PREDICTED AND OBSERVED RESPONSES IN BLUP ESTIMATES OF GENETIC GAIN

J.W.James
Centre for Advanced Technologies in Animal Genetics and Reproduction (Reprogen), Faculty of Veterinary Science, University of Sydney, NSW 2006.

SUMMARY

For balanced single-generation selection lines, the BLUP estimate of genetic gain is well known to be exactly equal to the predicted response if there is no control line. With a control line, the estimated genetic gain is a weighted average of the predicted and observed responses. The relative weight given to observed response is greater for high heritability, large family size and intense selection.
Keywords: BLUP, response to selection, genetic gain

INTRODUCTION

In recent years, BLUP has been very extensively used to compute estimated breeding values (EBVs), and for estimates of genetic gain which are readily derived from the EBVs. It has long been known (Thompson, 1979) that such estimates may be strongly influenced by the initial assumptions made, and in general a combination of assumptions and data yields the estimated genetic gain. One example of this is the analysis of a sheep selection experiment by Blair and Pollack (1984), where the estimated genetic trend depended strongly on the assumed heritability.

Complex data structures such as those observed in practice are too difficult to analyse mathematically, but simple structures have been studied by Thompson (1986), Sorensen and Johansson (1992) and Ollivier (1999), and among the results obtained have been the relative weights given to observed and predicted responses. In this paper an extension of a model analysed by Sorensen and Johansson (1992) and Ollivier (1999) will be treated, but attention will be limited to the relative weights.

MODEL

The base population is assumed to consist of m males and m females, all unrelated and not inbred. From among these, q animals of each sex are selected on their phenotype for the relevant trait and pair mated to produce n male and n female progeny per mated pair. Thus the size of the base population is $2m$ and that of the progeny population is $2qn$, these sizes being possibly different. This allows the effects of selection intensity and family size to be separated, whereas when the two generations are equal in size the selection intensity is the reciprocal of the number of progeny of one sex. Phenotypic records of all $2m + 2qn$ individuals are available, for simplicity assumed corrected for the known effect of sex. The assumed heritability is h^2 and we define $k = (1 - h^2)/h^2$.

RESULTS AND DISCUSSION

There are two cases to be considered: with or without a control population. If there is no control, two means must be fitted in the model with the result that the estimated genetic gain is given by Sh^2, where S is the observed selection differential. This is intuitively obvious, since there is no way of