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Problems of Generalization of Selection Indices

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Summary. The present investigation was undertaken to study the problem of generalization of the selection index in plant breeding. It was found that specific selection indices brought about the maximum genetic advance, provided that they were used for selection in the specific populations. If these indices were used as "foreign indices" the gain was negligible. The general selection indices, which were based on corrected pooled information from different experiments, were found to be as efficient as the specific indices. The problems of sampling, specific populations and base population of a crop species, and the application of general indices in a practical breeding programme have been discussed in detail.

All breeding procedures involve selection. The efficacy of any breeding procedure depends, therefore, upon its ability to spot the genotypes with higher genetic potentialities. Knowledge of the genetic constitution of yield and other components associated with it is essential to decide the type of breeding procedure expected to give maximum genetic gain during selection. In addition, information about the genetic correlations between different economic traits is needed when dealing with the quantitative traits. A selection index, which is advocated as an objective method of simultaneous selection for several traits, accounts for both the inheritance pattern of individual traits and the genetic correlation between them.

The use and construction of selection indices in plant and animal improvement for different purposes is recommended in most of the literature. Conversely, only a few reports are available indicating its application in practical breeding programmes. The literature also shows that a number of theoretical as well as practical problems still exist, for the use of selection indices is almost impracticable in breeding work (Cochran 1951, Robinson et al. 1951, Kempthorne 1957, Sumpf 1967, Singh 1969).

The parameters, especially the genetical, obtained from a particular population are functions of the gene action involved and the genotypic constitution controlling the traits in question. The prevailing environmental conditions in which the organism is growing and developing are additional factors which influence these parameters. Thus, an index constructed incorporating these parameters is specific for a particular situation. If such a specific index is used for selecting desirable genotypes in other populations with other parameter combinations, we shall call it a "foreign index". Now the following questions arise:

1. How effective is the foreign index in comparison with the specific ones?

2. What is the possibility of constructing a general index which would be effective for a range of populations?

The aim of the present investigation was to find answers to these questions by conducting a quantitative genetic analysis in rye and white mustard. The parameters in each case obtained from two different experiments were used to construct specific and general indices. The performance of these indices was then compared.

Material and Method

Using two separate samples of randomly selected plants of the variety 'Brucker Harrach' of rye (*Secale cereale* L.), full and half sib families were produced* and the genetic and phenotypic parameters were estimated using the North-Carolina-experiment I with hierarchical structure including 10 blocks, 4 males per block, 4 females per male, 10 progenies per plot and 2 replications per cross. The samples will be referred to as sample 1967 and sample 1968. Similar estimates were also obtained for a local variety of white mustard (*Sinapsis alba* L.).* Details of the variance and covariance analysis and estimation of parameters have been given elsewhere (Singh 1969). The variances and covariances, both phenotypic and genotypic, were used to construct specific and general indices for rye and white mustard in the manner described below.

Assuming that the genetic worth or "merit" (H) of an individual and its corresponding phenotypic value (I) are defined as follows:

$$H = \sum_{i=1}^{n} a_i G_i \quad \text{and} \quad I = \sum_{i=1}^{n} b_i P_i ,$$

the idea of index construction is to find the estimates of b_i in such a manner that the correlation between H and I i.e. $r_{(H,I)}$ becomes maximum. Here, G_i is the genotypic value of a given character, and a_i the corresponding relative economic weight. The expression for determining the values, b_i's, which maximize the correlation $r_{(H,I)}$ was given by Smith (1936) as follows:

$$b_j = \sum C_{ij} A_i ,$$

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where C_{ij} are the elements of the inverted phenotypic variance and covariance matrix, and $A_i = \sum_j a_i G_{ij}$ with G_{ij}, which are the genotypic variances and covariances.

The construction of a general index was proposed by Hanson and Johanson (1957), the estimates of b_i's being obtained by solving simultaneous equations of the following from:

$$b_i = \sum_j \sum_k \left(\frac{1}{V_{pk}}\right)^{1/2} \left(\frac{W_k}{V_{pk}}\right)^{1/2} b_j P_{ijk} = \sum_j \sum_k \left(\frac{1}{V_{pk}}\right)^{1/2} a_i G_{ijk}$$

or

$$\sum_j \sum_k b_j C_k P_{ijk} = \sum_j \sum_k a_i D_k G_{ijk} \qquad \begin{matrix}(i = 1, 2, \ldots, n)\\(j = 1, 2, \ldots, n)\end{matrix}$$

where $C_k = \frac{W_k}{(V_{pk})^{3/2}}$ and $D_k = \left(\frac{1}{V_{pk}}\right)^{1/2}$

$$W_k = \sum_i \sum_j b_i a_i G_{ij}$$

and

$$V_k = \sum_i \sum_j b_i b_j P_{ij},$$

k means k^{th} population.

