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A STUDY OF THE VARIABILITY OF ESTIMATES OF HERITABILITY AND THEIR STANDARD ERRORS DERIVED BY PATERNAL HALF-SIB TECHNIQUES USING SIMULATED DATA

A thesis presented in partial fulfilment of the requirements for the degree of Doctor of Philosophy in Animal Science at Massey University

JOHN MARTIN RENDEL

ABSTRACT

Data sets were generated that varied in the number of sires (20, 50, 100, 150 and 200) and progeny per sire (a mean of 20, 50, 70 and 100). These data sets were generated for balanced data and, in an effort to approximate actual flock data, unbalanced data based on a normal distribution of progeny per sire with standard deviations of 2, 5 and 7. In addition, data sets were generated with a standard deviation of 14, 25 and 29 progeny per sire, but for data set size of 100 sires with a mean of 100 progeny per sire, only. Also, numbers of progeny per sire and numbers of sires from 6 actual flocks were used to generate data sets. The sets were generated to conform with a 1-way random model with the sire variance set at 0.6783 and error variance at 11.0106, giving a paternal half-sib heritability of 0.2321. Each combination of number of sire and progeny per sire was generated 100 times (i.e. 100 replicates) at each level of unbalance. Sire and error variances and heritabilities were estimated, as well as their standard errors, for each replicate using Henderson's Method 1 (HM), Maximum Likelihood (ML) and Restricted Maximum Likelihood (REML).

There was good agreement between the population heritabilities and sire and error variances, and the corresponding mean of the replicates that made up each data set. There was also little difference between the results of the 3 methods of estimating the variance components. The Mean Squared Error (MSE) was similar for each method except for the data sets based on the flocks where the MSE of the sire variances for HM was larger than those for ML and REML. The MSE was largest for data sets consisting of 20 sires and 50 sires with a mean of 20 progeny per sire.

The standard errors of the heritability and sire and error variances appear to be good indicators of the variation of estimates within data sets regardless of the level of unbalance or method of estimation.

The differences between heritability estimates from 31 flocks for weaning weight of Coopworth lambs was shown to be greater than that estimated by the standard error. The implications of this are discussed with respect to the problems of pooling estimates from various sources.

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ACKNOWLEDGEMENTS

It is with pleasure that I extend gratitude to my supervisors, Dr G.A. Wickham and Professor A.L. Rae, for their assistance and advice given during the course of the study. For his unerring help and willingness to discuss the study, a special thanks goes to Dr G.A. Wickham.

I thank Massey University for employment as a Junior Lecturer over the period of study. This was an invaluable experience.

To the Department of Animal Science staff and graduate students, thank you for providing a stimulating environment in which to work.

My thanks and appreciation goes to Alison Glass for entering the text into the word processor, and for her companionship over the last year.

To those who contributed to the thesis and my well being during the time of study, but are uncited in the acknowledgements, I offer the following:

> "We are a tired, nerve shaken, over-civilised people, finding out that going to the mountains is going home, that wildness is a necessity, that parks are fountains of life."

> > (John Muir, 1838-1914)

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