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

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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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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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CHAPTER ONE
INTRODUCTION

Selection has been the main method of genetic improvement in farm animals and rates of future genetic improvement will remain dependent on the efficiency of selection.

The rate of gain in a genetic improvement programme relies on the accurate prediction of the genetic merit of animals (breeding values). This in turn relies on the accurate estimation of genetic parameters. Breeding values obtained using Best Linear Unbiased Prediction (BLUP) procedures are not best linear unbiased predictors unless the variances of traits and covariances between traits specified in the programme are true population parameters (Kennedy, 1981).

In devising efficient schemes, genetic parameters such as heritabilities and genetic correlations are required. The population parameters that will apply while the scheme is functioning are never known. What is often available are estimates based on historical data from samples of various populations.

In recent years the number of these estimates has grown rapidly. Having many estimates of genetic parameters for traits has made the task of choosing the most appropriate parameter to apply in a breeding scheme more complex.

Most schemes for the genetic improvement of large farm animals have been operated on a nationwide or large region basis. It would seem desirable to combine genetic parameters estimated for a particular trait from groups of animals in that nation or region into some overall estimate to be used in a breeding scheme. One method of combining estimates is to weight by the inverse of their standard error. This weights the parameters that appear most accurate (low standard error) more heavily than inaccurate parameters (large standard error).

The majority of methods that estimate the standard error of paternal half-sib heritabilities are based on Pearson's (1897) approximate variance of a ratio. This requires the variances of the individual variance components to be known. In order to estimate the variances of variance components, the population variance needs to be known, which is unlikely. The population variance component is therefore replaced by an estimate, often the estimate for which the variance is required. This could lead to the variances of variance components, and hence the standard error of the heritability estimate, being biased.

It was the purpose of this study investigate the effect of the method of variance component estimation, size of the data set and levels of unbalance, which are realistic for the animal breeding situation, on the accuracy of variance components and heritabilities in estimating population values, and also the accuracy of standard errors of variance components and heritabilities.

CHAPTER TWO
REVIEW OF LITERATURE

2.1. Introduction

The estimation of genetic parameters in the case of paternal half-sib analyses requires the estimation of variance components.

This review will cover the estimation of genetic variances using Analysis of Variance, Maximum Likelihood and Restricted Maximum Likelihood techniques. The estimation of sampling variances of the estimates will also be reviewed. Likewise, the estimation of sampling variances of heritabilities derived from paternal half-sib analyses, obtained by different techniques of estimating variance components will be discussed.

2.2. Estimation of Variance Components

2.2.1 Balanced Data

Balanced data sets have equal numbers of observations in every subclass. There is one universally accepted method of estimating variance components from such data. This involves equating the expected values of the mean squares from an appropriate analysis of variance, to their calculated mean squares. The equations are then solved for the unknown variance component. This is called the analysis of variance (ANOVA) method (Searle, 1971a).

Variance components estimated from balanced data by equating expected mean squares to their calculated value have several desirable properties (Searle, 1971b,1974):

(i) They are unbiased
(ii) Under normality, sampling variances are available
(iii) They are easy to compute
(iv) They have minimum variance among all quadratic unbiased estimators
(v) Under normality they have minimum variance among all unbiased estimators

A disadvantage of the ANOVA method is that it is possible to get negative estimates of variance components (Thompson 1962; Searle 1971b, 1974).

Fisher (1928) was one of the first to describe the ANOVA method for the 1-way random model. The resulting variance components were used to estimate the intraclass correlation coefficient. Daniels (1939) used the ANOVA method to obtain variance components from a 2-way model with interaction and a 3-way model without interaction. Winsor and Clarke (1940) estimated variance components from a 3-way model with interaction. Ganguli (1941) extended the ANOVA method to a 4-way nested classification.

2.2.2 Unbalanced Data

Hammersley (1949) recognised that the unbalanced data sets (ie data with unequal number of observations in subclasses, including some with no observations) were more representative of 'real world' situation of estimating variance components.

The estimation of variance components from unbalanced data is more complex than in the balanced case. Hammersley (1949) notes "The mathematics necessary to obtain the required formulae for the general case involves the manipulation of double series, in which the limits of numeration for one of the two suffixes depends arbitrarily upon the value of the other suffix. These series are finite, and they need to be combined as quartic polynomials; and hence the domain over which the analysis extends is an 'irregular' eight dimensional lattice. So far as I know, none of the conventional methods of the tensor calculus or the algebra of sets is sufficiently powerful to yield a solution without excessive algebraic labour; and I have therefore employed what may be called 'dummy Kronecker-deltas' to solve the problem". Likewise, Searle (1971b) states "all the methods (for estimating variance components from unbalanced data) involve relatively cumbersome algebra; discussion of unbalanced data can therefore easily deteriorate into a welter of symbols.....". Further "However, with regard to the latter (unbalanced data) the literature only covers special cases to calculate expected mean squares from an ANOVA table and indicates that new and laborious 'algebraic heroics' are required every time a new unbalanced body of data is encountered" (Hartley 1967).

Several methods are available to estimate variance components from unbalanced data, but as yet, none is universally accepted (Searle 1974). The methods that will be discussed are Henderson's methods 1, 2 and 3; maximum likelihood; and restricted maximum likelihood.

2.2.2.1 Henderson's Methods

Henderson's (1953) methods of estimating variance components all involve calculating mean squares of some kind, obtaining their expected values, equating mean squares to their expectations and solving linear equations for the unknown variance components (Searle 1968).

Henderson's (1953) Method 1 (HM1) involves calculating the sums of squares analogous to those used for analysis of variance of balanced data. The sums of squares are then equated to their expected values. The advantages of HM1 are that the resulting estimates are relatively easy to calculate and are unbiased for random models (Searle 1974). But HM1 does not give unbiased estimates of variance components for mixed models with unbalanced data. Hence it is inappropriate for mixed models (Searle 1968). Henderson (1984) notes that the bias due to the fixed effects can be evaluated.

Henderson's (1953) Method 2 (HM2) is designed to correct the deficiency of obtaining biased estimation of variance components when HM1 is used with mixed models (Searle, 1971b). HM2 first uses the data to estimate fixed effects treating the random effects as fixed. The data are then adjusted using these fixed effects, and variance components estimated from the data using HM1 with appropriate adjustments made to the expectations of sums of squares (Searle 1971a; 1974; Kennedy 1981). The resulting variance component estimates are unbiased providing there are no interactions between the random and fixed effects. Thus a disadvantage of HM2 is that the model cannot contain interactions between fixed and random effects (Searle 1968).

Henderson's (1953) Method 3 (HM3) uses reductions in sums of squares due to fitting different subgroups of factors in the models, rather than analysis of variance sums of squares as HM1 and HM2 use. The expected values of the reductions in sums of squares are equated with the reduction in sums of squares, and the variance components estimated (Searle 1968; 1971a). The importance of HM3 is that it yields variance components that are unaffected and uncomplicated by the fixed effects, provided the random effects are not confounded with the fixed effects. HM3 is the preferred method of mixed models. A disadvantage of HM3 is that, in the mixed model, more reductions can be derived than there are variance components to estimate (Searle 1968), hence in unbalanced designs, estimates will not be invariant to the choice of reductions (Henderson 1984). Another disadvantage of HM3 is that, in models with large numbers of effects, generalized inverses of very large matrices may be required (Searle 1968). This is unlikely to be a problem with today's computers.

Henderson's (1953) methods all yield unbiased, translation invariant estimates of the variance components provided the model is appropriate to the method (Kennedy, 1981). But if selection is being undertaken in herds/flocks for which variance components will be estimated, the estimation derived using Henderson's (1953) methods will be biased (Kennedy 1981).

2.2.2.2 Maximum Likelihood Techniques

The maximum likelihood (ML) estimator of Θ (a vector of unknown parameters), say $\hat{\Theta}$, is the value of Θ in Ω, the parameter space, which maximizes $\mathcal{L}(\Theta)$, the likelihood function . In words, Θ defines the density from which the sample, y, is 'most likely' to have come (Quaas 1976).

ML estimation of variance components from the unbalanced mixed linear model was described by Hartley and Rao (1967). ML estimators of variance components are translation invariant, functions of every sufficient statistic, consistent and asymptotically normal and efficient (Kennedy, 1981). A major disadvantage of the ML technique of estimating variance components in a mixed model is that the resulting estimators are biased (Quaas, 1976). Harville (1977) stated that the ML estimates do not generally coincide with ANOVA estimates for balanced data. The estimates are also generally biased downwards (Patterson and Thompson, 1974; Corbeil and Searle, 1976; Swallow and Monahan, 1984). Also the ML estimators of variance components do not take into account the loss of degrees of freedom due to the estimation of the fixed effects (Corbeil and Searle, 1976).

Patterson and Thompson (1974) stated that more general methods were required for estimating variance components from unbalanced data and these methods need the desirable properties of efficiency and unbiasedness. Also the methods must reduce to ANOVA in the completely balanced case and so at least give continuity in practice.

For the unbalanced mixed linear model, Patterson and Thompson (1971, 1974) maximised the likelihood of the vector of observations not with respect to each element of the fixed effects and with respect to each of the variance components, but with respect to a component that is free of fixed effects. This procedure was called Modified Maximum Likelihood by Patterson and Thompson (1971, 1974) but Corbeil and Searle (1976) refer to the method as Restricted Maximum Likelihood (REML) as maximization is taking place over a restricted parameter set. [Robinson (1987) has recently referred to the procedure as Residual Maximum Likelihood].

REML estimates of variance components have some desirable properties. The estimates are not only invariant to the fixed effects in the model but are also free of the estimates of fixed effects (Corbeil and Searle, 1976). With balanced data, the REML estimates are identical to the ANOVA estimates, a property not shared by ML.

Thompson (1982) notes that the ML and REML procedures also have the property of estimating the base population parameters free of bias due to selection. Simulation studies have verified this (e.g. Rothschild et al, 1979). Henderson (1986) states 'this property is a compelling argument for using these methods in data arising from selection'.

A disadvantage of using REML (and ML) with unbalanced data is that in order to solve the equations an iterative procedure is required. Thus efficient computer algorithms are essential.

2.3. Estimation of Standard Error of Variance Components

2.3.1 ANOVA Type Methods

For balanced data, Daniels (1939) noted that the procedure for estimating the standard error of a random factor is straight-forward, as the mean squares (MS) in the analysis of variance are independently distributed as $\frac{\chi^2}{f}E(MS)$ with variances estimated by $\frac{MS^2}{2(f+2)}$, f being the corresponding degrees of freedom. The variances of the variance components are then obtained by combining the variances of the appropriate mean squares. Satterthwaite (1941) suggested the divisor for the variance of the MS should be f, not f+2. Thus for any estimated variance component, say

$$\hat{\sigma}^2 = a_1MS_1 + a_2MS_2 + \cdots + a_kMS_k$$

where $MS_i (i=1,2,\ldots,k)$ is a mean square based on f_i degrees of freedom, and a_i are the appropriate multipliers to obtain the estimated variance components for the linear combination of mean squares, $\hat{\sigma}^2$ has sampling variance,

$$V(\hat{\sigma}^2) = \frac{2a_1^2[E(MS_1)]^2}{f_1} + \frac{2a_2^2[E(MS_2)]^2}{f_2} + \cdots + \frac{2a_k^2[E(MS_k)]^2}{f_k}$$

It is therefore possible to write out and estimate (replacing expected values, as these are very rarely known, with their estimated values) the sampling variance of any estimated variance component in a balanced, fully random, multiple, classification model (Crump, 1951). But for the standard error of $\hat{\sigma}^2$ to be of value, the distribution of $\hat{\sigma}^2$ should not differ greatly from normal (Daniels, 1939).

Hammersley (1949) addressed the problem of estimating the standard error of variance components obtained from the 1-way unbalanced classification with a model:

$$y_{ij} = \mu + \alpha_i + \epsilon_{ij}$$

where

y_{ij} = j^{th} observation in the i^{th} class

μ = general mean

α_i = the effect of the i^{th} class ($i=1,2,\ldots,c$) containing n_i observations. The α_i's are from a normally distributed population with mean 0 and variance σ_a^2

ϵ_{ij} = random residual, from a normally distributed population with mean 0 and variance σ_e^2, that are mutually independent and independent of the α_i's.

Hammersley showed that an unbiased estimate of the between class variance is

$$\hat{\sigma}_a^2 = \frac{N(c-1)}{(N^2 - s_2)}(MSA - MSE)$$

where N = total number of observations

c = number of classes

MSA = mean square between classes

MSE = mean square within classes

and

$s_j = \sum_{a=1}^{k} n_i^j$; n_i being the number of observation in the i^{th} class.

Also,

$$\begin{aligned} \text{Var (SSA)} &= E\,(SSA^2) - \{E(SSA)\}^2 \\ &= \sigma_a^4\{2(s_2 - \frac{2s_3}{N} + \frac{s_2^2}{N^2}) + \Gamma_2(s_2 - \frac{2s_3}{N} + \frac{s_4}{N^2})\} \\ &\quad + 4\sigma_e^2\sigma_a^2(N - \frac{s_2}{N}) + \sigma_e^4\{2(c-1) + \gamma_2(s_{-1} + \frac{1-2c}{N})\} \end{aligned}$$

and,

$$\text{Var (SSE)} = \sigma_e^4\{2(N-c)+\gamma_2(s_{-1}+N-2c)\}$$

and,

$$\text{Cov (SSA, SSE)} = \sigma_e^4\gamma_2(c - 1 + \frac{c}{N} - s_{-1})$$

where SSE = sum of squares for the error

SSA = sum of squares between classes

$\Gamma_2\sigma_a^4$ = fourth cumulant of the distribution between classes

$\gamma_2\sigma_e^4$ = fourth cumulant of the distribution within classes

The results given for Var(SSE) and Cov(SSA,SSE) and the last term for Var(SSA) have been given by Pearson (1931, cited by Hammersley, 1949). Also, if the within class source is distributed normally, Cov(SSA,SSE)=0 and hence in the general case Cov(SSA,SSE) contains only a term in $\sigma_e^2\gamma_2$.

Thus,

$$\text{Var}(\hat{\sigma}_a^2) = \frac{N^2(c-1)^2}{(N^2-s_2)^2}\left\{\frac{\text{Var(SSA)}}{(c-1)^2} - \frac{2\text{Cov(SSA,SSE)}}{(c-1)(N-c)} + \frac{\text{Var(SSE)}}{(N-c)^2}\right\}$$

$$= \frac{2\sigma_a^4}{(N^2-s_2)^2}\left\{(N^2s_2 - 2Ns_2 + s_2^2) + \tfrac{1}{2}\Gamma_2(N^2s_2 - 2Ns_3 + s_4)\right\}$$

$$+ \frac{4\sigma_e^2\sigma_a^2N}{(N^2-s_2)} + \frac{2\sigma_e^4N^2(N-1)}{(N^2-s_2)^2(N-c)}\left\{(c - 1 + \tfrac{1}{2}\gamma_2\frac{(N-1)}{(N-c)}(s_{-1} - \frac{c^2}{N})\right\}.$$

When class numbers are equal, the above reduces to

$$\mathrm{Var}(\hat{\sigma}_a^2) = \frac{2(N\sigma_a^2 + c\sigma_e^2)^2}{N^2(c-1)} + \frac{2(c\sigma_e^2)^2}{N^2(N-c)} + \frac{\sigma_a^4\Gamma^2}{c}$$

If σ_a^2 is replaced by $\hat{\sigma}_a^2$ (since $E(\hat{\sigma}_a^2)=\sigma_a^2$) and σ_e^2 is replaced by MSE (since $E(MSE)=\sigma_e^2$), and, as is usual in estimating the standard error of a variance, Γ_2 and γ_2 are neglected, then for the unbalanced case,

$$\mathrm{Var}(\hat{\sigma}_a^2) = \frac{2}{(N^2-s_2)^2}\left\{(N^2s_2 - 2Ns_3 + s_2^2)\hat{\sigma}_a^4 + 2N(N^2 - s_2)\hat{\sigma}_a^2MSE\right.$$

$$\left. + \frac{N^2(N-1)(c-1)}{(N-c)}MSE^2\right\}$$

and for the balanced case,

$$\mathrm{Var}(\hat{\sigma}_a^2) = \frac{2}{N^2}\left(\frac{MSA^2}{c-1} + \frac{MSE^2}{N-c}\right)$$

which is the same as derived by Daniels (1939) for balanced data.

Henderson (1953) commented that the relative sizes of the sampling variances of the estimates obtained by Henderson's 3 methods are not known.

Searle (1956) developed matrix methods to deal with the unbalanced 1-way random classification. The model was,

$$y_{ij} = \mu + \alpha_i + \epsilon_{ij}$$

where

y_{ij} = jth observation in the ith class

μ = general mean

α_i = the effect of the ith class (i=1,2,...,c) containing n_i observations. The α_i's are from a normally distributed population with mean 0 and variance σ_a^2

ϵ_{ij} = random residual, from a normally distributed population with mean 0 and variance σ_e^2, that are mutually independent and independent of the α_i's..

It was assumed by Searle (1956) that the y_{ij}'s are a set of multivariate normally distributed random variables with variance-covariance matrix V and vector of means 0.

If y is a function of the x's, $y = x^T F x$ is defined by the symmetric matrix F, then it can be shown that,

$$\kappa_r^{(y)} = 2^{r-1}(r-1)!\ \mathrm{trace}(VF)^2$$

where $\kappa_r^{(y)}$ is the r^{th} cumulant of y.

For r=2, this gives the result,

$$\mathrm{variance}\ (y) = 2\ \mathrm{trace}(VF)^2$$

If x^T is defined as a row vector of observations $(x_{11},\ldots,x_{1n_1},\ldots,x_{c1},\ldots,x_{cn_c})$ and V as a square matrix of order N, the only nonzero elements being c square submatrices of order n_i $(i = 1,\ldots,c)$ lying along the diagonal, each with diagonal term $\sigma_a^2 + \sigma_e^2$ and non diagonal term σ_a^2. The quadratic form for $(N-c)\hat{\sigma}_e^2$ can be expressed as,

$$(N-c)\hat{\sigma}_e^2 = x^T F x$$

which leads to

$$\mathrm{Var}(\hat{\sigma}_e^2) = \frac{2\sigma_e^4}{N-c}\ .$$

Similarly,

$$\mathrm{Var}(\hat{\sigma}_a^2) = \frac{2}{f^2}\left\{\frac{\sigma_e^4(N-1)}{(c-1)(N-c)} + \frac{2\sigma_e^2\sigma_a^2(N^2 - s_2)}{N(c-1)^2} + \frac{\sigma_a^4(N^2 s_2 + s_2^2 - 2Ns_3)}{N^2(c-1)^2}\right\}$$

where $s_j = \sum_{i=1}^{c} n_i^j$

$$f = \frac{c-1}{N - \frac{s_2}{N}}$$

which can be shown to be equivalent to the equation obtained by Hammersley (1949).

Searle (1956) estimates

$$\mathrm{Cov}(\hat{\sigma}_a^2,\hat{\sigma}_e^2) = -\frac{1}{f}\mathrm{var}(\hat{\sigma}_e^2)$$

which gives

$$\mathrm{var}(\hat{\sigma}_a^2 + \hat{\sigma}_e^2) = (1-\frac{2}{f})\mathrm{var}(\hat{\sigma}_e^2) + \mathrm{var}(\hat{\sigma}_a^2)$$

Smith (1956) also derived the sampling variances in a 1-way random unbalanced classification. The variance of $\hat{\sigma}_e^2$ was

$$\mathrm{var}(\hat{\sigma}_e^2) = \frac{2\hat{\sigma}_e^4}{N-c}$$

and the variance of $\hat{\sigma}_b^2$ was

$$\mathrm{var}(\hat{\sigma}_a^2) = \frac{\mathrm{var}(SSA) + k_1^2\mathrm{var}(\hat{\sigma}_e^2)}{k_2^2}$$

where $k_1 = c-1$

$$k_2 = N - \frac{s_2}{N}$$

and

$$\mathrm{var(SSA)} = 2\hat{\sigma}_e^4\, k_1 + 4\hat{\sigma}_e^2\hat{\sigma}_a^2\, k_2 + 2\hat{\sigma}_a^4(s_2 - \frac{2s_3}{N} + \frac{s_2^2}{N^2}).$$

The $\mathrm{var}(\hat{\sigma}_a^2)$ derived by Smith (1956) can be shown to be the same as that derived by Searle (1956). Thus it appears as if Searle (1956) and Smith (1956) both independently obtained the sampling variance of the between classes variance component for a 1-way random model, Smith appearing to be unaware of Daniels (1939) results and both authors being unaware of Hammersley's (1949) paper. Smith and Searle derived the variances for differing ends - Smith to derive the sampling variance of the intra class correlation and Searle to show the advantages of matrix algebra.

Searle (1958) obtained the sampling variances for variance components (estimated by HM1) in the unbalanced 2-way classification with interaction. The model was

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \epsilon_{ijk}$$

where

$k = 1,2,\ldots,n_{ij}$; $i = 1,2,\ldots,a$ and $j = 1,2,\ldots,b$

μ is a general mean

α_i and β_j are main effects

$(\alpha\beta)_{ij}$ is an interaction term

ϵ_{ijk} is a residual error

All terms (except μ) are taken as being normally distributed with zero means, and variance σ_a^2, σ_b^2, σ_{ab}^2 and σ_e^2, respectively.

For a sample of N observations in N' cells of this 2-way classification, an analysis of variance can be written as

TERM	df	SUMS OF SQUARES	
Between A classes	$a-1$	$T_a - T_f$	$=S_a$
Between B classes	$b-1$	$T_b - T_f$	$=S_b$
Interaction AxB	$N'-a-b+1$	$T_{ab} - T_a - T_b + T_f$	$=S_{ab}$
Residual	$N-N'$	$T_o - T_{ab}$	$=S_w$
TOTAL	$N-1$	$T_o - T_f$	

where T's are uncorrected sums of squares. With $n_{i.} = \sum_{j=1}^{b} n_{ij}$, $n_{.j} = \sum_{i=1}^{a} n_{ij}$ and using the customary notation for means,

$$T_a = \sum_{i=1}^{a} n_{i.}\bar{y}_{i..}^2 \qquad T_b = \sum_{j=1}^{b} n_{.j}\bar{y}_{.j.}^2 \qquad T_{ab} = \sum_{i=1}^{a}\sum_{j=1}^{b} n_{ij}\bar{y}_{ij.}^2$$

$$T_o = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n_{ij}} y_{ijk}^2 \qquad T_f = N\,\bar{y}_{\dots}^2$$

HM1 equates the first four lines of the above table to its expected value. Thus,

$$\begin{aligned}
T_a - T_f &= S_a &&= (N - k_1)\hat{\sigma}_a^2 + (k_{12} - k_2)\hat{\sigma}_b^2 + (k_{12} - k_3)\hat{\sigma}_{ab}^2 \\
&&&\quad + (a-1)\hat{\sigma}_e^2 \\
T_b - T_f &= S_b &&= (k_{21} - k_1)\hat{\sigma}_a^2 + (N - k_2)\hat{\sigma}_b^2 + (k_{21} - k_3)\hat{\sigma}_{ab}^2 \\
&&&\quad + (b-1)\hat{\sigma}_e^2 \\
T_{ab} - T_a - T_b + T_f &= S_{ab} &&= (k_1 - k_{21})\hat{\sigma}_a^2 + (k_2 - k_{12})\hat{\sigma}_b^2 \\
&&&\quad + (N - k_{12} - k_{21} + k_3)\hat{\sigma}_{ab}^2 + (N' - a - b + 1)\hat{\sigma}_e^2 \\
T_o - T_{ab} &= S_w &&= (N - N')\hat{\sigma}_e^2
\end{aligned}$$

where the k's, are functions of the n_{ij}'s, namely

$$k_{12} = \sum_{i=1}^{a} \frac{\sum_{j=1}^{b} n_{ij}^2}{n_{i\cdot}} \qquad k_{21} = \sum_{j=1}^{b} \frac{\sum_{i=1}^{a} n_{ij}^2}{n_{\cdot j}}$$

$$k_1 = \frac{1}{N}\sum_{i=1}^{a} n_{i\cdot}^2 \qquad k_2 = \frac{1}{N}\sum_{j=1}^{b} n_{\cdot j}^2 \qquad k_3 = \frac{1}{N}\sum_{i=1}^{a}\sum_{j=1}^{b} n_{ij}^2$$

In the analysis of variance S_w has a χ^2 distribution with $N-N'$ degrees of freedom. Hence

$$\text{var}(\hat{\sigma}_e^2) = \frac{2\sigma_e^4}{N-N'}$$

Writing P for the matrix of coefficients of $\hat{\sigma}_a^2$, $\hat{\sigma}_b^2$ and $\hat{\sigma}_{ab}^2$, then the equations of the expected value of the sum of squares can be written as,

$$\begin{bmatrix} 1 & 0 & 0 & -1 \\ 0 & 1 & 0 & -1 \\ -1 & -1 & 1 & 1 \end{bmatrix} \begin{bmatrix} T_a \\ T_b \\ T_{ab} \\ T_f \end{bmatrix} = P \begin{bmatrix} \hat{\sigma}_a^2 \\ \hat{\sigma}_b^2 \\ \hat{\sigma}_{ab}^2 \end{bmatrix} + \hat{\sigma}_e^2 \begin{bmatrix} a-1 \\ b-1 \\ N'-a-b+1 \end{bmatrix}$$

which can be rewritten as,

$$Ht = Pv + \hat{\sigma}_e^2 m$$

Hence the equation for estimating the variance components is (Bush and Anderson, 1963):

$$v = P^{-1}(Ht - \hat{\sigma}_e^2 m)$$

The variance-covariance matrix of $\hat{\sigma}_a^2$, $\hat{\sigma}_b^2$, $\hat{\sigma}_{ab}^2$ and $\text{var}(vv^T)$ can be expressed in terms of the variance-covariance matrix of the T's, $\text{var}(tt^T)$, as $\hat{\sigma}_e^2$ is independent of the terms in Ht. Thus,

$$\text{var}(vv^T) = P^{-1}\{H\text{var}(tt^T)H^T + mm^T\text{var}(\hat{\sigma}_e^2)\}P^{-1T}$$

and

$$\mathrm{Cov}(\hat{\sigma}_e^2, v) = -P^{-1} m \,\mathrm{var}(\hat{\sigma}_e^2)$$

The only unknown term in these expressions is $\mathrm{var}(tt^T)$. Searle (1978) obtained these expressions by solving the equation $\mathrm{var}(y) = 2\ \mathrm{trace}(VF)^2$. The equations obtained reduced with balanced data, to the well known ANOVA case (Searle, 1958).

Searle (1958) notes that 'estimates with any optimum properties have not been obtained, and it would mean that the only feasible estimation procedure in a practical case would be that of replacing the variance components in these formulae by their estimates.'

Searle (1961) derived sampling variances for variance components for the unbalanced 2-way nested classification, using the matrix methods set out by Searle (1958). Mahamunulu (1963) did likewise in deriving sampling variances of variance components in the unbalanced 3-way nested classification.

Low (1964) estimates the sampling variances of variance components from the adjusted analysis for a non-orthogonal 2-way classification without interaction. The model is,

$$Y = \mu j + X_1\beta + X_2\alpha + \epsilon$$

where

Y = vector of N observations
μ = a constant
j = a vector of N 1's
X_1 = an N × b incidence matrix of the β_j's
β = a b × 1 vector having elements β_j
X_2 = an N × t incidence matrix of the α_i's
α = a t × 1 vector having elements α_i
ϵ = an N × 1 vector of residual error terms.

The analysis of variance can be written as

TERM	df	SUM OF SQUARES
β unadjusted	$b-1$	$T_b - T_f$
α adjusted for β	$t-1$	T_{aa}
Residual	$N-b-t+1$	T_e
TOTAL	$N-1$	$T_o - T_f$

where $T_b = \sum n_{.j}\bar{y}^2_{.j.} = Y^T X_1 (X_1^T X_1)^{-1} X_1^T Y$

$T_o = \sum_i \sum_j \sum_k y^2_{ijk} = Y^T I\, Y$ where I is an identity matrix

$T_f = N\bar{y}^2_{...} = \frac{Y^T J Y}{N}$ J being a N x N matrix of 1's

[The expectations, variances and covariances of T_b, $T_o$and T_f were obtained by Searle, 1958].

The estimates of the variance components were then obtained. Low (1964) commented that, "these estimates (using 'adjusted' mean squares) will usually be more efficient than those using 'unadjusted' mean squares". The variance of the variance components were then derived by Low (1964) using exactly the same methods as described by Searle (1958, 1961). Low (1964) also showed how the procedure may be extended when an interaction term is added to the model.

Perhaps the first consideration of estimating variances of variance components in a mixed model was in a 3-way classification, consisting of 1 fixed effect and 2 random effects (Blischke, 1966). Blischke (1966) used HM2 (Henderson, 1953) to estimate the variance components. The model was,

$$y_{ijhg} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \gamma_h + \epsilon_{ijhg}$$

where μ is the overall mean

α_i and β_j are random effects assumed to be mutually independent, normally distributed with zero means and variances σ^2_a and σ^2_b

$(\alpha\beta)_{ij}$ is the interaction between α_i and β_j, being mutually independent, normally distributed random variable with mean zero and variance σ^2_{ab}.

γ_h is an unknown fixed effect

ϵ_{ijhg} is the random residual error, being mutually independent, normally distributed with mean zero and variance σ^2_b.

and y_{ijhg} is the g^{th} observation on the ijh^{th} combination of factor levels, with $i = 1,\ldots,I$, $j = 1,\ldots,J$, $h = 1,\ldots,H$, and $g = 1,\ldots,n_{ijh}$.

To estimate γ, γ_h is set to 0 as only $H-1$ effects are estimable. To estimate $\gamma_1,\ldots,\gamma_{h-1}$, the quantities,

$$\zeta_h = y_{..h.} - \sum_i \sum_j \frac{n_{ijh} y_{ij..}}{n_{ij.}}$$

are equated to their expectations. Blischke (1966) found

$$E(\zeta_h) = \sum_{h'} C_{hh'} \gamma_{h'}$$

where $$C_{hh'} = n_{\cdot\cdot h} - \sum_i \sum_j \frac{n_{ijh}^2}{n_{ij\cdot}} \text{ if } h = h'$$
$$= - \sum_i \sum_j \frac{n_{ijh} n_{ijh'}}{n_{ij\cdot}} \text{ if } h \neq h'$$

Thus,
$$\hat{\gamma}_h = \sum_{h'=1}^{H-1} C^{hh'} \zeta_{h'}$$

where $C^{hh'}$ is the h, h'^{th} element of the inverse of the $(H-1) \times (H-1)$ matrix $C = (C_{hh'})$.
The (i,j) cell totals are adjusted for the estimated fixed effects by computing
$$\overset{*}{y}_{ij} = y_{ij\cdot\cdot} - \sum_h n_{ijh} \hat{\gamma}_h$$
HM1 is then applied to $\overset{*}{y}_{ij}$.

The sums of squares used in estimating the variance components are (Blischke, 1966):

$$T_a^* = \sum_i \frac{\overset{*}{y}_{i\cdot}^2}{n_{i\cdot\cdot}} \qquad T_b^* = \sum_j \frac{\overset{*}{y}_{\cdot j}^2}{n_{\cdot j\cdot}} \qquad T_{ab}^* = \sum_i \sum_j \frac{\overset{*}{y}_{ij}^2}{n_{ij\cdot}}$$

$$T_f^* = \frac{\overset{*}{y}_{\cdot\cdot}^2}{N} \qquad T_{ab} = \sum_i \sum_j \frac{y_{ij\cdot\cdot}^2}{n_{ij\cdot}} \qquad T_o = \sum_i \sum_j \sum_h \sum_g y_{ijhg}^2$$

where $N = n_{\cdots}$.
Thus the estimate of the error variance is

$$\hat{\sigma}_e^2 = \frac{T_o - T_{ab} - \sum_h \hat{\gamma} \zeta_h}{N - N' - H + 1},$$

where N' is the number of i,j combinations for which $n_{ij\cdot}$ is greater than zero.
The estimates $\hat{\sigma}_a^2$, $\hat{\sigma}_b^2$ and $\hat{\sigma}_{ab}^2$ are linear combinations of the T*'s and $\hat{\sigma}^2$. If
$$t' = (T_a^* \; T_b^* \; T_{ab}^* \; T_f^*)$$
and
$$v' = (\hat{\sigma}_a^2 \; \hat{\sigma}_b^2 \; \hat{\sigma}_{ab}^2)$$
then $$H = \begin{bmatrix} 1 & 0 & 0 & -1 \\ 0 & 1 & 0 & -1 \\ 1 & 1 & -1 & -1 \end{bmatrix}$$

$$m = \begin{bmatrix} I + K_a - K_f - 1 \\ I + K_a - K_f - 1 \\ -N' - K_{ab} + I + K_a + J + K_b - K_f - 1 \end{bmatrix}$$

Where K_a, K_b, and K_f are functions of the n_{ijh}'s and P is the matrix of k coefficients of $\hat{\sigma}_a^2$, $\hat{\sigma}_b^2$ and $\hat{\sigma}_{ab}^2$, the k coefficients also being functions of the n_{ijh}'s. Thus the vector of estimated variance components is

$$\mathrm{Var}(\hat{\sigma}^2_e) = \frac{2\sigma^4_e}{N - N' - H + 1}.$$

The sampling variance of the estimated error variance is

$$v = P^{-1}(Ht - \hat{\sigma}^2_e m).$$

and the sampling variance-covariance matrix of the remaining estimated variance component is

$$\mathrm{var}(vv^T) = P^{-1}\{H\mathrm{var}(tt^T)H^T + mm^T\mathrm{var}(\hat{\sigma}^2_e)\}P^{-1T}$$

and also the covariance between the estimated error variance and remaining estimated variance components is,

$$\mathrm{Cov}(\hat{\sigma}^2_e, v) = -P^{-1}m\mathrm{var}(\hat{\sigma}^2_e)$$

Blischke (1966) estimated the variance of the uncorrected sums of squares (var(tt′)).