The following symbols have been used:

$I_{67}^{(Sp)}$; $I_{68}^{(Sp)}$; $I_{64}^{(Sp)}$; $I_{65}^{(Sp)}$	Specific indices of the samples 1967 and 1968 in rye and of the samples 1964 and 1965 in white mustard, respectively.
$I^{(Gen)}$	General index.
$I^{(F)}$	Foreign index i.e. a specific index used in a non-specific population for selection.
$\Delta G^{(F)}$	Genetic advance expected through a foreign index.
$\Delta G^{(Sp)}$	Genetic advance expected through a specific index.
ΔG^k	Genetic advance expected through a general index in the k^{th} population.
b_i; $b^{(Sp)}$; $b^{(k)}$	The coefficients which maximize the correlation between H and I.

Results

First of all the results obtained in rye will be discussed. On the basis of the few examples cited here, a comparison of the specific indices with general indices will be attempted. The two characters, tiller number and plant height, were included in an index. Two indices, one for the sample 1967 and the other for the sample 1968, were constructed separately. As is obvious from the table 1, the plant height was evaluated much higher in both the samples. The tiller number was negatively weighed in 1967. The $b^{(k)}$ value for plant height was also high in the general index. This indicates that plant height is more significant a character, as it contributes more during selection compared to tiller number.

The expected genetic advance for 1967, i.e. $\Delta G_{67}^{(Sp)}$, is almost double that of $\Delta G_{68}^{(Sp)}$. However, if selection is made on the basis of the general index which includes the corrected $b_i^{(k)}$, the gains $\Delta G_{67}^{(k)}$ and $\Delta G_{68}^{(k)}$ are much in accordance with their respective values of the specific index. This means that $\Delta G_{6-1}^{(k)}$ was very near to the $\Delta G_{67}^{(Sp)}$ and $\Delta G_{68}^{(k)}$ to $\Delta G_{68}^{(Sp)}$.

Table 1. *Comparison of b values and genetic advance (ΔG) obtained in rye by different selection indices with the characters number of tillers and plant height*

Characters, in the index included

b_i	no. of tillers	plant height
$b_{67}^{(Sp)}$	−0.0015	0.0789
$b_{68}^{(Sp)}$	0.0080	0.0410
$b^{(k)}$	0.0035	0.0623

Genetic Advance

Sample	Sp. Index $\Delta G^{(Sp)}/s$	Foreign Index $\Delta G^{(F)}/s$	Gen. Index $\Delta G^{(k)}/s$
Sample 1967	0.762	0.759	0.761
Sample 1968	0.355	0.035	0.355

If, however, the b_{67} are used with the parameters of 68 as foreign index and $\Delta G_{68}^{(F)}$ is calculated, the expected genetic advance is very low (about 10%). On the other hand, $\Delta G_{67}^{(F)}$, calculated on the basis of b_{68} and the parameters of the sample 1967, is almost equal to the gain obtained by the specific index $I_{67}^{(Sp)}$.

In another example, the three characters, leaf-width, tiller number and plant height, were included in the index. Table 2 shows that the b's were very different in the two samples, but it is clear that the order of significance of these three characters with respect to their b values remained the same in both populations. The highest value of b was for leaf width, followed by plant height and tiller number.

The values for expected genetic advance, $\Delta G^{(Sp)}$, were different for the two populations, as can be seen from table 2. The performance of the general index was well comparable with the performance of the specific indices in their respective populations. If the specific indices were used as foreign indices, the performance of $I_{67}^{(Sp)}$ was very poor, as shown by a very low value of $\Delta G_{68}^{(F)}$ (about 83%). $I_{68}^{(Sp)}$, used as foreign index in the population 1967, performed as well as $I_{67}^{(Sp)}$ in its specific population.

