On the Expected Response to Combined Selection

Ahmed Mostageer

Animal Breeding Department, Faculty of Agriculture, Cairo University, Egypt.

THE EXPRESSION of the amount of genetic progress gained by combined selection is derived by a simple method different from the "path coefficient". The method introduced depends on estimating the herilability of combined selection upon the fact that the accuracy of assessing the breeding value of an individual using two uncorrelated pieces of information is equal to the sum of the two accuracies of this assessment arrived at using each of these 2 pieces separately.

The Derivation

Combined selection is a kind of individual selection in which the breeder uses, for estimating the breeding value of the individual, the mean performance $\overline{(P)}$ of the family to which i contributes beside the deviation of the individual's own performance (P_i) from $\overline{P}$.

In idiscussing the method to derive the expected genetic response to combined selection, Lush (1947) in his original paper used the path coefficient as the tool. Tantawy (1968) described the derivation by this method in some detail. In this work, a simpler method is presented that does not require the application of the "path coefficient".

The performance of any individual in the following discussion will be assumed to be already taken as a deviation from the population mean. Thus we say

$$E (P_i)^2 = \sigma_p^2 \quad \dots \dots \dots \dots \dots \dots \dots \dots \quad (1)$$

where E denotes expectation and σ_p^2 is the phenotypic variance. We shall further assume that the mean of the breeding values in the population is equal to zero and thus

$$E (A_i^2) = \sigma_g^2 \quad \dots \dots \dots \dots \dots \dots \dots \dots \dots \quad (2)$$

where A_i is the breeding value of the individual i and σ_g^2 is the additive genetic variance. Since no covariance is supposed to exist between the breeding value A_i of the individual and the deviation of A_i from P_i, we can write the expected covariance between A_i and P_i as

$$E\ (A_i \cdot P_i)\ =\ \sigma_g^2 \quad \dotsb \quad (3)$$

A family is defined as "a group of individuals bearing a certain genetic relationship (r_g) to each other by virtue of common descent" Lerner (1958). Using the two members i and j of a family it could be stated that

$$E\ (A_i \cdot A_j)\ =\ r_g\ \sigma_g^2 \quad \dotsb \quad (4)$$
and
$$E\ (A_i \cdot P_j)\ =\ r_g\ \sigma_g^2 \quad \dotsb \quad (5)$$

Further, we assume that

$$E\ (P_i \cdot P_j)\ =\ r_p\ \sigma_p^2 \quad \dotsb \quad (6)$$

; where r_p is the phenotypic correlation between members of a family.

Now, suppose we wish to estimate the breeding value of any individual i using only the mean performance $\bar{P}$ of the family of n members to which he contributes. We need to assess both the regression coefficient to be used on $\bar{P}$ and the accuracy of the estimate, i.e., the squared correlation coefficient. The expected covariance between these two traits could be determined as follows :

$$E\ (A_i \cdot \bar{P}) = E\ \left(A_i \cdot \frac{P_1 + P_2 + \ldots + P_i + \ldots + P_n}{n} \right)$$

$$= E\left(A_i \cdot \frac{P_i}{n} \right) + E\left(A_i \cdot \frac{n-1}{n}\ P_j \right)$$

$$= \frac{\sigma_g^2}{n}\ (1 + (n-1)\ r_g) \dotsb \quad (7)$$

$\bar{P}$ (using relations 3 and 5).

The variance of $\bar{P}$ is expected to be :

$$E\ (\bar{p})^2\ =\ E\left(\frac{P_1 + P_2 + \ldots + P_n}{n} \right)^2$$

$$= \frac{1}{n^2}\ \left(nE\ (P_i^2) + n\ (n-1)\ E\ (P_i \cdot P_j) \right)$$

$$= \frac{\sigma^2_p}{n} \left(1 + (n-1) r_p\right) \quad \cdots \cdots \cdots \quad (8)$$

(Using relations 1 and 6). Thus the regression coefficient to be used on the mean performance of the family be equal to (7) / (8), or

$$b = h^2 \frac{1 + (n-1) r_g}{1 + (n-1) r_p} = h^2_f \ ,$$

h^2 being the individual heritability and h^2_f the family heritability. The accuracy of course is equal to this value of b multiplied by the regression coefficient of $\bar{P}$ over A_i, or

$$r^2 = h^2_j \frac{1 + (n-1) r_g}{n} \quad \cdots \cdots \cdots \cdots \quad (9)$$

