

A SIMULATION STUDY OF THE EFFECTS OF ASSORTATIVE MATING ON THE RESPONSE TO SELECTION

Ein Modellversuch zur Untersuchung des Einflusses von gelenkter Paarung
auf die Selektionswirkung

Un estudio de simulación del efecto del apareamiento afín sobre
la respuesta a la selección

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Assortative mating, or the mating of selected males and females according to rank, have long been practised in animal breeding. Theoretically this should lead to an increased response for the following reasons: Like inbreeding, assortative mating causes an increase in homozygosity and total population variance (WRICHT, 1921, and FISCHER, 1918). Both these factors should speed up the response since the homozygosity due to assortative mating affects only the *loci* concerned with the trait under selection (in contrast to homozygosity due to inbreeding) whilst the increase in variance should lead to a greater selection differential. However, CROW and FELSENSTEIN (1968) points out that in the case of a multifactorial trait the increase in homozygosity is so slight as to be negligible. The increase in variance on the other hand is quite large.

The only published experimental evidence on a comparison of the response under assortative mating with that under random mating is by McBRIDE and ROBERTSON (1963). They found that assortative mating increased the response to selection for a higher number of abdominal bristles in *Drosophila melanogaster*.

Since the mathematical treatment of assortative mating combined with selection becomes extremely unwieldy in the case of a multifactorial trait, this simulation study was done to compare the responses obtained with random mating, positive assortative mating and negative assortative mating of the selected parents.

PARAMETER COMBINATIONS

Five replicate runs for each of three different gene models were done for all combinations of population sizes 32 and 160, heritabilities 0.20 and 0.50, and selection intensities of one-eighth and one-half. The three gene models used were:

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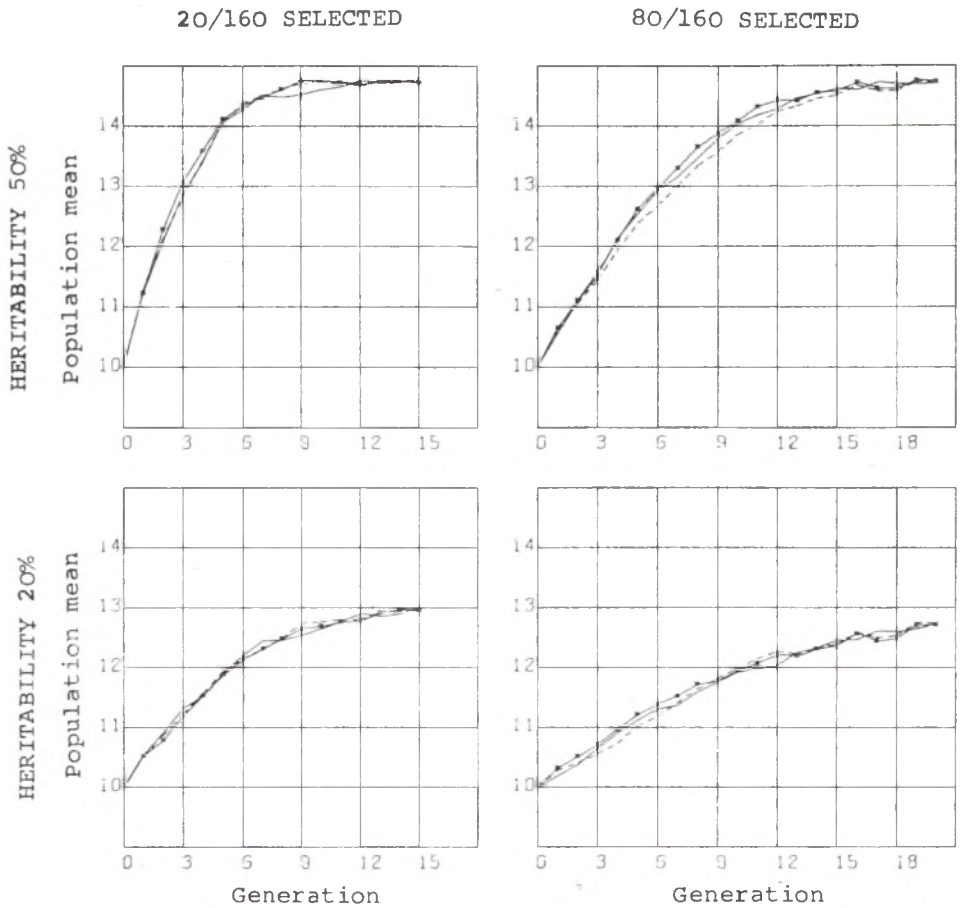


FIG. 1. Response to selection. Additive model with 10 *loci*. The smooth curve refers to random mating, the curve marked with asterisks to positive assortative mating and the dotted line to negative assortative mating.