Blischke (1968) derived the sampling variances of estimated variance components for an unbalanced, random 1-way classification, estimated by HM1 based on the method used by Searle (1958).

Henderson (1971) summarized the estimation of both variance components and sampling variances of variance components using Henderson (1953) methods. This is the first derivation of sample variances of variance components estimated by HM3. The model used was,

$$y = X\beta + Zu + \epsilon$$

where Z = an incidence matrix of random effects. Z can be partitioned as $[Z_1 \vdots Z_2 \vdots \ldots \vdots Z_s]$ with Z_i being a N x q_i matrix (where N is the total number of observations and q_i is the number of observations making up Z_i), with every row containing one element 1 and all other elements 0. Consequently $Z_i^T Z_i$ is diagonal, its trace is N, and its rank is q_i for $i = 1,\ldots,s$ random effects.

u = an unknown matrix of non-observable random effects.

X = an incidence matrix of fixed effects (including the mean).

β = an unknown matrix of fixed effects.

ϵ = a vector of the residual error effects.

With the mixed model, β^T can be partitioned into $[\mu \vdots \beta_1^T \vdots \beta_2^T \vdots \ldots \vdots \beta_t^T \vdots \beta_c^T]$ and X into $[1 \vdots X_1 \vdots X_2 \vdots \ldots \vdots X_t \vdots X_c]$, where $\beta_1, \beta_2, \ldots, \beta_t$ refer to classification type effects (design variables) and β_c to conventional regression coefficients (covariates). Thus the least squares equations are:

$$\begin{bmatrix} X^TX & X^TZ_1 & \cdots & X^TZ_s \\ Z_1^TX & Z_1^TZ_1 & \cdots & Z_1^TZ_2 \\ \vdots & \vdots & \ddots & \vdots \\ Z_s^TX & Z_s^TZ_1 & \cdots & Z_s^TZ_s \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}_1 \\ \vdots \\ \hat{u}_s \end{bmatrix} = \begin{bmatrix} X^Ty \\ Z_1^Ty \\ \vdots \\ Z_s^Ty \end{bmatrix}$$

or say

$$W^TW\hat{\gamma} = W^Ty$$

where $\hat{\gamma}$ is any solution to the above equations regarding u as fixed.

Thus, an estimate of the error variance ($\hat{\sigma}_e^2$) is:

$$\hat{\sigma}_e^2 = \frac{y^Ty - \hat{\gamma}^TW^Ty}{N - \text{rank}(W)} .$$

When ϵ is normally distributed, the variance of $\hat{\sigma}_e^2$ is:

$$\text{var}(\hat{\sigma}_e^2) = \frac{2\sigma_e^4}{N - \text{rank}(W)} .$$

The reduction in sums of squares is,

$$R(SS) = \hat{\gamma}^TW^Ty$$

and the expectation of such a reduction is

$$E[R(SS)] = \beta^TX^TX\beta + \sum_g N\sigma_g^2 + \sum_h \lambda_h\sigma_h^2 + \text{rank}(W^TW)\sigma_e^2$$

where σ_g^2 refers to variances of all factors and interactions that were included in the reductions.

σ_h^2 refers to all other variances.

$\lambda_h = \text{tr}(W^TW)^- W^TZ_hZ_h^TW$.

The estimates of σ_i^2 can be stated as,

$$\hat{\sigma}_i^2 = \lambda_{ie}\hat{\sigma}_e^2 + \sum_{j=1}^{s+1}\lambda_{ij}r^TQ_jr$$

where r^TQ_jr are the s+1 quadratics in the right hand side of the least squares equations.

Then the estimates can be written as

$$\hat{\sigma}_i^2 = \lambda_{ie}\hat{\sigma}_e^2 + r^TQ_ir$$

where $$Q_i = \sum_{j=1}^{s+1}\lambda_{ij}r^TQ_jr$$

Thus the sampling variance of $\hat{\sigma}_i^2$ is

$$\text{var}(\hat{\sigma}_i^2) = \frac{2\lambda_{ie}^2\sigma_e^4}{\text{df for } \sigma_e^2} + 2\text{tr}(Q_iV)^2$$

where V = variance-covariance of r, the right hand side of the least square equations.

Similarly,

$$\mathrm{Cov}(\hat{\sigma}_i^2, \hat{\sigma}_g^2) = \frac{2\lambda_{ie}\lambda_{ke}\sigma_e^4}{\mathrm{df}} + 2\mathrm{tr}(\mathrm{Q}_i\mathrm{V}\mathrm{Q}_g\mathrm{V})$$

and

$$\mathrm{Cov}(\hat{\sigma}_i^2, \hat{\sigma}_e^2) = \frac{2\lambda_{ie}\sigma_e^4}{\mathrm{df}} .$$

To obtain the values for the λ's, the HM3 estimates can be shown to come from the solution to (Henderson, 1971):

$$\left[\begin{array}{ccccc} 1 & \vdots & 0 & \vdots & 0 \\ \hline \mathrm{f} & \vdots & \mathrm{C} & \vdots & 1_{s+1} \end{array}\right] \begin{bmatrix} \hat{\sigma}_e^2 \\ \hat{\sigma}^2 \\ \beta^{\mathrm{T}}\mathrm{X}^{\mathrm{T}}\mathrm{X}\beta \end{bmatrix} = \begin{bmatrix} \hat{\sigma}^2 \\ \mathrm{r} \end{bmatrix}$$

where 0 is a row vector of 0's

f is s+1 column vector of ranks of coefficient matrices used in computing the s+1 reduction in SS

C is the s+1 by s matrix of coefficients of σ_i^2 in the s+1 reductions

1_{s+1} is a s+1 column vector of 1's

$\hat{\sigma}^2$ is the column vector of $\hat{\sigma}_1^2, \hat{\sigma}_2^2, \cdots, \hat{\sigma}_s^2$

r is the s+1 column vector of reductions.

The inverse of the coefficient matrix of the equation above then provides λ_{ie} and λ_{ij}.

If the least square equations are rewritten as

$$\begin{bmatrix} \mathrm{W}^{\mathrm{T}}\mathrm{X} & \mathrm{W}^{\mathrm{T}}\mathrm{Z}_1 & \cdots\cdots & \mathrm{W}^{\mathrm{T}}\mathrm{Z}_s \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{\mathrm{u}}_1 \\ \vdots \\ \hat{\mathrm{u}}_s \end{bmatrix}$$

where $\mathrm{W} = \begin{bmatrix} \mathrm{X} & \vdots & \mathrm{Z}_1 & \vdots \cdots\cdots \vdots & \mathrm{Z}_s \end{bmatrix}$

then V can be obtained as:

$$\begin{aligned} \mathrm{V} &= \mathrm{W}^{\mathrm{T}}\mathrm{W}\sigma_e^2 + \sum_i \mathrm{W}^{\mathrm{T}}\mathrm{Z}_i\mathrm{Z}_i^{\mathrm{T}}\mathrm{W}\sigma_i^2 \\ &= \sum_{i=0}^{s} \mathrm{V}_i\sigma_i^2 \end{aligned}$$

where $\sigma_0^2 = \sigma_e^2$

$$V_0 = W^T W$$

$$V_1 = W^T Z_1 Z_1^T W$$

etc.

Some assumed values of σ_e^2 and σ_i^2 are required for the calculation of the sampling variances of variance components. Often, the estimated variance components are substituted for population values (Henderson, 1971). But Mahamunulu (1963) noted that by replacing the population parameter estimates by their estimates, the estimation of the sampling variances will generally be biased. To overcome this bias, Mahamunulu (1963) suggested that for every product of the type $\sigma_x^2 \sigma_y^2$ be replaced by $\hat{\sigma}_x^2 \hat{\sigma}_y^2 - \mathrm{Cov}(\hat{\sigma}_x^2, \hat{\sigma}_y^2)$ whenever x and y are different, and term of the type σ_a^4 be replaced by $(\hat{\sigma}_a^2)^2 - \mathrm{var}(\hat{\sigma}_a^2)$. Then the required estimates can be obtained by solving a series of simultaneous equations. There appears to be no record of this procedure being adopted in the literature.

2.3.2 ML Methods

The large-sample variance-covariance matrix of parameters estimated by ML techniques of any model, is the inverse of the information matrix (Corbeil and Searle, 1976; Searle, 1970, 1979). This matrix is minus the expected value of the matrix of second order partial derivatives (the Hessian matrix) with respect to those parameters of the logarithm of the likelihood (Searle, 1970).

For the mixed model

$$y = X\beta + Zu$$

where y = the vector of N observations

β = a px1 vector of fixed effects, that includes the general mean, μ

u = a vector of random effects, that include the error terms, ϵ

X and Z are known matrices, often, but not always design matrices,

with the random effects having zero mean and a covariance matrix A, that involves q variance components, one of which is the error variance, and u is distributed as N(0,A). Hence

$$\begin{aligned} \mathrm{var}(y) &= \mathrm{var}(Zu) \\ &= ZAZ^T \\ &= V \end{aligned}$$

then the covariance matrix required is,

$$V_{ml} = \begin{bmatrix} \mathrm{var}(\tilde{\beta}) & \mathrm{cov}(\tilde{\beta}\tilde{\sigma}^2) \\ \mathrm{cov}(\tilde{\sigma}^2\tilde{\beta}) & \mathrm{var}(\tilde{\sigma}^2) \end{bmatrix}$$

$$= \begin{bmatrix} X^{T}V^{-1}X & 0 \\ 0 & \{t_{ij}\} \end{bmatrix}^{-1}$$

with $\{t_{ij}\} = (\log|V|)_{ij} + \mathrm{tr}[V(V^{-1})_{ij}]$

where the subscripts on the right hand side of the equation denote partial differentiation with respect to σ_i^2 and σ_j^2 (Searle, 1970).

Searle (1970) further simplified $\mathrm{var}(\bar{\sigma}^2)$ to

$$\begin{aligned} \mathrm{var}(\bar{\sigma}^2) &= 2\{\mathrm{tr}[V^{-1}(V)_i V^{-1}(V)_i]\}^{-1} \\ &= 2\{\mathrm{tr}[V^{-1}\frac{\partial V}{\partial \sigma_i^2} V^{-1}\frac{\partial V}{\partial \sigma_i^2}]\}^{-1} \text{ for } i=1,2,\ldots,q. \end{aligned}$$

Thus the large-sample variance of the variance components are entirely free of fixed effects and solely a function of the covariance matrix V of the observations y and hence no matter what the fixed effects are, or how they occur, they in no way effect $\mathrm{var}(\bar{\sigma}^2)$ (Searle 1970, 1971a,b).

The information matrix for the REML equations is (Searle, 1979):

$$I(\dot{\sigma}^2) = \frac{1}{2}\begin{bmatrix} \mathrm{tr}(P^2) & \{\mathrm{tr}(Z_j^T P^2 Z_j)\}^T \\ \{\mathrm{tr}(Z_j^T P^2 Z_j)\}^T & \{\mathrm{tr}[Z_i^T P Z_j (Z_i^T P Z_j)^T]\} \end{bmatrix} \text{ for } i,j=1,\ldots,c$$

where c = the number of variance components

and $P = L(L^T V L)^{-1} L^T$ with L being the matrix such that the original model,

$y = X\alpha + Zb + \epsilon \sim N(X\alpha, V)$ becomes $L^T y = L^T Zb + L^T\epsilon \sim N(0, L^T V L)$.

Hence

$$\begin{bmatrix} \mathrm{var}(\dot{\sigma}_e^2) & \mathrm{cov}(\dot{\sigma}_j^2, \dot{\sigma}_i^2) \\ \mathrm{cov}(\dot{\sigma}_i^2, \dot{\sigma}_j^2) & \mathrm{var}(\dot{\sigma}_i^2) \end{bmatrix} = [I(\dot{\sigma}^2)]^{-1} \text{ for } i,j=1,\ldots,c.$$

When deriving large-sample variances of variance components, what constitutes a large-sample? The usual case of asymptotic properties of ML estimates relates to a sample size of n as n → ∞, but the analogue of this for many-factored classifications is not obvious when the property of unbalancedness of data is to be retained (Searle, 1970). Hartley and Rao (1967) suggested that the number of levels for at least one factor must tend to infinity, and so long as there is at least one random effect in the model, this is appropriate. When there are several such factors the number of levels in each must tend to infinity (Searle, 1970).

2.4. Estimation of Heritabilities

Heritability is, according to Hill (1974) arguably the most important concept in the application of genetics to animal breeding as it can be used to predict the rate of response to selection, and, along with genetic correlations, it is used to formulate weightings for traits in multi-trait selection schemes.

Heritability of a trait in Lush's narrow sense, can be described as the ratio of additive genetic variance to phenotypic variance (Falconer, 1981). The most often used method of estimating heritability in this sense is the analysis of paternal half-sibs to estimate both the additive genetic variance, and total variance. These variances are then combined to form the heritability as

$$h^2 = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2+\hat{\sigma}_e^2}$$

$$= 4t$$

where $\hat{\sigma}_s^2$ = estimate of sire variance

$\hat{\sigma}_e^2$ = estimate of residual error variance

t = estimate of the population intra-class correlation, ρ.

Fisher (1928) appears to be the first to obtain the intra-class correlation using variance components. He used the ANOVA method of equating mean squares or sums of squares to their expected values, and solving for the unknown variance components.

2.4.1 Sampling Variance of Heritability Estimated by Paternal Half-sib

To obtain the sampling variance of the heritability estimate, estimates from the intra-class correlation, the sampling variance of the intra-class correlation is required.

The variance of t may be estimated using the approximate formula for the variance of a ratio (Pearson, 1897),

$$\mathrm{var}(\tfrac{y}{x}) \simeq \left(\frac{\mu_y}{\mu_x}\right)^2\left(\frac{\sigma_y^2}{\mu_y^2} + \frac{\sigma_x^2}{\mu_x^2} - 2\frac{\sigma_{xy}}{\mu_x\mu_y}\right)$$

where μ_x and μ_y are the population means of x and y.

σ_x^2 and σ_y^2 are the population variances of x and y

and σ_{xy} is the population covariance between x and y.

Fisher (1928) derived the large-sample variance of the ANOVA estimate of t, t_a, as:

$$\mathrm{var}(t_a) = \frac{2(1-\rho)^2[1+(n-1)\rho]^2}{n(n-1)(k-1)}$$

where there are k sib-groups with n observations per family and ρ is the population intraclass correlation. Donner and Koval (1983) compared the sampling variance obtained by Fisher's

(1928) approximation with that derived from the exact sampling distribution of t_a. They showed that for moderately large number of sib groups ($k \geq 30$) Fisher's approximation was highly accurate. There were 2 or 4 observations per sib group.

Smith (1956) obtained an approximate error variance of t as

$$\mathrm{var}(t_a) = \left(\frac{\partial t_a}{\partial \hat{\sigma}_e^2}\right)^2 \mathrm{var}(\hat{\sigma}_e^2) + 2\left(\frac{\partial t_a}{\partial \hat{\sigma}_e^2}\right)\left(\frac{\partial t_a}{\partial \hat{\sigma}_s^2}\right)\mathrm{cov}(\hat{\sigma}_e^2, \hat{\sigma}_s^2) + \left(\frac{\partial t_a}{\partial \hat{\sigma}_s^2}\right)^2 \mathrm{var}(\hat{\sigma}_s^2)$$

For the unbalanced 1-way analysis of variance, Smith (1956) obtained the variance of t_a as

$$\begin{aligned} \mathrm{var}(t_a) &= \Big\{[(1 - t_a)k_1 + t_a k_2]\,\frac{2\hat{\sigma}_e^4}{(N - c)} \\ &\quad + (1 - t_a)^2\,[2\hat{\sigma}_e^4\,k_1 + 4\hat{\sigma}_e^2\hat{\sigma}_s^2\,k_2 + \hat{\sigma}_s^4(s_2 - \frac{2s_3}{N} + \frac{s_2^2}{N^2})]\Big\} \\ &\quad /\; k_2^2(\hat{\sigma}_e^2 + \hat{\sigma}_s^2)^2 \end{aligned}$$

where $k_1 = c - 1$

$k_2 = N - \frac{s_2}{N}$

$s_i = \sum_j n_j^i$

N = total number of observations

Hence

$$\begin{aligned} \mathrm{var}(\hat{h}_a^2) &= \mathrm{var}(4t_a) \\ &= 16\mathrm{var}(t_a)\,. \end{aligned}$$

Smith (1956) suggested how the method could be extended for models containing more variance components.

Swiger, Harvey, Everson and Gregory (1964) derived an estimate for the variance of the intra-class correlation using a random 1-way unbalanced classification and analysis of variance estimation of the variance components. Swiger et al (1964) obtained the approximate large-sample variance as

$$\mathrm{var}(t_a) \simeq \frac{2(N - 1)(1 - t_a)^2[1 + (k - 1)t_a]^2}{k^2(N - s)(s - 1)}\,.$$

Donner and Koval (1980) derived the ML estimation of the intra-class correlation. This involved minimizing the function

$$-2\ell n = N(1 + \ell n\sigma^2 + \ell n 2\pi) + (N - c)\ell n(1 - \rho) + \sum_{i=1}^{2} \ell n W_i$$

where c = the number of sib groups

and $W_i = 1 + (n_i - 1)\rho$

with respect to ρ to yield the maximum likelihood estimator t_m.

The large-sample variance of t_m can be obtained by inverting the information matrix (Donner and Koval, 1980), to give

$$\mathrm{var}(t_m) = \frac{2N(1-t_m)^2}{N\sum_{i=1}^{k} n_i(n_i-1)\hat{V}_i\hat{W}^{-2} - t_m^2\{\sum_{i=1}^{k} n_i(n_i-1)\hat{W}_i^{-1}\}^2}$$

where $\hat{W}_i = 1 + (n_i - 1)t_m$

$\hat{V}_i = 1 + (n_i - 1)t_m^2$.

The variance of the heritability can then be estimated as

$$\begin{aligned}\mathrm{var}(\hat{h}_m^2) &= \mathrm{var}(4t_m) \\ &= 16\mathrm{var}(t_m).\end{aligned}$$

With Pearson's (1897) variance of a ratio, provided that the appropriate variances and covariances of the variance components are known, the variance of a heritability can be obtained regardless of the method used to estimate the variance components or the number of variances in the intra-class correlation. A limitation is that the method is approximate.

Chapter 3
Materials and Methods

The study involved Monte-Carlo simulation. Data sets were generated with the required number of sires and appropriate number of progeny per sire, coming from a population with known genetic and environmental parameters.

Data sets were set up comprising of 20, 50, 100, 150 and 200 sires with, for balanced data, 20, 50 ,70 and 100 progeny per sire. Unbalanced data sets were also created, these comprising of a mean of 20, 50, 70 and 100 progeny per sire. A normal distribution about the mean number of progeny was assumed, and distributions set up with standard deviations of 2, 5 and 7 progeny per sire (SD2, SD5 and SD7 respectively), using the programme shown in Appendix 1. The distributions of progeny usually had to be altered to give the correct total numbers of observations, or to get the standard deviation closer to what was required. It was not possible to set up a distribution of 20 sires having a standard deviation of 7 progeny per sire. The distribution achieved at each level of unbalance is shown in Tables 3.1, 3.2 and 3.3. The Tables also show an estimate of the unbalancedness of the data, γ, which was derived by Ahrens and Pincus (1981) as:

$$\gamma = \frac{\mathrm{m}}{\overline{\mathrm{n}} \sum_{j=1}^{m} \frac{1}{\mathrm{n}_j}}$$

where m = number of sires

n_j= number of observations on the j^{th} sire (j=1,2,...,m)

$\overline{\mathrm{n}}$ = average number of observations per sire

Obviously, γ falls between 0 and 1, a value of 1 indicating balanced data and a value approaching 0 indicating highly unbalanced data. The data were not heavily unbalanced, based on γ, when compared with data from flocks that have been used in genetic parameter estimation (data from 31 flocks that was used by Rendel (1985) for the estimation of variance components and heritability of weaning weight of lambs had γ range from 0.3887 to 0.8889). Therefore, data sets of 100 sires with a mean of 100 progeny per sire (as they were considered representative of the data sets) were set up assuming a normal distribution of progeny per sire about the mean (100) and standard deviations of 15, 25 and 29. The γ's achieved (Table 3.4) did not approach the flock values and, as the normal distribution had been extended to the limit (for SD29 there was 1 sire in every class except for the mean which had 2), another approach was required. This involved selecting 6 flocks from those used to estimate lamb weaning weight genetic parameters by Rendel (1985) that were representative of numbers of sires, mean number of progeny per sire, and γ. The distribution of number of progeny per sire is shown in Fig. 3.1. The standard deviation of the number of progeny per sire, and γ are shown in Table 3.5.

Table 3.1 The minimum and maximum number of progeny per sire, actual standard deviation and estimate of unbalance (γ) for data sets from data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	MIN	16	15	15	14	15
		MAX	24	25	25	26	25
		SD	1.97	2.03	2.02	2.05	1.99
		γ	0.9906	0.9897	0.9898	0.9897	0.9900
	50	MIN	46	45	45	44	45
		MAX	54	55	55	56	55
		SD	1.97	2.03	2.02	2.05	1.99
		γ	0.9985	0.9984	0.9984	0.9983	0.9984
	70	MIN	67	65	65	64	65
		MAX	74	75	75	76	75
		SD	1.97	2.03	2.02	2.05	1.99
		γ	0.9992	0.9992	0.9992	0.9991	0.9992
	100	MIN	96	95	95	94	95
		MAX	104	105	105	106	105
		SD	1.97	2.03	2.02	2.05	1.99
		γ	0.9996	0.9996	0.9996	0.9996	0.9996

Table 3.2 The minimum and maximum number of progeny per sire, actual standard deviation and estimate of unbalance (γ) for data sets from data type SD5.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	MIN	11	9	8	7	7
		MAX	29	31	32	33	33
		SD	4.83	5.08	4.89	5.00	4.86
		γ	0.9379	0.9178	0.9326	0.9278	0.9328
	50	MIN	41	39	38	37	37
		MAX	59	61	62	63	63
		SD	4.83	5.08	4.89	5.00	4.86
		γ	0.9910	0.9897	0.9904	0.9899	0.9904
	70	MIN	61	59	58	57	57
		MAX	79	81	82	83	83
		SD	4.83	5.08	4.89	5.00	4.86
		γ	0.9954	0.9948	0.9951	0.9949	0.9952
	100	MIN	91	89	88	87	87
		MAX	109	111	112	113	113
		SD	4.83	5.08	4.89	5.00	4.86
		γ	0.9978	0.9975	0.9976	0.9975	0.9976

Table 3.3 The minimum and maximum number of progeny per sire, actual standard deviation and estimate of unbalance (γ) for data sets from data type SD7.

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny per Sire	20	MIN		6	4	3	2
		MAX		34	36	37	38
		SD		6.76	6.93	6.93	6.93
		γ		0.8583	0.8398	0.8315	0.8180
	50	MIN		36	34	33	32
		MAX		64	65	67	68
		SD		6.76	6.93	6.93	6.93
		γ		0.9815	0.9804	0.9803	0.9802
	70	MIN		56—	54	53	52
		MAX		84	86	87	88
		SD		6.76	6.93	6.93	6.93
		γ		0.9907	0.9901	0.9901	0.9901
	100	MIN		86	84	83	82
		MAX		114	116	117	118
		SD		6.76	6.93	6.93	6.93
		γ		0.9955	0.9952	0.9952	0.9952

Table 3.4 The minimum and maximum number of progeny per sire, actual standard deviation and estimate of unbalance (γ) for data types SD15, SD25 and SD 29.

	MIN	MAX	SD	γ
SD15	71	129	14.26	0.9793
SD25	55	145	25.19	0.9329
SD29	51	149	28.58	0.9130

Table 3.5 The number of sires (SIRES), mean number of progeny per sire (MEAN), minimum (MIN) and maximum (MAX) number of progeny per sire, standard deviation of progeny per sire (SD) and estimate of unbalance (γ) for flocks A to F.

	SIRES	MEAN	MIN	MAX	SD	γ
A	105	63.61	14	263	27.99	0.8610
B	44	81.59	10	183	37.99	0.6735
C	84	81.51	6	196	45.08	0.5235
D	60	99.03	6	271	67.08	0.4015
E	60	97.61	6	226	61.53	0.3910
F	87	101.75	6	199	51.25	0.3887

Figure 3.1 Distribution of the number of progeny per sire of the data sets based on the six commercial flocks.

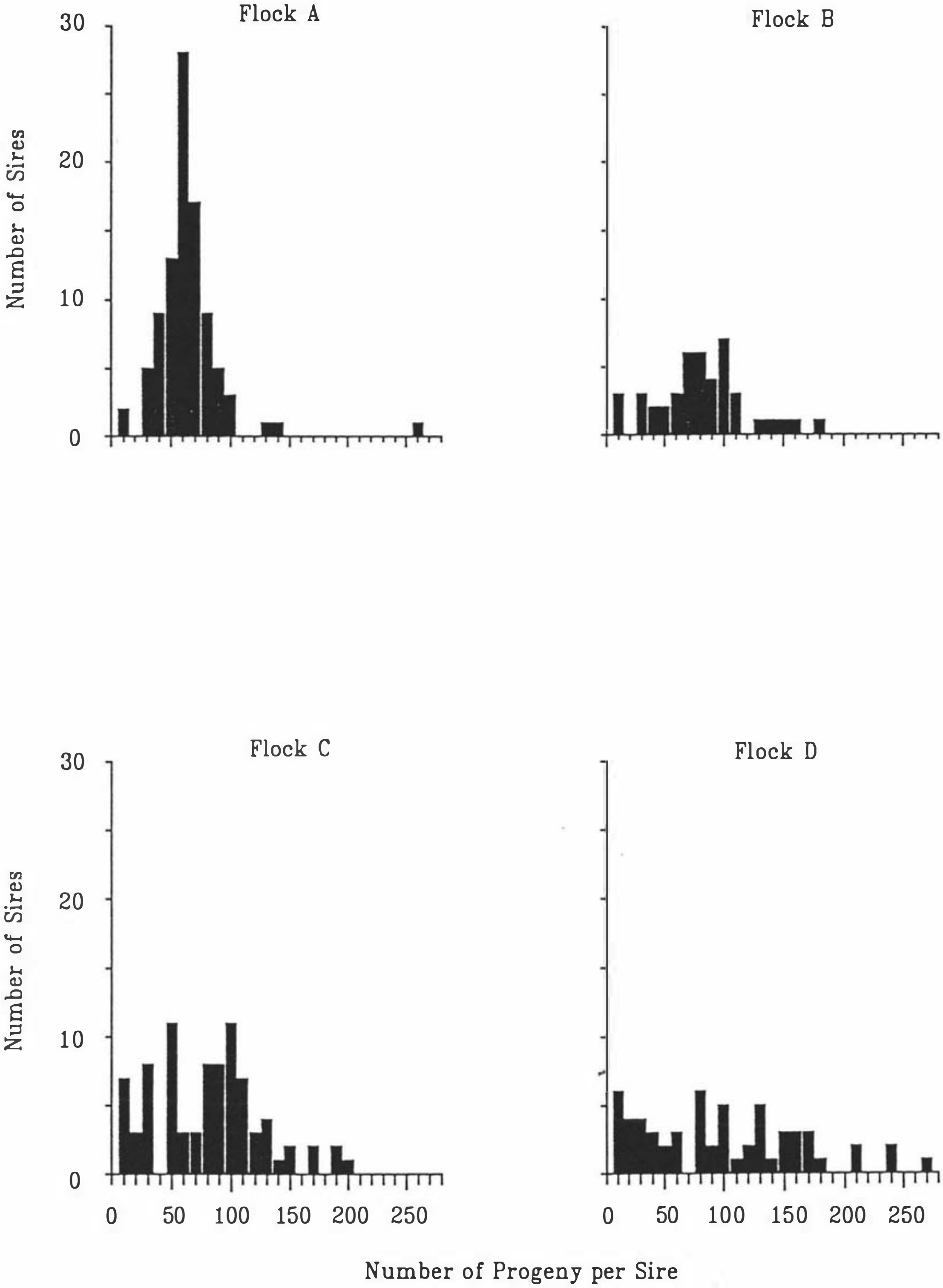
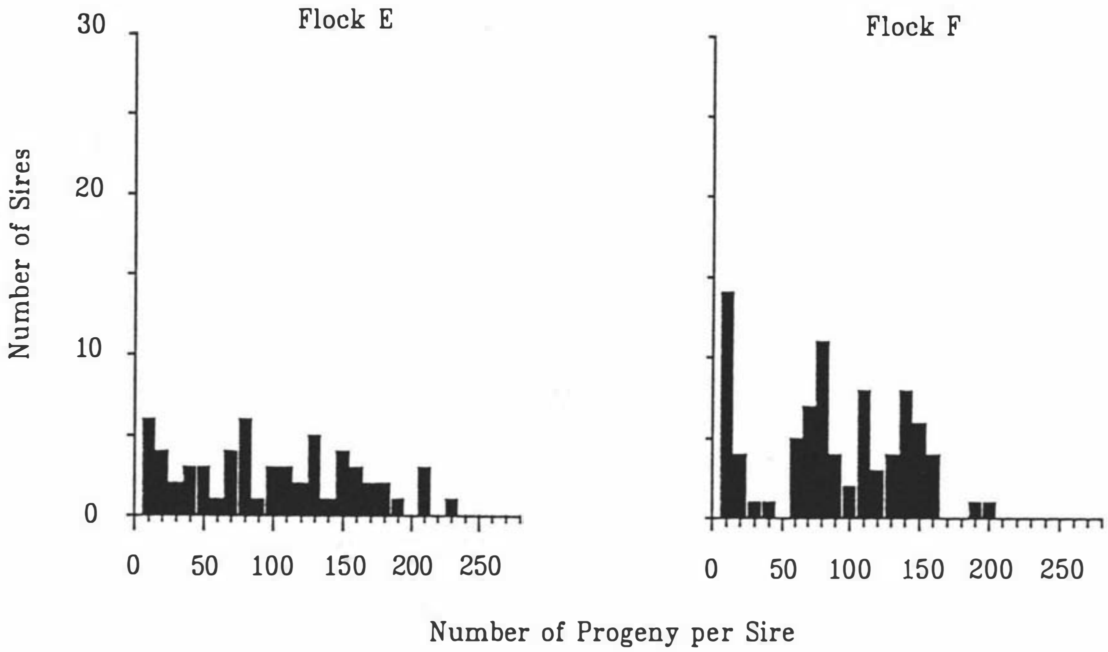


Figure 3.1 Continued.



The observations in each group were based on the model:

$$y_{ij} = \mu + s_i + \epsilon_{ij}$$

where y_{ij} = the j^{th} observation on the i^{th} sire

μ = the general mean

s_i = the random effect of the i^{th} sire assumed to be normally and independently distributed with mean 0 and variance σ_s^2

ϵ_{ij} = the random residual effect assumed to be normally and independently distributed with mean 0 and variance σ_e^2. Furthermore the sire andresidual terms are assumed to be independent.

The observations were generated using a random number generator that returned pseudo-random numbers from a normal distribution. The random number generator was chosen from the NAG (1983) library as these would have been widely used and tested. The routine used was based on the method of Brent (1974, cited by NAG, 1983). The sire variance was set at 0.6783 and the error variance 11.0106, these being variances actually obtained for lamb weaning weight in a flock from Rendel (1985). A value of 18 was used for the general mean. Each number of sire and progeny per sire combination was generated 100 times (i.e. 100 replicates) at each level of unbalance. This was the maximum number of replicates used in simulation studies of heritabilities reported by Rönningen (1974), although more recently Rothschild et al (1979) used 200 replicates and Lin and McAllister (1984) used 10.

