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Combined selection in early generation testing of self-pollinated plants

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ABSTRACT

Seven selection indexes based on the phenotypic value of the individual and the mean performance of its family were assessed for their application in breeding of self-pollinated plants. There is no clear superiority from one index to another although some show one or more negative aspects, such as favoring the selection of a top performing plant from an inferior family in detriment of an excellent plant from a superior family.

INTRODUCTION

Combined selection is a technique used to identify individuals with better additive genetic value in a population under selection, using information from the individual itself and its relatives. Such procedure should increase the efficiency of the selection process, maximizing the expected genetic gain. This selection procedure was discussed first by Lush (1947a,b) and can be used successfully in both animal and plant breeding (Bueno Filho, 1992 and Morais, 1992). Its main limitation may be a marked reduction in the genetic variability in the population, with one or few selection cycles, because of the great decrease in its effective size resulting from the selection of many related individuals (Morais, 1992). However, this can be overcome by defining a maximum number of individuals to be selected in the same family (Morais, 1992).

Early generation testing in the breeding of self-pollinated plants was proposed to make selection based on quantitative traits, which generally have reduced heritability compared to qualitatively traits more efficient in the initial segregant generations (Fehr, 1987). The experimental assessment of the segregant families will allow identification of those with a superior genotypic value for one or more polygenic traits, such as yield. This helps to assure the selection in the following generations of one or more lines with performance superior to that of the initial parents.

The use of combined selection in early generation testing should allow the identification of plants with desirable additive genetic value, which are selected as parents of the families to be analyzed in the following generation. This work will discuss the use of combined selection for assessment of F_3 families using various indexes, estimators of individual additive genetic value, which consider the phenotypic value of the individual and the mean phenotypic value of the individual's family.

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THEORETICAL CONSIDERATIONS

Analysis of variance

An experiment will be considered with f F_3 families, obtained from selfed F_2 plants, derived from the cross of two parental lines, the two parental lines, referred as P_1 and P_2, and the F_1 generation, in b complete blocks with p plants in each plot. The F_2 generation is the base population, which is in Hardy-Weinberg equilibrium, non-inbred and made up of unrelated individuals (Wricke and Weber, 1986). Table I shows the expected mean squares of the analysis of variance.

Components of the genotypic variance of F3 generation

The variance component σ_f^2 is the variance of the genotypic means of the F_3 families. The variance component σ_w^2 is the mean variance of the phenotypic values of the plants within the same F_3 family. Thus, if the genotypic value is independent of the environmental effect, $\sigma_w^2 = \sigma_{gw}^2 + \sigma_{ew}^2$. The variance component σ_{gw}^2 is the mean variance of the genotypic values of the plants in the same F_3 family and σ_{ew}^2 is the variance of the environmental effects.

Considering absence of epistasis and that the genes in the polygenic system under study assort independently, then (Wricke and Weber, 1986; pp. 72-73):

$$\sigma_f^2 = \sigma_A^2 + \frac{1}{4}\sigma_D^2$$

$$\sigma_w^2 = \frac{1}{2}\sigma_A^2 + \frac{1}{2}\sigma_D^2 + \sigma_{ew}^2 ,$$

where σ_A^2 and σ_D^2 are the additive and due to dominance genetic variances in the F_2 generation, respectively.

Selection indexes

The following indexes will be analyzed, all considering the information from the individual and its family:

$$I_1 = \hat{b}_1 (Y_{ilk} - \overline{Y}_{il.}) + \hat{b}_2 (\overline{Y}_{il.} - \overline{Y}_{.l.})$$

$$I_2 = \hat{b}_1 (Y_{ilk} - \overline{Y}_{il.}) + \hat{b}_2 (\overline{Y}_{i..} - \overline{Y}_{...})$$

$$I_3 = \hat{b}_1 (Y_{ilk} - \overline{Y}_{.l.}) + \hat{b}_2 (\overline{Y}_{il.} - \overline{Y}_{.l.})$$

$$I_4 = \hat{b}_1 (Y_{ilk} - \overline{Y}_{.l.}) + \hat{b}_2 (\overline{Y}_{i..} - \overline{Y}_{...})$$

$$I_5 = \hat{b}_1 (Y_{ilk} - \overline{Y}_{i..}) + \hat{b}_2 (\overline{Y}_{il.} - \overline{Y}_{.l.})$$

$$I_6 = \hat{b}_1 (Y_{ilk} - \overline{Y}_{i..}) + \hat{b}_2 (\overline{Y}_{i..} - \overline{Y}_{...})$$

$$I_7 = \hat{b}_1 Y_{ilk} + \hat{b}_2 \overline{Y}_{i..}$$

where Y_{ilk} is the observation of the dependent variable taken on the kth plant of the ith family, in the lth block.

