ESTIMATE OF THE GENETIC LOAD DISCLOSED BY INBREEDING

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ASSUMING that only one of the mean number n of common ancestors per consanguineous couple carries a rare deleterious recessive mutation, the mean probability of homozygosis for this mutation in the inbred offspring is given by $F_i/2n$, where F_i is the mean coefficient of inbreeding of the inbred zygotes. The probability of nonhomozygosis for the same allele is $1 - (F_i/2n)$. Assuming that the considered common ancestor carries not one, as postulated above, but two deleterious recessive mutations (*i.e.*, an average of one per gamete), then the probability γ of nonhomozygosis for at least one of such mutations will be

$$\gamma = [1 - (F_i/2n)]^2 \quad (1)$$

If B is the mean number of deleterious mutations per gamete from the n common ancestors, the total probability of nonhomozygosis for any of these mutations is given by

$$\gamma_t = [1 - (F_i/2n)]^{2nB} \quad (2)$$

The probability x of homozygosis for at least one of the B mutations is

$$x = 1 - [1 - (F_i/2n)]^{2nB} \quad (3)$$

From this formula,

$$B = \frac{\log(1-x)}{2n \log[1 - (F_i/2n)]} \quad (4)$$

An estimate of x can be obtained by subtracting the amount of damage M_c in a suitable control sample ($F = 0$) from the weighted mean M_i of the damages verified in all the inbred subsamples, and dividing the result by $(1 - M_c)$. The term $(M_i - M_c)/(1 - M_c)$ measures the excess of damage produced by the action of inbreeding in the fraction $(1 - M_c)$ of the inbred zygotes. This term is, therefore, a reliable estimate of the real effect of inbreeding.

If S_c and S_i are the incidences of survivors or normals in the control and inbred samples, respectively, x may also be written as follows:

$$x = (S_c - S_i)/S_c \quad (5)$$

Substituting for this x in formula (4), we obtain

$$B = \frac{\log[1 - (S_c - S_i)/S_c]}{2n \log[1 - (F_i/2n)]} = \frac{\log(S_i/S_c)}{2n \log[1 - (F_i/2n)]} \quad (6)$$

The reliability of the estimates obtained with formula (6) does not depend on

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a reliable estimate of n , when $F_i/2n$ is a small fraction. In practice, n may be assumed to be equal to 2. Formula (6) turns out to be

$$B = \frac{\log (S_i/S_c)}{4 \log [1-(F_i/4)]} \quad (7)$$

In practice, this formula may be accepted as equivalent to the simplified equation

$$B = \frac{\log (S_i/S_c)}{-0.4343F_i} \quad (8)$$

These formulas have been applied to simple models representing various situations of inbreeding effect. The results obtained with formula (8) proved to be identical to those obtained with the method of MORTON, CROW and MULLER (1956). This problem will be discussed in a paper now in press (FREIRE-MAIA 1964).

When only one inbred subsample composed of first cousin unions ($F = 1/16$) is used, as preferred by some authors in human genetics, formula (7) may be expressed: $B = [\log(S_i/S_c)]/-0.0273576$.

When a control group ($F = 0$) is not available, two subsamples (or groups of subsamples) with different values of F may be used. Assuming that N_1 is a sample characterized by F_1 and showing a damage measured by M_1 , and N_2 is another sample characterized by F_2 and with a damage measured by M_2 , being $F_2 > F_1$, the difference between both damages divided by $(1-M_1)$ may be assumed to be produced by a coefficient of inbreeding equal to the difference between the two values of F , i.e., F_2-F_1 . Therefore, for such situations, our formula (7) turns out to be

$$B = \frac{\log (S_2/S_1)}{4 \log [1-(F_2-F_1)/4]} \quad (9)$$

Since our present method is based on the difference d between two means (M_i and M_c , or M_1 and M_2), an estimate of the variance s_B^2 of B may be obtained as the product of the variance of d by B/d . A detailed formula for estimating s_B^2 is:

$$s_B^2 = B^2 \left(\frac{M_i S_i}{N_i} + \frac{M_c S_c}{N_c} \right) / (M_i - M_c)^2 \quad (10)$$

This formula leads to estimates of s_B^2 either identical or rather close to those obtained on the basis of the theory of MORTON *et al.* (1956) (cf. FREIRE-MAIA 1964).

Some of the animal data which have been analysed by PISANI and KERR (1961) according to the method of MORTON *et al.* (1956) have been reanalysed according to our formula (7). In one instance, no estimate of the error was possible since no information on the number of observations was given. Estimates of B_{FO} , i.e., the regression coefficient based on the comparison of the noninbred sample with the average of all the inbred groups, will be also added for comparison. The estimates are as follows, in the order: (1) our present approach; (2) B of MORTON *et al.*; (3) B_{FO} (please refer to the indicated tables of PISANI and KERR (1961) for the data):

Table 1. Barred Plymouth Rocks (hatchability): 3.29; 3.40; 3.38.

Table 7. White Leghorns (hatchability): 0.75 ± 0.21 ; 0.75 ± 0.32 ; 0.78 ± 0.22 .

Table 19. Poland China hogs (early mortality): 0.29 ± 0.11 ; 0.20 ± 0.27 ; 0.32 ± 0.12 .

Our formulas (7) and (9) have also been applied to data from human populations and led to results which are similar to those obtained with the method of MORTON *et al.* (FREIRE-MAIA, GUARACIABA and QUELCE-SALGADO 1964; FREIRE-MAIA 1964). KERR (1963, personal communication) used formula (6) and the approach of MORTON *et al.* with data on inbreeding effect on mortality in bees and also found that they lead to equivalent estimates.

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SUMMARY

Formulas for the estimate of the genetic load revealed in inbred individuals and its variance are presented. They lead to results which are equivalent to those obtained with the aid of the theory of MORTON, CROW and MULLER (1956).

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