Now let us estimate the breeding value A_i of the individual i using only the deviation of his own performance P_i from the mean performance of the family of n members to which he contributes. The covariance between these two characters is expected to be

$$E\left(A_i \cdot (P_i - \bar{P})\right) = E(A_i \cdot P_i) - E\left(A_i \cdot \bar{P}\right)$$

$$= \sigma^2_g - \frac{\sigma^2_g}{n} \left(1 + (n-1) r_g\right)$$

$$= \frac{\sigma^2_g}{n} (n-1) (1 - r_g) \quad \cdots \cdots \cdots \quad (10)$$

(using relations 3 and 7). The expected variance of the value used for estimation, i.e., $P_i - \bar{P}$, will be

$$E (P_i - \bar{P})^2 = E(P_i)^2 + E(\bar{P})^2 (P_i)^2 - 2E(P_i \cdot \bar{P}).$$

We need now to get the estimate of the covariance between P_i and $\bar{P}$. we have

$$E(P_i \cdot \bar{P}) = E\left(P_i \cdot \frac{P_1 + P_2 + \ldots + P_i + \ldots + P_n}{n}\right)$$

$$= \frac{1}{n} E(P_i)^2 + \frac{n-1}{n} E(P_i \cdot P_j)$$

$$= \frac{\sigma^2_p}{n} \left(1 + (n-1) r_p\right) \quad\quad\quad (11)$$

That is to say that, the variance of the observed mean of the family is equal to the covariance between the performance of any randomly chosen individual contributing to the mean and that mean. This is a very useful identity that has very wide applications in the field of animal breeding. Now, using relations 2, 8 and 11 to solve for the required variance we get.

$$E\,(P_i - \bar{P})^2 = \sigma_p^2 - \frac{\sigma_p^2}{n}\,(1 + (n-1)\,r_p)$$

$$= \frac{\sigma_p^2}{n}\,(n-1)\,(1-r_p) \quad \cdots \cdots \cdots \quad (12)$$

The regression coefficient to be applied to the deviation $P_i - \bar{P}$ will then be equal to

$$b = h^2\,\frac{1-r_g}{1-r_p} = h_w^2 \; ,$$

; where h_w^2 is the heritability within families. The accuracy will then be equal to

$$r^2 = h_w^2\,\frac{(n-1)\,(1-r_g)}{n} \quad \cdots \cdots \cdots \cdots \quad (13)$$

Now, if these two pieces of information, namely $\bar{P}$ and $P_i - \bar{P}$, are not correlated, the accuracy of estimating the breeding value of i using them together will be the sum of the two accuracies arrived at using each piece separately. This is comparable to the case in which the breeder evaluates the additive genetic merit of an individual using the performances of his two uncorrelated parents. Since $E(P_i.\bar{P}) = E(\bar{P})^2$ as shown above, the covariance between the two bits of information used in combined selection is equal to zero. Thus the accuracy r_c^2 of estimating the breeding values of individuals using combined selection will be

$$r_c^2 = h^2\,\frac{(1 + (n-1)\,r_g)^2}{n(1 + (n-1)\,r_p)} + h^2\,\frac{(n-1)\,(1-r_g)^2}{n\,(1-r_p)}$$

$$= h^2\left(1 + \frac{(r_g - r_p)^2}{1-r_p} \cdot \frac{n-1}{1 + (n-1)\,r_p}\right)$$

This is the heritability of combined selection. The amount of genetic progress (Δ_g) obtained will then be

$$\Delta_g = \bar{\imath}\,\sigma_g\,r_c \quad\quad \text{or}$$

$$= \bar{\imath}\,\sigma_p\,h^2\,\sqrt{1 + \frac{(r_g - r_p)^2}{1-r} \cdot \frac{n-1}{1 + (n-1)\,r_p}}$$

$\bar{\imath}$ being the intensity of selection.

References

Lerner, I.M. (1958)   *"The Genetic Basis of Selection"*. John Wiley & Sons, Inc.

Lush, J., L., (1947) Family merit and individval merit as bases for selection Part I.   *Amer. Nat.*, 81 , 241.

Tantawy, A. O. (1968)   *"Population Genetics"*. (In Arabic). Dar-el-Maaref.

الاستجابة المتوقعة للانتخاب المشترك

أحمد مستجير

كلية الزراعة ، جامعة القاهرة

استخرجت كمية التحسين الوراثى المتوقع الناتجة من استعمال الانتخاب المشترك بطريقة مبسطة مختلفة عن طريقة «معامل المرور» الشائعة الاستعمال ٠ وتعتمد هذه الطريقة فى تقدير العمق الوراثى للانتخاب المشترك على حقيقة أن درجة الدقة فى تقدير القيمة التربوية للفرد باستعمال مصدرين غير مرتبطين من مصادر البيانات تساوى حاصل جمع درجتى الدقة الناتجة من استعمال كلاهما منفردا فى التقدير ٠