The sire and error variances were estimated for each replicate by Hendersons Method 1 (HM) using REG (Gilmour, 1985), Maximum Likelihood (ML) using SAS (SAS Institute, 1985) and Restricted Maximum Likelihood (REML) using a programme supplied by K. Meyer. The stopping criterion was set at a difference of 4×10^{-8} between 2 successive likelihoods for ML, and a change of 0.005% in the sire variance between 2 successive rounds of iteration for REML. If convergence did not occur with the REML and ML methods then the replicate was recorded as having a missing value for the variance components.

Standard errors of the variance components were calculated for HM by methods outlined by Searle (1971a) and for ML and REML by inverting the information matrix (Searle, 1979), as described in sections 2.3.1 and 2.3.2 of Chapter 2. The standard errors are large sample standard errors.

The heritability was also estimated for each replicate, as 4 times the intraclass correlation. The standard errors of the heritability estimates were also estimated. The HM standard errors were approximate (see section 2.4.1 of chapter 2) as derived by Swiger et al (1964) which is based on the variance of a ratio as derived by Pearson (1897). The approximate standard error of the REML estimate (see section 2.4.1 of chapter 2) was also the variance of a ratio. The standard error of the ML heritability was calculated as outlined by Donner and Koval (1980), who calculated the sampling variance of the intra-class correlation estimated by ML (see section 2.4.1 of chapter 2).

The mean of the variance component and heritability estimates were calculated from the 100 replicates for each set of sires and progeny per sire, for each level of unbalance. These were compared to the population values to assess how accurate differing sets of sire and progeny per sire were in estimating the population parameters.

Likewise, the mean of the standard error estimates of the variance component and heritability estimates were calculated for each of the sire and progeny per sire combinations. The means of the standard errors were compared with the standard deviation of the 100 replicates, in order to establish if the standard errors actually reflected the amount of variation present within each sire, progeny per sire combination.

To assess if the data sets gave unbiased estimates of heritability and sire and error variances, confidence intervals for HM estimates from a one-way random model were calculated. Exact confidence intervals for balanced data were (Searle, 1971a):

$$\Pr\left\{ \frac{\mathrm{SSE}}{\chi^2_{a(n-1),u}} \leq \sigma^2_e \leq \frac{\mathrm{SSE}}{\chi^2_{a(n-1),l}} \right\} = 1-\alpha$$

$$\Pr\left\{ \frac{\mathrm{SSA}(1-\frac{\mathrm{F}_u}{\mathrm{F}})}{\mathrm{n}\chi^2_{a-1,u}} \leq \sigma^2_s \leq \frac{\mathrm{SSA}(1-\frac{\mathrm{F}_l}{\mathrm{F}})}{\mathrm{n}\chi^2_{a-1,l}} \right\} = 1-2\alpha$$

$$\Pr\left\{ \frac{\frac{\mathrm{F}}{\mathrm{F}_u}-1}{\mathrm{n}+\frac{\mathrm{F}}{\mathrm{F}_u}-1} \leq \frac{\sigma^2_s}{\sigma^2_s+\sigma^2_e} \leq \frac{\frac{\mathrm{F}}{\mathrm{F}_l}-1}{\mathrm{n}+\frac{\mathrm{F}}{\mathrm{F}_l}-1} \right\} = 1-\alpha$$

where

SSE = Sum of squares error

SSA = Sum of squares sire

n = number of progeny per sire

a−1 = sire degrees of freedom

$\mathrm{F} = \frac{\text{Mean square sire}}{\text{Mean square error}}$

$\Pr\{\chi^2_{n,l} \leq \chi^2_{(n)} \leq \chi^2_{n,u}\} = 1-\alpha$

$\Pr\{ \mathrm{F}_l \leq \mathrm{F}_{[a-1,a(n-1)]} \leq \mathrm{F}_u \} = 1-\alpha$

The confidence intervals were constructed for each replicate and the number of intervals that did not contain the population parameter were noted for each data set.

With unbalanced data the distribution of the analogous sum of squares, used by HM 1 to estimate the variance components, do not, under normality assumptions, follow a χ^2 distribution. The form of the distribution is unknown. The exception is the error sum of squares which do follow a χ^2 distribution as with balanced data. The error sum of squares also have zero covariance with (i.e. independent of) other sum of squares, a property not shared by other analogous sum of squares (Searle, 1971a). Therefore the confidence intervals for the error variances from unbalanced data could be constructed in the manner outlined above.

The distribution of the population standard errors was also unknown. Unlike the heritability and variance estimates it was not possible to obtain the population standard deviation of the standard errors. Hence the standard error estimates could not be analysed statistically. A graphical presentation was therefore used.

Another method that was used to assess the accuracy of estimation was to calculate the mean squared error (MSE) for each set of sires and average number of progeny per sire. The MSE is defined as:

$$\mathrm{MSE} = \frac{\sum_{i=1}^{n}(V_i - a)^2}{n}$$

where

V_i = estimate of the parameter from the i^{th} replicate

a = parameter population value

n = number of replicates that make up the group (usually 100).

For variance component and heritability estimates, a is the population value. For the standard errors of the parameters, a is the standard deviation of the estimates in each set of sires and progeny per sire.

CHAPTER FOUR

RESULTS AND DISCUSSION

The heritability of a trait, rather than the variance components from which it was calculated, is usually reported in the literature. Hence the results for the heritabilities will be presented and discussed followed by the sire and error variances.

4.1 Heritabilities

4.1.1 Heritability Estimates

The mean of the HM heritability estimates for each number of sires, mean number of progeny per sire and level of unbalance data sets were compared with the population heritability in Fig. 4.1. As expected heritabilities estimated by HM for balanced data (SD0) agreed well with the population value. Fig. 4.1 suggests that data sets consisting of 20 sires with 20 or 50 progeny per sire and data sets of 50 sires with 20 progeny per sire did not allow accurate estimates of the population heritability. The difference between the mean heritability estimates and population value for those data sets (0.022, −0.020 and −0.023, respectively) were large compared with other data sets. The 90% confidence intervals for HM showed that over half of the data sets had the population heritability (0.2321) falling outside the confidence intervals for the replicates, with a frequency greater than the expected 10% (Table 4.1). The data sets consisting of 20 progeny per sire had the fewest infringements, whereas those consisting of 50, 70 and 100 progeny per sire had approximately equal numbers of infringements. This suggests that either the estimates are biased or the confidence intervals of the heritability estimates are too narrow for balanced data with more than 20 progeny per sire. As there was good agreement between the mean heritability estimates and the population values for nearly all the data sets, it would seem unlikely that the estimates are biased. It is unlikely that the random number generator is not giving random numbers, as it comes from a well used and documented statistical algorithm library. Therefore, the confidence intervals may be too narrow.

The results from the balanced data, using HM are in good agreement with those in the literature. Olausson and Rönningen (1975) reported that bias of ±0.03 in the estimation of the paternal half-sib heritability for a simulation with a balanced design of 50 sires with 50 progeny per sire and 50 replicates and a population heritability of 0.1 and 0.5. Likewise, paternal half-sib heritability estimates reported by Rönningen (1972) for a simulation of balanced data sets of 100 sires with 30, 50 and 100 progeny per sire and population heritabilities of 0.1 and 0.3, had a bias between 0 and 0.01. There were 100 replicates.

Figure 4.1 Mean heritability estimated by HM for data sets from data types SD0, SD2, SD5 and SD7 and with population heritability 0.2321.

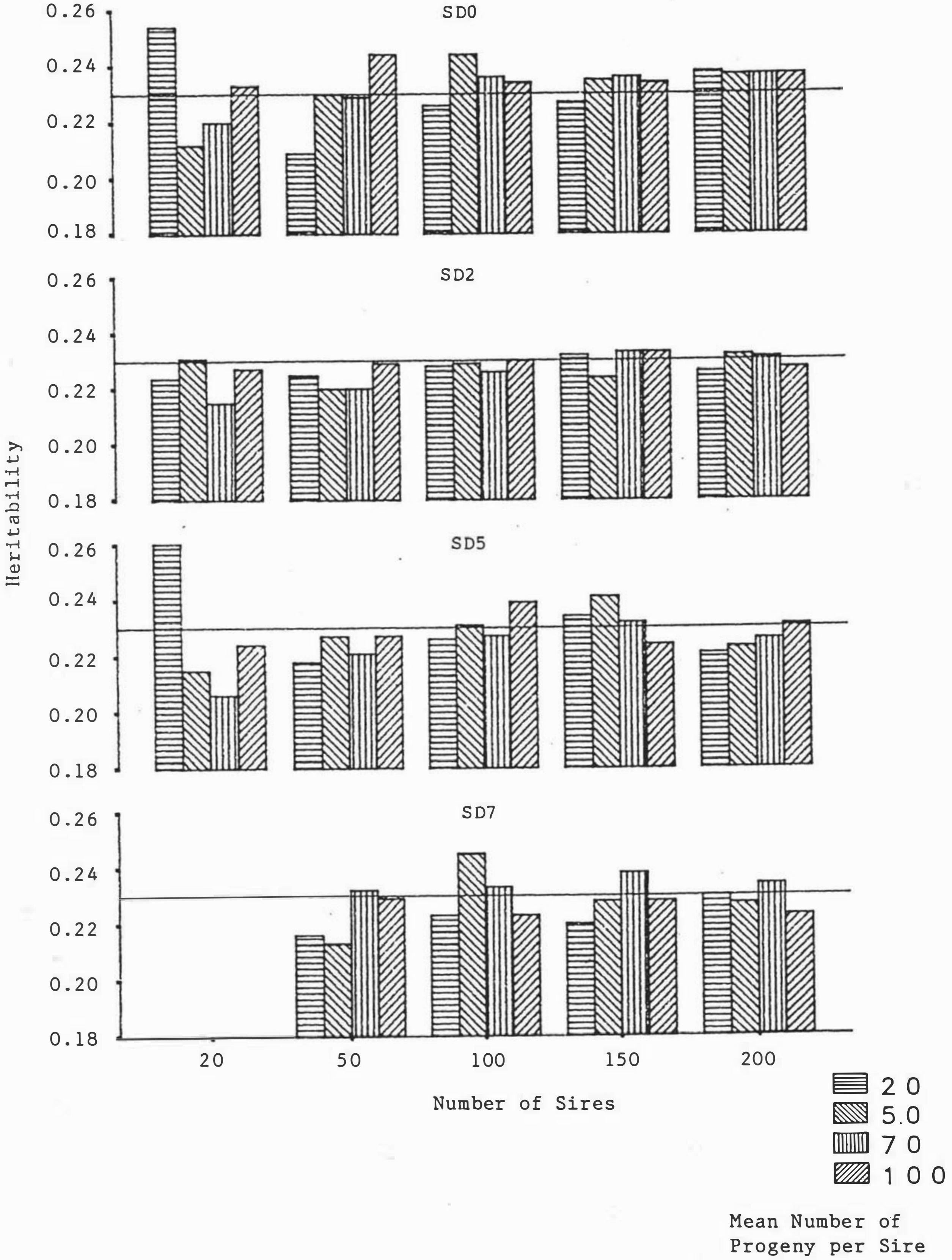


Table 4.1 Number of replicates from HM heritability estimates that have the population heritability falling above and below the 90% confidence intervals for data type SD0.

Number of Progeny per Sire	Number of Sires 20	50	100	150	200
20	5,4	5,2	2,0	0,5	0,13
50	2,0	8,8	3,9	0,9	7,11
70	12,0	3,3	10,8	0,3	1,13
100	3,7	2,3	1,0	6,7	6,15

Rothschild et al (1979), for a simulation involving 100 sires and 50 daughters per sire with 200 replicates, reported that the difference between the true heritability (0.3) and the estimated, using HM1, was 0.0004.

Heritability estimates from the unbalanced data type SD2 using HM, were close to the population value (Fig. 4.1). The figure shows that the data set consisting of 20 sires and a mean of 70 progeny per sire to be the least accurate in estimating the population heritability, having a deviation from the population value of −0.017. Why this occurred is uncertain, but as it appears not to be part of a trend, it is probably due to random variation. Confidence intervals were not constructed due to the distribution being unknown for unbalanced data.

The data type SD5 had heritability estimates that appeared to be further from the population value (Fig. 4.1) than with the data type SD2. This was evident for data sets of 20 sires with a mean of 20, 50 or 70 progeny per sire, and 50 sires with a mean of 20 progeny per sire which had deviations from the population heritability of 0.03, −0.017, −0.026 and −0.014 respectively. These data sets may be of insufficient size for accurate estimation of heritabilities.

The data type SD7 had several data sets that had mean heritability estimates that appeared to be different from the population value (Fig. 4.1). These were 50 sires with a mean of 20 or 50 progeny per sire and 100 sires with a mean of 50 progeny per sire which had deviations of −0.016, −0.019 and 0.013 respectively.

Rothschild et al (1979) reported, for a simulation of unbalanced data with 200 replicates and 100 sires with a mean of 25 daughters per sire, a difference of 0.004 between the population heritability (0.24) and the mean of the estimated heritabilities. This difference is similar to that achieved for unbalanced data with 100 sires and a mean of 20 progeny per sire in this study. Rothschild et al (1979) do not quantify the level of unbalance.

The more unbalanced data types SD14, SD25 and SD29 had mean HM heritability estimates (Table 4.2) that were similar to those from data sets of 100 sires and a mean of 100 progeny per sire for previous data types.

The mean HM heritability of the 6 data types based on numbers of sires and progeny per sire from actual flocks (Table 4.3) were similar to those based on previous data types, showing little difference from the population heritability. There was no relationship between the degree of unbalance and the mean heritability estimates.

Table 4.2 The mean of the data set heritabilities, estimated using HM, ML and REML, for data types SD14, SD25 and SD 29.

	HM	ML	REML
SD14	0.2302	0.2270	0.2295
SD25	0.2221	0.2188	0.2213
SD29	0.2457	0.2402	0.2429

Table 4.3 The mean of the data set heritabilities, estimated using HM, ML and REML, for flocks A, B, C, D, E and F.

	γ	HM	ML	REML
A	0.8610	0.2365	0.2326	
B	0.6735	0.2405	0.2301	0.2363
C	0.5235	0.2294	0.2241	0.2275
D	0.4015	0.2302	0.2231	0.2277
E	0.3910	0.2432	0.2322	0.2369
F	0.3887	0.2354	0.2329	0.2365

Figure 4.2 Mean heritability estimated by ML for data sets from data types SD0, SD2, SD5 and SD7 and with population heritability 0.2321.

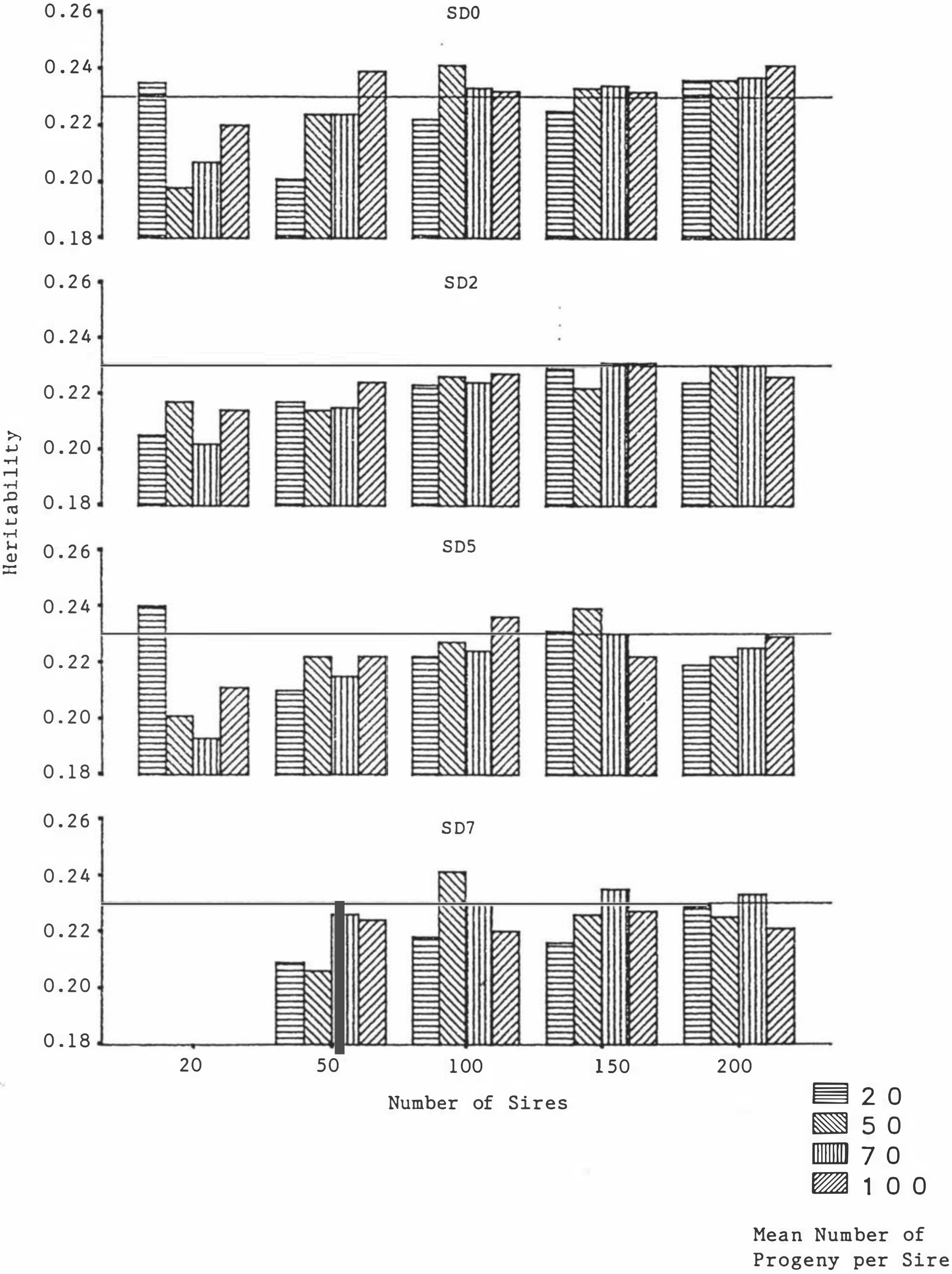
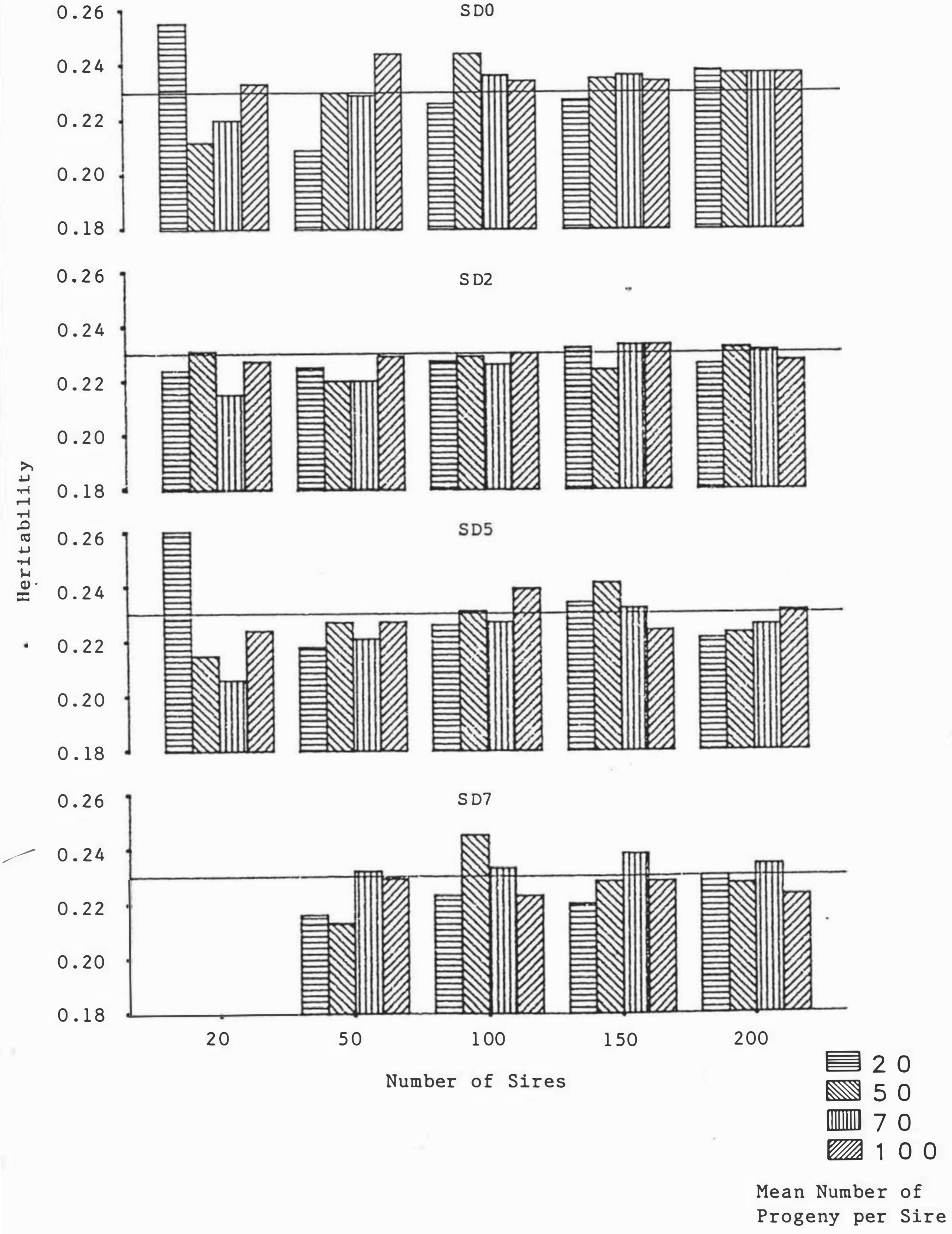


Figure 4.3 Mean heritability estimated by REML for data sets from data types SD0, SD2, SD5 and SD7 and with population heritability 0.2321.



As expected the REML and ML heritability estimates were very similar to the HM estimates for all data types, the differences between the population value and mean of the data sets rarely being greater than ±0.01 (which for practical purposes is unimportant). In flock A it was not possible to get a REML estimate, as the solutions to the equations went outside the parameter space during iteration. This is a deficiency of the algorithm used, not of REML. The data sets SD0, SD2, SD5 and SD7 showed a similar relationship between numbers of sires and progeny for ML (Fig. 4.2) and REML (Fig. 4.3) as for HM. Rothschild et al (1979) showed no difference between the ML and HM estimates for balanced data for a simulation with a 1-way random model. With unbalanced data (the extent of which was not quantified) they showed a difference of 0.001, which is smaller than reported in this study.

The MSE's of the heritability estimates for data types SD0, SD2, SD5 and SD7 were similar for the 3 methods of estimation and showed no consistent effect due to data unbalance (Tables 4.4, 4.5, 4.6). Not surprisingly, HM and REML methods had the same MSE's for balanced data (SD0) except for the data set of 20 sires with 20 progeny per sire, where the negative heritability estimates that occurred with HM were constrained to be non-negative for REML. The data types SD14, SD25 and SD29, which comprised the data set 100 sires with a mean of 100 progeny per sire, showed similar MSE's for the 3 methods of estimation (Table 4.7) and were similar to data types SD0, SD2, SD5 and SD7. The data types of flocks A, B, C, D, E and F had MSE's of heritabilities that were larger for HM than for ML or REML (Table 4.8). This may indicate that HM has a larger error in estimating the heritability, or it may be a reflection on the algorithm used to solve the equations needed to obtain the ML and REML estimates. The stopping criterion may have been too large and the point of maximum likelihood had not been reached. Flocks B and E had large MSE's of the heritability, relative to the other flocks, which appears to be independent of the level of unbalance. This may be due to the data structure, but the 2 flocks had little that made them different from the other flocks as far as the distribution of progeny per sire (Fig. 3.1) was concerned. The MSE's also showed that data sets consisting of 20 sires and data sets of 50 sires and a mean of 20 progeny per sire were less accurate in the estimation of the population heritability relative to other data sets.

Lin and M^{c}Allister (1984) reported MSE's of heritability estimates, from unbalanced data, were larger for ML than for HM or REML, for a population heritability of 0.4 and 120 sires with 5 to 100 progeny per sire. There were 10 replicates. The model used by Lin and M^{c}Allister for their simulation included a fixed effect due to herd (480 herds) and as ML does not account for the loss of degrees of freedom due to the fixed effects (Searle, 1979), the larger MSE's would be expected.

Table 4.4 Mean squared errors ($\times 10^3$) of HM heritability estimates for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	17.493	5.202	2.842	1.780	2.307
	SD2	16.401	9.854	2.988	2.730	1.430
	SD5	22.327	6.377	3.837	2.249	1.831
	SD7		6.469	3.264	2.705	1.432
50	SD0	6.454	3.887	2.189	1.503	0.997
	SD2	9.717	4.043	1.526	1.280	0.688
	SD5	7.211	3.842	2.397	1.395	0.868
	SD7		3.222	1.753	1.407	1.198
70	SD0	6.621	2.407	1.882	1.183	1.064
	SD2	6.511	2.771	1.459	0.880	0.669
	SD5	6.616	2.064	1.448	1.100	1.245
	SD7		2.735	2.056	1.388	0.367
100	SD0	6.057	2.058	1.150	0.795	0.871
	SD2	7.573	2.470	1.019	0.964	0.614
	SD5	5.610	2.472	1.127	0.645	0.619
	SD7		2.050	1.542	0.735	0.646

Table 4.5 Mean squared errors ($\times 10^3$) of ML heritability estimates for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	15.196	5.460	2.861	1.793	2.269
	SD2	15.363	9.646	2.958	2.709	1.449
	SD5	19.812	6.441	3.888	2.187	1.819
	SD7		6.259	3.391	2.791	1.403
50	SD0	6.682	3.810	2.094	1.480	0.976
	SD2	9.145	4.064	1.543	1.303	0.686
	SD5	7.256	3.809	2.274	1.303	0.900
	SD7		3.383	1.613	1.411	1.225
70	SD0	6.548	2.382	1.838	1.161	1.050^{1}
	SD2	6.556	2.822	1.478	0.872	0.664
	SD5	6.890	2.127	1.442	1.102	1.248
	SD7		2.635	1.946	1.295	0.372
100	SD0	5.688	1.895	1.126	0.783	0.767^{2}
	SD2	7.181	2.446	1.019	0.951	0.619
	SD5	5.502	2.442	1.071	0.667	0.616
	SD7		2.083	1.573	0.728	0.652^{1}

1 = 98 observations 2 = 87 observations

Table 4.6 Mean squared errors ($\times 10^3$) of REML heritability estimates for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires 20	50	100	150	200
20	SD0	17.137	5.202	2.842	1.779	2.307
	SD2	16.051	9.764	2.952	2.731	1.431
	SD5	22.206	6.335	3.885	2.210	1.788
	SD7		6.153	3.343	2.739	1.405
50	SD0	6.454	3.887	2.189	1.503	0.997
	SD2	9.695	4.026	1.540	1.281	0.688
	SD5	7.163	3.854	2.293	1.348	0.880
	SD7		3.231	1.701	1.409	1.218
70	SD0	6.621	2.407	1.882	1.183	1.064
	SD2	6.473	2.761	1.465	0.881	0.667
	SD5	6.581	2.045	1.428	1.110	1.240
	SD7		2.691	1.976	1.324	0.380
100	SD0	6.057	2.058	1.151	0.795	0.871
	SD2	7.515	2.473	1.019	0.962	0.611
	SD5	5.608	2.449	1.118	0.644	0.616
	SD7		2.099	1.543	0.721	0.645

Table 4.7 Mean squared errors ($\times 10^3$) of HM, ML and REML heritability estimates for data types SD14, SD25 and SD29.

	HM	ML	REML
SD14	1.226	1.137	1.136
SD25	1.879	1.820	1.789
SD29	1.721	1.381	1.454

Table 4.8 Mean squared errors ($\times 10^3$) of HM, ML and REML heritability estimates for flocks A, B, C, D, E and F.

	HM	ML	REML
A	1.684	1.562	
B	3.621	3.090	3.234
C	1.969	1.524	1.515
D	2.749	1.894	1.884
E	4.892	3.745	3.877
F	1.798	1.498	1.548

Rothschild et al (1979) had similar MSE's for heritabilities estimated by HM and ML for balanced data. With unbalanced data the MSE's were slightly larger for heritability estimates using HM than ML. The MSE's reported by Rothschild et al (1979) were larger than this study by 10^2. This may be a reflection of the relatively small error variances (0.9250 and 0.9875) used by Rothschild et al (1979) in their simulation.

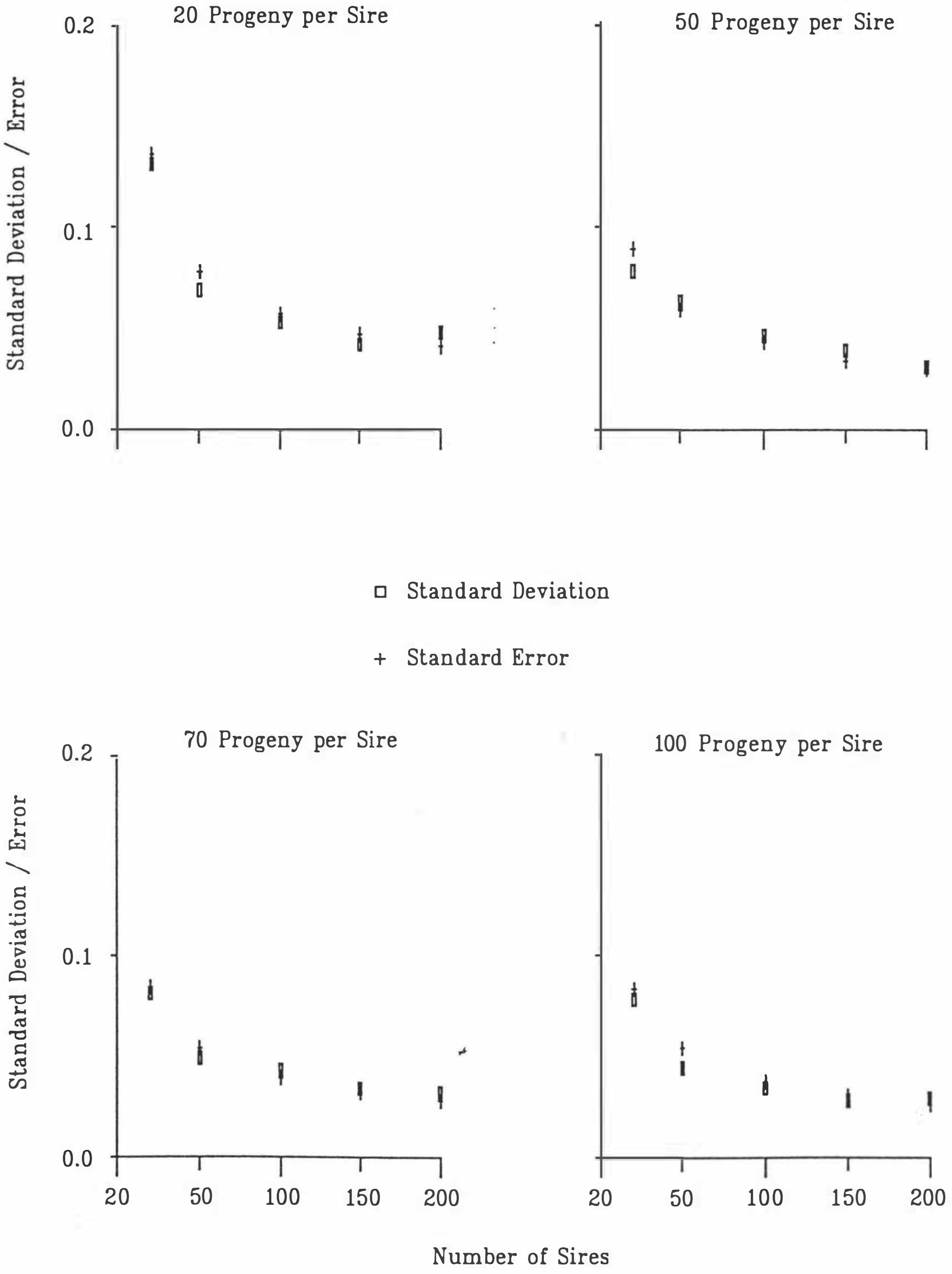
Kennedy (1981) noted that predictions of breeding values from models with only one random factor tend to be fairly robust to the heritability estimates used. When more than one random factor is involved or the predictions are multi-trait, then this may not necessarily be the case. As it is usually the rankings of individuals that is of importance and not the actual breeding value, it is unlikely that small changes in heritability estimates used will alter the rankings.