Table I - Expected mean squares of the analysis of variance of observations of plants.

Source of variation	Degrees of freedom	E(Mean square)
Blocks (B)	b - 1	-
Treatments (T)	(f + 2)	-
Homogeneous populations (P_1, P_2 and F_1)(P)	2	-
Families (F)	f - 1	$\sigma_w^2 + p\sigma_e^2 + bp\sigma_f^2$
Between groups	1	-
Error (B x T)	((f + 2)(b - 1))	-
Error 1 (B x P)	2(b - 1)	$\sigma_{ew}^2 + p\sigma_e^2$
Error 2 (B x F)	(f - 1)(b - 1)	$\sigma_w^2 + p\sigma_e^2$
Error 3	b - 1	-
Between plants/homogeneous populations block	3b(p - 1)	σ_{ew}^2
Between plants/families block	fb(p - 1)	σ_w^2

All the following results were obtained considering only the F_3 families.

Estimation of the coefficients

Let A_{ilk} be the additive genetic value of the ilkth plant and $I_{ilk} = b_1 y_1 + b_2 y_2$ be the additive genetic value of the same plant, predicted by the index, where y_1 and y_2 are the individual and family merits, respectively. The index coefficients may be estimated to maximize the correlation between the additive genetic value (A) and the index (I) (Hazel, 1943) or to minimize the variance of the difference between the additive genetic value and the index (Wricke and Weber, 1986). The values b_1 and b_2 that minimize the function z = V(A - I) are:

$$\hat{b}_1 = \frac{v_2 c_2 - c_1 c_3}{v_1 v_2 - c_1^2}$$

$$\hat{b}_2 = \frac{v_1 c_3 - c_1 c_2}{v_1 v_2 - c_1^2}$$

where

$$v_1 = V(y_1)$$

$$v_2 = V(y_2)$$

$$c_1 = Cov(y_1, y_2)$$

$$c_2 = Cov(A, y_1)$$

$$c_3 = Cov(A, y_2)$$

RESULTS AND DISCUSSION

Analysis of the index I_1

This index establishes stratification for individual selection and for the definition of the family merit. However, when defining merit of the individual as the difference among its phenotypic value and the average phenotypic value of its family in the block, the following can occur: a plant with exceptional phenotypic value, belonging to a family also with excellent mean, can be screened out because its merit is near zero. In this situation the index I_1 should favor selection of superior plants in families of inferior performance. This can happen more frequently in cases where the weight of the individual merit is greater than that of the family merit. The use of this index, therefore, should result in greater variability in the derived generations compared to those indexes which determine the selection of many plants in few families of outstanding performance.

The following relationships hold for the index I_1:

$$\hat{b}_1 = \left(\frac{\frac{3}{2}\sigma_A^2}{\sigma_w^2} \right)(1 - r_1)$$

$$\hat{b}_2 = \left(\frac{\frac{3}{2}\sigma_A^2}{\sigma_f^2 + \sigma_e^2 + \frac{\sigma_w^2}{p}} \right) \cdot \frac{1}{p}\left[1 + (p-1)r_1\right]$$

where:

$$r_1 = \frac{\sigma_A^2}{\frac{3}{2}\sigma_A^2} = \frac{2}{3}$$

is the correlation between additive genetic values of plants in the same F_3 family.

For details about the derivation of $\hat{b}_1$, $\hat{b}_2$ and r_1, see Appendix.

Once the base population is defined, the values of $\hat{b}_1$ and $\hat{b}_2$ will depend essentially on the experimental conditions, that is, on the magnitudes of the residual variance (σ_e^2), estimated by (error 2 mean square - between plants/families block mean square)/p, and the environmental variance between plants (σ_{ew}^2), and on the number of plants in each plot (p). Other indexes shown will also be affected by the number of families (f) and (or) by the number of replications (b) and/or by the value of the variance component due to block effect, estimated by (blocks mean square - error mean square)/fp.

For an assessment of the variation of the weights of the individual ($\hat{b}_1$) and family ($\hat{b}_2$) merits under different experimental conditions, it was considered that 100 F_3 families were evaluated in an experiment with four replications and 10 plants per plot. The following assumptions were made: σ_D^2 corresponds to 1/10 of σ_A^2 (average degree of dominance of, approximately, 0.45, indicating partial dominance); σ_e^2 and σ_{ew}^2 vary between zero and a value 10 times greater than σ_A^2; and σ_b^2 is either equal to zero or ten times greater than σ_A^2.

