationship between W and R or between W and T we use:

$$W = f_1(R) \quad \text{or} \quad W = f_2(T) \tag{8}$$

We are especially interested in whether or not there are linear relationships between W and some R's or between W and some T's.

Table 1. Characteristics of yield datasets from German registration trials carried out from 1985 to 1989

Crop	Year	Number of genotypes	Number of environments	Number of replications
Faba bean	1985	14	9	4
	1986	31	9	4
	1987	32	9	4
	1988	35	10	4
	1989	35	10	4
Fodder beet	1985	19	7	4
	1986	22	6	4
	1987	21	8	4
	1988	17	8	4
	1989	20	9	4
Sugar beet	1985	78	11	4
	1986	73	11	4
	1987	86	9	4
	1988	71	9	4
	1989	67	11	4
Oats	1985	32	12	4
	1986	33	12	4
	1987	20	12	4
	1988	14	18	4
	1989a	33	12	4
	1989b	15	9	4
	1989c	17	16	4
Winter rape	1985	32	8	4
	1986	35	11	4
	1987	35	10	4
	1988	42	9	4
	1989	41	10	4

Each dataset provides, of course, only one value for an investigation of these relationships. To obtain more 'points' for a determination of these relationships, one can combine the results of different years (for the same agricultural crop). In this paper, however, we even combine the results for different agricultural crops. This approach may be justified by the following two arguments: (1) The parameters *W*, *T* and *R* are expressed as ratios. They are standardized measures that are independent from the absolute numerical level of the specific underlying dataset. (2) We are convinced that the relationships between *W* and *R* or between *W* and *T* reflect a general relationship that is valid for each two-way dataset obtained by testing a set of genotypes in different environments – irrespective of specific experimental conditions like plant material, growing conditions, etc.

The relationships between *W* and each ratio *R* or between W and each ratio *T* will be investigated (1) by the calculation of Spearman's rank correlation r_S between *W* and each of the diverse ratios (3) and (4) and (2) by a simple linear regression between *W* and each of the ratios.

Results

The estimates (1) of the different variance components and (2) of $\bar{\rho}$ and *W* for the 27 datasets from Table 1 are presented in Table 2. In this paper we are not concerned with these variance components 'per se'. Therefore, no detailed discussion of their numerical magnitude and their interrelations shall be given. Only some simple conclusions are mentioned:

1) The variance component for 'environments' is of predominant importance – with extremely increased numerical values compared to all other variance components (for each crop in each year).

2) The variance component for genotype × environment interactions is lower than the variance component for experimental error

$$\sigma_e^2 > \sigma_o^2 > \sigma_{ge}^2 \tag{9}$$

(exception: faba bean 1985).

3) The variance component for genotypes is lower than the variance component for experimental error

$$\sigma_e^2 > \sigma_o^2 > \sigma_g^2 \tag{10}$$

(exceptions: faba bean 1985; fodder beet 1985, 1987 and 1988; sugar beet 1985).

4) The relationship between the numerical magnitudes of σ_g^2 and σ_{ge}^2 is not unique. σ_g^2 may be lower or larger than σ_{ge}^2, but in most cases we have: $\sigma_g^2 > \sigma_{ge}^2$.

5) The inequality

$$\sigma_e^2 > \sigma_o^2 > \sigma_g^2 > \sigma_{ge}^2 \tag{11}$$

is valid for 16 of the 27 datasets from Table 2.

Table 2. Estimates of the variance components and of $\bar{\rho}$ and W for the five agricultural crops in the different years

Crop	Year	$\hat{\sigma}_g^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_{ge}^2$	$\hat{\sigma}_o^2$	$\hat{\sigma}_v^2$	$\hat{\bar{\rho}}$	$\hat{W}$
Faba bean	1985	20.27	118.66	26.63	18.02	31.13	0.37	0.44
	1986	16.23	229.01	13.76	39.65	23.68	0.38	0.45
	1987	19.12	73.06	15.12	22.94	20.85	0.40	0.47
	1988	13.67	189.37	16.39	19.21	21.20	0.33	0.40
	1989	11.20	86.33	13.86	18.68	18.53	0.40	0.46
Fodder beet	1985	102.80	502.44	20.54	51.28	33.36	0.75	0.78
	1986	41.59	225.06	9.17	43.04	19.93	0.68	0.73
	1987	101.20	233.12	11.23	31.48	19.10	0.84	0.86
	1988	88.39	168.03	16.12	32.92	24.34	0.78	0.81
	1989	74.45	624.68	22.36	112.09	50.38	0.59	0.64
Sugar beet	1985	13.80	76.03	1.23	12.57	4.37	0.76	0.79
	1986	10.19	84.27	0.29	21.87	5.76	0.65	0.69
	1987	11.85	30.63	0.24	13.33	3.58	0.74	0.77
	1988	11.49	54.86	1.19	14.92	4.92	0.64	0.68
	1989	9.37	92.57	0.00	31.81	7.95	0.60	0.63
Oats	1985	3.45	127.14	1.92	23.46	7.79	0.29	0.35
	1986	9.56	101.40	5.14	13.22	8.45	0.29	0.35
	1987	3.14	217.07	5.52	8.13	7.55	0.23	0.30
	1988	3.56	84.50	3.96	17.53	8.34	0.29	0.33
	1989a	6.95	129.48	4.39	9.58	6.78	0.53	0.57
	1989b	9.16	243.10	2.75	16.45	6.86	0.55	0.60
	1989c	9.41	85.44	4.26	16.76	8.45	0.50	0.53
Winter rape	1985	12.34	32.15	9.78	16.09	13.80	0.39	0.47
	1986	9.14	41.51	4.62	15.60	8.52	0.50	0.54
	1987	11.60	63.00	5.50	12.59	8.65	0.51	0.56
	1988	5.91	18.84	7.10	9.29	9.42	0.34	0.41
	1989	4.71	42.36	5.75	15.33	9.59	0.34	0.40

