

CHOICE OF EVALUATION-SELECTION SYSTEM TO MAXIMIZE GENETIC RESPONSE AT THE SAME LEVEL OF INBREEDING

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SUMMARY

A stochastic simulation was used to compare genetic and inbreeding responses for different genetic evaluation-selection systems, viz; selection 1) at random, 2) on true breeding value (TBV), 3) on phenotype, 4) on BLUP estimated breeding value (EBV) and 5) on BLUP EBVH, using a false high heritability estimate. An algorithm to adjust the EBV of a selection candidate for the average relationship with those already selected was also used. The relation of the genetic response to inbreeding response at generation 10 is shown graphically for a range in the number of sires used. Comparisons show a gradual increase in the inbreeding (for the same number of sires) from random selection, selection on TBV, on phenotype, on EBVH and to the highest level with EBV, from co-selection of relatives. When the number of sires is fixed (and small--less than 20), it is possible to get substantial reductions in inbreeding for small reductions in response using EBVH, compared with selection on EBV. However, similar results can be obtained simply by increasing the number of sires used. Put in this graphical form for comparison, only modest gains in genetic response at the same level of inbreeding were obtained by the alternative evaluation-selection systems, and no single system seems generally optimum.

INTRODUCTION

More intense selection and increased accuracy of selection through use of information on relatives both lead to higher genetic response, but also lead to higher rates of inbreeding. It is, therefore, important to compare genetic evaluation selection strategies for response at the same level of inbreeding (Quinton et al., 1992). This can be done graphically, relating the genetic response with the level of inbreeding for a range in the numbers of sires used. The aim of this paper is to illustrate graphs for a range of genetic evaluation-selection systems to ascertain if there is any generally optimum system.

METHODS

A single trait was simulated stochastically using an infinite model of gene effects. The procedure has been described in Quinton et al., 1992. Differing from simulation studies reported by other authors, the number of sires per generation was varied to give the graph for genetic response on inbreeding. The population consisted of 1,024 progeny per generation, bred by 256 dams and either 8, 16, 32 or 64 sires. Responses were accumulated over 10 generations. Some 100 replicates were run for each case, so the mean responses were well estimated.

Selection was either; 1) on true breeding value (the extreme case), 2) on phenotype, 3) on BLUP estimated breeding value (EBV) using the true heritability (0.25), 4) on BLUP EBVH using a false (high) heritability (Grundty and Hill, 1993; Verrier et al., 1993) and 5) at random.

An algorithm to adjust the EBV of a selection candidate (i) for its average relationship (R_i) with those already selected, as proposed by Goddard and Smith (1990), was also used. This (EBVA) took the form of $EBV_i (1-kR_i)$, with k varied from 0.5 to 2.0.

RESULTS AND DISCUSSION

The results are given in graphical form to show the relation of genetic response to inbreeding response over a range of situations. Figure 1 shows that, with selection on true breeding value, high rates of genetic response (Sehested and Mao, 1992) can be obtained without high rates of inbreeding. This augers well for more accurate selection based on genetic markers associations (Zhang and Smith, 1992), or on marker (genetic) similarity (Nejati-Javaremi et al., 1994). The inbreeding from random selection, relative to the others, shows the proportion of inbreeding that is automatic due to the limited number of sires used. The levels of inbreeding (with the same number of sires selected) increase gradually with selection on TBV, on phenotype, on EBVH and are highest with EBV, from the co-selection of relatives.

Comparison of the evaluation-selection systems are usually made for a fixed number of sires (eg. Grundy and Hill, 1993; Brisbane and Gibson, 1993). For example, in Figure 1 with 8 sires, by using EBVH (0.65) instead of EBV (0.25), a reduction of inbreeding from .294 to .188 (a 36% reduction) for a reduction in genetic response from 3.69 to 3.61 s.d. units (a 2% reduction) was obtained. This seems a worthwhile change. However, it can be matched simply by increasing the number of sires selected on EBV from 8 to 16, and similarly for other cases. Thus, it is important to compare systems at the same level of inbreeding as is feasible with the graphical form presented. When compared in this form, differences between the systems are small.

Figure 2 shows graphs for some other cases including the algorithm (EBVH) adjusting EBV for the average relationship of the selection candidate with individuals already selected (with $k = 1$). The results in the two figures show that it is difficult to deviate far from the average graph of response and inbreeding. No single system is optimum for maximizing the genetic response at all levels of inbreeding. The optimum seems to depend on the situation studied, on the population size (Smith and Quinton, 1993; Verrier et al., 1993), on the number of generations, on the level of inbreeding targeted, on the heritability, and on other factors.

CONCLUSIONS

A graphical approach relating the genetic response to inbreeding for different numbers of sires selected is recommended in choosing among evaluation systems. It appears difficult to obtain systems which improve much on the general graph for response and inbreeding, and the optimum system seems to depend on the situation studied.