Figure 1 shows the graphic which describes the relationship between the weights of the family and individual merits ($\hat{b}_2/\hat{b}_1$), in relation to the index I_1. When the residual and environmental variances are close to zero, the coefficients $\hat{b}_1$ and $\hat{b}_2$ have approximately the same magnitude with slight superiority of the family merit weight.

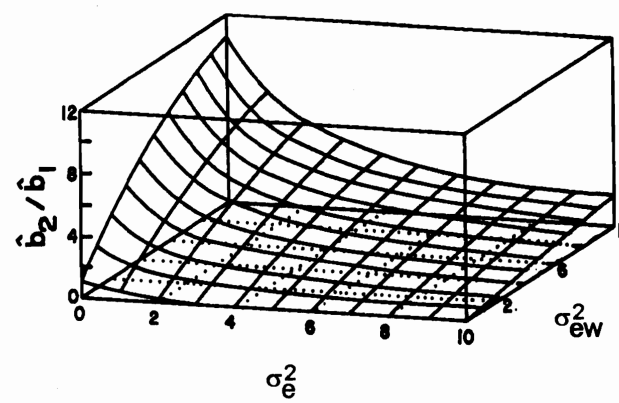

Figure 1 - Relationship between the weights of the family merit ($\hat{b}_2$) and of the individual merit ($\hat{b}_1$) under different experimental conditions, for the index I_1.

When the residual variance has a much lower value than the environmental variance within family, the family merit weight becomes greater than the individual merit weight. On the other hand, if σ_e^2 is much greater than σ_{ew}^2, the weight of the individual merit will be larger than the weight of the family merit.

When the two variances are of large magnitude compared to the additive genetic variance, the family merit weight tends to be greater than the coefficient of the individual value. These results indicate that the index I_1 correctly weights the merits of the individual and its family.

Analysis of the index I_2

This index establishes stratification for individual selection, and has the same characteristics of the index I_1. Thus, its use can favor selection of superior plants in inferior families in detriment to good plants in excellent families, when the weight of the individual information is greater than the coefficient of the family merit.

The following relationships hold for the index I_2:

$$\hat{b}_I = \left(\frac{\frac{3}{2}\sigma_A^2}{\sigma_w^2} \right) (1 - r_I)$$

$$\hat{b}_2 = \left(\frac{\frac{3}{2}\sigma_A^2}{\sigma_f^2 + \frac{\sigma_e^2}{b} + \frac{\sigma_w^2}{bp}} \right) \cdot \frac{1}{bp} \left[1 + (bp-1) r_I \right]$$

Figure 2 shows the relationship between the family and individual merit weights in different experimental conditions. The behavior is similar to that described for the index I_1: the individual merit weight should only be greater than the coefficient of the family merit when the environmental variance within family is near to zero, regardless of whether the residual variance is small or large. For this index, family information may weight more heavily than in index I_1. As in the former index, the I_2 weights adequately the information of the individual and its family.

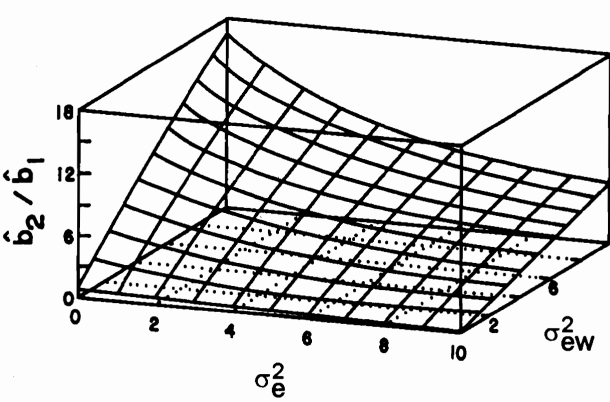

Figure 2 - Relationship between the weights of the family merit ($\hat{b}_2$) and of the individual merit ($\hat{b}_I$) under different experimental conditions, for the index I_2.

Analysis of the index I_3

This index establishes another type of stratification for individual selection: the block rather than the family in the block. There is also stratification in the characterization of the family merit. When the individual merit is defined as the difference between its performance and the mean of the F_3 plants under the same environmental condition (same block) the inconvenience of the indexes I_1 and I_2 are overcome. With the index I_3 the plants with superior performance in the good families will have individual merit different from zero.

Compared to the indexes I_1 and I_2, the index I_3 should lead to the selection of good plants in families with desirable mean or superior performance, instead of exceptional plants in inferior families.