The $\bar{\rho}$-values vary from 0.23 up to 0.84, while Kendall's W takes numerical values between 0.30 and 0.86. W is significant in all datasets (at an error probability of 0.1%).

All possible ratios of R and T have been investigated (210 R's and 42 T's). The rank correlations r_S between W and each of these ratios and, additionally, the parameters of a simple linear regression (regression coefficient, intercept, coefficient of determination) are presented in Table 3 for those ratios R and T with larger r_S and larger coefficients of determination. (The results for all other ratios can be obtained from the authors on request.)

All numerical values of Table 3 are significantly different from zero (at an error probability of 0.1%), with only two exceptions: The intercepts for nos. 5 and 16 are non-significant. The largest coefficients of determination are obtained for no. 2 and for no. 5 – with a numerical value of 0.91 in both cases. The rank correlations are – 0.93 for no. 2 and 0.93 for no. 5. No larger rank correlation was observed among the 252 different ratios. Both ratios no. 2 and no. 5 are, of course, not independent from each other: ratio no. 2 + ratio no. 5 = 1. We, therefore, concentrate on only one of them, i.e. no. 5.

The regression equation

W = regression coefficient × ratio + intercept

for no. 5 is:

$$W = \underbrace{0.96}_{\cong 1} \frac{\sigma_g^2}{\sigma_g^2 + \sigma_v^2} + \underbrace{0.04}_{\cong 0} \tag{12}$$

This regression equation leads to the approximation

$$W \cong \frac{\sigma_g^2}{\sigma_g^2 + \sigma_v^2} \tag{13}$$

This expression (13) gives a quite clear and even simple relationship between the non-parametric coefficient of concordance W and the parametric ratio $\sigma_g^2/(\sigma_g^2 + \sigma_v^2)$. This result answers Comstock's question and comment given above. Furthermore, it provides a clear and meaningful interpretation of W, since (13) can be rewritten as:

$$W \cong \frac{1}{1 + \dfrac{\sigma_v^2}{\sigma_g^2}} \tag{14}$$

W depends on only one parameter: the ratio σ_v^2/σ_g^2 of both variance components (see also Discussion).

Table 3. Rank correlation, regression coefficient, intercept and coefficient of determination for the relation between W and different variance ratios R and T