4.1.2 Standard Errors of the Heritability Estimates

The mean of the approximate sample standard error of the heritability estimate should equal the standard deviation of a large number of samples from a Monte Carlo simulation if the large sample standard error is an accurate estimate of the actual variation present. This arises as the standard error is the standard deviation of n estimates of the mean (Snedecor and Cochran, 1980).

The approximate standard errors of the HM heritability estimates give a close approximation of the standard deviation of the replicate estimates (Fig. 4.4) and hence appear reasonable indicators of the reliability of heritability estimates for balanced data (SD0). There was little difference in the accuracy with which the HM approximate standard error estimated the actual variability with either increasing numbers of sires or increasing numbers of progeny per sire. There was no difference greater than 0.011 between the mean of the approximate standard error estimates and the standard deviation of the HM heritability estimates. This is probably within sufficient accuracy as the majority of the literature presents the heritability to two decimal places. Funkhouser and Grossman (1982) reported a maximum difference of 0.006 between the sampling variance of the HM heritability and the expected variability based on Pearson's (1897) approximate variance of a ratio, for a 2-way random model. They simulated a heritability of 0.2 with 10, 30 and 75 sires, each with 2 dams with 6, 10 and 8 progeny per sire respectively. These combinations were replicated 100 times. The smaller difference obtained by Funkhouser and Grossman (1982) may have been due to the different model used.

Figure 4.4 Mean HM heritability approximate sample standard error and standard deviation of the replicate HM heritability estimates from data sets of the data type SD0.



Jensen and Barr (1965) showed a maximum difference of 0.014 for balanced data. The simulation used a heritability of 0.2 and a 2-way random model with interaction. Data sets were made up of 25, 50 and 100 sires with 5, 10 and 20 herds and 2,4 and 8 progeny per sire per herd.

The unbalanced data type SD2 gave close agreement between the mean heritability standard error and the standard deviation of the replicate heritability estimates. These were very similar to Fig. 4.4. The majority of the differences between the mean approximate standard error of the HM heritability and the standard deviation of the heritability estimates were less than 0.01 except for 50 sires with a mean of 20 progeny per sire where the difference was −0.019. Hence, the differences were probably not practically important. The large standard deviation of the heritability estimates for 50 sires with a mean of 20 progeny per sire was probably a chance effect as the other data sets with a mean of 20 progeny per sire were in good agreement with the mean standard error.

The unbalanced data types SD5 and SD7 showed close agreement between the mean of the approximate HM heritability standard error and the standard deviation of the replicate heritability estimates. These were very similar to Fig 4.4. The differences between the mean approximate standard error of the heritability estimates and the standard deviation of the estimates were small, not exceeding 0.01. Hence, differences between the mean approximate standard error and the standard deviation of the heritabilities are for practical purposes not important.

REML and ML showed similar relationships to HM in the accuracy with which the approximate standard error of the heritability estimate was able to measure the standard deviation of the replicate estimates for data types SD0, SD2, SD5 and SD7. The difference between the mean of the standard errors and the standard deviation of the replicate heritabilities for the ML estimates, was most often less than or equal to the HM estimate. The ML heritability estimates were usually less variable than the HM estimates, especially in the data sets with relatively low numbers of sires and progeny per sire. An exception was for balanced data (SD0) where the data set containing 200 sires with 100 progeny per sire had a larger difference for ML than HM or REML. This could be due to there only being 87 observations in this group, the remaining 13 not being estimated due to the iterative procedure not converging. A relatively large discrepancy exists between the REML estimate, and the ML and HM estimates for the data type SD2 with data sets consisting of 20 sires with a mean of 20 progeny per sire. This could possibly be due to the mean of the REML standard errors being calculated on 99 replicates, although it would seem unlikely that 1 replicate in 100 would make such a large difference.

The standard errors of the HM, ML and REML heritabilities of data types SD14, SD25 and SD29 were very similar to the standard deviation of the heritability estimates of the replicates (Fig. 4.5).

There was also very close agreement between the HM heritability standard error and the standard deviation of the 100 replicates based on the six flocks, except for flock E (Fig. 4.6). With flock E the standard error underestimated the standard deviation by 0.0206. This was independent of unbalance as flock D which showed a similar level of unbalance as E, was unaffected. No feature of the data structure of flock E could be recognised as the cause of the discrepancy. The ML and REML estimates showed a similar relationship between the mean standard error and the standard deviation of the replicates to that of HM (Fig. 4.6).

Jensen and Barr (1965), using a 2-way random model with interaction for the simulation, showed differences between the mean standard error of the data sets and the standard deviation of the heritability estimates for HM of up to 0.056 for unbalanced data based on a uniform distribution and up to 0.145 for unbalanced data based on an exponential distribution. These large differences occurred in data sets that had 5 herds with 2, 4 and 8 progeny per sire per herd. The differences were smaller for those data sets with 10 and 20 herds, not exceeding 0.023 for the uniform based and 0.048 for the exponential based data sets. A possible reason for the larger differences reported by Jensen and Barr (1965) than occurred in this study, is that a 2-way model was used, with a proportion of the sires not having progeny in some herds. This proportion was larger in the exponential distribution than in the uniform distribution.

The MSE's of the heritability approximate standard errors for data types SD0, SD2, SD5 and SD7 (Table 4.9, 4.10, 4.11) were similar between methods, except for data sets with 20 or 50 sires, where the MSE's of the ML estimates were smaller (more accurate) than the HM or REML estimates. The REML MSE's for data sets of 20 sires with a mean of 20 progeny per sire were larger than either the ML or HM estimates. If there was to be an effect of unbalance on the accuracy of the approximate standard error in estimating the actual variability of the heritability estimates it would be expected to show in data sets with a mean of 20 progeny per sire (Table 3.1, 3.2, 3.3) as these had the greatest level of unbalance. However there were no trends within these data sets. The data sets consisting of 20 sires and data sets with 50 sires and a mean of 20 progeny per sire were less accurate in estimating the actual parameter variation relative to other data sets. As would be expected, the MSE's for the REML estimates were the same as those from HM estimates for balanced data and where the HM

Figure 4.5 Mean heritabilty standard error and standard deviation of the replicate heritability estimates from data types SD14, SD25 and SD29.

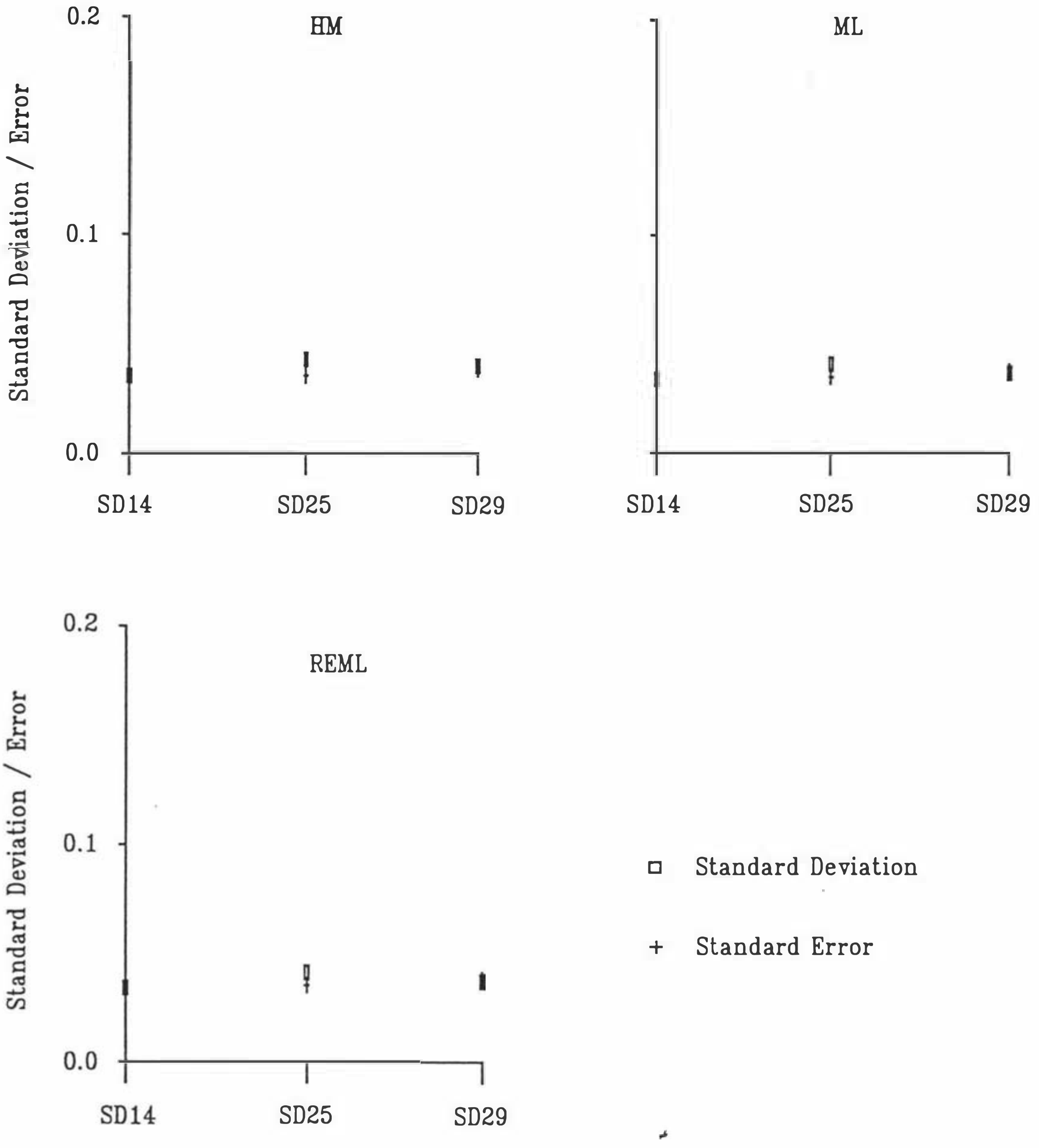
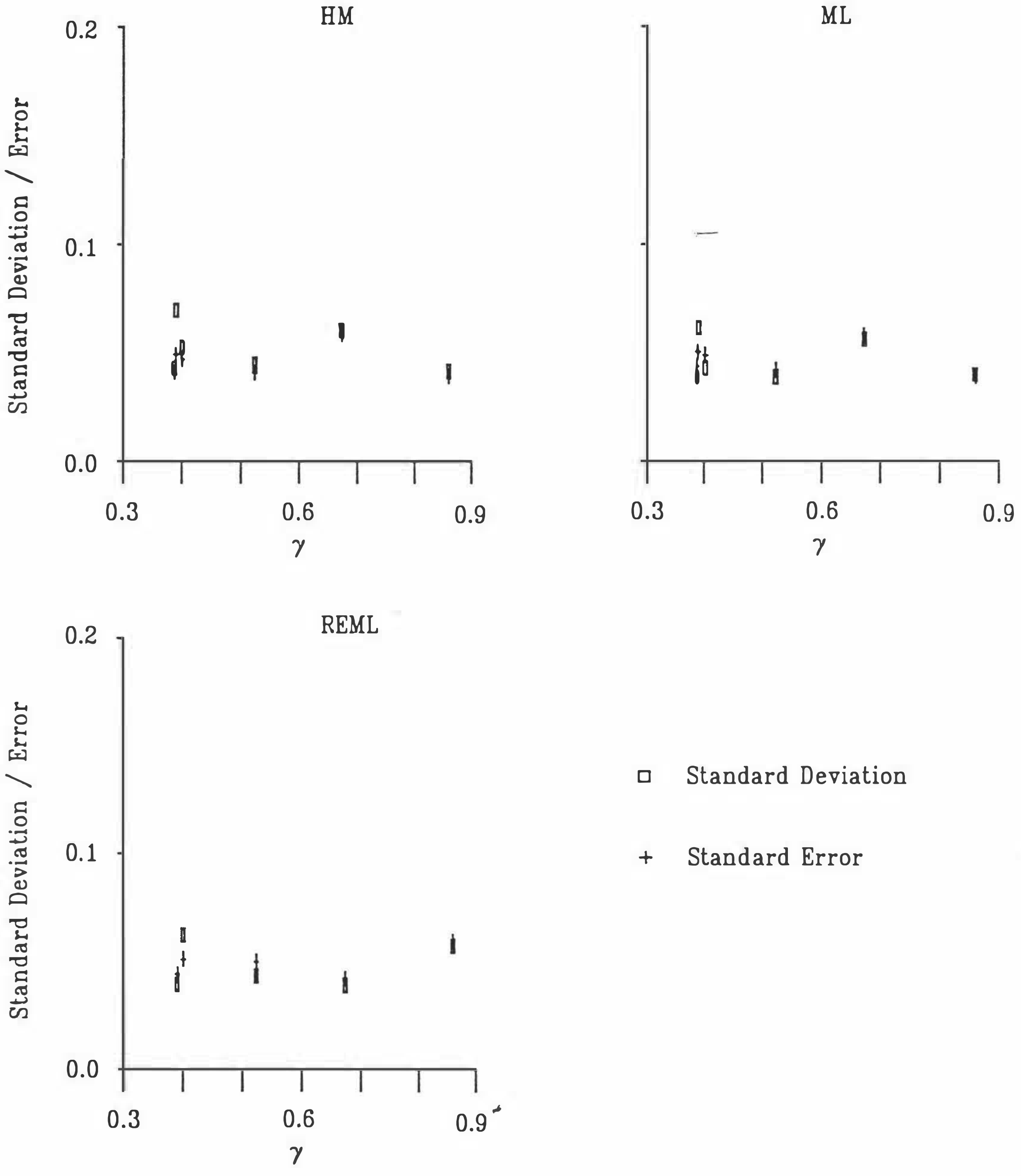


Figure 4.6 Mean heritabilty standard error and standard deviation of the replicate heritability estimates from flocks A to F plotted against gamma.



estimates were non-negative.

The MSE's of the heritability standard error estimates for SD14, SD25 and SD29 (Table 4.12) were similar to those from the data sets of 100 sires with a mean of 100 progeny per sire for data types SD0, SD2, SD5 and SD7. The MSE's of SD25 were larger than SD15 and SD29, but not unexpectedly large when compared with variation that occurred with SD0, SD2, SD5 and SD7. The three methods gave similar MSE's.

Table 4.9 Mean squared errors ($\times 10^4$) of HM heritability approximate standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires				
		20	50	100	150	200
20	SD0	11.503	2.144	0.512	0.352	0.599
	SD2	11.115	6.186	0.450	0.541	0.166
	SD5	14.431	1.615	0.745	0.196	0.146
	SD7		1.636	0.419	0.464	0.163
50	SD0	5.868	1.328	0.366	0.373	0.095
	SD2	7.378	1.529	0.261	0.155	0.135
	SD5	5.662	1.297	0.968	0.155	0.060
	SD7		0.904	0.322	0.298	0.390
70	SD0	5.396	0.975	0.480	0.186	0.300
	SD2	5.000	0.814	0.215	0.115	0.063
	SD5	4.779	1.305	0.214	0.149	0.782
	SD7		0.871	0.791	0.392	0.708
100	SD0	4.937	1.490	0.238	0.102	0.177
	SD2	6.238	0.771	0.314	0.121	0.051
	SD5	4.669	0.768	0.337	0.263	0.050
	SD7		0.941	0.326	0.122	0.052

Table 4.10 Mean squared errors (x10^4) of ML heritability approximate standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	9.904	1.933	0.485	0.336	0.607
	SD2	9.762	6.087	0.447	0.548	0.162
	SD5	14.133	1.631	0.786	0.197	0.127
	SD7		1.697	0.466	0.459	0.221
50	SD0	4.846	1.316	0.370	0.380	0.098
	SD2	6.833	1.505	0.244	0.158	0.130
	SD5	4.836	1.289	0.810	0.138	0.059
	SD7		0.846	0.320	0.295	0.423
70	SD0	4.673	0.884	0.488	0.189	0.303^1
	SD2	4.299	0.765	0.212	0.110	0.062
	SD5	4.131	1.209	0.205	0.157	0.769
	SD7		0.813	0.673	0.319	0.648
100	SD0	4.244	1.338	0.224	0.098	0.052^2
	SD2	5.741	0.728	0.294	0.121	0.050
	SD5	3.970	0.719	0.320	0.258	0.049
	SD7		0.813	0.326	0.127	0.060^1

1 = 98 observations 2 = 87 observations

Table 4.11 Mean squared errors (x10^4) of REML heritability approximate standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	15.003^1	2.144	0.512	0.353	0.599
	SD2	70.702^1	5.994	0.460	0.546	0.169
	SD5	42.094	1.606	0.789	0.191	0.132
	SD7		1.829	0.471	0.431	0.236
50	SD0	5.868	1.328	0.366	0.373	0.095
	SD2	7.370	1.509	0.258	0.155	0.135
	SD5	5.663	1.292	0.798	0.138	0.061
	SD7		0.902	0.336	0.293	0.418
70	SD0	5.397	0.975	0.480	0.186	0.300
	SD2	4.968	0.810	0.217	0.115	0.064
	SD5	4.764	1.340	0.211	0.155	0.764
	SD7		0.874	0.658	0.315	0.665
100	SD0	4.937	1.491	0.238	0.102	0.177
	SD2	6.169	0.772	0.313	0.121	0.051
	SD5	4.664	0.764	0.342	0.268	0.050
	SD7		0.901	0.323	0.134	0.052

1 = 99 observations

The standard error MSE's of the flocks (Table 4.13) are similar for the 3 methods of heritability estimation. They are also similar to those obtained for the SD series of data types with similar numbers of sires and progeny per sire. The exception is flock E, which has a large MSE relative to other flocks. This reflects the discrepancy between the standard error and standard deviation of the replicates that has already been alluded to.

Table 4.12 Mean squared errors ($\times 10^4$) of HM, ML and REML heritability approximate standard errors for the data types SD14, SD25 and SD29.

	HM	ML	REML
SD14	0.194	0.209	0.220
SD25	0.824	0.621	0.613
SD29	0.253	0.208	0.213

Table 4.13 Mean squared errors ($\times 10^3$) of HM, ML and REML heritability approximate standard errors for flocks A, B, C, D, E and F.

	HM	ML	REML
A	0.275	0.233	
B	1.253	1.144	1.273
C	0.513	0.396	0.418
D	1.043	0.861	0.921
E	5.456	2.377	2.369
F	0.349	0.498	0.561

4.2 Sire Variance

4.2.1 Variance Estimates

The mean of the HM, ML and REML sire variance estimates for each number of sires, mean number of progeny and the SD of progeny number was compared with the population variance in Figs. 4.7, 4.8 and 4.9, respectively. As expected, sire variance estimates with balanced data (SD0), approached the actual population value (0.6783) with increasing numbers of sires and number of progeny per sire. As numbers of sires increased, the number of progeny required to get an estimate approaching the population value of the sire variance decreased. The three methods gave similar results with discrepancies occurring only in data sets with 20 sires and a mean of 20 progeny per sire. This occurred as REML and ML estimates are required to fall within a non-negative parameter space, whereas the HM estimates may be negative. Rothschild et al (1979) showed no difference between HM, ML and the population sire variance of 0.075 for balanced data.

The differences between the population sire variance and the estimated sire variance was usually not large although some differences did reach 0.09 (20 sires with 50 progeny per sire and 50 sires with 20 progeny per sire, for ML). In several data sets, greater than 10% of the replicates had 90% confidence intervals of the HM sire variance that did not cover the population sire variance (Table 4.14). These were spread evenly over the data sets. Confidence intervals were not constructed for the ML or REML estimates.

The HM, ML and REML sire variance estimates for the slightly unbalanced data type SD2 approximated the population value closely (Fig. 4.7, 4.8 and 4.9). The greatest difference between the population sire variance and the mean estimated value was 0.092 for the data set with 20 sires and a mean of 70 progeny per sire and the variance estimated using ML.

The SD5 unbalanced data with 20 sires had a large variability in the sire variances for all 3 methods of estimation (Fig. 4.7, 4.8, 4.9). The data set having 20 sires with a mean of 20 progeny per sire appeared to overestimate the population sire variance while those with 20 sires and means of 50 or 70 progeny per sire underestimated the sire variance. For HM estimates the largest deviation (0.103) from the population value arise from sets based on 20 sires with a mean of 20 progeny. This is probably due to the relatively small size of the data set and the random variation this allows.

Figure 4.7 Mean sire variances estimated by HM for data sets from data types SD0, SD2, SD5 and SD7 and with population sire variance 0.6783.

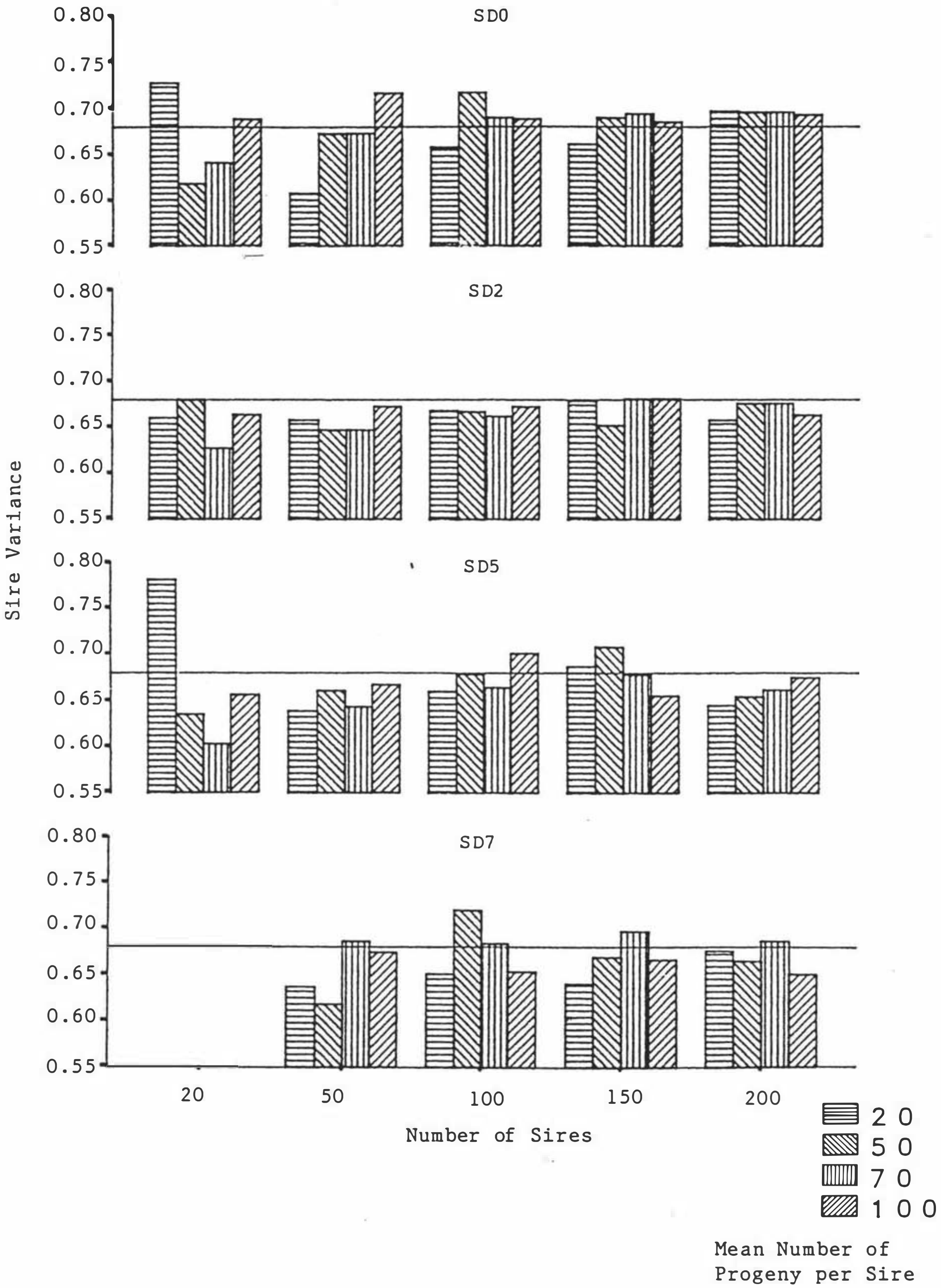


Figure 4.8 Mean sire variances estimated by ML for data sets from data types SD0, SD2, SD5 and SD7 and with population sire variance 0.6783.

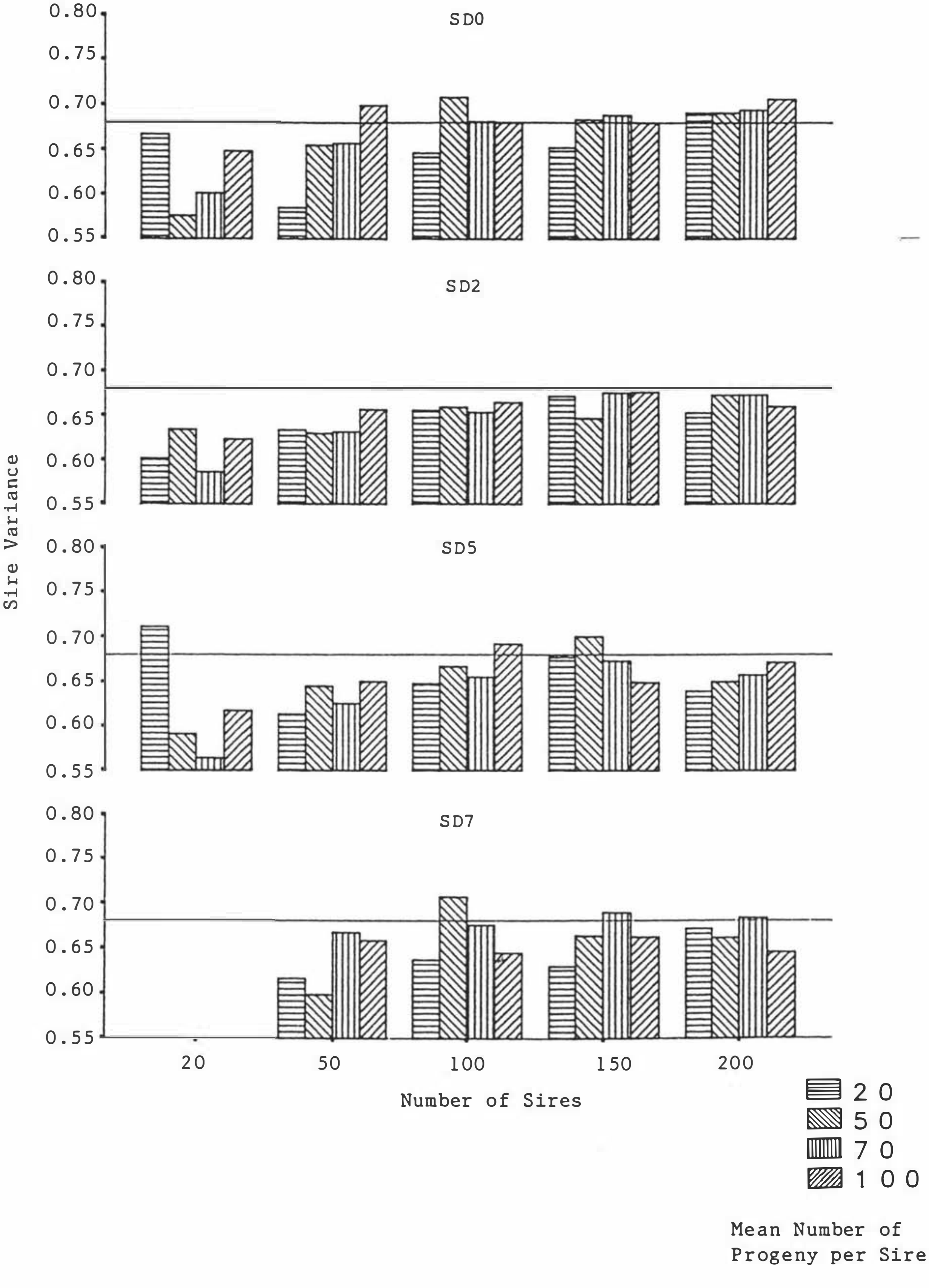


Figure 4.9 Mean sire variances estimated by REML for data sets from data types SD0, SD2, SD5 and SD7 and with population sire varance 0.6783.

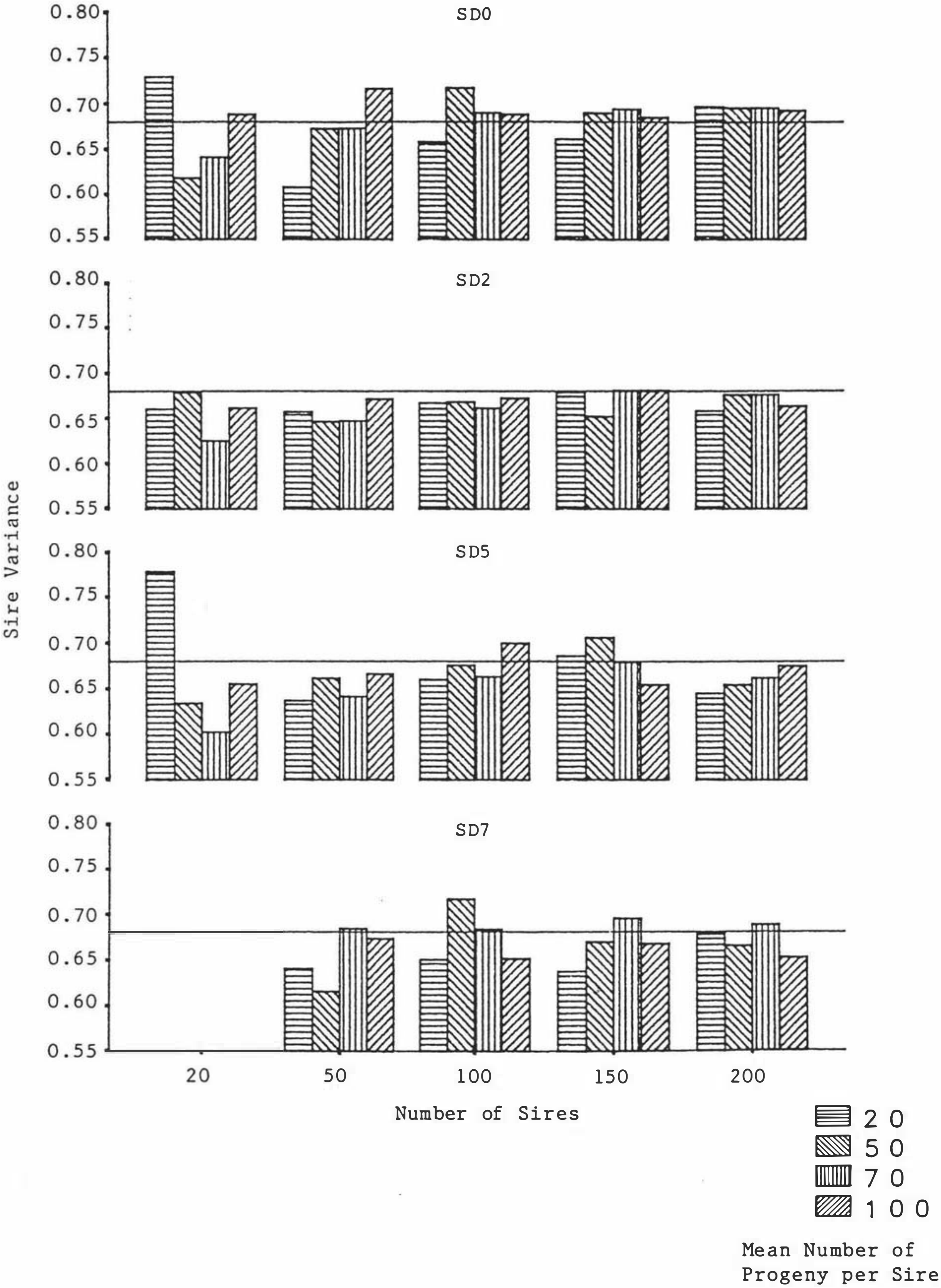


Table 4.14 Number of replicates from HM sire variance estimates that have the population sire variance falling above and below the 90% confidence intervals for data type SD0.

Number of Progeny per Sire	Number of Sires: 20	50	100	150	200
20	4,1	1,2	0,0	0,0	0,10
50	2,0	7,0	3,4	0,2	0,2
70	9,0	0,3	9,8	0,4	2,12
100	3,4	0,1	1,0	0,0	0,10

Estimates of sire variance using all methods with the unbalanced SD7 data were similar to the estimates from the preceding levels of unbalance (Fig. 4.7, 4.8, 4.9) and there was no unduly large deviations from the population value.