The following relationships hold for the index I_3:

$$\hat{b}_I = \left(\frac{\frac{3}{2}\sigma_A^2}{\sigma_w^2} \right) (1 - r_I)$$

$$\hat{b}_2 = \left(\frac{\frac{3}{2}\sigma_A^2}{\sigma_f^2 + \sigma_e^2 + \frac{\sigma_w^2}{p}} \right) \cdot \frac{1}{p} \left[1 + (p-1) r_I \right] - \hat{b}_I$$

Under different experimental conditions, the relationship $\hat{b}_2/\hat{b}_I$ has a behavior similar to that described for the index I_1, as shown in Figure 3. However, the weight of the family merit may be negative when the environmental variance among plants in the same family is near zero or very small compared to the additive genetic variance. When $\hat{b}_2$ is negative, the index I_3 may favor selection of good plants in families with inferior performance (negative family merit) in detriment to good plants in families with desirable performance (positive family merit).

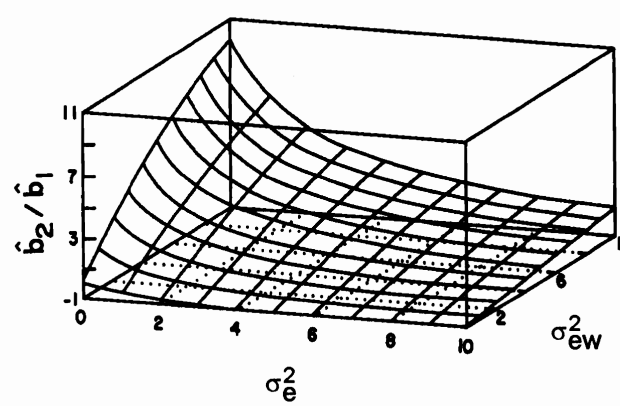

Figure 3 - Relationship between the weights of the family merit ($\hat{b}_2$) and of the individual merit ($\hat{b}_I$) under different experimental conditions, for the index I_3.

When the residual variance is close to zero or is of magnitude much smaller than σ^2_{ew}, the weight of the family merit should be greater than the weight of the individual merit. On the other hand, in the cases where the residual variance is much superior to the additive genetic variance, the weight of the individual information will be greater than the family merit coefficient, regardless of the magnitude of σ^2_{ew}.

Disregarding the cases where $\hat{b}_2$ is negative, the index I_3 also attributes appropriate weights to the information of the individual and its family.

Analysis of the index I_4

Like index I_3, this also stratifies at the block level for individual selection, although it does not establish stratification in the definition of the family merit. It does not, therefore, have the limitations of the indexes I_1 and I_2.

The following relationships hold for the index I_4:

$$\hat{b}_I = \left[\frac{\frac{3}{2}\sigma^2_A}{\frac{p(f-1)(b-1)}{b(fp-1)-(f-1)}\sigma^2_e + \sigma^2_w} \right](1-r_I)$$

$$\hat{b}_2 = \left(\frac{\frac{3}{2}\sigma^2_A}{\sigma^2_f + \frac{\sigma^2_e}{b} + \frac{\sigma^2_w}{bp}} \right) \cdot \frac{1}{bp}\left[1+(bp-1)r_I\right] - \hat{b}_I$$

Figure 4 shows the value of the relationship $\hat{b}_2/\hat{b}_I$ under different experimental conditions. It shows that the index I_4 attributes, almost always, a greater weight to the family information even when σ^2_e is large and σ^2_{ew} is near to zero. Only when the residual variance and the environmental variance within the same family are close to zero is the weight of the individual information greater than the weight of the family merit.

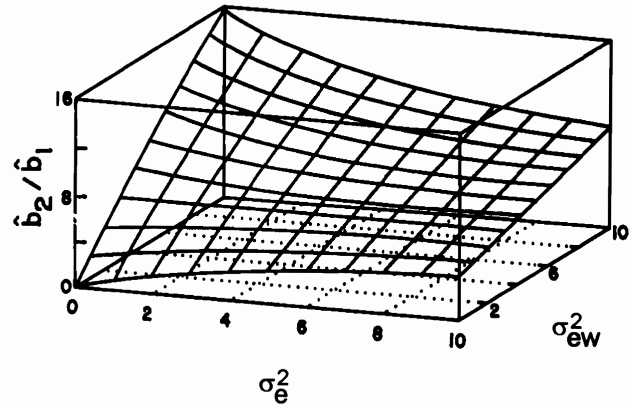

Figure 4 - Relationship between the weights of the family merit ($\hat{b}_2$) and of the individual merit ($\hat{b}_I$) under different experimental conditions, for the index I_4.