In another comparison, three other characters, i.e. leaf, stem and ear green matter, were included. In this case also, the b values were very different in the

Table 2. *Comparison of b values and genetic advance (ΔG) obtained in rye by different selection indices with the characters width of primary leaves, number of tillers and plant height*

Characters, in the index included

b_i	Width of primary leaves	No. of tillers	plant height
$b_{67}^{(Sp)}$	0.48110	0.00199	0.07802
$b_{68}^{(Sp)}$	0.6870	0.0040	0.0390
$b^{(k)}$	0.73061	0.00153	0.06009

Genetic Advance

Sample	Sp. Index $\Delta G^{(Sp)}/s$	Foreign Index $\Delta G^{(F)}/s$	Gen. Index $\Delta G^{(k)}/s$
Sample 1967	0.765	0.756	0.764
Sample 1968	0.380	0.035	0.376

Table 3. *Comparison of b-values and genetic advance (ΔG) obtained in rye by different selection indices with the characters leaf, stem and ear green matter*

Characters, in the index included

b_j	Leaf green matter	Stem green matter	Ear green matter
$b_{67}^{(Sp)}$	0.0836	0.0077	−0.1564
$b_{68}^{(Sp)}$	0.0035	−0.0145	0.1582
$b^{(k)}$	0.0376	−0.0074	0.0509

Genetic Advance

Sample	Sp. Index $\Delta G^{(Sp)}/s$	Foreign Index $\Delta G^{(F)}/s$	Gen. Index $\Delta G^{(k)}/s$
Sample 1967	0.4712	−0.0468	0.2398
Sample 1968	0.4150	−0.0828	0.2894

two populations (table 3). In the 1967 sample the b value for leaf green matter was very high, whereas it was negative for ear green matter. In 1968 the ear green matter had the highest b value, and the leaf green matter a relatively low value, while the stem green matter was negatively valued. On the basis of $b_s^{(k)}$, the order of merit was ear green matter, leaf green matter and stem green matter.

The values for selection advance, $\Delta G^{(Sp)}$, were also equal (table 3). The selection advance, $\Delta G_{67}^{(k)}$ was 50.8%. The values for $\Delta G^{(F)}$ were negative in both the populations indicating no genetic progress in either case.

The results obtained in white mustard will now be discussed. Two indices each with two characters were constructed. In the first case, the number of branches per plant and the number of siliqua per branch were considered. The b_i values for these two characters were very different from each other (table 4). The number of branches was negatively weighted in 1964, whereas the number of siliqua per branch had a very high positive value for b in 1965. The corrected values, $b_i^{(k)}$, were approximately the same for both the characters.

The values for selection advance for all the indices have been listed in table 4. As can be seen, $\Delta G_{65}^{(Sp)}$ was very high. The performance of the general index was comparable with the performance of $I_{64}^{(Sp)}$ (i.e. $\Delta G_{64}^{(k)} \approx \Delta G_{64}^{(Sp)}$). The efficiency of the general index for selection in the population of 1965 was only 71% of the efficiency of the specific index, $I_{65}^{(Sp)}$. If, however, the Index $I_{64}^{(Sp)}$ in 1965 and Index $I_{65}^{(Sp)}$ in 1964 were used as foreign indices, the performance in both cases was very poor (table 4).

Table 4. *Comparison of b-values and genetic advance (ΔG) obtained in white mustard by different selection indices with the characters number of branches/plant and number of siliqua/branch*

Characters, in the index included

b_i	No. of branches per plant	No. of siliqua per plant
$b_{64}^{(Sp)}$	−0.0465	0.0331
$b_{65}^{(Sp)}$	0.1414	0.0195
$b^{(k)}$	0.03007	0.02513

Genetic Advance

Sample	Sp. Index $\Delta G^{(Sp)}/s$	Foreign Index $\Delta G^{(F)}/s$	Gen. Index $\Delta G^{(k)}/s$
Sample 1964	0.0761	−0.0600	0.0809
Sample 1965	0.1479	0.0255	0.1048

Another comparison of indices was made in which 1000-grain weight and grain yield were included. As is evident from table 5, b_i values were again very different in the two populations. The character 1000-grain weight, which was relatively high in the sample of 1964, had a negative value in 1965. The genetic gain expected in the 1965 sample, i.e. $\Delta G_{65}^{(Sp)}$, was, however, as much as double the corresponding value in 1964 (table 5). This indicates that the character 1000-grain weight is not a very decisive factor in yield estimates. The general index produced the same genetic progress as expected from $I_{65}^{(Sp)}$. Both $\Delta G_{64}^{(k)}$ and $\Delta G_{64}^{(Sp)}$ are approximately zero, indicating that no progress is expected when selection is made through these indices.