Number	Ratios	Rank correlation r_S	Linear regression		
			Regression coefficient	Intercept	Coefficient of determination
	Ratios T				
1	σ_v^2/σ_g^2	−0.93	−0.22	0.79	0.81
2	$\sigma_v^2/\sigma_g^2+\sigma_v^2$	−0.93	−0.96	1.01	0.91
3	$\sigma_e^2+\sigma_v^2/\sigma_g^2+\sigma_e^2$	−0.87	−1.47	1.99	0.74
4	σ_g^2/σ_v^2	0.93	0.12	0.37	0.80
5	$\sigma_g^2/\sigma_g^2+\sigma_v^2$	0.93	0.96	0.04	0.91
6	$\sigma_g^2+\sigma_v^2/\sigma_v^2$	0.93	0.12	0.25	0.80
7	$\sigma_g^2+\sigma_v^2/\sigma_g^2$	−0.93	−0.22	1.01	0.81
8	$\sigma_g^2+\sigma_e^2/\sigma_e^2+\sigma_v^2$	0.87	1.22	−0.70	0.71
	Ratios R				
9	σ_{ge}^2/σ_g^2	−0.84	−0.28	0.72	0.69
10	$\sigma_{ge}^2/\sigma_g^2+\sigma_{ge}^2$	−0.84	−0.73	0.79	0.74
11	$\sigma_{ge}^2+\sigma_o^2/\sigma_g^2+\sigma_o^2$	−0.91	−0.64	1.08	0.85
12	$\sigma_{ge}^2+\sigma_o^2/\sigma_g^2+\sigma_{ge}^2+\sigma_o^2$	−0.81	−0.99	1.21	0.73
13	$\sigma_e^2+\sigma_{ge}^2/\sigma_g^2+\sigma_e^2$	−0.87	−1.54	1.99	0.75
14	$\sigma_e^2+\sigma_{ge}^2+\sigma_o^2/\sigma_g^2+\sigma_e^2+\sigma_o^2$	−0.86	−1.82	2.27	0.77
15	$\sigma_g^2/\sigma_{ge}^2+\sigma_o^2$	0.81	0.25	0.40	0.61
16	$\sigma_g^2/\sigma_g^2+\sigma_{ge}^2$	0.84	0.73	0.06	0.74
17	$\sigma_g^2/\sigma_g^2+\sigma_{ge}^2+\sigma_o^2$	0.81	0.99	0.21	0.73
18	$\sigma_g^2+\sigma_o^2/\sigma_{ge}^2+\sigma_o^2$	0.91	0.27	0.19	0.76
19	$\sigma_g^2+\sigma_e^2/\sigma_e^2+\sigma_{ge}^2$	0.87	1.13	−0.68	0.71
20	$\sigma_g^2+\sigma_e^2+\sigma_o^2/\sigma_e^2+\sigma_{ge}^2+\sigma_o^2$	0.86	1.40	−0.95	0.73

Discussion

The main result (14) can be easily explained by considering Fig. 1a and b for two genotypes and two environments: In both figures the effects $v_{ij}(i=1,2;\ j=1,2)$ are the same, but the differences between the two genotypic effects are different (large in Fig. 1a, small in Fig. 1b).

In Fig. 1a the interaction does not cause a rank change because it is small in relation to the difference between the genotypic effects. More precisely, the rank-interaction in Fig. 1b (at environment 1) occurs because the absolute value of $(v_{11}-v_{21})$ is larger than that of (g_2-g_1):

$$
\begin{aligned}
y_{21}-y_{11} &= (\mu+g_2+e_1+v_{21})-(\mu+g_1+e_1+v_{11}) \\
&= (g_2-g_1)+(v_{21}-v_{11}) > 0 \text{ in Fig. 1a} \\
&\qquad\qquad\qquad\qquad\quad > 0 \text{ in Fig. 1b} \qquad (15)
\end{aligned}
$$

and this leads to

$$
\left.\begin{aligned}
(g_2-g_1) &> (v_{11}-v_{21}) \quad \text{in Fig. 1a} \\
(g_2-g_1) &< (v_{11}-v_{21}) \quad \text{in Fig. 1b}
\end{aligned}\right\} \qquad (16)
$$

In terms of variances, σ_v^2 is the same in both figures, while σ_g^2 is larger in Fig. 1a than in Fig. 1b.

These considerations make plausible that rank-interaction is more likely to occur the smaller σ_g^2 is relative to σ_v^2, or the larger σ_v^2 is relative to σ_g^2. The similarity respective dissimilarity of the rank orders of the genotypes in the different environments will therefore be determined by the ratio σ_v^2/σ_g^2. This conclusion is in perfect accordance with the approximation of Eq. 14.

Therefore, a high rank correlation of W with σ_v^2/σ_g^2 (no. 1 from Table 3) is expected.

Note that $\sigma_v^2=\sigma_{ge}^2+\sigma_o^2/L$. Thus, high rank correlations are also expected for variance ratios involving one of the two components of σ_v^2, namely $\sigma_o^2/L\sigma_g^2$ and σ_{ge}^2/σ_g^2 (see: no. 9 in Table 3).

If the ratio of two variance components is substituted by the relative share of one component in the total of the two, the rank correlation remains unaffected while the coefficient of determination improves (see: nos. 2, 5, 10 from Table 3). Many other ratios from Table 3 are of particular interest: for example no. 11: $\sigma_{ge}^2+\sigma_o^2/\sigma_g^2+\sigma_o^2$ with a rank correlation of $r_S=-0.91$ and a coefficient of determination of 0.85.