Although it is not subject to the inconveniences of the previous indexes, this index shows a contradictory aspect, since if the environmental variance among plants in the same family is small, compared to the value of σ^2_A, and the residual variance is large, it is expected that $\hat{b}_2 < \hat{b}_I$. However, this should not occur when the index I_4 is used since, in general, it gives greater weight to family information.

Analysis of the index I_5

A characteristic of this index is to disregard any stratification in individual selection, although it considers stratification at the level of the block in the definition of the family merit. Individual merit is the difference between the phenotypic value of the plant and the average of its family in the experiment. Therefore, plants with superior performance in excellent families may have individual merit close to zero.

The following relationships hold for the index I_5:

$$\hat{b}_I = \frac{\left(\frac{bp-1}{bp}\right)\left(\sigma^2_f+\sigma^2_e+\frac{\sigma^2_w}{p}\right)\left(\frac{3}{2}\sigma^2_A\right)(1-r_I) - \left[\frac{(f-1)(b-1)}{fb}\right]\left(\sigma^2_e+\frac{\sigma^2_w}{p}\right)\left(\frac{\frac{3}{2}\sigma^2_A}{p}\right)\left[1+(p-1)r_I\right]}{\left[\left(\frac{b-1}{b}\right)(\sigma^2_b+\sigma^2_e)+\left(\frac{bp-1}{bp}\right)\sigma^2_w\right]\left(\sigma^2_f+\sigma^2_e+\frac{\sigma^2_w}{p}\right) - \left(\frac{f-1}{f}\right)\left(\frac{b-1}{b}\right)^2\left(\sigma^2_e+\frac{\sigma^2_w}{p}\right)^2}$$

$$\hat{b}_2 = \frac{\left[\left(\frac{b-1}{b}\right)(\sigma^2_b+\sigma^2_e)+\left(\frac{bp-1}{bp}\right)\sigma^2_w\right]\left(\frac{\frac{3}{2}\sigma^2_A}{p}\right)\left[1+(p-1)r_I\right] - \left(\frac{(bp-1)(b-1)}{b^2p}\right)\left(\sigma^2_e+\frac{\sigma^2_w}{p}\right)\left(\frac{3}{2}\sigma^2_A\right)(1-r_I)}{\left[\left(\frac{b-1}{b}\right)(\sigma^2_b+\sigma^2_e)+\left(\frac{bp-1}{bp}\right)\sigma^2_w\right]\left(\sigma^2_f+\sigma^2_e+\frac{\sigma^2_w}{p}\right) - \left(\frac{f-1}{f}\right)\left(\frac{b-1}{b}\right)^2\left(\sigma^2_e+\frac{\sigma^2_w}{p}\right)^2}$$

Table II - Some values for the relationship between the family merit ($\hat{b}_2$) and the individual merit ($\hat{b}_1$) weights under different experimental conditions, for the index I_5.

σ^2_e	σ^2_{ew}			
	0	$9.5\sigma^2_A$	$9.6\sigma^2_A$	$10\sigma^2_A$
0	1.12[a]	48.14	49.32	54.39
	17.41[b]	86.35	88.08	95.51
$0.7\sigma^2_A$	3.01	7434.00	-6667.96	-809.40
	31.24	13164.19	-11758.50	-1404.54
$10\sigma^2_A$	-1.95	-5.20	-5.23	-5.35
	-5.18	-8.10	-8.13	-8.23

[a]When $\sigma^2_b = 0$.

[b]When $\sigma^2_b = 10\sigma^2_A$.

Therefore, the two coefficients of the index are a function of σ^2_b. Table II shows values of the relationship $\hat{b}_2/\hat{b}_1$ in some particular cases.

When the residual and environmental variances are near to zero or when σ^2_e is close to zero and σ^2_{ew} is much larger to the additive genetic variance, the weight of the family merit is greater than the coefficient of the individual merit, regardless of the value of σ^2_b, mainly in the second case (Table II). When residual variance is large, comparatively to σ^2_A, $\hat{b}_2$ is negative and its absolute value is greater than $\hat{b}_1$. This superiority is proportional to σ^2_{ew} and σ^2_b (Table II). Depending on the value of the environmental variance within family, when σ^2_e is in the interval $[(0.6)\ \sigma^2_A, (1.7)\ \sigma^2_A]$, the value of $\hat{b}_2$ can be thousands of times greater than $\hat{b}_1$ or negative and thousands of times greater than $\hat{b}_1$. The absolute value of the relationship $\hat{b}_2/\hat{b}_1$ is proportional to the variance component due to block effect (Table II).

