

SHORT PAPER

Comparing the means of inbred lines with the base population: a model with overdominant loci

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SUMMARY

For one-, two- and n -locus models of a quantitative trait assumed to be determined by overdominant loci, it is shown that the mean of an inbred line will be equal to or larger than the mean of the base population if the original gene frequencies satisfy a condition which is generally a function of the degree of overdominance and of the genotypic values.

1. INTRODUCTION

It has been proposed by Bowman & Falconer (1960) and by Falconer (1971) that the residual variance often found at the selection limit for a quantitative character might not be due mainly to overdominance. In the earlier paper they studied the litter size of lines of mice under inbreeding, and in the second one the author submitted lines of mice, at the selection limit for high litter size, to inbreeding and selection. Summarizing the results of these two experiments Falconer stated recently (1977): 'If overdominant loci were an important source of variation it would be impossible to produce inbred lines with means equal to the original population.' Working on the same trait, Eklund & Bradford (1977) observed that inbred lines of mice and the base population had the same means and concluded also that overdominant loci could not have any major effect on litter size.

Using a one-locus model of inheritance, and building it up to n loci, this paper shows that there are conditions in which overdominance can yield an inbred line with a phenotypic mean equal to, or even larger than, the mean of the base population.

2. RESULTS

Let us assume for simplicity that the trait is under the control of a single locus with two alleles and that the base population is large and panmictic. Genotypic values and frequencies are assigned to each genotype as follows:

Genotype	A_1A_1	A_1A_2	A_2A_2
Genotypic value	$+a$	$+ka$	$-a$
Genotypic frequency	p^2	$2p(1-p)$	$(1-p)^2$

where k , the degree of dominance, is larger than one. M_0 , the mean of the population, is

$$M_0 = a(2p - 1 + 2p(1 - p)k).$$

After lines have been made up from the base population and completely inbred without selection, the phenotypic means, M_1 , are expected to be equal to $+a$ (in a proportion p of lines) or to $-a$ (in a proportion $1 - p$ of lines). Obviously the latter outcome is always smaller than the value of the original phenotypic mean. However, when inbreeding leads to fixation of the allele A_1 , it is interesting to compare M_0 and M_1 :

$$M_1 = M_0$$

if and only if
which yields

$$a(2p - 1 + 2p(1 - p)k) = a$$

$$(kp - 1)(p - 1) = 0. \tag{1}$$

The only non-trivial solution of (1) is $p = 1/k$, a value between 0 and 1. Therefore, when the degree of dominance, k , is larger than one, if the frequency of the allele A_1 , p , is $1/k$ in the base population, the inbred lines fixed for A_1 and the original population are expected to have the same mean. It follows that the mean M_1 is expected to be greater than M_0 when p is smaller than $1/k$.

Next, if one starts selection on the same base population, one may reach a selection plateau caused by overdominance, at which the equilibrium frequency of A_1 is p_e . Under random mating the plateaued population can be described as a new base population, with p_e replacing p . Inbreeding coupled with selection towards higher value of the trait will cause the lines made up from this population to shift towards A_1 and eventually to become fixed for A_1 with a probability larger than p_e . The condition for the mean of such a fixed line to be larger than or equal to the mean of the plateaued population is homologous to the one found before, provided the quantitative character is not fitness itself. The reviewer showed that if the character is fitness, then $p_e = (1 + k)/2k$ and the inbred lines will have smaller means than the equilibrium population when there is overdominance. Therefore, if one considers a trait, like litter size, which is an important component of fitness, the equilibrium gene frequency should be close to the value of p_e given above and one would expect to observe only few superior inbred means under the overdominant model.

Now let us add a second locus ($B_1/B_2, p', k', b$) to the one-locus system, and, in absence of epistasis, the mean of the base population becomes

$$M_0 = a(2p - 1 + 2p(1 - p)k) + b(2p' - 1 + 2p'(1 - p')k').$$

Then, M_1 , the mean of the line fixed for A_1 and B_1 , will be equal to M_0 if and only if

$$a(2p - 1 + 2p(1 - p)k) + b(2p' - 1 + 2p'(1 - p')k') = a + b. \tag{2}$$

It can be shown that (2) is equivalent to

$$ka \left(p - \frac{1+k}{2k} \right)^2 + k'b' \left(p' - \frac{1+k'}{2k'} \right)^2 = \frac{a(1-k)^2}{4k} + \frac{b(1-k')^2}{4k'}. \tag{3}$$

Since $ka, k'b, \frac{a(1-k)^2}{4k}$ and $\frac{b(1-k')^2}{4k'}$

are positive, (3) is the general equation of an ellipse (a circle if $a = b$ and $k = k'$) in p and p' . The points of the ellipse which are found in the unit square, have coordinates that satisfy (2).

Finally, the results derived for the two-locus model can be generalized safely to a system of n overdominant loci (a_1 to a_n , p_1 to p_n and k_1 to k_n , measuring respectively the genotypic value, the gene frequency and the degree of dominance at each locus, with $k_i > 1$, $\forall i$) to yield the general condition

$$\sum_{i=1}^{i=n} k_i a_i \left(p_i - \frac{1+k_i}{2k_i} \right)^2 = \sum_{i=1}^{i=n} \frac{a(1-k_i)^2}{4k_i}$$

which has to be satisfied for M_1 and M_0 to be equal. We should note that this general condition was derived for the most extreme outcome of the inbreeding process: the fixation of all n favourable alleles. Homologous conditions could be derived when inbreeding leads to the fixation of $n-1$, $n-2$, ... favourable alleles, and the existence of the corresponding sets of p values could be determined numerically.

3. DISCUSSION

Without loss of generality, we will discuss only the one-locus model. Although p , the frequency of the best allele in the unselected base population, is unknown it is likely to have an intermediate value. However, when the new base population is at a selection plateau, it is expected that p_e , the equilibrium gene frequency, will be larger than p , since selection has been effective. In general then, (1) will hold for small values of k , that is for slightly overdominant loci.

Provided condition (1) is satisfied, one would expect a proportion p of inbred lines to have a mean equal to the mean of the base population and the remaining lines to have a smaller mean. Only the first part of this prediction was fulfilled directly in the experiments on litter size. However a large proportion of lines was discontinued because of fertility problems. One might argue that this result was also possibly due partly to the random fixation of detrimental alleles for litter size and, therefore, that it satisfied the second part of the prediction indirectly. A more definitive evaluation of the importance of overdominance could be attained by using a character which is not relevant to fitness.

Overall, the results show that the importance of overdominant loci, as causes of residual variation at the selection limit, cannot always be assessed safely just by comparing the mean of the original population and the means of inbred lines constituted from the base population: it is possible for the means to have the same value when the trait is determined by slightly overdominant loci.

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