- I) Additive model: 10 *loci* with two alleles each, equal effects and independent segregation.
- II) Dominance model: the same as above but with one allele completely dominant over the other at all *loci*.
- III) Multiple allele model: the same as the additive model, but with all 10 *loci* on one «chromosome» and no recombination between *loci*. This is equivalent to a one *locus* eleven alleles system (ROBERTSON, 1970) and can also serve as an illustration of the effect of extreme linkage in the case of 10 *loci* with 2 alleles each.

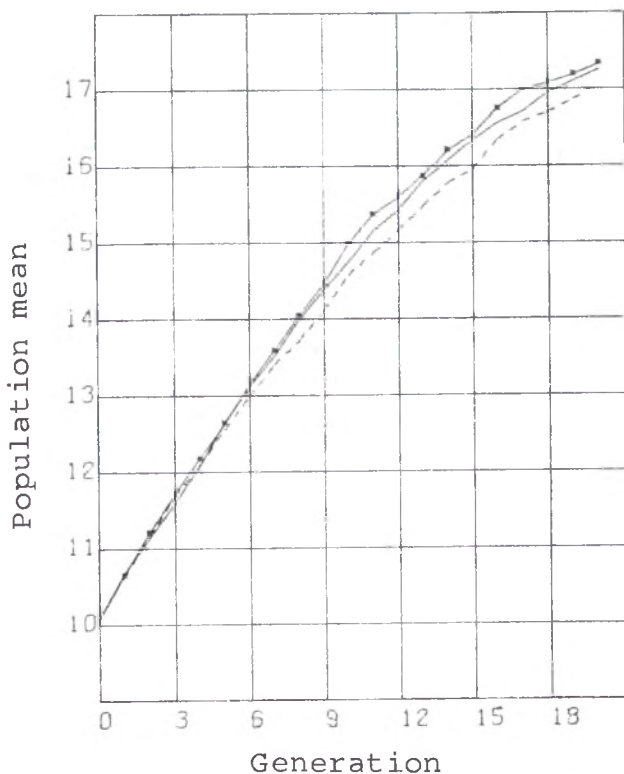


FIG. 2. Response to selection. Additive model with 30 loci, heritability 50 % and 80/160 selected.

The approach throughout was to start with a base population in linkage equilibrium, equal gene frequencies for all alleles, a phenotypic mean of ten units and a phenotypic coefficient of variation of 0,15. For each run the three different gene models started off with base populations with identical genotypes, although the genotypic values of the dominance model naturally differed from those of the other two models.

RESULTS AND DISCUSSION

The runs with small populations gave completely irregular results replicate runs with the same parameter combinations giving quite diverse response patterns. With population size 160 the pattern that one would expect from the work of McBRIDE and ROBERTSON (1963) was slightly apparent in only one case, namely a high heritability (0.50) low selection intensity ($\frac{1}{2}$) independent segregation and

equal additive gene effects. Even in this case the differences in response was only very slight, as shown in figure 1.

Since the increase in variance caused by assortative mating increases with the number of *loci* (CROW and FELSENSTEIN, 1968) the number of *loci* was increased, first to 30 and then to 60 *loci*. With 30 *loci* the population size was kept at 160 and runs were done at both the previous selection intensities, but only one heritability namely 0.50. With a high selection intensity the three mating systems did not differ in response. At a selection intensity of one-half, the tendency observed in figure 1 was slightly enhanced as can be seen in figure 2. Each curve represent the average of five replicate runs.

The number of *loci* was then increased to and the population size brought down to 100 to cut down running time. Selection were done at two intensities, namely 20/100 and 50/100. The results obtained with five replicate runs is shown in figure 3.