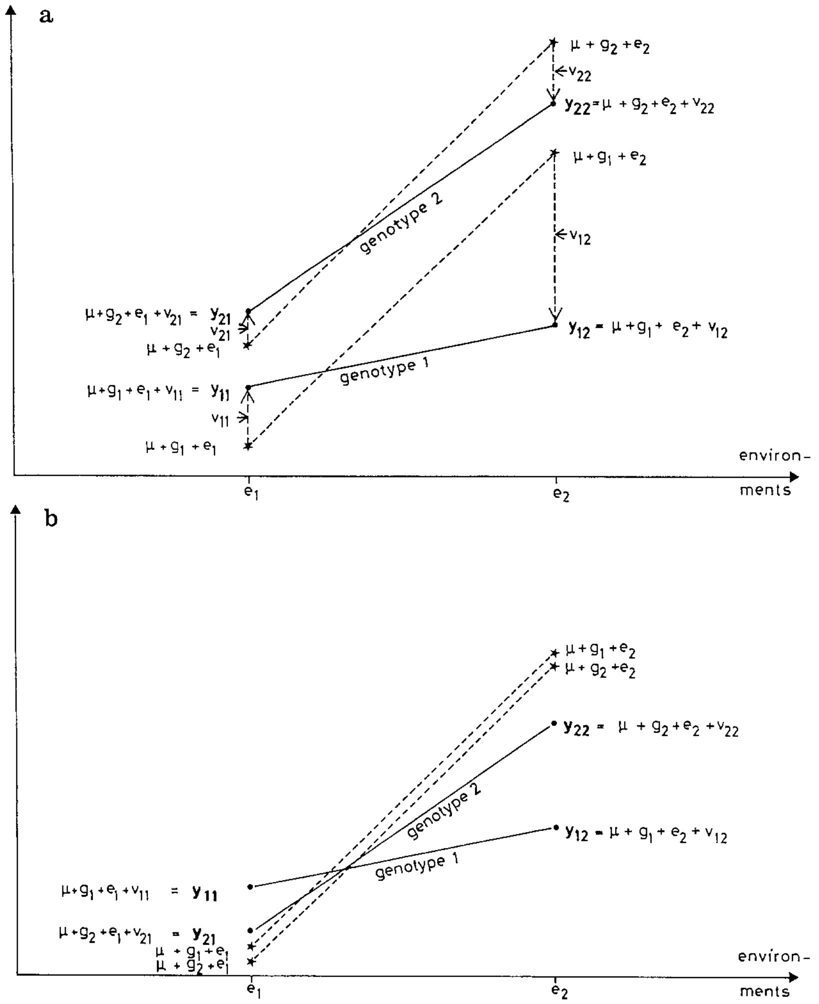

Fig. 1. a Schematic representation for two genotypes and two environments (without rank change). **b** Schematic representation for two genotypes and two environments (with rank change)

The linear regression

$$W = (-0.64)\frac{\sigma_{ge}^2 + \sigma_o^2}{\sigma_g^2 + \sigma_o^2} + 1.08 \qquad (17)$$

provides the approximation

$$\frac{0.36 - W}{0.64} \cong \frac{\sigma_{ge}^2 - \sigma_g^2}{\sigma_g^2 + \sigma_o^2} \qquad (18)$$

and it can be concluded:

$$\sigma_{ge}^2 \cong \sigma_g^2 \Leftrightarrow W \cong 0.36 \qquad (19)$$

(where the sign $\Leftrightarrow$ means "if and only if").

The empirical results from Table 2 are in approximate agreement with these findings: For example oats data 1988 with $\sigma_g^2 = 3.56$, $\sigma_{ge}^2 = 3.96$ and $W = 0.33$ (Table 2).

Albeit interesting, in this paper no further ratios will be discussed. The approximate functional relationship between W and the ratio of the two variance components in Eq. 14 provides an interesting further interpretation of Kendall's W: by Eq. 14 one obtains:

$$\frac{1 - W}{W} = \frac{\text{measure of discordance}}{\text{measure of concordance}} \cong \frac{\sigma_v^2}{\sigma_g^2} \qquad (20)$$

This means: the discordance $(1 - W)$ expressed in units of the concordance (W) equals the ratio of the two variance components σ_v^2 and σ_g^2.

For $\sigma_v^2 = 0$ it follows that $W = 1$ (perfect concordance). $\sigma_v^2 = 0$ is equivalent to $\sigma_{ge}^2 = \sigma_o^2 = 0$. For zero variance components for interaction and for error one obtains identical rank orders of the genotypes in the different environments ($W = 1$), i.e. maximum association. Relationship 14, therefore, is in perfect agreement with the expectations.

The linear regressions of Table 3 are based on the 27 experimental values of W, R and T. The empirical W's are not dispersed over the total interval from 0 up to 1; they are in a restricted interval from 0.30 up to 0.86. There may be some difficulties and/or uncertainties if one considers the calculated linear regressions as a valid functional relationship for the complete interval from 0 to 1.

Further improvements may be achieved by generalizations of the expressions for R and for T in Eqs. 3 and 4. In our previous investigations the coefficients c_i, $i = 1, 2, \ldots, 8$ and k_i, $i = 1, 2, \ldots, 6$ were only assigned the numerical values 0 or 1. If we allow arbitrary values for c_i and for k_i that may be theoretically determined or estimated from the data by some criterion of optimality, improvements in the previous results may be possible. Such generalizations, however, will not be discussed in this paper.

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