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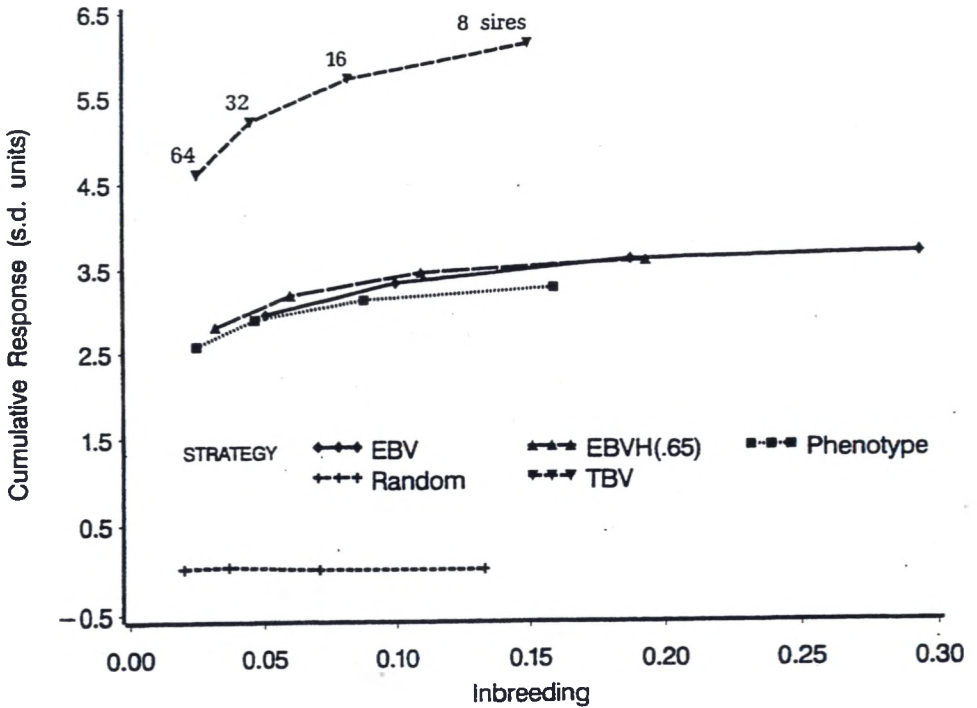


Figure 1.

Cumulative genetic response and inbreeding from 10 generations of selection on true breeding value (TBV), on phenotype, on BLUP estimated breeding value (EBV) [using the true heritability (0.25)], on BLUP estimated breeding value [using a high (false) heritability (0.65) (EBVH.65)], and random selection. 1,024 progeny are born per generation from 256 dams and either 8, 16, 32 or 64 sires, the marked points on the graphs. 100 replicates.

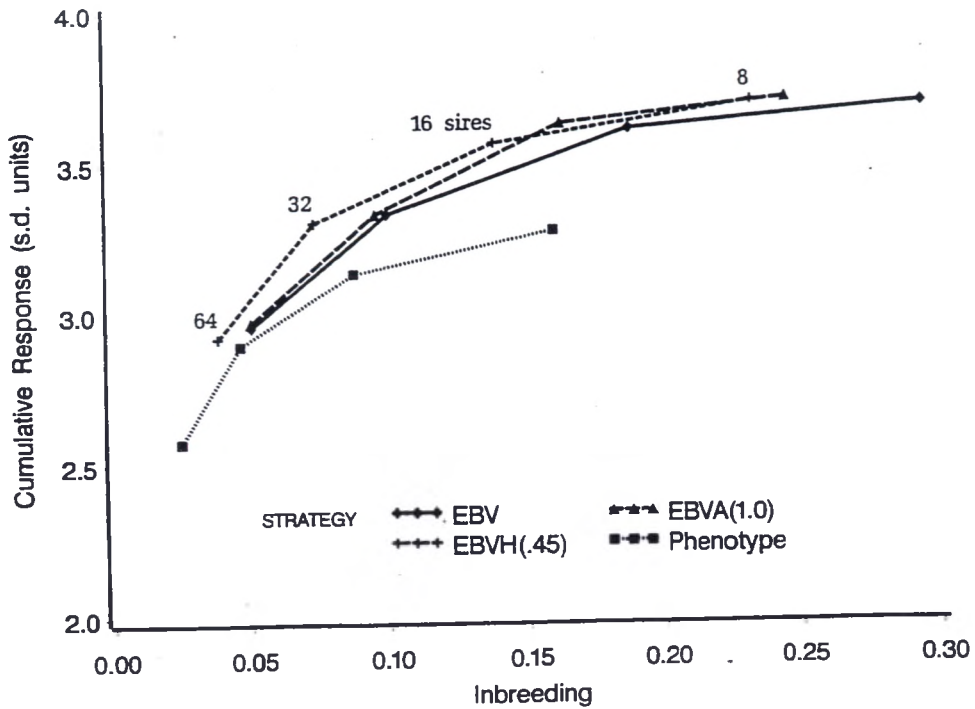


Figure 2.

Cumulative genetic response and inbreeding for different evaluation-selection systems, for comparison with results in Figure 1. The methods of selection are on phenotype, on BLUP estimated breeding value (EBV), on BLUP estimated breeding value (using a high (false) heritability (0.45) EBVH(.45)), and on the algorithm adjusted EBV (EBVA (k = 1.0)).