Therefore, when $\hat{b}_2/\hat{b}_1$ is much superior to one, this index should lead to the selection of all plants of the best families. When the coefficient of the family merit is negative and of magnitude much greater than the weight of the individual merit, the index I_5 will lead to the selection of all plants of the families with inferior performance (negative family merit or reduced family merit).

Analysis of the index I6

This index does not establish stratification for individual selection nor for the definition of the family merit. Also, with the use of the index I_6, plants with good performance in families with desirable performance may have individual merit close to zero.

The following relationships hold for the index I_6:

$$\hat{b}_1 = \left[\frac{\frac{3}{2}\sigma^2_A}{\left(\frac{bp-p}{bp-1}\right)\left(\sigma^2_b+\sigma^2_e\right)+\sigma^2_w}\right](1-r_1)$$

$$\hat{b}_2 = \left(\frac{\frac{3}{2}\sigma^2_A}{\sigma^2_f+\frac{\sigma^2_e}{b}+\frac{\sigma^2_w}{bp}}\right)\cdot\frac{1}{bp}\left[1+(bp-1)r_1\right]$$

Thus, only the weight of the individual merit depends on σ^2_b. The graphs in Figure 5 show how the relationship $\hat{b}_2/\hat{b}_1$ varies under different experimental conditions, in two distinct situation: $\sigma^2_b = 0$ (Figure 5a) and $\sigma^2_b = 10\sigma^2_A$ (Figure 5b).

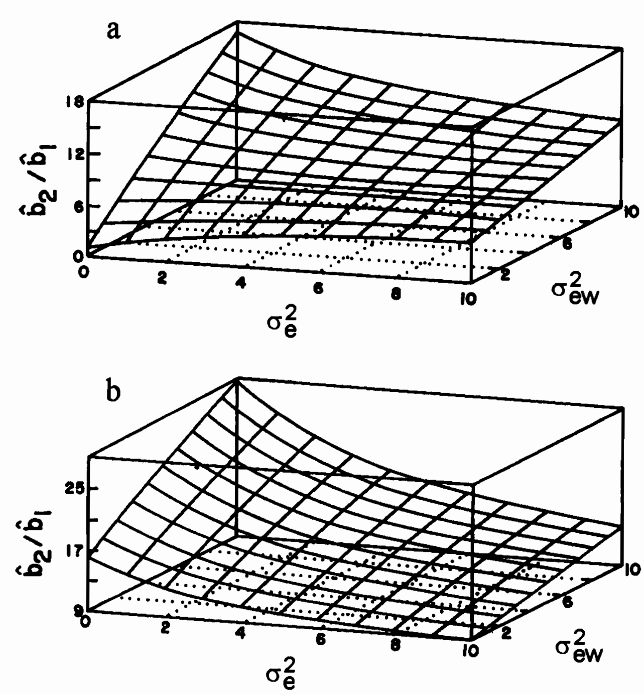

Figure 5 - Relationship between the weights of the family merit ($\hat{b}_2$) and of the individual merit ($\hat{b}_1$) under different experimental conditions, considering $\sigma^2_b = 0$ (a) and $\sigma^2_b = 10\sigma^2_A$ (b), for the index I_6

When the variance component σ^2_b is equal to zero, the index I_6 gives a family merit weight always superior to the coefficient of the individual merit, regardless of the values of σ^2_e and σ^2_{ew}. Therefore, even though the environmental variance among plants in the same family is minimal or close to zero and the residual variance has a magnitude much greater than the additive genetic variance, this index will give greater weight to the family merit. The weights $\hat{b}_2$ and $\hat{b}_I$ will have approximately the same value only when σ^2_e and σ^2_{ew} are close to zero.

If σ^2_b is much larger than the additive genetic variance, the weight of the family merit becomes even greater than the coefficient of the individual merit. Thus, the existence of variation among blocks makes $\hat{b}_2$ much greater than $\hat{b}_I$, regardless of the values of σ^2_e and σ^2_{ew}. This may lead to the selection of many plants from the same family, when it has a desirable performance.

Analysis of the index I_7

Differing from the six previous indexes, I_7 takes the individual and its family performance into account without any stratification for selection. Due to the definition of the individual merit, an exceptional plant belonging to a family with a highly desirable phenotypic value, will always be selected when this index is used.