It is to be expected that data sets consisting of either 20 sires or a mean of 20 progeny per sire would have shown any effect of data unbalance as these had the greatest change, as measured by γ, from SD0 to SD7 (Tables 3.1, 3.2, 3.3). However, there was no consistent effect of increasing unbalance on the sire variance estimated by HM, ML or REML (Fig. 4.7, 4.8, 4.9).

The three methods of variance component estimation gave sire variances close to the population value for SD14, SD25 and SD29 (Table 4.15) and for the six flocks (Table 4.16). Estimates of REML sire variances for flock A were not possible as the algorithm could not solve the equations, and keep the solutions in the parameter space. This is a fault of the algorithm, and not a problem with REML.

Table 4.15 The mean of the data set sire variances, estimated using HM, ML and REML, for data types SD14, SD25 and SD 29.

	HM	ML	REML
SD14	0.6752	0.6650	0.6729
SD25	0.6489	0.6385	0.6461
SD29	0.7221	0.7049	0.7132

Table 4.16 The mean of the data set sire variances, estimated using HM, ML and REML, for flocks A, B, C, D, E and F.

	γ	HM	ML	REML
A	0.8610	0.6931	0.6804	
B	0.6735	0.7062	0.6738	0.6934
C	0.5235	0.6726	0.6562	0.6664
D	0.4015	0.6760	0.6530	0.6673
E	0.3910	0.7174	0.6821	0.6968
F	0.3887	0.6914	0.6834	0.6944

The ML estimates of the sire variance tended to be smaller than either the REML or HM estimates. It would be expected that they would be similar as the only fixed effect is the mean which accounts for 1 degree of freedom, and this for 100 sires should have little effect on the sire variance. The stopping criterion for the ML algorithm may be set too large and iterating stops before the point of maximum likelihood is reached.

Rothschild et al (1979), for a simulation involving balanced data, reported no differences between the ML and HM estimates of sire variance. Both methods underestimated the population sire variance by 0.001.

Swallow and Monahan (1984), for a similar ratio of $\frac{\sigma_s^2}{\sigma_e^2}$, also showed that a ML method consistently underestimated the population value of sire variance to a greater extent than ANOVA and REML. However they were dealing with relatively few observations within a random effect (3 to 9) and relatively few observations in total (15 to 45). The degree of unbalance was quite severe in some data sets (e.g. 7 groups with 1 observation each, and 2 with 19 each).

The MSE's of the sire variances estimated by the three different methods for data types SD0, SD2, SD5 and SD7 (Tables 4.17, 4.18, 4.19) showed no trend in the effect of unbalance. What the MSE's also highlight was that the ML estimates, for data sets with 20 sires, were more accurate at estimating the true sire variance than either HM or REML. The MSE's also indicate that data sets with 20 sires and 50 sires with a mean of 20 progeny per sire were less accurate in estimating the population sire variance than larger sized data sets.

Table 4.17 Mean squared errors ($\times 10^2$) of HM sire variances for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires 20	50	100	150	200
20	SD0	14.597	4.710	2.538	1.570	2.122
	SD2	15.102	9.180	2.876	2.543	1.334
	SD5	22.433	5.976	3.678	2.207	1.776
	SD7		6.560	3.270	2.610	1.350
50	SD0	6.203	3.612	2.228	1.477	0.974
	SD2	9.159	3.803	1.399	1.207	0.646
	SD5	7.020	3.643	2.286	1.399	0.770
	SD7		3.024	1.734	1.371	1.196
70	SD0	5.901	2.270	1.842	1.227	1.071
	SD2	6.105	2.563	1.359	0.842	0.649
	SD5	6.004	1.898	1.274	0.999	1.161
	SD7		2.911	1.958	1.284	0.364
100	SD0	6.328	2.099	1.132	0.740	0.841
	SD2	7.333	2.330	1.007	0.904	0.592
	SD5	5.472	2.318	1.059	0.628	0.620
	SD7		1.797	1.481	0.702	0.611

Table 4.18 Mean squared errors ($\times 10^2$) of ML sire variances for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires 20	50	100	150	200
20	SD0	12.624	4.924	2.554	1.586	2.082
	SD2	13.851	8.899	2.828	2.515	1.351
	SD5	19.073	5.925	3.703	2.131	1.764
	SD7		6.258	3.365	2.670	1.321
50	SD0	6.312	3.520	2.123	1.448	0.951
	SD2	8.446	3.783	1.412	1.227	0.644
	SD5	6.871	3.601	2.148	1.302	0.797
	SD7		3.156	1.584	1.365	1.222
70	SD0	5.798	2.225	1.793	1.196	1.053[2]
	SD2	6.069	2.583	1.372	0.832	0.644
	SD5	6.171	1.957	1.260	0.997	1.161
	SD7		2.753	1.841	1.190	0.365
100	SD0	5.794	1.925	1.101	0.726	0.758[1]
	SD2	6.841	2.284	1.003	0.890	0.596
	SD5	5.260	2.264	1.003	0.647	0.615
	SD7		1.809	1.499	0.697	0.612[2]

1=87 observations 2=98 observations

Table 4.19 Mean squared errors ($\times 10^2$) of REML sire variances for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires: 20	50	100	150	200
20	SD	14.311	4.710	2.539	1.570	2.123
	SD2	14.790	9.088	2.842	2.544	1.335
	SD5	22.012	5.883	3.718	2.164	1.736
	SD7		6.270	3.346	2.627	1.330
50	SD0	6.203	3.612	2.228	1.477	0.974
	SD2	9.137	3.786	1.413	1.208	0.646
	SD5	6.969	3.657	2.178	1.349	0.781
	SD7		3.020	1.677	1.369	1.221
70	SD0	5.901	2.270	1.842	1.227	1.071
	SD2	6.065	2.552	1.365	0.843	0.647
	SD5	5.968	1.881	1.252	1.009	1.157
	SD7		2.858	1.880	1.222	0.375
100	SD0	6.328	2.099	1.133	0.740	0.841
	SD2	7.268	2.331	1.007	0.902	0.589
	SD5	5.463	2.290	1.052	0.627	0.617
	SD7		1.841	1.480	0.691	0.611

Table 4.20 Mean squared errors ($\times 10^2$) of HM, ML and REML sire variances for the data types SD14, SD25 and SD29.

	HM	ML	REML
SD14	1.267	1.165	1.173
SD25	1.756	1.695	1.670
SD29	1.656	1.326	1.402

The MSE's of the sire variance for data types SD14, SD25 and SD29 (Table 4.20) were similar to those for the data type SD7 with a data set of 100 sires and a mean of 100 progeny per sire. There was no difference between the MSE's due to method.

The flock sire-variance MSE's showed no relationship with unbalance (Table 4.21). Flocks B and E had the largest MSE's, but they were similar to those for data types SD0, SD2, SD5 and SD7 with similar numbers of sires and progeny per sire. The MSE's from HM were larger than those from either ML or REML.

The MSE's reported by Rothschild et al (1979), for balanced and unbalanced data, were similar to those reported in this study for HM and ML. Lin and M^{c}Allister (1984) reported larger MSE's, this probably being due to there being only 10 replicates.

Table 4.21 Mean squared errors ($\times 10^2$) of HM, ML and REML sire variances for flocks A, B, C, D, E and F.

	HM	ML	REML
A	1.661	1.497	
B	3.486	2.973	3.141
C	1.896	1.456	1.457
D	2.835	1.862	1.870
E	4.986	3.702	3.861
F	1.757	1.427	1.486

4.2.2 Standard Errors of the Sire Variance Estimates.

The mean of the large sample standard error of the HM sire variance from balanced data (SD0) underestimated the standard deviation of the replicates for data sets with a mean of 20 progeny per sire, except for data sets with 200 sires (Fig. 4.10). The underestimation did not exceed 0.031 and hence is small enough not to be important, practically. The remaining data sets showed close agreement between the mean large sample standard error and the standard deviation of the replicate sire variances. Hence the large sample standard error was an accurate measure of the variability of the HM sire variance estimates.

The mean of the HM sire variance large sample standard errors for unbalanced data type SD2 agree closely with the standard deviation of the HM sire variance, with the exception of the data set with 50 sires and a mean of 20 progeny per sire. In this data set the large sample standard error underestimated the actual standard deviation by 0.058. As the other data sets in the proximity had close agreement between the 2 measures, the difference was probably due to random variation. The relationship between the standard errors and the standard deviation was similar to Fig. 4.10.

Figure 4.10 Mean HM sire variance large sample standard error and standard deviation of the replicate HM sire variance estimates from data sets of the data type SD0.

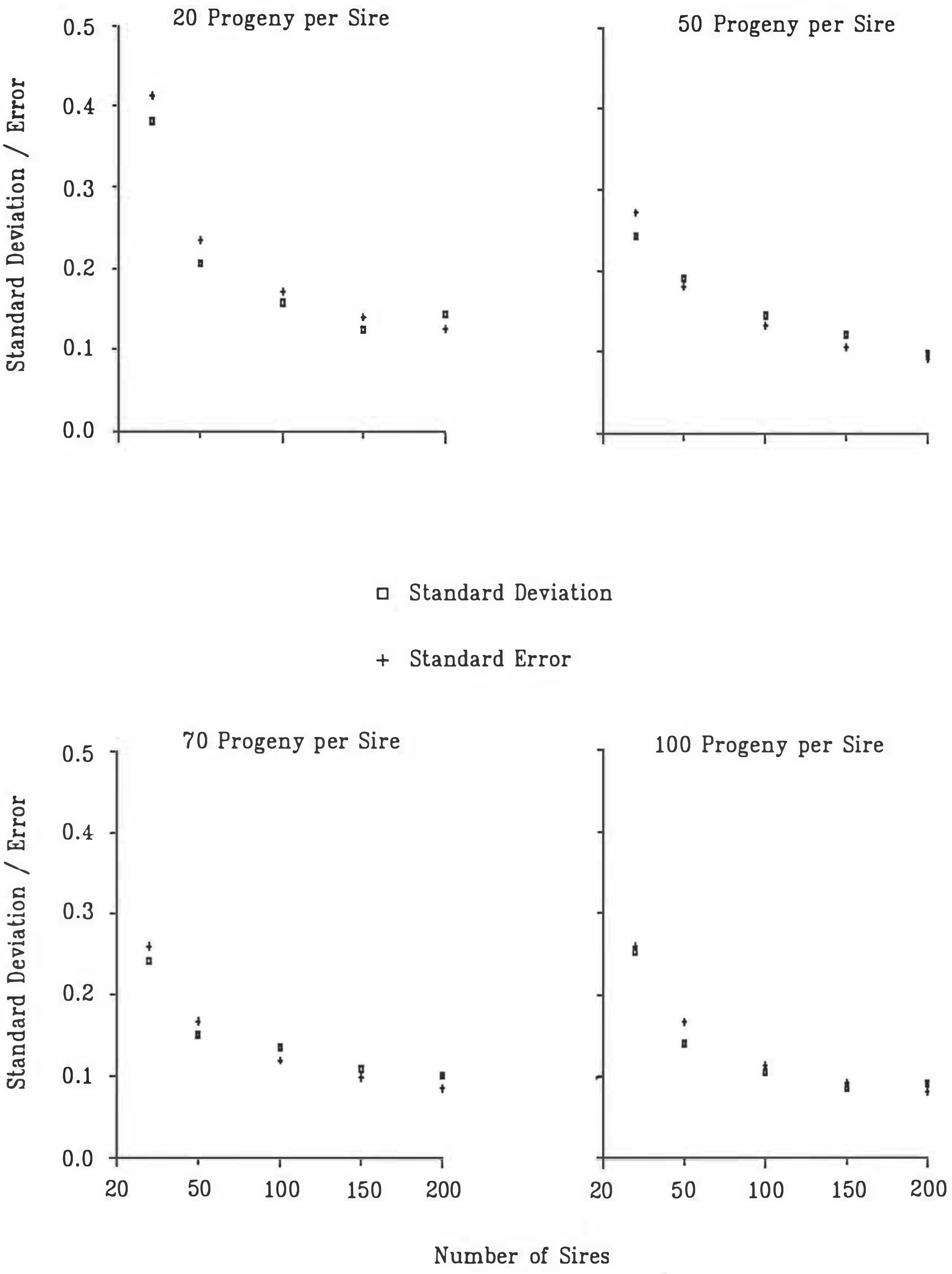
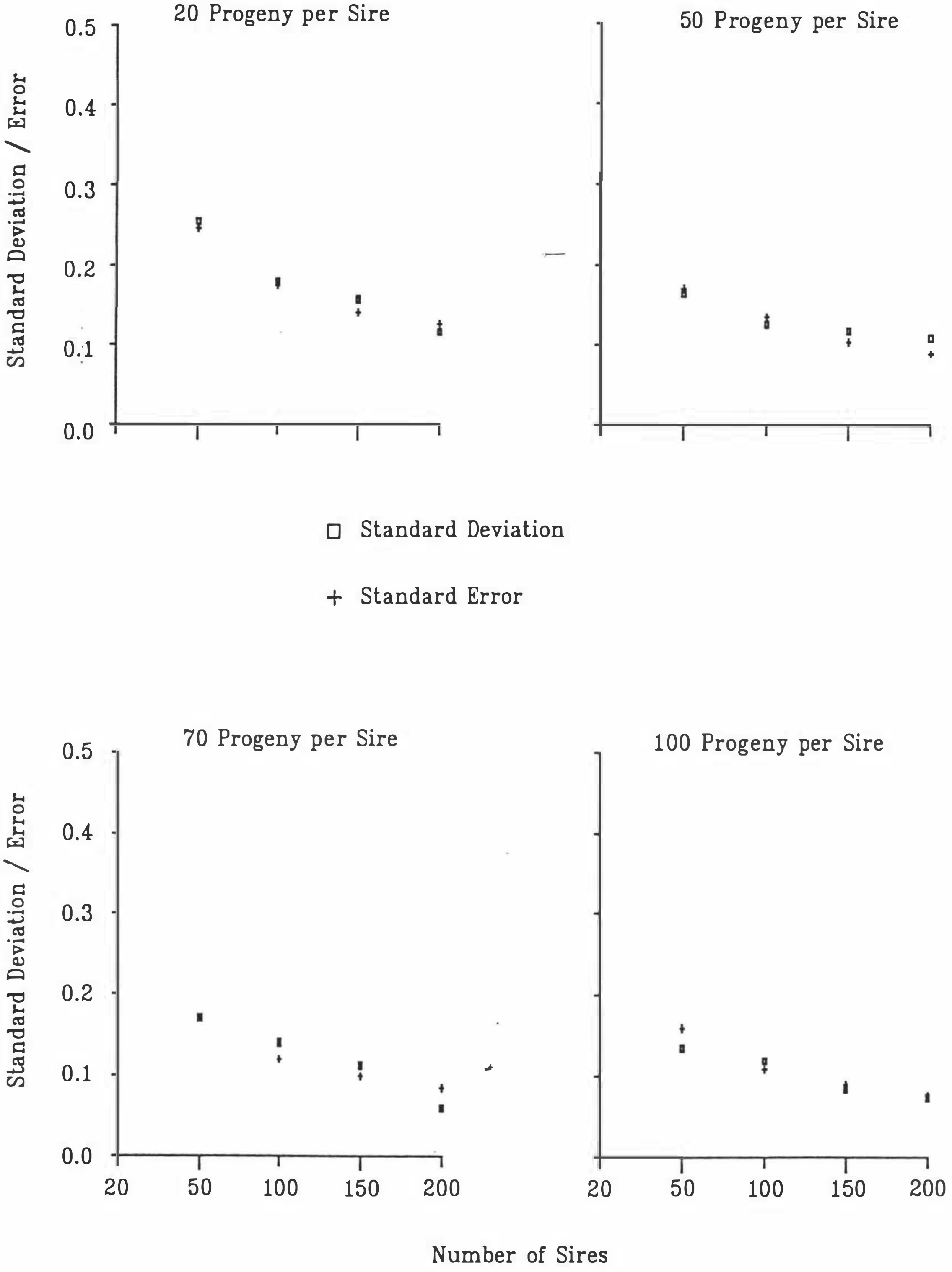


Figure 4.11 Mean HM sire variance large sample standard error and standard deviation of the replicate HM sire variance estimates from data sets of the data type SD7.



The more unbalanced data types, SD5 and SD7, gave good agreement between the mean large sample standard error and the standard deviation of the HM sire variance estimates (SD5 was similar to Fig. 4.10 and SD7 is shown in Fig. 4.11). The differences did not exceed 0.03 which for practical purposes is unimportant.

The accuracy with which the variation about the REML sire variance was estimated by the large sample sampling standard deviation was almost identical to that obtained for HM estimates. The exceptions were for 20 sires with a mean of 20 progeny per sire for the data sets from SD0, SD2 and SD5, and to a lesser extent from 50 sires with a mean of 20 progeny per sire from SD7. These REML differences were larger than the HM differences for SD2, but smaller for data sets from SD5 and SD7.

The trend in the relationship between the large sample standard error and the standard deviation of the ML sire variances was very similar to that observed for the REML and HM estimates for data sets with 50 sires or more. The differences between the large sample standard error and actual standard deviation of the sire variance estimates with data sets of 20 sires were less for ML than the HM and REML methods. This appears due to both the large sample standard error of the sire variances and the standard deviation of the replicates being smaller for ML than HM or REML. Also the mean sample standard error of the ML sire variance was smaller than the corresponding HM or REML sample standard error by more than the corresponding differences in the standard deviation of the replicates.

With data types SD14, SD25 and SD29 the standard error of the sire variance closely estimated the standard deviation of the actual sire variances for the three methods (Fig. 4.12). The same was true with the flock data types (Fig 4.13), with the exception of flock E where the standard error underestimated the standard deviation of the replicates by 0.0471. This may be an effect of data structure , although there appears to be very little that makes flock E different from the other 5. It is not an effect of unbalance as flocks D and F, which had similar levels of unbalance, did not show any discrepancies.

The MSE's of the large sample standard errors about the actual parameter standard deviations for data types SD0, SD2, SD5 and SD7 (Table 4.22, 4.23, 4.24) were smaller for the ML estimates than for the HM and REML estimates. Also, the MSE's of the REML standard errors were larger than either ML or HM for the data sets of 20 sires with a mean of 20 progeny per sire. There were, however, no consistent trends in the effect of unbalance on the MSE's of the sire variance standard errors. The MSE's of data sets of 20 sires and data sets

Figure 4.12 Mean sire variance standard error and standard deviation of the replicate sire variance estimates from data types SD14, SD25 and SD29.

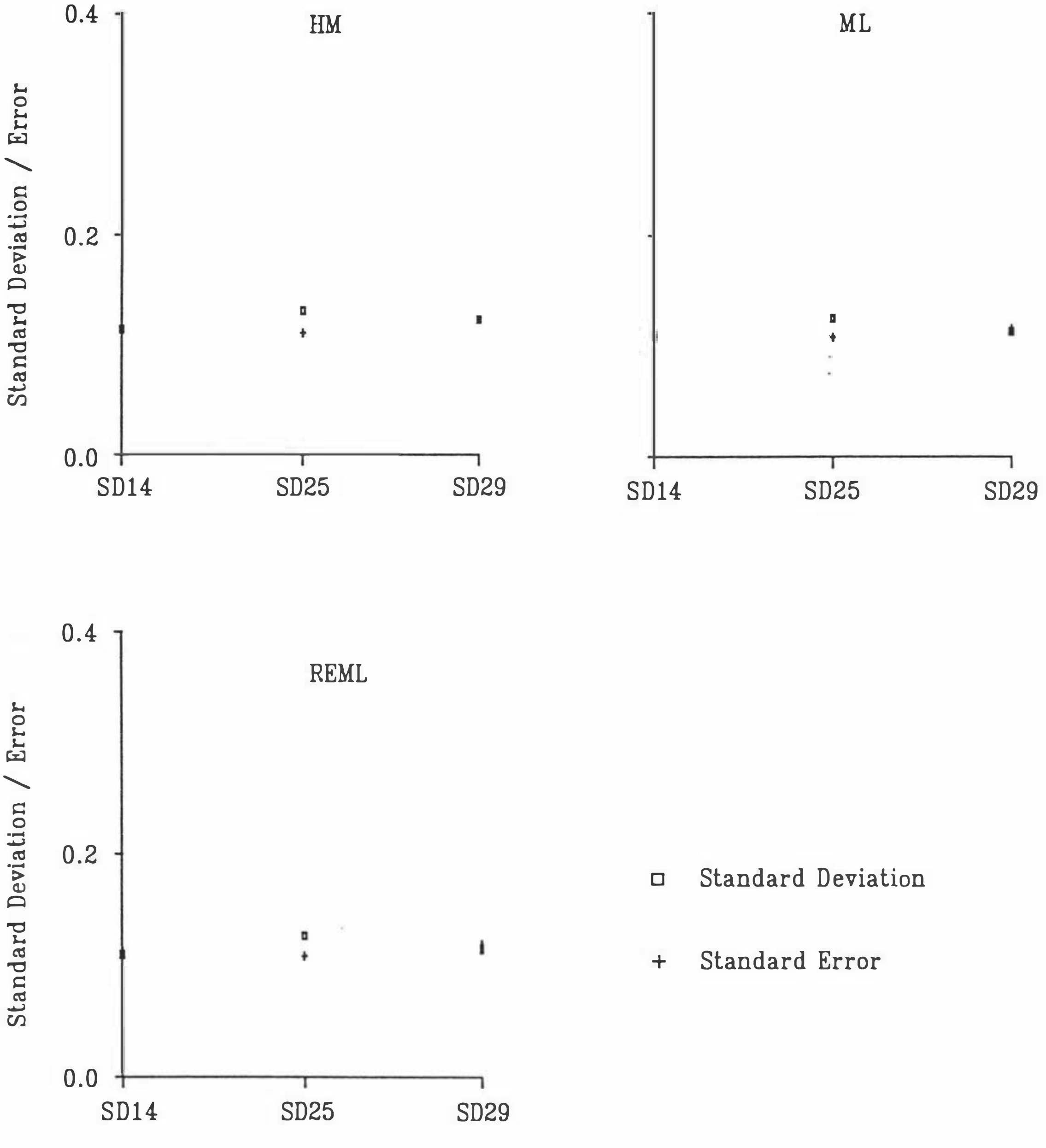


Figure 4.13 Mean sire variance standard error and standard deviation of the replicate sire variance estimates from flocks A to F plotted against gamma.

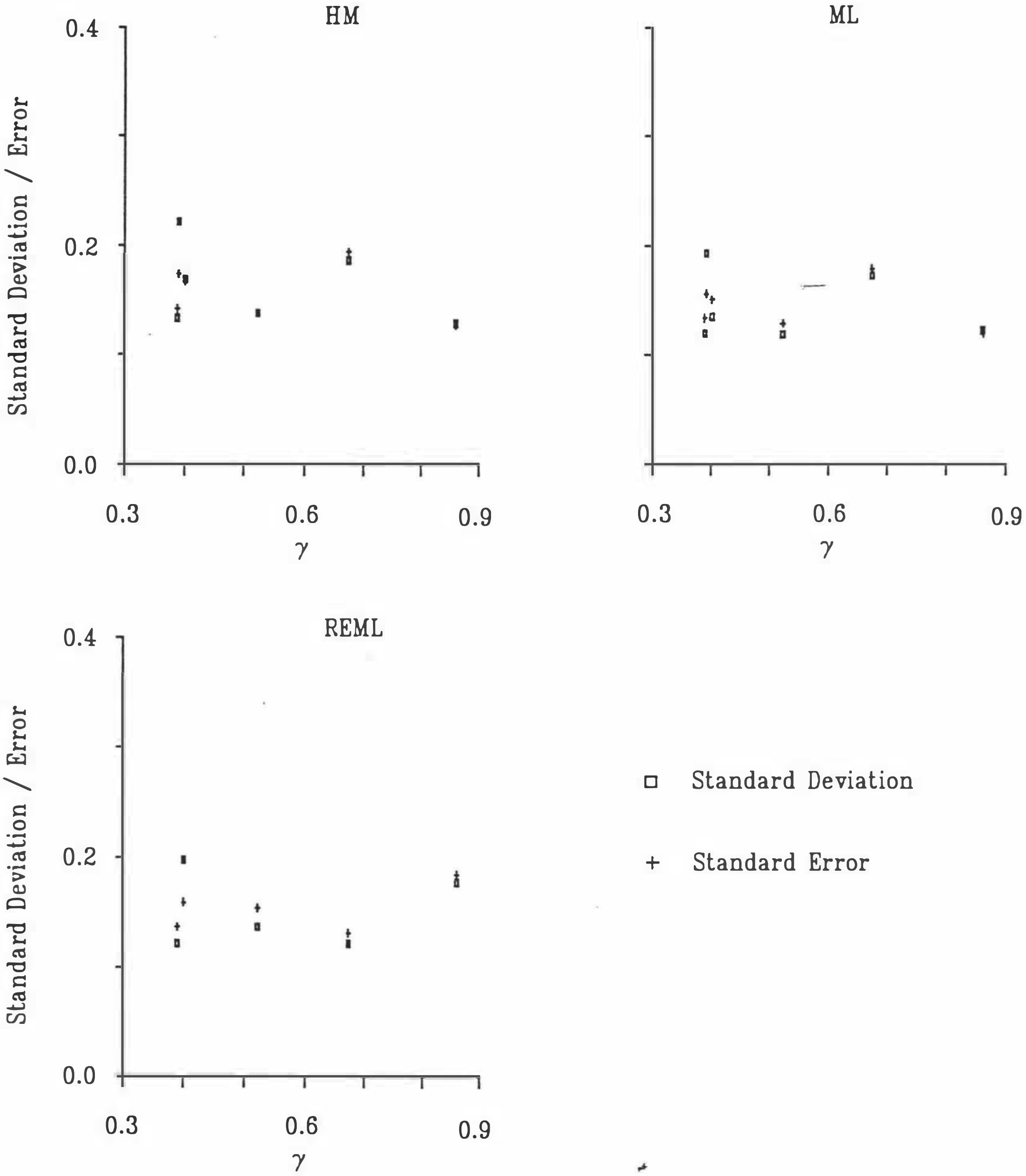


Table 4.22 Mean squared errors ($\times 10^3$) of HM sire variance standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	15.186	2.534	0.672	0.454	0.577
	SD2	15.470	7.102	0.613	0.624	0.189
	SD5	23.873	2.486	1.079	0.322	0.245
	SD7		2.985	0.768	0.643	0.236
50	SD0	7.008	1.568	0.556	0.459	0.130
	SD2	9.658	1.832	0.339	0.188	0.149
	SD5	7.529	1.646	1.027	0.231	0.082
	SD7		1.140	0.401	0.370	0.509
70	SD0	6.353	1.201	0.611	0.294	0.387
	SD2	6.265	1.028	0.269	0.138	0.073
	SD5	5.864	1.509	0.271	0.144	0.726
	SD7		1.218	0.815	0.337	0.663
100	SD0	6.755	1.487	0.275	0.134	0.194
	SD2	8.136	0.970	0.316	0.135	0.060
	SD5	5.953	0.961	0.414	0.238	0.063
	SD7		1.309	0.407	0.138	0.062

Table 4.23 Mean squared errors ($\times 10^3$) of ML sire variance standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	12.486	2.277	0.631	0.431	0.584
	SD2	12.883	6.854	0.588	0.629	0.180
	SD5	20.512	2.282	1.129	0.304	0.220
	SD7		2.658	0.804	0.667	0.238
50	SD0	5.728	1.514	0.557	0.459	0.131
	SD2	8.467	1.772	0.316	0.191	0.142
	SD5	6.225	1.608	0.870	0.207	0.075
	SD7		1.027	0.375	0.376	0.572
70	SD0	5.290	1.084	0.614	0.299	0.383^2
	SD2	5.230	0.950	0.261	0.131	0.071
	SD5	4.862	1.369	0.259	0.148	0.721
	SD7		1.119	0.707	0.281	0.602
100	SD0	5.758	1.332	0.261	0.127	0.072^1
	SD2	7.167	0.900	0.296	0.134	0.059
	SD5	4.956	0.885	0.384	0.231	0.060
	SD7		1.104	0.404	0.137	0.069^2

1 = 87 observations 2 = 98 observations

Table 4.24 Mean squared errors ($\times 10^3$) of REML sire variance standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires				
		20	50	100	150	200
20	SD0	18.205[1]	2.534	0.672	0.454	0.578
	SD2	66.178[1]	6.912	0.606	0.631	0.187
	SD5	44.050	2.311	1.140	0.294	0.226
	SD7		2.864	0.811	0.636	0.251
50	SD0	7.007	1.565	0.556	0.456	0.129
	SD2	9.637	1.812	0.334	0.189	0.148
	SD5	7.419	1.648	0.865	0.207	0.078
	SD7		1.103	0.393	0.373	0.568
70	SD0	6.349	1.200	0.612	0.296	0.388
	SD2	6.204	1.023	0.269	0.137	0.073
	SD5	5.801	1.519	0.272	0.149	0.718
	SD7		1.186	0.699	0.279	0.617
100	SD0	6.754	1.489	0.275	0.133	0.192
	SD2	8.025	0.969	0.314	0.135	0.061
	SD5	5.921	0.953	0.411	0.242	0.063
	SD7		1.234	0.404	0.145	0.061

1 = 99 observations

with 50 sires and a mean of 20 progeny per sire were greater than for the larger data sets, indicating that if MSE is used as a criterion, smaller data sets have the variation in sire variance components estimated with less accuracy than larger data sets.

The MSE's of the sire variance standard errors for data types SD14, SD25 and SD29 (Table 4.25) are similar to those for the data sets of 100 sires with a mean of 100 progeny per sire obtained for data types SD0, SD2, SD5 and SD7. Hence there is little relationship between the level of unbalance and the MSE's of the standard errors. There is also little difference in the MSE's between the three methods of sire variance estimation.

The MSE's of the sire variance standard errors for the six flocks (Table 4.26) is also in good agreement with those obtained for SD0, SD2, SD5 and SD7. The MSE's of flock E are larger than those from the other five flocks, but this does not appear to be due to the level of unbalance. There is little difference in the MSE's between the three methods of variance component estimation, but the HM MSE's do tend to be larger than either REML or ML. This is a probably due to the algorithms used in ML and REML not having reached the point of maximum likelihood and is unlikely to be a real effect due to method of variance component estimation.

Table 4.25 Mean squared errors ($\times 10^3$) of HM, ML and REML sire variance approximate standard errors for the data types SD14, SD25 and SD29.

	HM	ML	REML
SD14	0.264	0.238	0.244
SD25	0.739	0.628	0.622
SD29	0.319	0.266	0.275

Table 4.26 Mean squared errors ($\times 10^3$) of HM, ML and REML sire variance approximate standard errors for flocks A, B, C, D, E and F.

	HM	ML	REML
A	0.374	0.297	
B	1.987	1.455	1.632
C	0.590	0.459	0.483
D	1.398	0.922	0.968
E	4.488	2.797	2.825
F	0.639	0.593	0.659

4.3 Error Variances

4.3.1 Variance Estimates

HM, ML and REML estimates of error variances all approach the population value (11.0106) closely with most data sets from data types SD0, SD2, SD5 and SD7 (Fig. 4.14, 4.15, 4.16). The major exception in the balanced data (SD0) was the data set of 20 sires with 20 progeny per sire, where the population error variance was underestimated by 0.310, 0.313 and 0.312 respectively. This underestimate was probably a reflection of the small numbers in the data sets and hence random variation. A large proportion of the data sets for data types SD0, SD2,

Figure 4.14 Mean error variances estimated by HM for data sets from data types SD0, SD2, SD5 and SD7 and population error variance 11.0106.

