CORRECTION FOR REGRESSION ON A SECONDARY TRAIT AS A METHOD OF INCREASING THE EFFICIENCY OF SELECTIVE BREEDING

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Summary

A revised estimate is given for the efficiency of a selection index investigated by Rendel (1954) which corrects the variations in a particular trait for linear regression on another.

I. INTRODUCTION

A recent report (Rendel 1954) suggested that the efficiency of selective breeding for a trait of incomplete heritability may be increased by basing selection on an index which corrects the variations of the primary trait for measurable variations introduced by environmental agencies. It was shown that if trait A is correlated only environmentally with B and B has no economic value, the optimum index for improvement of A as a linear combination of A and B is

\[ I = A - bB, \]

where \( b \) is the phenotypic regression of A on B. The purpose of this note is to reexamine the efficiency of such an index in the case discussed by Rendel when A and B are also genetically correlated.

II. THEORY

The genetic gain in character A when selection is based on an index I is given by \( R_{G_A} \) where \( R_{G_A} \) is the correlation between I and genotype of A, \( \sigma_{G_A} \) is the genetic standard deviation of A, and the gains are measured per unit standard deviation in the selection differential (Hazel 1943). Here, of course, the usual assumptions are made regarding additivity and independence of genetic and environmental variations. If individual phenotype A is the criterion of selection, then

\[ R_{G_A} = h_A \sigma_{G_A}, \]

where \( h_A^2 \) is the heritability of A. Thus the gain from phenotypic selection is \( h_A \sigma_{G_A} \) and the efficiency of index selection relative to this is

\[ R_{G_A}/h_A = \text{cov}(G_A, I)/h_A \sigma_{G_A} \sigma_I. \]

Since

\[ I = A - bB, \]

then

\[ \text{cov}(G_A, I) = \text{cov}(G_A, A - bB) = \text{cov}(G_A, G_A - bG_B) = \sigma_{G_A}^2 - br_G \sigma_{G_A} \sigma_{G_B}, \]

which reduces to

\[ \sigma_{G_A}^2 (1 - r_P r_G h_B/h_A), \]

where \( r_P \) and \( r_G \) are the phenotypic and genetic correlations of A and B and \( h_B^2 \) is

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the heritability of \( B \). The well-known result of correcting the variance of one variable for regression on another gives \( \sigma^2 = \sigma^2 \sqrt{1-r^2} \). Since also \( h_A = \sigma G / \sigma_A \), the relative efficiency of index selection reduces to

\[
E = \frac{1-r^2 \sigma^2 G / h_A}{\sqrt{1-r^2}}
\]

rather than \( \frac{1-r^2}{\sqrt{1-r^2}} \) as given by Rendel.

It may be noted that Rendel’s result would follow if \( b \) in the expression \( \text{cov}(G_A, G_A-b_G I) \) were the genetic regression coefficient. There are, however, other considerations involved with respect to his analysis. The gain from phenotypic selection for \( A \) may be written as \( h_A^2 \sigma_A \). It was then assumed, or at least implied, that the gain in \( A \) from selection on the index is \( h_I^2 \sigma_I \), the product of heritability and standard deviation of the index. Heritability of the index is the ratio of its genetic to phenotypic variance, the latter being, as above, by \( \sigma_I^2 = \sigma_I^2 (1-r^2) \). It does not follow that genetic variance of the index is \( \sigma_I G^2 = \sigma_G^2 (1-r^2) \), since once again the genetic regression is not used in the correction \( I = A - b B \). The true value is

\[
\sigma_I^2 = \sigma_G^2 + b^2 \sigma_G^2 - 2b \text{cov}(G_A, G_B)
\]

\[
= \sigma_G^2 - \sigma_G^2 (1+r^2) \sigma_G^2 / h_A^2 - 2r \sigma_G h_B / h_A
\]

From these expressions the true value of \( h_I^2 \) may be derived. However, it must be emphasized that \( h_I^2 \sigma_I \) measures the gain in the index and not in \( A \). Gain in \( A \) is given by \( b_G I \), where \( b_G I \) is the regression of genotype of \( A \) on genotype of \( I \). But

\[
b_G I = \frac{\text{cov}(G_A, I)}{\sigma_G^2} \cdot \frac{\sigma_I^2}{\sigma_I} = \frac{\text{cov}(G_A, I)}{\sigma_I}
\]

so that estimation of \( \sigma_I^2 \) is unnecessary. Since \( \text{cov}(G_A, I) = \text{cov}(G_A, I) \) the gain from index selection is \( R_G \) as before.

The corrected formula may give either a greater or lesser efficiency than that indicated by Rendel, but it is evident that judicious consideration of phenotypic and genetic correlations and heritabilities of the traits concerned is necessary to evaluate the precision of the method—not only whether it exceeds that of phenotypic selection but whether the relative gain is worth while compared with that from optimum indices for genetically correlated traits.

### III. References