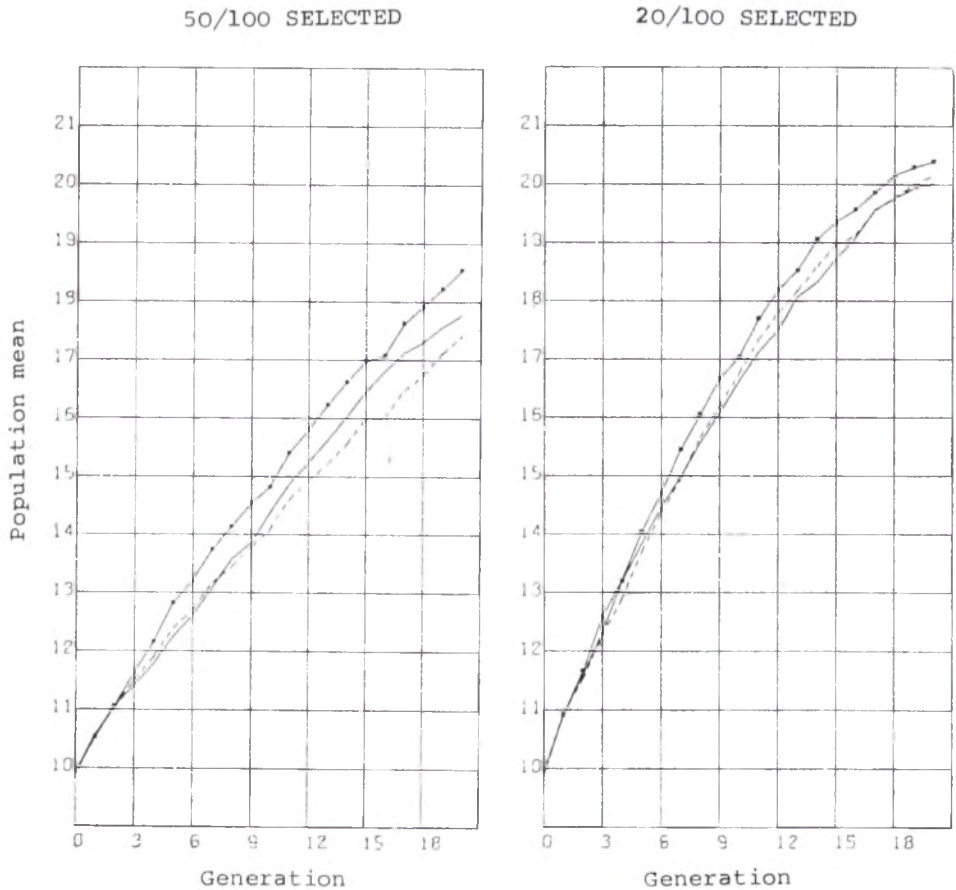


FIG. 3. Response to selection. Additive model with 60 *loci* and heritability 50 %

There is now a much greater differentiation between the three response curves, and for the first time the response with assortative mating was better than with random mating when selection was done at a relatively high intensity.

Bearing in mind that any conclusions drawn from this kind of study apply only to the parameters specified, the results do give us a few pointers as to the conditions under which assortative mating of selected parents may give a better selection response than random mating. These are a high heritability, not too small a population, a large number of *loci* governing the trait under selection, and a fairly low intensity of selection. These conditions may be quite common in many animal breeding situations.

SUMMARY

A simulation study was done to compare the selection responses obtained with random mating versus assortative mating in the case of a polygenic trait. It was found that with equal additive gene effects and independent segregation, the conditions required for significant differences in response were a large number of *loci* affecting the trait, high heritability and low selection intensity. Under these conditions positive assortative mating gave the best response, followed by random mating and negative assortive mating in that order.

ZUSAMMENFASSUNG

Mit Hilfe eines Modellversuches wurden die Selektionswirkungen auf poligene Merkmale nach zufälliger und gelenkter Paarung miteinander verglichen. Die Resultate zeigten, das bei gleichen additiven Genwirkungen und unabhängiger Spaltung eine grosse Anzahl das Merkmal beeinflussender *Loci*, hohe Erbllichkeit und niedrige Selektionsintensität nötig waren, um signifikante Unterschiede der Selektionswirkungen zu erhalten. Unter diesen Bedingungen zeigte die positiv gelenkte Paarung die beste Selektionswirkung, gefolgt von zufälliger und dann von negativ gelenkter Paarung.

RESUMEN

Se ha realizado un estudio de simulación para comparar las respuestas a la selección obtenidas con cruzamientos al azar frente a cruzamientos afines en el caso de un carácter poligénico. Se encontró que con efectos genéticos aditivos iguales y segregación independiente, las condiciones requeridas para las diferencias significativas en la respuesta eran: un gran número de *loci* responsables del carácter, una elevada heredabilidad y una baja intensidad de selección. Bajo estas condiciones, el cruce positivo afín dio la mejor respuesta, seguido por el cruzamiento al azar y por el cruce negativo, por este orden.

REFERENCES

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