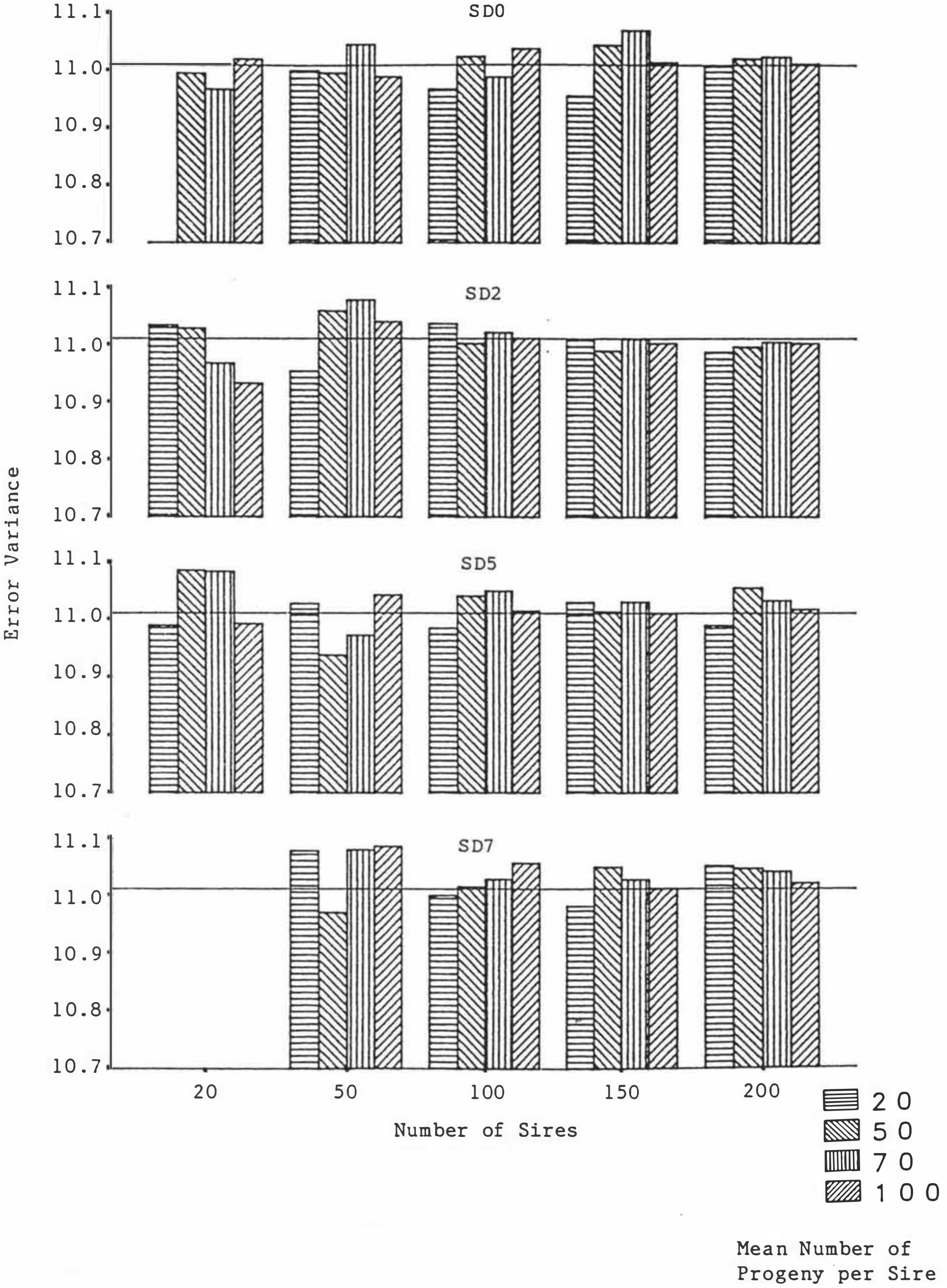


Figure 4.15 Mean error variances estimated by ML for data sets from data types SD0, SD2, SD5 and SD7 and population error variance 11.0106.

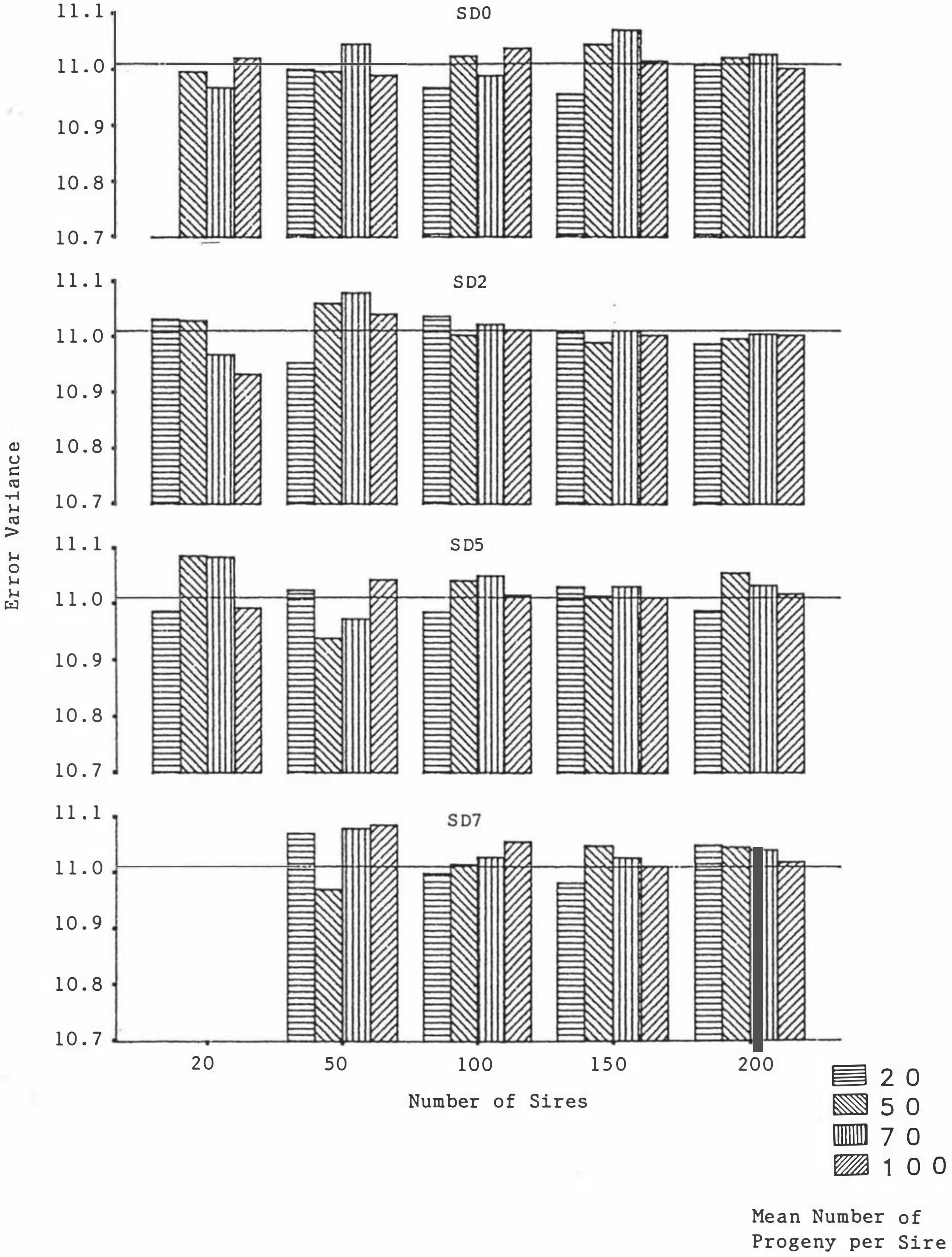
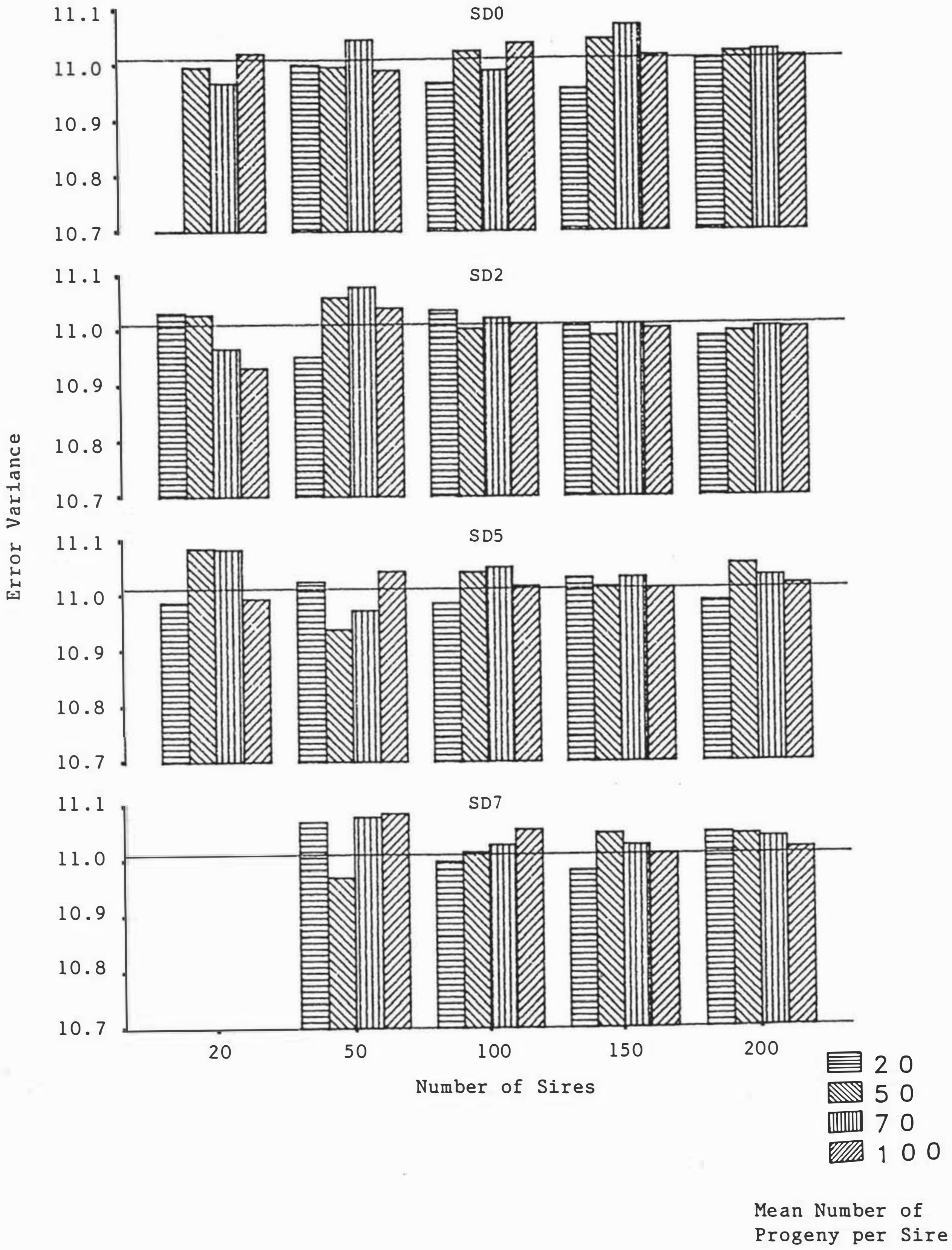


Figure 4.16 Mean error variances estimated by REML for data sets from data types SD0, SD2, SD5 and SD7 and population error variance 11.0106.



SD5 and SD7 had HM error variance confidence intervals that did not contain the population sire variance at a frequency greater than the expected 10% (Table 4.27). The close agreement between the population and estimated sire variances indicate that the confidence intervals may be too narrow and perhaps not a true reflection of the bounds encountered.

The data types SD14, SD25 and SD29 along with flocks A to F also had close agreement between the mean of the estimated sire variance and the population value for all methods (Tables 4.28, 4.29). There was very little difference between estimates due to method of estimation and there was no effect of unbalance.

Swallow and Monahan (1984) reported close agreement between the HM, ML and REML estimates of error variance and the population values for all levels of unbalance used, except for data sets with six or less random levels where biases in ML were large. Similarly, the HM and ML estimates obtained by Rothschild et al (1979) agreed well with the population values.

The MSE's of the error variances for data types SD0, SD2, SD5 and SD7 (Tables 4.30, 4.31, 4.32) also showed no effect of unbalance on the accuracy with which the sample error variance estimate the population error variance. All methods of estimating the sire variance gave similar MSE's. Data sets consisting of 20 sires and those with 50 sires and a mean of 20 progeny per sire generally gave less accurate estimates (i.e. larger MSE's) of the population error variance than other data sets.

Data types SD14, SD25 and SD 29 had MSE's (Table 4.33) similar to those obtained for data sets of 100 sires with a mean of 100 progeny per sire for data types SD0, SD2, SD5 and SD7. There were no differences between the methods of estimation. Flocks A to F also had MSE's (Table 4.34) similar to data types SD0, SD2, SD5 and SD7 with approximately the same numbers of sires and progeny per sire. Hence data unbalance had no effect on MSE's of error variances. Method of estimation also had no effect on the MSE's.

The sire variance MSE's reported by Swallow and Monahan (1984) were similar for HM, ML and REML. They were also similar to the MSE's in this study for data sets of comparable size. Rothschild et al (1979) showed little difference between HM and ML sire-variance MSE's. The MSE's reported by Rothschild et al (1979) were smaller by 10^2 than the estimates in this study. This may be due to the population error variance being 0.925 and 0.9875, compared with 11.0106 used in this study.

Table 4.27 Number of replicates from HM error variance estimates that have the population error variance falling above and below the 90% confidence intervals for data types SD0, SD2, SD5 and SD7.

Number of Sires

			20	50	100	150	200
Number of Progeny per Sire	20	SD0	19,7	4,3	7,7	11,3	6,8
		SD2	6,5	6,2	6,8	5,4	6,3
		SD5	6,3	6,9	8,9	6,1	5,6
		SD7		3,7	9,11	10,1	3,12
	50	SD0	2,9	4,6	4,10	11,1	13,8
		SD2	6,7	1,11	5,4	7,3	3,3
		SD5	2,7	9,2	2,11	4,10	5,15
		SD7		7,7	3,11	9,10	5,14
	70	SD0	6,7	9,11	6,11	4,14	4,11
		SD2	8,2	3,7	4,7	1,1	5,3
		SD5	5,11	6,4	6,11	6,9	0,4
		SD7		4,11	4,10	6,10	0,4
	100	SD0	5,6	2,3	1,0	6,7	6,15
		SD2	7,4	5,3	4,7	3,4	7,5
		SD5	3,1	4,8	5,12	11,6	3,4
		SD7		1,15	3,15	6,4	4,2

Table 4.28 The mean of the data set error variances, estimated using HM, ML and REML, for data types SD14, SD25 and SD 29.

	HM	ML	REML
SD14	11.0313	11.0313	11.0313
SD25	11.0156	11.0155	11.0155
SD29	11.0198	11.0196	11.0196

Table 4.29 The mean of the data set error variances, estimated using HM, ML and REML, for flocks A, B, C, D, E and F.

	γ	HM	ML	REML
A	0.8610	11.0094	11.0086	
B	0.6735	10.9999	10.9989	10.9989
C	0.5235	11.0335	11.0316	11.0316
D	0.4015	11.0238	11.0233	11.0233
E	0.3910	11.0133	11.0119	11.0120
F	0.3887	11.0347	11.0350	11.0350

Table 4.30 Mean squared errors ($\times 10^1$) of HM error variances for data sets from data types SD0, SD2, SD5 and SD7.

		Number of Sires				
Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	10.246	2.666	1.212	0.957	0.631
	SD2	6.844	2.305	1.361	0.817	0.648
	SD5	6.156	3.403	1.277	0.725	0.623
	SD7		2.034	1.458	0.724	0.706
50	SD0	2.832	0.924	0.520	0.398	0.331
	SD2	2.747	0.934	0.438	0.288	0.180
	SD5	1.928	0.984	0.539	0.411	0.316
	SD7		1.154	0.511	0.423	0.307
70	SD0	2.091	0.864	0.377	0.323	0.179
	SD2	1.941	0.653	0.332	0.151	0.167
	SD5	1.923	0.646	0.383	0.285	0.142
	SD7		0.690	0.406	0.275	0.131
100	SD0	1.290	0.366	0.311	0.139	0.086
	SD2	1.287	0.367	0.241	0.122	0.117
	SD5	0.914	0.512	0.290	0.178	0.078
	SD7		0.826	0.315	0.152	0.087

Table 4.31 Mean squared errors $(\times 10^1)$ of ML error variances for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	10.243	2.666	1.212	0.957	0.631
	SD2	6.806	2.312	1.359	0.816	0.647
	SD5	6.128	3.404	1.261	0.730	0.617
	SD7		2.026	1.462	0.716	0.690
50	SD0	2.832	0.924	0.520	0.398	0.331
	SD2	2.749	0.934	0.438	0.288	0.180
	SD5	1.928	0.985	0.538	0.411	0.316
	SD7		1.150	0.511	0.423	0.308
70	SD0	2.091	0.864	0.377	0.323	0.178[1]
	SD2	1.941	0.653	0.332	0.151	0.167
	SD5	1.923	0.646	0.383	0.285	0.142
	SD7		0.690	0.406	0.275	0.131
100	SD0	1.290	0.366	0.311	0.139	0.085[2]
	SD2	1.287	0.367	0.242	0.122	0.117
	SD5	0.914	0.512	0.290	0.178	0.078
	SD7		0.826	0.315	0.152	0.088[1]

1 = 98 observations 2 = 87 observations

Table 4.32 Mean squared errors $(\times 10^1)$ of REML error variances for data sets from data types SD0, SD2, SD5 and SD7.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	SD0	10.243	2.666	1.212	0.957	0.631
	SD2	6.815	2.311	1.359	0.816	0.647
	SD5	6.131	3.404	1.261	0.730	0.617
	SD7		2.026	1.462	0.716	0.690
50	SD0	2.832	0.924	0.520	0.398	0.331
	SD2	2.748	0.934	0.438	0.288	0.180
	SD5	1.928	0.985	0.538	0.411	0.316
	SD7		1.150	0.511	0.423	0.308
70	SD0	2.091	0.864	0.377	0.323	0.179
	SD2	1.941	0.653	0.332	0.151	0.167
	SD5	1.923	0.646	0.383	0.285	0.142
	SD7		0.690	0.406	0.275	0.131
100	SD0	1.290	0.366	0.311	0.139	0.086
	SD2	1.287	0.367	0.242	0.122	0.117
	SD5	0.914	0.512	0.290	0.178	0.078
	SD7		0.826	0.315	0.152	0.087

Table 4.33 Mean squared errors ($\times 10^1$) of HM, ML and REML error variances for the data types SD14, SD25 and SD29.

	HM	ML	REML
SD14	0.283	0.283	0.283
SD25	0.282	0.282	0.282
SD29	0.245	0.245	0.245

Table 4.34 Mean squared errors ($\times 10^1$) of HM, ML and REML error variances for flocks A, B, C, D, E and F.

	HM	ML	REML
A	0.493	0.489	
B	0.698	0.698	0.698
C	0.345	0.344	0.344
D	0.640	0.636	0.636
E	0.382	0.380	0.380
F	0.372	0.369	0.369

Lin and M^{c}Allister (1984) reported the MSE of the ML error variance to be larger by 100 times that of the HM3 and REML estimates. Lin and M^{c}Allister (1984) suggested that this large difference came about due to the ML estimator of the error variance being biased as the total number of records are used as the degrees of freedom to compute the error variance without taking into account the degrees of freedom associated with fitting the fixed effects in the model. In the current study there was only 1 degree of freedom for fixed effects, whereas their study had 480. The MSE's obtained by Lin and M^{c}Allister were approximately 10 times larger than those in this study. This is most likely to be due to the current study using 100 replicates whereas Lin and M^{c}Allister (1984) used 10.

4.3.2 Standard Errors of Error Variance Estimates

The approximate sample standard error of the error variance estimated for HM gave a good measure of the variation present in the error variances for data type SD0 (Fig 4.17). The relationships were similar for SD2, SD5 and SD7. The results from ML and REML were very similar to HM. The difference between the large sample standard error and the standard deviation of the error variances was greatest for data sets consisting of 20 sires with 20 progeny per sire from balanced data (−0.19). As the remaining data sets and data types had relatively small differences this large difference was probably due to the small number of observations and the subsequent random variation.

The data types SD14, SD25 and SD29 likewise had close agreement between sample standard errors and the standard deviation of the replicate error variances, irrespective of the method of estimation (Fig. 4.18). Similarly, flocks A to F also showed good agreement (Fig 4.19), irrespective of method of estimation. Thus there is no effect of level of unbalance on error variance standard errors.

The MSE's of the error variance standard errors for data types SD0, SD2, SD5 and SD7 (Tables 4.35, 4.36, 4.37) showed little difference due to the 3 methods or between the data types. As expected, the data sets with limited data (20 sires with a mean of 20 or 50 progeny per sire, and 50 sires with a mean of 20 progeny per sire) were less accurate in the estimation of the standard errors of the error variance than the other data sets.

The data sets SD15, SD25 and SD29 had MSE's of the sire variance standard error (Table 4.38) similar to those for data sets of 100 sires with a mean of 100 progeny per sire from the data types SD0, SD2, SD5 and SD7. MSE's for HM, ML and REML were almost identical.

The MSE's of the error variance standard error of flocks A to F (Table 4.39) also had good agreement with data types SD0, SD2, SD5 and SD7 for similar data set sizes. The exception was flock D which had a relatively large MSE. As several of the data sets from the SD series that were in close proximity to the size of flock D had similarly large MSE's, this is probably not a reflection on the data set structure. There was also little difference between methods. Hence the level of unbalance had no effect on the MSE's of the error variance standard errors.

Figure 4.17 Mean HM error variance large sample standard error and standard deviation of the replicate HM error variance estimates from data sets of the data type SD0.

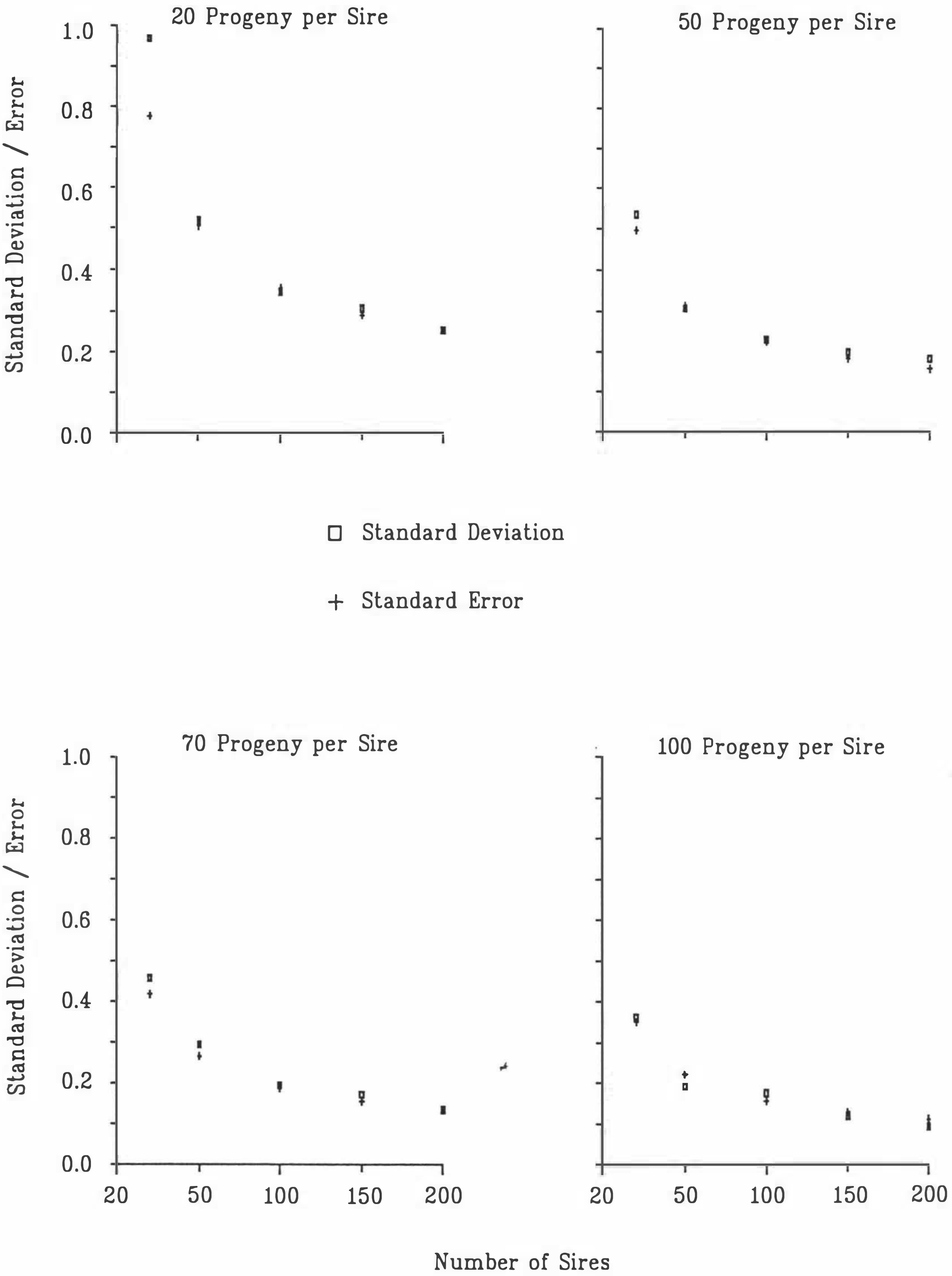


Figure 4.18 Mean error variance standard error and standard deviation of the replicate error variance estimates from data types SD14, SD25 and SD29.

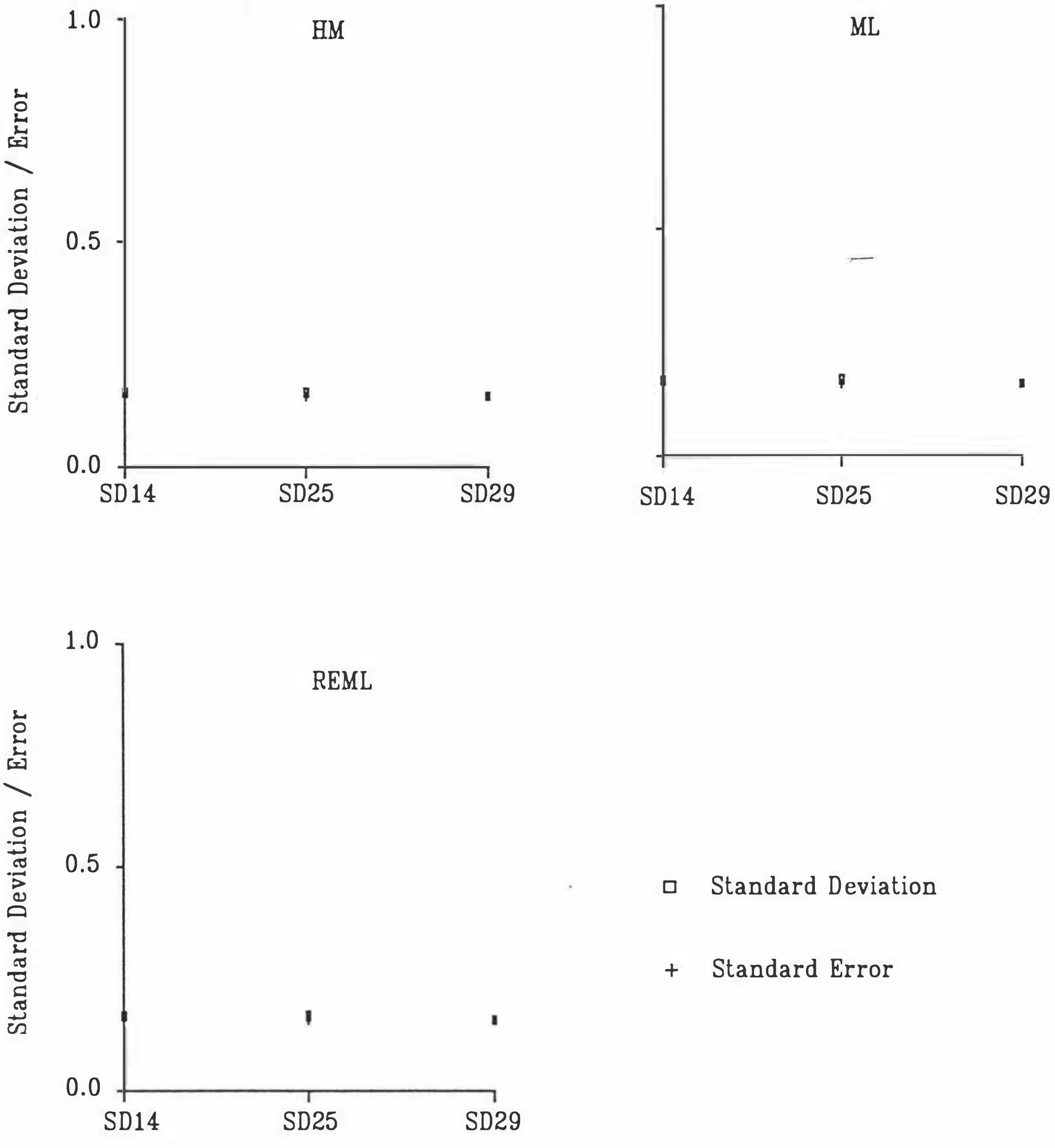


Figure 4.19 Mean error variance standard error and standard deviation of the replicate error variance estimates from flocks A to F plotted against gamma.

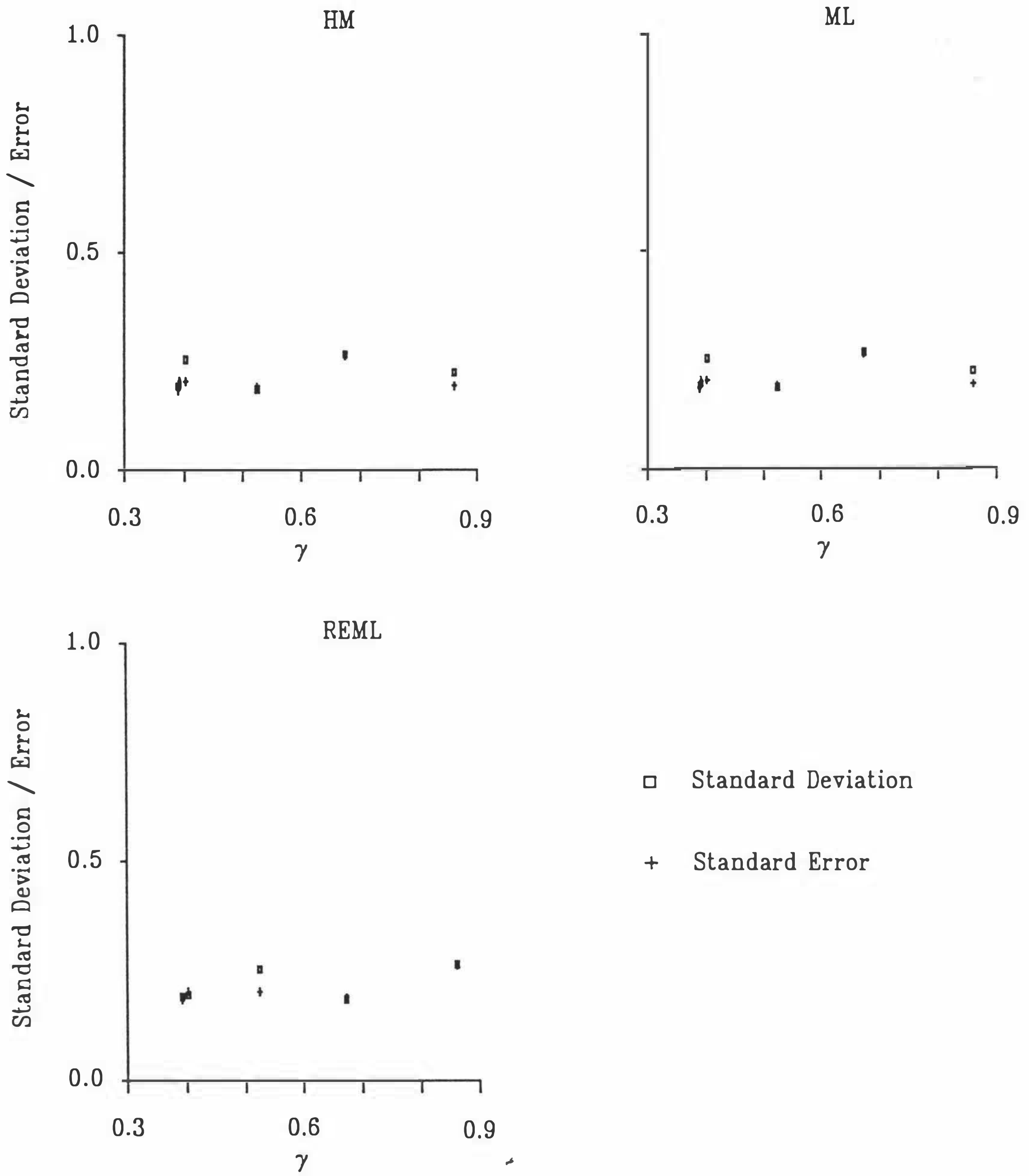


Table 4.35 Mean squared errors ($\times 10^3$) of HM error variance standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires 20	50	100	150	200
20	SD0	41.786	0.760	0.200	0.312	0.033
	SD2	4.538	1.034	0.284	0.076	0.040
	SD5	3.318	7.144	0.137	0.539	0.037
	SD7		3.992	0.865	0.540	0.147
50	SD0	2.011	0.157	0.057	0.246	0.635
	SD2	1.360	0.236	0.165	0.152	0.540
	SD5	4.692	0.111	0.091	0.496	0.242
	SD7		0.744	0.043	0.448	0.232
70	SD0	1.905	0.798	0.059	0.292	0.003
	SD2	0.812	0.392	0.033	0.873	0.010
	SD5	0.441	0.174	0.033	0.240	0.230
	SD7		0.170	0.208	0.165	0.472
100	SD0	0.243	0.902	0.339	0.094	0.315
	SD2	0.144	1.010	0.005	0.282	0.005
	SD5	2.216	0.032	0.221	0.042	0.491
	SD7		3.217	0.246	0.018	0.303

Table 4.36 Mean squared errors ($\times 10^3$) of ML error variance standard errors for data sets from data types SD0, SD2, SD5 and SD7.