The results obtained in rye and white mustard can be summarized as follows: the specific indices are most effective followed by the general indices; the foreign indices are, the least effective. These statements are in full agreement with the results obtained by Hanson and Johnson (1957) and Caldwell and Weber (1965).

Hanson and Johnson compared the performance of general indices with specific ones in soybean. The results have been summarized in table 6. One can clearly see that the genetic gain expected with the help of the general index, i.e. $\Delta G^{(k)}$, is almost the same (13,06) as that obtained with the specific index (14,26). However, the performance of this specific

Table 5. *Comparison of b-value and genetic advance (ΔG) obtained in white mustard by different selection indices with the characters 1000-grain weight and grain yield*

Characters, in the index included

b_i	1000 grain weight	grain yield
$b_{64}^{(Sp)}$	0.1287	0.0493
$b_{65}^{(Sp)}$	−0.5203	0.0163
$b^{(k)}$	−0.1699	0.0443

Genetic Advance

Sample	Sp. Index $\Delta G^{(Sp)}/s$	Foreign Index $\Delta G^{(F)}/s$	Gen. Index $\Delta G^{(k)}/s$
Sample 1964	0.1544	−0.1016	−0.0183
Sample 1965	0.3459	−0.2393	0.3013

Table 6. *Comparison of genetic advances obtained by different selection indices in soyabean*

Genetic Advance

Population	Sp. Index $\Delta G^{(Sp)}/s$	Foreign $\Delta G^{(F)}/s$	Gen. Index $\Delta G^{(k)}/s$
Population 1	14.26	7.55	13.06
Population 2	13.08	12.70	12.71

index as foreign index is comparatively poor, as the genetic gain, $\Delta G^{(F)}$, is only 7.55, which is 57% of the expected gain obtained by the specific index. In population 2, the general index is as good as the specific index. The performance of this index as foreign index is also satisfactory.

Discussion

The results indicate that the specific indices are the most effective in selection. The general index brings about the same genetic progress as the specific one. Further, if the specific indices are used for selection in a population other than their own, the expected gain seems to be insignificant. Now the question arises as to which population is the specific population for an index. In the present investigation the working was a random mating variety of rye 'Brucker Harrach'. Parameters were estimated in two separate samples of this population and two indices, one for each sample, were constructed. When the indices were used in their respective samples the expected genetic gains were maximum. However, the gain was negligible when the index constructed from one sample was used for selecting superior genotypes in another sample of the same population. The nominal selection gains obtained by the foreign indices indicate that the parameters of the two samples are very different from each other. This is a further proof that the two samples for estimating the parameters needed for the calculation of the b_i's and taken from the same base population did not contain similar genotypes. These two samples can, therefore, be regarded as two different populations.

This means that an index based on a relatively small sample of individuals as the base for parameter estimation will not be effective, or will be less effective for selection in the initial population of which the sample was a part. It also shows that the individuals of a sample form a population of their own. Perhaps this sample is not big enough to represent the initial population of the variety 'Brucker Harrach'. Thus, the index $I_{67}^{(Sp)}$ is specific for the sample of individuals which have been involved in crossing and testing for the purpose of estimating parameters in 1967. The same holds true for $I_{68}^{(Sp)}$.

It can, therefore, be said that for selection in the population 'Brucker Harrach', an index should be constructed based on the parameters obtained from a large representative sample of individuals taken from the base population. Years and locations should also be given due consideration so as to avoid the bias expected from their interaction with the genotypes. The size of the sample which may be representative for a base population depends upon the type of material being used and on the number of the expected to be responsible for the expression of the character.

Another point which needs emphasis is that, although the general index may be advocated for selection in the base population of 'Brucker Harrach', its generality for selection in a population of rye other than 'Brucker Harrach' may be challenged. Its effectiveness in any other population again may depend upon the similarity in genetic constitution of the population in question with that of 'Brucker Harrach'.

These problems can, however, be solved, provided that a base population representing the total gene pool of the species in question is constituted by incorporating all possible idiotypes and equilibrium in the population is established (Singh 1969). From this base population a number of small manageable samples may be studied separately, parameters estimated from the pooled information of all the samples, and indices constructed. These indices should, from time to time, be brought up-to-date by incorporating new information gained during the selection programme, so that they may act as an efficient selection procedure for a longer period.

Literature

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