The following relationships hold for the index I_7:

$$\hat{b}_I = \left[\frac{\frac{3}{2}\sigma^2_A}{\left(\frac{bp-p}{bp-1}\right)\left(\sigma^2_b+\sigma^2_e\right)+\sigma^2_w}\right](1-r_I)$$

$$\hat{b}_2 = \left(\frac{\frac{3}{2}\sigma^2_A}{\sigma^2_f+\frac{\sigma^2_b}{b}+\frac{\sigma^2_e}{b}+\frac{\sigma^2_w}{bp}}\right)\cdot\frac{1}{bp}\left[1+(bp-1)r_I\right]-\hat{b}_I$$

The two weights are function of the σ^2_b component. The graphs in Figure 6 show the variation of the $\hat{b}_2/\hat{b}_I$ values when σ^2_b = 0 (Figure 6a) and for σ^2_b = 10 σ^2_A (Figure 6b), under different experimental conditions.

The results are essentially the same already reported for the index I_6, except that if the variance components σ^2_b, σ^2_e and σ^2_{ew}, are close to zero, the weight of the individual merit will be greater than the weight of the family merit. In other situations the index I_7 will give more weight to the family merit even when the residual variance is much larger than σ^2_A and the environmental variance within family is minimum.

When the component of variance due to block effect is much greater than the additive genetic variance, the coefficient of the family merit will always be greater than the weight of the individual merit. Therefore, in the

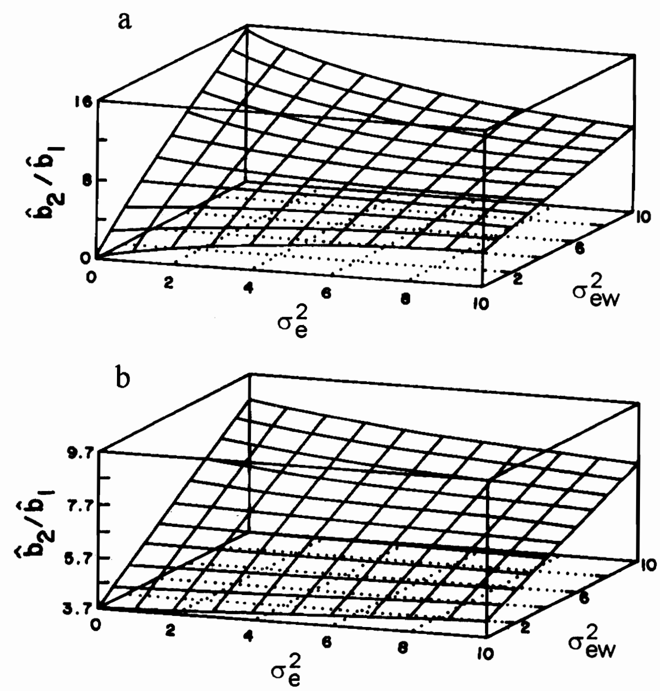

Figure 6 - Relationship between the weights of the family merit ($\hat{b}_2$) and of the individual merit ($\hat{b}_I$) under different experimental conditions, considering σ^2_b = 0 (a) and σ^2_b = 10σ^2_A (b), for the index I_7.

same way that the index I_6, the use of the index I_7 should favor selection of many plants in families with outstanding performance, specially if there is variation among blocks.

CONCLUSION

All of the assessed indexes present one or more limitations or questionable aspects, making it difficult to choose among them. Indexes I_4 and I_7 may be suitable options for any experimental situation, as with the use of one or the other there is no risk of not choosing good plants in superior families in exchange for selecting exceptional plants in families with inferior performance. There is such risk with the use of the indexes I_1, I_2, I_3, I_5 and I_6.

Apparently the index I_4 has two advantages in relation to the index I_7. It establishes stratification at the block level for individual selection and its weights are independent of the variance component due to block effect. The main characteristic of these two indexes, as already seen, is to give greater weight to family information whenever there is residual variance and/or environmental variance among plants in the same family. This may be desirable in early generation testing involving quantitative traits with low heritability.

A probable consequence of the use of these two indexes is the selection of many related plants, from the same family. This may cause a pronounced reduction in the genetic variability in the following generation, as many F_4 families will have as common ancestor the same F_2 plant, or still, the F_4 families will be derived from few F_2 plants. However, this may not be undesirable if the selected F_3 are those with better genetic value in the population. If the selected plants are heterozygous and have desirable additive genetic value, it is possible, through gene recombination, to obtain genotypes with higher performance in the following generations, ensuring the success of the program.

A questionable situation regarding the indexes I_4 and I_7 occurs when the environmental variance within families is close to zero. In this case the individual information is more important or as important as the family information, depending on the size of the residual variance. This expectation is not completely satisfied with the use of any of these indexes because, even when σ^2_{ew} is equal to zero and σ^2_e has a much larger value than the additive genetic variance, the value of $\hat{b}_2$ will always be greater than $\hat{b}_1$. However, as already stated, a greater weighting of the family information may be suitable, whatever the experimental conditions, in the case of selection based on polygenic traits.