Mean Number of Progeny Per Sire		Number of Sires 20	50	100	150	200
20	SD0	41.443	0.759	0.200	0.312	0.033
	SD2	4.402	1.001	0.280	0.078	0.040
	SD5	3.322	7.231	0.132	0.496	0.044
	SD7		3.885	0.914	0.595	0.098
50	SD0	2.012	0.157	0.057	0.246	0.635
	SD2	1.368	0.236	0.166	0.153	0.540
	SD5	4.697	0.108	0.090	0.497	0.241
	SD7		0.708	0.043	0.449	0.236
70	SD0	1.905	0.798	0.059	0.292	0.003[1]
	SD2	0.812	0.393	0.033	0.873	0.010
	SD5	0.441	0.174	0.033	0.239	0.228
	SD7		0.170	0.208	0.167	0.473
100	SD0	0.243	0.902	0.339	0.094	0.337[2]
	SD2	0.144	1.010	0.005	0.282	0.005
	SD5	2.217	0.032	0.221	0.042	0.491
	SD7		3.205	0.245	0.018	0.286[1]

1 = 98 observations   2 = 87 observations

Table 4.37 Mean squared errors ($\times 10^3$) of REML error variance standard errors for data sets from data types SD0, SD2, SD5 and SD7.

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	SD0	68.784	0.760	0.200	0.313	0.033
		SD2	43.891[1]	1.003	0.281	0.077	0.040
		SD5	16.632	7.239	0.131	0.499	0.044
		SD7		3.873	0.913	0.595	0.098
	50	SD0	2.011	0.157	0.057	0.246	0.636
		SD2	1.367	0.236	0.166	0.153	0.539
		SD5	4.696	0.109	0.090	0.497	0.241
		SD7		0.710	0.044	0.450	0.237
	70	SD0	1.905	0.798	0.058	0.292	0.003
		SD2	0.812	0.392	0.033	0.873	0.010
		SD5	0.442	0.174	0.033	0.239	0.230
		SD7		0.170	0.208	0.167	0.474
	100	SD0	0.243	0.902	0.339	0.094	0.317
		SD2	0.144	1.011	0.005	0.282	0.006
		SD5	2.217	0.032	0.222	0.042	0.490
		SD7		3.206	0.246	0.018	0.303

1=99 observations

Table 4.38 Mean squared errors ($\times 10^3$) of HM, ML and REML error variance standard errors for the data types SD14, SD25 and SD29.

	HM	ML	REML
SD14	0.127	0.125	0.125
SD25	0.152	0.152	0.152
SD29	0.005	0.005	0.005

Table 4.39 Mean squared errors ($\times 10^3$) of HM, ML and REML error variance standard errors for flocks A, B, C, D, E and F.

	HM	ML	REML
A	0.980	0.929	
B	0.056	0.056	0.056
C	0.029	0.030	0.030
D	2.586	2.515	2.516
E	0.080	0.087	0.087
F	0.093	0.083	0.083

4.4 General Discussion

The results presented in the previous three sections have shown that the level of data unbalance has little effect on the ability of HM, ML and REML to estimate accurately heritabilities, and sire and error variances in a random 1-way model. Both the approximate standard error of the heritability estimates and the large sample standard error of the sire and error variances closely approximated the actual variation in the estimates, unaffected by data unbalance or data set size. Thus, providing estimates of the parameters come from the same population, it would be expected that the variation between estimates would be reflected in their standard errors.

Rendel (1985) estimated the heritability (using Henderson's Method 3) of weaning weight from 31 flocks of Coopworth sheep spread throughout New Zealand (Table 4.40). The variance of the heritability estimates was 0.0260 (8 flocks that had unusually large or few sires and/or progeny per sire were not included) and the mean of the flocks squared standard errors (to give the variance) was 0.0017. Hence, the standard error only accounted for 6.5% of the variation between flocks in heritability estimates.

The inclusion of fixed effects in the model used by Rendel (1985) may have been a cause of this large unaccounted for variation. This is unlikely to have a large effect as HM3 estimates are invariant to the fixed effects (Searle, 1971).

Another factor may be differing levels of selective mating within the various flocks. Rams with characteristics deemed important by the stud-master may have been mated to ewes with similar characteristics. This may have the effect of inflating the sire variance and hence the heritability. Also it is plausible that dam age may be confounded with sires in some flocks. Sires may have been selectively mated to certain age group ewes (e.g. a "top" young ram may only be mated to 2-tooth ewes, or, a poorer ram may be mated solely to old ewes) and hence some of the sire variance is removed with the dam age effect.

The differences between the flocks may also be due to genetic differences. Wide between flock differences in frequencies of genes that affect the trait could be responsible for some of the difference. It is also possible that different genetic pathways have, inadvertently, been selected for in the different flocks, possibly due to different objectives in flocks. In flocks where the genes that are desirable are at high frequencies, the sire variance would tend to be low, thus the heritability would be low. Similarly, where desirable genes occur at low frequencies (except for genes that have large effects), the variance between sires would be expected to be low. If a gene, or several genes, with a major effect are present in a flock they will increase the genetic variance and the resulting heritability.

Table 4.40 Within-flock heritability estimates, standard errors of heritability estimates, number of observations and sires nested within-years for weaning weight (from Rendel, 1985).

Heritability	Standard Error	Number of Observations	Number of Sire-years
0.1490	0.0406	3843	44
0.1244	0.0454	2486	30
0.1029	0.0291	5142	44
0.0815	0.0242	4965	50
0.1352	0.0285	6335	83
0.1731	0.0332	8421	71
0.0726	0.0293	3139	31
0.1096	0.0323	3716	52
0.5451	0.0802	6847	83
0.1688	0.0324	7348	83
0.0728	0.0253	4370	42
0.0561	0.0236	3419	43
0.0558	0.0229	3725	56
0.0189	0.0227	2261	40
0.1648	0.0326	7913	73
0.1185	0.0294	5942	60
0.1000	0.0224	7967	72
0.2321	0.0496	5359	56
0.3966	0.1083	1724	33
0.0372	0.0183	4101	46
0.2010	0.0656	2384	30
0.7455	0.1077	7154	81
0.2910	0.0255	23633	315
0.1474	0.0444	2840	42
0.0929	0.0314	3439	46
0.0786	0.0339	2697	32
0.1343	0.0381	3671	48
0.0901	0.0219	6289	87
0.1657	0.0365	4760	71
0.1023	0.0255	5752	67
0.2614	0.0571	3373	64

Genotype-environment interactions may also have contributed to the differences in heritability estimates between flocks. Newman (1988) reported a heritability for weaning weight in Romney lambs of 0.2 (±0.17) at a control stocking rate, and 0.04 (±0.15) at a high stocking rate. Hence an environment provided for a flock may be such that the genotype of the sires are not expressed through their progeny. This would result in a decreased sire variance and hence a decreased heritability. There also may be differences within flocks in the treatment of progeny. Ewes may have been grouped according to mating sire and have lambed and reared their progeny in these groups. As these groups would be located on different areas of the farm, some may have received preferential treatment, or been exposed to different levels of environmental factors (e.g. disease, intestinal worms, etc.) than progeny from other sires. This would tend to inflate the sire variance and hence the heritability.

The sires would have probably been related in the flocks used to estimate the heritabilities. This would serve to deflate the sire variance and hence the heritability.

The differences in the heritability estimates between flocks, over and above that explained by the standard error, may have also been contributed to by differences in the accuracy of recording between flocks. Recording errors at weighing increase the error variance and hence may decrease the sire variance and therefore the heritability, whereas errors in pedigree identification could have a variable affect.

This leads to an important issue of what genetic parameters should be used when setting up a breeding programme? In the New Zealand sheep industry (indeed, in all New Zealand pastoral based livestock systems, except dairying) there is a move away from centralised, nationwide recording schemes toward within flock schemes that are microcomputer based (Callow et al, 1986)✓ Where several flocks have the same objectives, what genetic parameters should be used in the breeding scheme? It would be possible to estimate the parameters, for larger flocks, from past records, but would these be the "correct" parameters to use? An alternative would be to use either the same estimates for all flocks, or have groups of flocks with the same estimates. How are flocks that should be grouped together identified and how is an estimate obtained for such a group?

A pooled heritability estimate from a group of flocks could be obtained by calculating the mean of the estimates from different flocks. This would take no account of the number of sires and progeny per sire in flocks, which has been shown to be an important component of the variation in heritability estimates. An alternative is to calculate a weighted mean, using the inverse of the heritability standard error as the weight. This takes into account the variation in heritability estimates due to number of sires and number of progeny per sire. However, there is a strong positive correlation between the estimated heritability and the standard error as they are both derived from the same intra-class correlation (see section 2.4.1 of Chapter 2). This will result in the weighted mean being less than the unweighted mean. Also the between flock variation in estimates is not taken into account. Weighting the heritability estimates by the number of sires, or progeny per sire, or some combination of number of sires and number of progeny per sire is another alternative.

When pooling estimates the assumption is made that the estimates are samples from the same population. As heritabilities are functions of both the animals own genetic make-up and also the environment in which it lives (Falconer,1981), then flocks that constitute a population should have similar genetic structures and environmental conditions. Thus, heritabilities estimated from research flocks may only be applicable to that type of flock. This suggests that flocks be somehow grouped according to both the environment they operate in and their genetic structure.

The genetic correlations are equally as important as heritabilities in formulating breeding schemes. Large differences between flocks in the genetic correlations are also found (Rendel, unpub.). A study similar to this may identify if differences between flocks in genetic correlations are of the magnitude expected from the size of the standard errors.

The present study could be extended to include differing heritabilities, especially those close to zero. Also, distributions other than normal could be used to obtain the distribution of progeny per sire. A gamma distribution would allow distributions to be set up with longer tails at either end of the distribution of progeny per sire.

CHAPTER FIVE
CONCLUSIONS

The study has shown that heritabilities and sire and error variances estimated using HM, ML and REML were unaffected by the level of data unbalance. Relative to neighbouring sets, several data sets had large deviations from the population values. As these had a sporadic and infrequent occurrence throughout the different levels of unbalance, they were considered as random variation rather than part of a trend. The MSE's of the heritabilities and variance components showed that estimates from data sets containing 20 sires and 50 sires with a mean of 20 progeny per sire were the least accurate in estimating the parameters. The heritability and error-variance MSE's of the ML and REML estimates were lower than those from HM for the distributions based on the 6 flocks. This is probably a reflection on the algorithms used to solve the equations for ML and REML, especially as very little difference would be expected between the accuracy of the 3 methods in a 1-way model.

There was virtually no difference between the HM, ML and REML methods in the heritability and sire and error variance estimates with the present model. The results may have been different if selection and/or fixed effects had been included in the simulation.

The calculated standard error of the heritability estimates and the large sample standard error of the variance components were very close to the actual variation in these parameters for all three methods. There were several data sets that had relatively large deviations from the actual variation, but they were rare and sporadic occurrences.

The study indicated the standard errors are accurate estimators of the variation in heritability estimates that can arise from that variation that is common to the within and between flock component. However, there is additional variation that is peculiar to flocks, shown by the standard error of weaning weight heritability, estimated from 23 Coopworth sheep flocks of similar size, only accounting for 6.5% of the variation in heritability estimates between flocks.

These results apply to a specific set of population parameters. Comparisons with other results suggest that the conclusions made would probably follow a similar trend to those presented in this study if the population parameters were changed.

APPENDICES

Appendix 1 : Computer programmes used to generate data.

A.1.1 Programme (Fortran77) to obtain a normal distribution of number of progeny per sire for the required mean number of progeny and number of sires.

```
      program sire_freq

c  Program to generate numbers of progeny per sire
c  for unbalanced data

c  Requires input file consisting of:
c           mean number of progeny per sire              f3.0
c           standard deviation (to get unbalancedness)     f5.1
c           number of sires in data set              i4

c     uses NAGLIB


      real*8 s15abf,zupint,zloint,aupint,aloint
      real area(100),predsires(100),upint(100),loint(100),mprog,
     *     mnprog,sd
      integer ifail,ipredsires(100),ival(100)
      character star*1
      character*20 fname1,fname2
      parameter (star='*')

      call soua('Name of INPUT file... ')
      read(1,1000)fname1
      write(1,'(/)')
      call soua('Name for OUTPUT file... ')
      read(1,1000)fname2
      write(1,'(/)')
 1000 format(a20)

      open(30,file=fname1,status='old')
      open(35,file=fname2,status='unknown')
      m=:100200000
      write(35,'(a2/a2)')m,m
    1 ifail = 0
      icount = 0
      ineg = 0
      add = 0.0
      sumprob = 0.0
      read(30,*,end=999)mprog,sd,nsires
      improg = nint(mprog)
    2 icount=icount+1
      ival(icount)=nint(mprog+add)
      upint(icount) = ival(icount) + 0.5
      loint(icount) = ival(icount) - 0.5
      zupint = (upint(icount)-mprog)/sd
      zloint = (loint(icount)-mprog)/sd
      aupint = s15abf(zupint,ifail)
```

```
      aloint = s15abf(zloint,ifail)
      area(icount) = aupint-aloint
      predsires(icount) = nsires*area(icount)
      ipredsires(icount) = nint(predsires(icount))
      if(ineg.eq.1)then
c sum no sires
        sumprob = area(1)
        sumsires = ipredsires(1)
        sumprog = ival(1)*ipredsires(1)
        sumsquared = ival(1)*ival(1)*ipredsires(1)
        do 3 i=2,icount
c Multiplied by 2 because have got lower distribution
          sumprob = sumprob + (area(i)*2)
          sumsires = sumsires + (ipredsires(i)*2)
          lval = (2*mprog)-ival(i)
          sumprog = sumprog + (ival(i)*ipredsires(i)) +
     *                    (lval*ipredsires(i))
          sumsquared = sumsquared + (ival(i)*ival(i)*ipredsires(i)) +
     *              (lval*lval*ipredsires(i))
    3   continue
        mnprog = sumprog/sumsires
        sdprog = (sumsquared-(sumprog*sumprog/sumsires))/(sumsires-1)
        sdprog = sqrt(sdprog)
c write out info
        write(35,1002)improg,sd,nsires
 1002 format('1'/10x,
     *'Distribution Requested  ',i3,' mean number of progeny per sire'/
     *33x,f4.1,' Standard deviation of progeny per sire'/
     *34x,i3,' Number of sires'///
     *' Number of Progeny',3x,'Probability',4x,'Number of Sires',4x,
     *'Modifications',3x,'Histogram'/35x,'Unrounded Rounded'/'0')
        do 4 i=icount,2,-1
          lval = (2*mprog)-ival(i)
          write(35,1003)lval,area(i),predsires(i),ipredsires(i),
     *              (star,l=1,ipredsires(i))
    4   continue
        do 5 i=1,icount
          write(35,1003)ival(i),area(i),predsires(i),ipredsires(i),
     *              (star,l=1,ipredsires(i))
    5   continue
 1003 format(7x,i3,14x,f6.4,7x,f6.3,4x,i2,23x,80a1)
        isumsires = nint(sumsires)
        write(35,1004)sumprob,isumsires,mnprog,sdprog
 1004 format(/19x,'Sum',f8.4,16x,i3/35x,'Mean',7x,f6.2/35x,'Std Dev',
     *4x,f6.2)
        goto 1
      end if
      if(ipredsires(icount).lt.1)ineg=1
      add = add + 1.0
      goto 2

  999 close(30)
      close(35)
      stop
      end
```

A.1.2 Programme (Fortran77) to generate the progeny

```
      program sire_generator

c  Program to generate a set of progeny from sires
c  using a random number generator.

c   Load LIBRARY VAPPLB
c                         NAGLIB

      integer*2 infos(28),infoe(28),num,nsires(100),nprog(100)

      real*8 agvar,gvar,evar,envar,pvar,rmean,g05ddf

      character*20 outfile,infile
      parameter (gvar=0.6783,evar=11.0106,rmean=18.0)

      call timdat(infos,num)
      write(1,101)
  101 format('Name of file that contains number of classes and sire'/
     *'and progeny frequencies ... ',$)
      read(1,'(a20)')infile
      call soua('Name for output file...')
      read(1,'(a20)')outfile
      open(50,file=outfile,status='new')
      open(55,file=infile,status='old')

      read(55,*)nc
      read(55,*)(nprog(i),nsires(i),i=1,nc)
      close(55)
      icount = 0
      call g05ccf
      do 8 i=1,nc
        do 7 j=1,nsires(i)
c  set up genetic value for each sire
        agvar = g05ddf(dble(0.0),sqrt(gvar))
        icount=icount+1
          do 5 k=1,nprog(i)
c  set up enviro info and print out pheno info
            envar = g05ddf(dble(0.0),sqrt(evar))
            pvar = rmean + agvar + envar
            write(50,100)icount,pvar
    5     continue
    7   continue
    8 continue
  100 format(i4,5x,f6.3)
      close(50)
      num=28
      call timdat(infoe,num)
      icputime = infoe(7)-infos(7)
      iotime = infoe(9)-infos(9)
      write(1,110)infos(12),(infos(i),i=13,22),infos(2),infos(1),
     *infos(3),icputime,iotime
  110 format(//'USER NO',5X,'USER ID',15X,'DATE',5X,'CPU TIME',2X,
     *'I/O TIME'/I4,6X,10A2,2X,2(A2,'-'),A2,2X,2X,I3,8X,I3/)
      stop
      end
```

Appendix 2 : Raw Data Summaries

Table A.2.1 The mean, minimum, maximum and standard deviation of HM heritability estimates from data sets with a population heritability of 0.2321, each with 100 replicates, for balanced data (SD0).

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.2544	0.2090	0.2260	0.2274	0.2381
		min	−0.0242	0.0527	0.1434	0.1572	0.1703
		max	0.7341	0.4308	0.3187	0.3228	0.3377
		sd	0.1310	0.0687	0.0532	0.0421	0.0479
	50	mean	0.2118	0.2301	0.2437	0.2347	0.2372
		min	0.0450	0.1092	0.1436	0.1812	0.1801
		max	0.3629	0.3633	0.3631	0.3186	0.2965
		sd	0.0781	0.0626	0.0455	0.0389	0.0313
	70	mean	0.2198	0.2293	0.2358	0.2355	0.2374
		min	0.0091	0.1408	0.1531	0.1810	0.1666
		max	0.3423	0.3494	0.3633	0.3386	0.3091
		sd	0.0808	0.0492	0.0434	0.0344	0.0324
	100	mean	0.2327	0.2439	0.2343	0.2340	0.2366
		min	0.0710	0.1532	0.1616	0.1761	0.1834
		max	0.4229	0.3750	0.2914	0.2826	0.2951
		sd	0.0782	0.0440	0.0340	0.0283	0.0293

Table A.2.2 The mean, minimum, maximum and standard deviation of ML heritability estimates from data sets with a population heritability of 0.2321, each with 100 replicates, for balanced data (SD0).

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.2348	0.2014	0.2221	0.2248	0.2361
		min	0.0000	0.0477	0.1402	0.1549	0.1686
		max	0.6971	0.4199	0.3140	0.3197	0.3353
		sd	0.1239	0.0676	0.0528	0.0419	0.0477
	50	mean	0.1982	0.2244	0.2407	0.2328	0.2358
		min	0.0389	0.1056	0.1415	0.1796	0.1788
		max	0.3430	0.3553	0.3592	0.3162	0.2948
		sd	0.0748	0.0616	0.0452	0.0387	0.0312
	70	mean	0.2069	0.2240	0.2330	0.2337	0.2366[1]
		min	0.0058	0.1370	0.1511	0.1795	0.1655
		max	0.3242	0.3421	0.3595	0.3363	0.3075
		sd	0.0773	0.0484	0.0431	0.0342	0.0323
	100	mean	0.2200	0.2386	0.2317	0.2323	0.2409[2]
		min	0.0656	0.1495	0.1597	0.1747	0.1927
		max	0.4023	0.3675	0.2883	0.2807	0.2935
		sd	0.0748	0.0433	0.0337	0.0281	0.0264

1 = 98 replicates   2 = 87 replicates

Table A.2.3 The mean, minimum, maximum and standard deviation of REML heritability estimates from data sets with a population heritability of 0.2321, each with 100 replicates, for balanced data (SD0).

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.2551	0.2090	0.2260	0.2274	0.2381
		min	0.0000	0.0527	0.1434	0.1572	0.1703
		max	0.7341	0.4308	0.3187	0.3228	0.3377
		sd	0.1295	0.0687	0.0532	0.0421	0.0479
	50	mean	0.2118	0.2301	0.2437	0.2347	0.2372
		min	0.0450	0.1092	0.1436	0.1812	0.1801
		max	0.3629	0.3633	0.3631	0.3186	0.2965
		sd	0.0781	0.0626	0.0455	0.0389	0.0313
	70	mean	0.2198	0.2293	0.2358	0.2355	0.2374
		min	0.0091	0.1408	0.1531	0.1810	0.1666
		max	0.3423	0.3494	0.3633	0.3386	0.3091
		sd	0.0808	0.0492	0.0434	0.0344	0.0324
	100	mean	0.2327	0.2439	0.2343	0.2340	0.2366
		min	0.0710	0.1532	0.1616	0.1761	0.1834
		max	0.4229	0.3750	0.2914	0.2826	0.2951
		sd	0.0782	0.0440	0.0340	0.0283	0.0293

Table A.2.4 The mean, minimum, maximum and standard deviation of HM heritability approximate standard errors from data sets with a population heritability of 0.2321, each with 100 replicates, for balanced data (SD0).

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.1361	0.0780	0.0569	0.0466	0.0412
		min	0.0592	0.0511	0.0473	0.0399	0.0356
		max	0.2436	0.1126	0.0675	0.0554	0.0490
		sd	0.0337	0.0113	0.0061	0.0039	0.0038
	50	mean	0.0887	0.0586	0.0429	0.0341	0.0297
		min	0.0402	0.0371	0.0305	0.0288	0.0248
		max	0.1298	0.0809	0.0569	0.0422	0.0347
		sd	0.0219	0.0108	0.0055	0.0038	0.0027
	70	mean	0.0840	0.0542	0.0389	0.0317	0.0276
		min	0.0215	0.0385	0.0286	0.0262	0.0214
		max	0.1179	0.0746	0.0540	0.0418	0.0337
		sd	0.0231	0.0086	0.0053	0.0034	0.0028
	100	mean	0.0825	0.0536	0.0365	0.0298	0.0260
		min	0.0353	0.0374	0.0274	0.0239	0.0213
		max	0.1337	0.0757	0.0435	0.0346	0.0310
		sd	0.0219	0.0077	0.0042	0.0028	0.0026

Table A.2.5 The mean, minimum, maximum and standard deviation of ML heritability approximate standard errors from data sets with a population heritability of 0.2321, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.1280	0.0760	0.0562	0.0462	0.0409
	min	0.0649	0.0497	0.0466	0.0395	0.0354
	max	0.2310	0.1100	0.0666	0.0549	0.0487
	sd	0.0313	0.0111	0.0061	0.0039	0.0038
50	mean	0.0828	0.0570	0.0423	0.0338	0.0295
	min	0.0374	0.0361	0.0301	0.0285	0.0246
	max	0.1215	0.0788	0.0562	0.0419	0.0345
	sd	0.0206	0.0106	0.0054	0.0038	0.0027
70	mean	0.0784	0.0527	0.0384	0.0315	0.0275[1]
	min	0.0200	0.0374	0.0282	0.0260	0.0213
	max	0.1103	0.0726	0.0533	0.0414	0.0335
	sd	0.0217	0.0084	0.0052	0.0034	0.0028
100	mean	0.0770	0.0521	0.0360	0.0295	0.0263[2]
	min	0.0328	0.0364	0.0270	0.0236	0.0221
	max	0.1253	0.0737	0.0429	0.0343	0.0308
	sd	0.0206	0.0075	0.0042	0.0028	0.0023

1 = 98 replicates 2 = 87 replicates

Table A.2.6 The mean, minimum, maximum and standard deviation of REML heritability approximate standard errors from data sets with a population heritability of 0.2321, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.1350[1]	0.0780	0.0569	0.0466	0.0412
	min	0.0002	0.0511	0.0473	0.0399	0.0356
	max	0.2436	0.1126	0.0675	0.0554	0.0490
	sd	0.0385	0.0113	0.0062	0.0039	0.0038
50	mean	0.0887	0.0586	0.0429	0.0341	0.0297
	min	0.0402	0.0371	0.0305	0.0288	0.0248
	max	0.1298	0.0809	0.0569	0.0422	0.0347
	sd	0.0219	0.0108	0.0055	0.0038	0.0027
70	mean	0.0840	0.0542	0.0389	0.0317	0.0276
	min	0.0215	0.0385	0.0286	0.0262	0.0214
	max	0.1179	0.0746	0.0540	0.0418	0.0337
	sd	0.0231	0.0086	0.0053	0.0034	0.0028
100	mean	0.0825	0.0536	0.0365	0.0298	0.0260
	min	0.0353	0.0374	0.0274	0.0239	0.0213
	max	0.1337	0.0757	0.0435	0.0346	0.0310
	sd	0.0219	0.0077	0.0042	0.0028	0.0026

1 = 99 replicates

Table A.2.7 The mean, minimum, maximum and standard deviation of HM sire variance estimates from data sets with a population sire variance of 0.6783, each with 100 replicates, for balanced data (SD0).

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.7269	0.6081	0.6577	0.6605	0.6974
		min	−0.0669	0.1384	0.4075	0.4490	0.4864
		max	2.1416	1.2937	0.9417	0.9642	0.9970
		sd	0.3809	0.2064	0.1588	0.1247	0.1451
	50	mean	0.6184	0.6732	0.7172	0.6895	0.6956
		min	0.1355	0.3095	0.4173	0.5302	0.5165
		max	1.1655	1.0709	1.1038	0.9641	0.8678
		sd	0.2430	0.1909	0.1449	0.1216	0.0977
	70	mean	0.6409	0.6732	0.6897	0.6937	0.6964
		min	0.0257	0.4001	0.4471	0.5249	0.4832
		max	1.0218	1.0484	1.1157	1.0450	0.9238
		sd	0.2412	0.1513	0.1359	0.1102	0.1024
	100	mean	0.6877	0.7157	0.6877	0.6849	0.6930
		min	0.1917	0.4331	0.4656	0.5109	0.5355
		max	1.2859	1.1345	0.8790	0.8529	0.8756
		sd	0.2526	0.1407	0.1065	0.0862	0.0910

Table A.2.8 The mean, minimum, maximum and standard deviation of ML sire variance estimates from data sets with a population sire variance of 0.6783, each with 100 replicates, for balanced data (SD0).

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.6666	0.5849	0.6456	0.6524	0.6912
		min	0.0000	0.1252	0.3981	0.4424	0.4812
		max	2.0107	1.2571	0.9268	0.9541	0.9893
		sd	0.3569	0.2023	0.1572	0.1239	0.1444
	50	mean	0.5764	0.6553	0.7078	0.6834	0.6910
		min	0.1168	0.2988	0.4109	0.5251	0.5129
		max	1.0955	1.0449	1.0906	0.9562	0.8623
		sd	0.2308	0.1871	0.1434	0.1208	0.0972
	70	mean	0.6011	0.6566	0.6812	0.6880	0.6941[1]
		min	0.0164	0.3890	0.4411	0.5204	0.4799
		max	0.9629	1.0243	1.1030	1.0369	0.9183
		sd	0.2292	0.1483	0.1346	0.1095	0.1019
	100	mean	0.6478	0.6992	0.6797	0.6796	0.7056[2]
		min	0.1769	0.4223	0.4598	0.5068	0.5674
		max	1.2162	1.1096	0.8691	0.8465	0.8706
		sd	0.2400	0.1379	0.1055	0.0856	0.0831

1 = 98 replicates   2 = 87 replicates

Table A.2.9 The mean, minimum, maximum and standard deviation of REML sire variance estimates from data sets with a population sire variance of 0.6783, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7289	0.6081	0.6577	0.6605	0.6975
	min	0.0000	0.1384	0.4075	0.4490	0.4865
	max	2.1416	1.2936	0.9417	0.9643	0.9971
	sd	0.3768	0.2064	0.1588	0.1247	0.1451
50	mean	0.6184	0.6732	0.7172	0.6895	0.6956
	min	0.1355	0.3095	0.4173	0.5302	0.5165
	max	1.1655	1.0709	1.1038	0.9641	0.8678
	sd	0.2430	0.1909	0.1448	0.1216	0.0977
70	mean	0.6409	0.6732	0.6897	0.6937	0.6964
	min	0.0257	0.4001	0.4471	0.5249	0.4832
	max	1.0218	1.0484	1.1157	1.0450	0.9238
	sd	0.2412	0.1513	0.1359	0.1102	0.1024
100	mean	0.6877	0.7157	0.6877	0.6849	0.6930
	min	0.1918	0.4331	0.4656	0.5109	0.5355
	max	1.2859	1.1345	0.8790	0.8529	0.8756
	sd	0.2526	0.1407	0.1065	0.0862	0.0910

Table A.2.10 The mean, minimum, maximum and standard deviation of HM sire variance large sample standard errors from data sets with a population sire variance of 0.6783, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.4115	0.2354	0.1724	0.1408	0.1257
	min	0.1637	0.1349	0.1345	0.1158	0.1044
	max	0.8500	0.3704	0.2119	0.1761	0.1549
	sd	0.1200	0.0414	0.0222	0.0140	0.0142
50	mean	0.2722	0.1805	0.1334	0.1055	0.0919
	min	0.1217	0.1072	0.0911	0.0872	0.0735
	max	0.4544	0.2627	0.1884	0.1375	0.1091
	sd	0.0789	0.0384	0.0207	0.0142	0.0099
70	mean	0.2589	0.1679	0.1204	0.0988	0.0856
	min	0.0608	0.1127	0.0854	0.0787	0.0640
	max	0.3821	0.2435	0.1814	0.1396	0.1086
	sd	0.0781	0.0306	0.0193	0.0128	0.0103
100	mean	0.2589	0.1668	0.1135	0.0922	0.0805
	min	0.0964	0.1095	0.0819	0.0721	0.0648
	max	0.4525	0.2514	0.1411	0.1118	0.0990
	sd	0.0824	0.0285	0.0151	0.0100	0.0092

Table A.2.11 The mean, minimum, maximum and standard deviation of ML sire variance large sample standard errors from data sets with a population sire variance of 0.6783, each with 100 replicates, for balanced data (SD0).

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.3821	0.2284	0.1698	0.1393	0.1248
		min	0.1667	0.1308	0.1326	0.1145	0.1034
		max	0.7872	0.3594	0.2088	0.1741	0.1536
		sd	0.1094	0.0401	0.0218	0.0139	0.0142
	50	mean	0.2520	0.1752	0.1313	0.1045	0.0912
		min	0.1127	0.1039	0.0900	0.0866	0.0728
		max	0.4208	0.2548	0.1855	0.1360	0.1082
		sd	0.0730	0.0372	0.0204	0.0139	0.0098
	70	mean	0.2397	0.1629	0.1186	0.0977	0.0852[1]
		min	0.0566	0.1091	0.0843	0.0781	0.0640
		max	0.3538	0.2362	0.1786	0.1386	0.1082
		sd	0.0723	0.0297	0.0190	0.0127	0.0102
	100	mean	0.2397	0.1618	0.1117	0.0912	0.0815[2]
		min	0.0894	0.1063	0.0806	0.0714	0.0678
		max	0.4190	0.2439	0.1389	0.1109	0.0980
		sd	0.0763	0.0277	0.0150	0.0099	0.0084

1 = 98 replicates   2 = 87 replicates

Table A.2.12 The mean, minimum, maximum and standard deviation of REML sire variance large sample standard errors from data sets with a population sire variance of 0.6783, each with 100 replicates, for balanced data (SD0).