APPENDIX

The derivations of the values of $\hat{b}_1$ and $\hat{b}_2$, for all indexes, are tedious and repetitive. For instructive purposes, only the estimators for the index I_1 will be derived. The statistical model for the analysis of variance considering only the families is:

$$Y_{ilk} = \mu + F_i + B_l + e_{il} + (P\,|\,F\,|\,B)_{ilk}$$

where:

– μ is the mean of the F_3 generation;

– F_i is the effect of the ith family ($F_i \sim N(0, \sigma^2_f)$, independents);

– B_l is the effect of the lth block ($B_l \sim N(0, \sigma^2_b)$, independents);

– e_{il} is the error associated to the total of family i in the block l ($e_{il} \sim N(0, \sigma^2_e)$, independents);

– $(P\,|\,F\,|\,B)_{ilk}$ is the effect of the kth plant of the ith family, in the lth block ($(P\,|\,F\,|\,B)_{ilk} \sim N(0, \sigma^2_w)$, independents).

Considering that the random effects are independent variables the following results hold:

$$v_1 = v\left(Y_{ilk} - \mu - F_i - B_l - e_{il} - \frac{1}{p}\sum_k (P\,|\,F\,|\,B)_{ilk}\right) = \left(\frac{p-1}{p}\right)\sigma^2_w$$

$$v_2 = v\left(\bar{Y}_{il.} - \mu - \frac{1}{f}\sum_i F_i - B_l - \frac{1}{f}\sum_i e_{il} - \frac{1}{fp}\sum_i\sum_k (P\,|\,F\,|\,B)_{ilk}\right) = \left(\frac{f-1}{f}\right)\left(\sigma^2_f + \sigma^2_e + \frac{1}{p}\sigma^2_w\right)$$

$$c_1 = cov(Y_{ilk} - \bar{Y}_{il.}, \bar{Y}_{il.} - \bar{Y}_{.l.}) = 0$$

The demonstration of the values of c_2 and c_3 is more intuitive and requires additional considerations. It is important to note that A_{ilk} is the additive genetic value of an F_3 plant. Then $v(A_{ilk}) = \frac{3}{2}\sigma^2_A$. The phenotypic value of an F_3 individual can be defined as:

$$Y_{ilk} = \mu + A_{ilk} + D_{ilk} + E_{ilk}$$

where D_{ilk} is the genetic value due to dominance and E_{ilk} is the environmental effect.

Then, considering that genetic values and environmental effect are independent variables and since the allelic frequencies are equal and the genes have independent distribution, the covariance c_2 is:

$$c_2 = cov(A_{ilk}, Y_{ilk} - \bar{Y}_{il.}) = cov\left(A_{ilk}, Y_{ilk} - \mu - \frac{1}{p}\sum_{k'} A_{ilk'} - \frac{1}{p}\sum_{k'} D_{ilk'} - \frac{1}{p}\sum_{k'} E_{ilk'}\right) = \left[\frac{(p-1)(1-r_1)}{p}\right]\left(\frac{3}{2}\sigma^2_A\right)$$

The correlation between additive genetic values of plants in the same F_3 family (r_1) is easily obtained. The coefficient of coancestry between plants in the same F_3 family is (1/2). Then:

$$r_1 = \frac{cov(A_{ilk}, A_{ilk'})}{\sqrt{v(A_{ilk})\,v(A_{ilk'})}} = \frac{2(1/2)\sigma^2_A}{(3/2)\sigma^2_A} = \frac{2}{3}$$

Using the previous considerations and results, it can be demonstrated that:

$$c_3 = cov\left(A_{ilk}, \bar{Y}_{il.} - \frac{1}{fp}\sum_{i'}\sum_{k'} (\mu + A_{i'lk'} + D_{i'lk'} + E_{i'lk'})\right) = \left(\frac{f-1}{fp}\right)[1 + (p-1)r_1]\left(\frac{3}{2}\sigma^2_A\right)$$

After some algebraic operations the values of $\hat{b}_1$ and $\hat{b}_2$ are derived.

RESUMO

São apresentados os estimadores dos coeficientes de sete índices de seleção, que levam em consideração o valor

fenotípico do indivíduo e o desempenho médio de sua família, e discute-se o uso destes índices em teste de geração precoce, no melhoramento de plantas autógamas. Não há clara superioridade de nenhum índice, embora alguns apresentem um ou mais aspectos negativos, como favorecer à seleção de planta excepcional em família de desempenho inferior, em detrimento de planta com desempenho desejável, em família superior.

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