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.4087[1]	0.2354	0.1724	0.1408	0.1257
		min	0.0006	0.1347	0.1345	0.1156	0.1044
		max	0.8501	0.3704	0.2119	0.1760	0.1549
		sd	0.1318	0.0414	0.0222	0.0140	0.0143
	50	mean	0.2722	0.1806	0.1333	0.1055	0.0919
		min	0.1216	0.1073	0.0913	0.0874	0.0736
		max	0.4544	0.2626	0.1884	0.1376	0.1090
		sd	0.0788	0.0384	0.0207	0.0141	0.0098
	70	mean	0.2589	0.1679	0.1204	0.0987	0.0856
		min	0.0611	0.1126	0.0854	0.0787	0.0644
		max	0.3822	0.2435	0.1813	0.1398	0.1088
		sd	0.0781	0.0306	0.0193	0.0128	0.0103
	100	mean	0.2589	0.1668	0.1135	0.0921	0.0805
		min	0.0967	0.1095	0.0819	0.0721	0.0649
		max	0.4525	0.2514	0.1411	0.1118	0.0988
		sd	0.0824	0.0285	0.0152	0.0099	0.0091

1 = 99 replicates

Table A.2.13 The mean, minimum, maximum and standard deviation of HM error variance estimates from data sets with a population error variance of 11.0106, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	10.7004	11.0007	10.9679	10.9557	11.0072
	min	8.5873	9.3983	10.1508	10.3915	10.4298
	max	12.6026	11.9305	11.8654	11.5399	11.6256
	sd	0.9684	0.5188	0.3472	0.3060	0.2524
50	mean	10.9962	10.9969	11.0241	11.0445	11.0209
	min	9.6149	10.3729	10.5521	10.6030	10.6394
	max	12.2004	11.9377	11.4108	11.3737	11.3216
	sd	0.5346	0.3052	0.2287	0.1975	0.1825
70	mean	10.9675	11.0456	10.9886	11.0692	11.0236
	min	9.8614	10.3806	10.6948	10.7308	10.7954
	max	11.8029	11.6678	11.3972	11.4528	11.2760
	sd	0.4576	0.2933	0.1940	0.1708	0.1337
100	mean	11.0204	10.9900	11.0375	11.0149	11.0129
	min	10.1121	10.5964	10.6609	10.7731	10.7554
	max	11.9820	11.4815	11.3959	11.3096	11.2094
	sd	0.3609	0.1911	0.1751	0.1182	0.0929

Table A.2.14 The mean, minimum, maximum and standard deviation of ML error variance estimates from data sets with a population error variance of 11.0106, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	10.6976	11.0007	10.9679	10.9557	11.0072
	min	8.5873	9.3983	10.1508	10.3915	10.4298
	max	12.6026	11.9305	11.8654	11.5399	11.6256
	sd	0.9673	0.5188	0.3472	0.3060	0.2524
50	mean	10.9962	10.9969	11.0241	11.0445	11.0209
	min	9.6149	10.3729	10.5521	10.6030	10.6394
	max	12.2004	11.9377	11.4108	11.3737	11.3216
	sd	0.5346	0.3052	0.2287	0.1975	0.1825
70	mean	10.9675	11.0456	10.9886	11.0692	11.0267[1]
	min	9.8614	10.3806	10.6947	10.7308	10.7954
	max	11.8029	11.6678	11.3972	11.4528	11.2760
	sd	0.4576	0.2933	0.1940	0.1708	0.1332
100	mean	11.0204	10.9900	11.0375	11.0149	11.0021[2]
	min	10.1121	10.5964	10.6609	10.7731	10.7554
	max	11.9820	11.4815	11.3959	11.3096	11.2094
	sd	0.3609	0.1911	0.1751	0.1182	0.0922

1 = 98 replicates 2 = 87 replicates

Table A.2.15 The mean, minimum, maximum and standard deviation of REML error variance estimates from data sets with a population error variance of 11.0106, each with 100 replicates, for balanced data (SD0).

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	10.6985	11.0007	10.9679	10.9557	11.0072
		min	8.5873	9.3983	10.1508	10.3915	10.4298
		max	12.6026	11.9305	11.8653	11.5399	11.6256
		sd	0.9676	0.5188	0.3472	0.3060	0.2524
	50	mean	10.9962	10.9969	11.0241	11.0445	11.0209
		min	9.6149	10.3729	10.5521	10.6030	10.6394
		max	12.2004	11.9377	11.4108	11.3737	11.3216
		sd	0.5346	0.3052	0.2287	0.1975	0.1825
	70	mean	10.9675	11.0456	10.9886	11.0692	11.0236
		min	9.8614	10.3806	10.6948	10.7308	10.7954
		max	11.8029	11.6678	11.3972	11.4528	11.2760
		sd	0.4576	0.2933	0.1940	0.1708	0.1337
	100	mean	11.0204	10.9900	11.0375	11.0149	11.0129
		min	10.1121	10.5964	10.6609	10.7731	10.7554
		max	11.9820	11.4815	11.3959	11.3096	11.2094
		sd	0.3609	0.1911	0.1751	0.1182	0.0929

Table A.2.16 The mean, minimum, maximum and standard deviation of HM error variance large sample standard errors from data sets with a population error variance of 11.0106, each with 100 replicates, for balanced data (SD0).

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.7763	0.5048	0.3559	0.2902	0.2525
		min	0.6230	0.4313	0.3294	0.2753	0.2394
		max	0.9143	0.5474	0.3850	0.3058	0.2666
		sd	0.0703	0.0238	0.0113	0.0081	0.0058
	50	mean	0.4968	0.3142	0.2227	0.1822	0.1575
		min	0.4344	0.2963	0.2131	0.1749	0.1520
		max	0.5512	0.3410	0.2304	0.1876	0.1619
		sd	0.0242	0.0087	0.0046	0.0033	0.0026
	70	mean	0.4175	0.2659	0.1871	0.1539	0.1327
		min	0.3754	0.2500	0.1822	0.1493	0.1300
		max	0.4493	0.2809	0.1942	0.1591	0.1356
		sd	0.0174	0.0070	0.0033	0.0024	0.0016
	100	mean	0.3502	0.2209	0.1569	0.1278	0.1106
		min	0.3214	0.2131	0.1517	0.1249	0.1082
		max	0.3808	0.2309	0.1619	0.1311	0.1127
		sd	0.0115	0.0038	0.0025	0.0014	0.0009

Table A.2.17 The mean, minimum, maximum and standard deviation of ML error variance large sample standard errors from data sets with a population error variance of 11.0106, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7761	0.5047	0.3559	0.2902	0.2525
	min	0.6230	0.4313	0.3294	0.2753	0.2394
	max	0.9143	0.5474	0.3850	0.3058	0.2666
	sd	0.0702	0.0238	0.0113	0.0081	0.0058
50	mean	0.4968	0.3142	0.2227	0.1822	0.1575
	min	0.4344	0.2963	0.2131	0.1749	0.1520
	max	0.5512	0.3410	0.2304	0.1876	0.1619
	sd	0.0242	0.0087	0.0046	0.0033	0.0026
70	mean	0.4175	0.2659	0.1871	0.1539	0.1327[1]
	min	0.3754	0.2500	0.1822	0.1493	0.1300
	max	0.4493	0.2809	0.1942	0.1591	0.1356
	sd	0.0174	0.0070	0.0033	0.0024	0.0016
100	mean	0.3502	0.2209	0.1569	0.1278	0.1105[2]
	min	0.3214	0.2131	0.1517	0.1249	0.1082
	max	0.3808	0.2309	0.1619	0.1311	0.1127
	sd	0.0115	0.0038	0.0025	0.0014	0.0009

1 = 98 replicates   2 = 87 replicates

Table A.2.18 The mean, minimum, maximum and standard deviation of REML error variance large sample standard errors from data sets with a population error variance of 11.0106, each with 100 replicates, for balanced data (SD0).

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7521	0.5047	0.3558	0.2902	0.2525
	min	0.0006	0.4312	0.3293	0.2753	0.2393
	max	0.9143	0.5474	0.3850	0.3057	0.2667
	sd	0.1501	0.0238	0.0113	0.0081	0.0058
50	mean	0.4968	0.3142	0.2227	0.1822	0.1574
	min	0.4344	0.2964	0.2132	0.1749	0.1520
	max	0.5512	0.3411	0.2305	0.1876	0.1617
	sd	0.0242	0.0087	0.0046	0.0033	0.0026
70	mean	0.4175	0.2660	0.1871	0.1539	0.1327
	min	0.3754	0.2499	0.1821	0.1492	0.1300
	max	0.4493	0.2809	0.1940	0.1592	0.1357
	sd	0.0174	0.0071	0.0033	0.0024	0.0016
100	mean	0.3503	0.2209	0.1569	0.1278	0.1107
	min	0.3214	0.2130	0.1515	0.1250	0.1081
	max	0.3808	0.2308	0.1620	0.1312	0.1127
	sd	0.0115	0.0038	0.0025	0.0014	0.0009

Table A.2.19 The mean, minimum, maximum and standard deviation of HM heritability estimates from data sets with a population heritability of 0.2321, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
	20	mean	0.2239	0.2250	0.2276	0.2321	0.2258
		min	−0.0276	0.0477	0.0730	0.1136	0.1342
Mean		max	0.5970	0.4982	0.3635	0.4000	0.3180
		sd	0.1285	0.0995	0.0547	0.0525	0.0375
Number	50	mean	0.2312	0.2201	0.2286	0.2238	0.2317
		min	0.0297	0.0660	0.1561	0.1688	0.1609
of		max	0.5411	0.3812	0.3584	0.3602	0.3105
		sd	0.0991	0.0628	0.0391	0.0350	0.0264
Progeny	70	mean	0.2152	0.2204	0.2264	0.2328	0.2314
		min	0.0692	0.1136	0.1409	0.1674	0.1634
Per		max	0.4440	0.3737	0.3413	0.3089	0.2876
		sd	0.0793	0.0516	0.0380	0.0298	0.0260
Sire	100	mean	0.2269	0.2291	0.2298	0.2331	0.2272
		min	0.0597	0.0874	0.1574	0.1614	0.1635
		max	0.5763	0.3498	0.3172	0.3176	0.2979
		sd	0.0873	0.0499	0.0320	0.0312	0.0244

Table A.2.20 The mean, minimum, maximum and standard deviation of ML heritability estimates from data sets with a population heritability of 0.2321, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
	20	mean	0.2050	0.2168	0.2235	0.2294	0.2238
		min	0.0000	0.0366	0.0698	0.1127	0.1324
Mean		max	0.5645	0.4855	0.3513	0.3980	0.3157
		sd	0.1216	0.0975	0.0540	0.0522	0.0373
Number	50	mean	0.2165	0.2143	0.2258	0.2219	0.2302
		min	0.0237	0.0631	0.1539	0.1679	0.1599
of		max	0.5175	0.3733	0.3555	0.3574	0.3081
		sd	0.0948	0.0615	0.0390	0.0348	0.0262
Progeny	70	mean	0.2020	0.2150	0.2236	0.2309	0.2300
		min	0.0630	0.1101	0.1384	0.1660	0.1623
Per		max	0.4227	0.3667	0.3380	0.3055	0.2858
		sd	0.0755	0.0506	0.0377	0.0297	0.0258
Sire	100	mean	0.2141	0.2239	0.2272	0.2313	0.2260
		min	0.0548	0.0851	0.1552	0.1600	0.1626
		max	0.5451	0.3422	0.3142	0.3159	0.2964
		sd	0.0832	0.0490	0.0317	0.0310	0.0243

Table A.2.21 The mean, minimum, maximum and standard deviation of REML heritability estimates from data sets with a population heritability of 0.2321, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.2242	0.2246	0.2274	0.2321	0.2258
		min	0.0000	0.0416	0.0724	0.1147	0.1340
		max	0.5975	0.4974	0.3562	0.4015	0.3180
		sd	0.1271	0.0990	0.0544	0.0525	0.0375
	50	mean	0.2309	0.2198	0.2287	0.2238	0.2316
		min	0.0292	0.0660	0.1562	0.1695	0.1611
		max	0.5443	0.3816	0.3595	0.3600	0.3099
		sd	0.0990	0.0626	0.0393	0.0350	0.0264
	70	mean	0.2146	0.2202	0.2262	0.2327	0.2313
		min	0.0691	0.1133	0.1403	0.1674	0.1633
		max	0.4449	0.3745	0.3416	0.3077	0.2874
		sd	0.0789	0.0514	0.0380	0.0298	0.0259
	100	mean	0.2265	0.2289	0.2298	0.2330	0.2273
		min	0.0597	0.0876	0.1571	0.1613	0.1635
		max	0.5712	0.3493	0.3175	0.3180	0.2979
		sd	0.0869	0.0499	0.0320	0.0312	0.0244

Table A.2.22 The mean, minimum, maximum and standard deviation of HM heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.1283	0.0804	0.0571	0.0470	0.0402
		min	0.0582	0.0502	0.0385	0.0356	0.0325
		max	0.2170	0.1221	0.0723	0.0620	0.0475
		sd	0.0335	0.0160	0.0063	0.0049	0.0030
	50	mean	0.0939	0.0568	0.0411	0.0330	0.0293
		min	0.0355	0.0290	0.0321	0.0275	0.0231
		max	0.1729	0.0837	0.0564	0.0461	0.0359
		sd	0.0268	0.0109	0.0047	0.0034	0.0023
	70	mean	0.0827	0.0526	0.0378	0.0315	0.0271
		min	0.0402	0.0334	0.0271	0.0248	0.0211
		max	0.1437	0.0785	0.0515	0.0389	0.0319
		sd	0.0222	0.0090	0.0047	0.0030	0.0023
	100	mean	0.0808	0.0509	0.0360	0.0297	0.0252
		min	0.0318	0.0251	0.0269	0.0223	0.0195
		max	0.1704	0.0716	0.0466	0.0380	0.0312
		sd	0.0242	0.0088	0.0040	0.0031	0.0021

Table A.2.23 The mean, minimum, maximum and standard deviation of ML heritability approximate standard errors from data sets with a population heritability of 0.2321, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.1205	0.0784	0.0565	0.0467	0.0400
		min	0.0646	0.0476	0.0379	0.0354	0.0323
		max	0.2054	0.1194	0.0708	0.0618	0.0473
		sd	0.0314	0.0157	0.0062	0.0049	0.0031
	50	mean	0.0876	0.0553	0.0406	0.0327	0.0291
		min	0.0328	0.0282	0.0317	0.0273	0.0230
		max	0.1633	0.0817	0.0558	0.0457	0.0356
		sd	0.0252	0.0106	0.0047	0.0034	0.0022
	70	mean	0.0771	0.0512	0.0373	0.0312	0.0269
		min	0.0374	0.0325	0.0266	0.0246	0.0210
		max	0.1350	0.0766	0.0509	0.0385	0.0317
		sd	0.0208	0.0088	0.0046	0.0030	0.0022
	100	mean	0.0753	0.0495	0.0355	0.0294	0.0250
		min	0.0295	0.0244	0.0265	0.0221	0.0194
		max	0.1591	0.0696	0.0460	0.0377	0.0310
		sd	0.0227	0.0086	0.0039	0.0031	0.0021

Table A.2.24 The mean, minimum, maximum and standard deviation of REML heritability approximate standard errors from data sets with a population heritability of 0.2321, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.1366[1]	0.0803	0.0571	0.0470	0.0402
		min	0.0001	0.0505	0.0385	0.0354	0.0326
		max	0.8923	0.1229	0.0715	0.0624	0.0477
		sd	0.0840	0.0159	0.0063	0.0050	0.0031
	50	mean	0.0937	0.0568	0.0411	0.0330	0.0293
		min	0.0356	0.0290	0.0322	0.0276	0.0231
		max	0.1738	0.0839	0.0565	0.0461	0.0358
		sd	0.0268	0.0109	0.0048	0.0034	0.0023
	70	mean	0.0825	0.0526	0.0378	0.0315	0.0271
		min	0.0401	0.0333	0.0269	0.0248	0.0211
		max	0.1440	0.0786	0.0516	0.0388	0.0319
		sd	0.0221	0.0090	0.0047	0.0030	0.0022
	100	mean	0.0806	0.0509	0.0360	0.0296	0.0252
		min	0.0318	0.0252	0.0268	0.0223	0.0195
		max	0.1691	0.0715	0.0466	0.0380	0.0312
		sd	0.0241	0.0088	0.0040	0.0031	0.0021

1 = 99 replicates

Table A.2.25 The mean, minimum, maximum and standard deviation of HM sire variance estimates from data sets with a population sire variance of 0.6783, each with 100 replicates, for data type SD2.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.6598	0.6584	0.6678	0.6794	0.6579
	min	−0.0776	0.1344	0.2032	0.3248	0.3919
	max	1.8389	1.4647	1.1271	1.1753	0.9582
	sd	0.3901	0.3038	0.1701	0.1603	0.1143
50	mean	0.6803	0.6467	0.6675	0.6519	0.6764
	min	0.0832	0.1844	0.4597	0.4904	0.4736
	max	1.7073	1.1375	1.0463	1.0504	0.9318
	sd	0.3042	0.1934	0.1184	0.1072	0.0808
70	mean	0.6271	0.6473	0.6620	0.6809	0.6762
	min	0.1759	0.3261	0.4039	0.4821	0.4713
	max	1.3493	1.0882	1.0124	0.9187	0.8542
	sd	0.2429	0.1578	0.1160	0.0922	0.0809
100	mean	0.6627	0.6722	0.6721	0.6813	0.6631
	min	0.1651	0.2491	0.4550	0.4709	0.4710
	max	1.8382	1.0446	0.9392	0.9353	0.8869
	sd	0.2717	0.1533	0.1007	0.0955	0.0758

Table A.2.26 The mean, minimum, maximum and standard deviation of ML sire variance estimates from data sets with a population sire variance of 0.6783, each with 100 replicates, for data type SD2.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.6005	0.6329	0.6549	0.6713	0.6519
	min	0.0000	0.1030	0.1942	0.3222	0.3863
	max	1.7262	1.4427	1.1093	1.1687	0.9505
	sd	0.3658	0.2963	0.1674	0.1592	0.1137
50	mean	0.6342	0.6285	0.6588	0.6460	0.6717
	min	0.0664	0.1764	0.4528	0.4879	0.4707
	max	1.6043	1.1054	1.0372	1.0413	0.9239
	sd	0.2887	0.1890	0.1178	0.1065	0.0804
70	mean	0.5862	0.6307	0.6533	0.6751	0.6718
	min	0.1599	0.3157	0.3964	0.4778	0.4680
	max	1.2770	1.0659	1.0014	0.9078	0.8492
	sd	0.2297	0.1543	0.1150	0.0916	0.0804
100	mean	0.6230	0.6559	0.6641	0.6758	0.6593
	min	0.1512	0.2423	0.4484	0.4665	0.4682
	max	1.7229	1.0213	0.9318	0.9296	0.8821
	sd	0.2569	0.1502	0.0996	0.0948	0.0752

Table A.2.27 The mean, minimum, maximum and standard deviation of REML sire variance estimates from data sets with a population sire variance of 0.6783, each with 100 replicates, for data type SD2.

		Number of Sires				
Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.6603	0.6570	0.6671	0.6795	0.6579
	min	0.0000	0.1174	0.2017	0.3281	0.3910
	max	1.8456	1.4833	1.1264	1.1802	0.9582
	sd	0.3861	0.3022	0.1691	0.1603	0.1143
50	mean	0.6792	0.6459	0.6677	0.6518	0.6762
	min	0.0818	0.1845	0.4597	0.4927	0.4742
	max	1.7004	1.1324	1.0498	1.0497	0.9297
	sd	0.3038	0.1928	0.1190	0.1072	0.0808
70	mean	0.6253	0.6468	0.6615	0.6807	0.6760
	min	0.1757	0.3253	0.4020	0.4821	0.4711
	max	1.3524	1.0907	1.0131	0.9149	0.8543
	sd	0.2417	0.1574	0.1162	0.0922	0.0808
100	mean	0.6615	0.6715	0.6719	0.6811	0.6632
	min	0.1649	0.2495	0.4541	0.4704	0.4712
	max	1.8192	1.0444	0.9423	0.9365	0.8871
	sd	0.2704	0.1533	0.1006	0.0954	0.0756

Table A.2.28 The mean, minimum, maximum and standard deviation of HM sire variance large sample standard errors from data sets with a population sire variance of 0.6783, each with 100 replicates, for data type SD2.

		Number of Sires				
Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.3960	0.2454	0.1745	0.1435	0.1219
	min	0.1637	0.1421	0.1082	0.1030	0.0927
	max	0.7743	0.4032	0.2435	0.1985	0.1526
	sd	0.1249	0.0610	0.0245	0.0185	0.0115
50	mean	0.2926	0.1755	0.1263	0.1011	0.0900
	min	0.0995	0.0819	0.0975	0.0825	0.0700
	max	0.6268	0.2737	0.1792	0.1463	0.1158
	sd	0.0981	0.0391	0.0167	0.0124	0.0081
70	mean	0.2544	0.1628	0.1165	0.0972	0.0836
	min	0.1034	0.0980	0.0800	0.0742	0.0632
	max	0.4881	0.2504	0.1661	0.1245	0.1020
	sd	0.0787	0.0318	0.0165	0.0107	0.0081
100	mean	0.2506	0.1582	0.1112	0.0917	0.0775
	min	0.0889	0.0728	0.0806	0.0678	0.0583
	max	0.6319	0.2339	0.1497	0.1208	0.1000
	sd	0.0881	0.0309	0.0144	0.0110	0.0076

Table A.2.29 The mean, minimum, maximum and standard deviation of ML sire variance large sample standard errors from data sets with a population sire variance of 0.6783, each with 100 replicates, for data type SD2.

Mean Number of Progeny Per Sire			Number of Sires				
			20	50	100	150	200
	20	mean	0.3671	0.2378	0.1718	0.1420	0.1209
		min	0.1811	0.1342	0.1063	0.1025	0.0922
		max	0.7182	0.3943	0.2396	0.1970	0.1513
		sd	0.1141	0.0589	0.0240	0.0183	0.0114
	50	mean	0.2706	0.1701	0.1244	0.1001	0.0892
		min	0.0917	0.0794	0.0964	0.0819	0.0700
		max	0.5782	0.2642	0.1769	0.1449	0.1145
		sd	0.0907	0.0378	0.0166	0.0123	0.0080
	70	mean	0.2350	0.1578	0.1147	0.0962	0.0829
		min	0.0959	0.0949	0.0787	0.0735	0.0624
		max	0.4527	0.2433	0.1637	0.1229	0.1010
		sd	0.0725	0.0308	0.0162	0.0106	0.0081
	100	mean	0.2316	0.1533	0.1095	0.0907	0.0769
		min	0.0825	0.0707	0.0794	0.0671	0.0583
		max	0.5794	0.2267	0.1480	0.1200	0.0990
		sd	0.0812	0.0300	0.0141	0.0109	0.0075

Table A.2.30 The mean, minimum, maximum and standard deviation of REML sire variance large sample standard errors from data sets with a population sire variance of 0.6783, each with 100 replicates, for data type SD2.

Mean Number of Progeny Per Sire			Number of Sires				
			20	50	100	150	200
	20	mean	0.4201[1]	0.2447	0.1741	0.1433	0.1218
		min	0.0002	0.1426	0.1080	0.1027	0.0931
		max	2.6227	0.4087	0.2431	0.1993	0.1525
		sd	0.2563	0.0603	0.0242	0.0186	0.0115
	50	mean	0.2920	0.1752	0.1263	0.1011	0.0899
		min	0.0999	0.0819	0.0976	0.0832	0.0704
		max	0.6240	0.2726	0.1797	0.1463	0.1154
		sd	0.0979	0.0390	0.0168	0.0124	0.0081
	70	mean	0.2536	0.1627	0.1164	0.0971	0.0836
		min	0.1032	0.0979	0.0795	0.0742	0.0631
		max	0.4891	0.2510	0.1661	0.1241	0.1017
		sd	0.0783	0.0317	0.0165	0.0107	0.0081
	100	mean	0.2501	0.1580	0.1112	0.0917	0.0775
		min	0.0888	0.0730	0.0803	0.0675	0.0583
		max	0.6253	0.2337	0.1502	0.1211	0.1000
		sd	0.0877	0.0309	0.0143	0.0110	0.0076

1 = 99 replicates

Table A.2.31 The mean, minimum, maximum and standard deviation of HM error variance estimates from data sets with a population error variance of 11.0106, each with 100 replicates, for data type SD2.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	11.0339	10.9526	11.0356	11.0072	10.9865
	min	8.5927	9.2329	10.0765	10.3223	10.4113
	max	12.9590	11.8975	11.8412	11.6790	11.7917
	sd	0.8311	0.4790	0.3699	0.2873	0.2546
50	mean	11.0284	11.0593	11.0018	10.9891	10.9961
	min	9.3611	10.2542	10.5993	10.5375	10.7171
	max	12.3967	11.8726	11.4749	11.4081	11.3663
	sd	0.5265	0.3033	0.2101	0.1693	0.1339
70	mean	10.9675	11.0775	11.0208	11.0102	11.0042
	min	9.7404	10.4514	10.5354	10.6537	10.6861
	max	11.8155	11.6842	11.4280	11.3308	11.3126
	sd	0.4406	0.2478	0.1828	0.1236	0.1297
100	mean	10.9322	11.0388	11.0107	11.0024	11.0021
	min	10.0042	10.6014	10.5330	10.6767	10.7983
	max	11.8120	11.5198	11.3799	11.2420	11.3212
	sd	0.3519	0.1903	0.1562	0.1109	0.1085

Table A.2.32 The mean, minimum, maximum and standard deviation of ML error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD2.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	11.0311	10.9519	11.0346	11.0065	10.9860
	min	8.5893	9.2325	10.0806	10.3272	10.4129
	max	12.9362	11.9076	11.8393	11.6807	11.7928
	sd	0.8289	0.4796	0.3697	0.2871	0.2545
50	mean	11.0282	11.0592	11.0018	10.9891	10.9961
	min	9.3612	10.2536	10.5997	10.5379	10.7172
	max	12.3973	11.8723	11.4749	11.4078	11.3664
	sd	0.5266	0.3033	0.2101	0.1692	0.1339
70	mean	10.9673	11.0775	11.0208	11.0102	11.0041
	min	9.7404	10.4515	10.5353	10.6536	10.6861
	max	11.8152	11.6841	11.4281	11.3307	11.3126
	sd	0.4406	0.2478	0.1828	0.1236	0.1297
100	mean	10.9322	11.0387	11.0107	11.0024	11.0021
	min	10.0041	10.6014	10.5330	10.6767	10.7983
	max	11.8120	11.5198	11.3799	11.2420	11.3212
	sd	0.3519	0.1903	0.1562	0.1109	0.1085

Table A.2.33 The mean, minimum, maximum and standard deviation of REML error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	11.0319	10.9519	11.0346	11.0065	10.9860
		min	8.5896	9.2325	10.0805	10.3271	10.4129
		max	12.9384	11.9072	11.8393	11.6807	11.7928
		sd	0.8294	0.4796	0.3697	0.2871	0.2545
	50	mean	11.0282	11.0592	11.0018	10.9891	10.9961
		min	9.3612	10.2537	10.5997	10.5379	10.7172
		max	12.3972	11.8723	11.4749	11.4078	11.3664
		sd	0.5266	0.3033	0.2101	0.1692	0.1339
	70	mean	10.9674	11.0775	11.0208	11.0102	11.0041
		min	9.7404	10.4515	10.5353	10.6537	10.6861
		max	11.8153	11.6841	11.4281	11.3307	11.3126
		sd	0.4406	0.2478	0.1828	0.1236	0.1297
	100	mean	10.9322	11.0387	11.0107	11.0024	11.0021
		min	10.0041	10.6014	10.5330	10.6767	10.7983
		max	11.8120	11.5198	11.3799	11.2420	11.3212
		sd	0.3519	0.1903	0.1562	0.1109	0.1085

Table A.2.34 The mean, minimum, maximum and standard deviation of HM error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.8005	0.5025	0.3580	0.2916	0.2521
		min	0.6234	0.4237	0.3270	0.2735	0.2387
		max	0.9402	0.5459	0.3842	0.3094	0.2706
		sd	0.0603	0.0220	0.0120	0.0076	0.0058
	50	mean	0.4982	0.3160	0.2223	0.1813	0.1571
		min	0.4228	0.2929	0.2142	0.1738	0.1530
		max	0.5600	0.3393	0.2317	0.1881	0.1625
		sd	0.0238	0.0087	0.0042	0.0028	0.0019
	70	mean	0.4175	0.2667	0.1876	0.1530	0.1325
		min	0.3708	0.2516	0.1794	0.1480	0.1285
		max	0.4498	0.2812	0.1947	0.1575	0.1360
		sd	0.0168	0.0060	0.0031	0.0017	0.0016
	100	mean	0.3474	0.2219	0.1565	0.1277	0.1106
		min	0.3180	0.2131	0.1497	0.1241	0.1086
		max	0.3754	0.2315	0.1619	0.1304	0.1136
		sd	0.0112	0.0038	0.0022	0.0013	0.0011

Table A.2.35 The mean, minimum, maximum and standard deviation of ML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD2.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.8002	0.5025	0.3580	0.2916	0.2520
	min	0.6231	0.4236	0.3271	0.2735	0.2390
	max	0.9383	0.5464	0.3841	0.3094	0.2706
	sd	0.0601	0.0220	0.0120	0.0076	0.0058
50	mean	0.4982	0.3160	0.2223	0.1813	0.1571
	min	0.4228	0.2929	0.2142	0.1738	0.1530
	max	0.5601	0.3393	0.2317	0.1881	0.1625
	sd	0.0238	0.0087	0.0042	0.0028	0.0019
70	mean	0.4175	0.2667	0.1876	0.1530	0.1325
	min	0.3708	0.2516	0.1794	0.1480	0.1285
	max	0.4498	0.2812	0.1947	0.1575	0.1360
	sd	0.0168	0.0060	0.0031	0.0017	0.0016
100	mean	0.3474	0.2219	0.1565	0.1277	0.1106
	min	0.3180	0.2131	0.1497	0.1241	0.1086
	max	0.3754	0.2315	0.1619	0.1304	0.1136
	sd	0.0112	0.0038	0.0022	0.0013	0.0011

Table A.2.36 The mean, minimum, maximum and standard deviation of REML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD2.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.8097[1]	0.5024	0.3580	0.2915	0.2520
	min	0.0002	0.4236	0.3272	0.2737	0.2389
	max	2.6227	0.5468	0.3840	0.3095	0.2705
	sd	0.2096	0.0220	0.0120	0.0076	0.0058
50	mean	0.4982	0.3160	0.2223	0.1813	0.1571
	min	0.4229	0.2929	0.2142	0.1738	0.1531
	max	0.5601	0.3392	0.2318	0.1882	0.1624
	sd	0.0238	0.0087	0.0042	0.0028	0.0019
70	mean	0.4175	0.2667	0.1876	0.1531	0.1325
	min	0.3708	0.2516	0.1794	0.1481	0.1286
	max	0.4498	0.2813	0.1946	0.1575	0.1362
	sd	0.0168	0.0060	0.0031	0.0017	0.0016
100	mean	0.3475	0.2219	0.1565	0.1277	0.1106
	min	0.3179	0.2131	0.1497	0.1239	0.1085
	max	0.3754	0.2316	0.1617	0.1305	0.1138
	sd	0.0112	0.0038	0.0022	0.0013	0.0011

1 = 99 replicates

Table A.2.37 The mean, minimum, maximum and standard deviation of HM heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.2616	0.2181	0.2258	0.2339	0.2213
	min	−0.0041	0.0757	0.1299	0.1564	0.1220
	max	0.6717	0.4532	0.4389	0.3807	0.3371
	sd	0.1472	0.0790	0.0619	0.0476	0.0416
50	mean	0.2152	0.2271	0.2311	0.2412	0.2234
	min	0.0538	0.1165	0.1236	0.1631	0.1540
	max	0.4744	0.4385	0.3447	0.3018	0.2780
	sd	0.0836	0.0621	0.0492	0.0364	0.0283
70	mean	0.2057	0.2213	0.2266	0.2317	0.2262
	min	0.0326	0.1538	0.1466	0.1684	0.1623
	max	0.3964	0.3364	0.3182	0.2984	0.2915
	sd	0.0773	0.0444	0.0378	0.0333	0.0350
100	mean	0.2238	0.2272	0.2391	0.2243	0.2307
	min	0.0697	0.1216	0.1490	0.1724	0.1650
	max	0.3919	0.3307	0.2926	0.2910	0.2817
	sd	0.0748	0.0497	0.0330	0.0243	0.0250

Table A.2.38 The mean, minimum, maximum and standard deviation of ML heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.2399	0.2098	0.2219	0.2309	0.2194
	min	0.0000	0.0658	0.1261	0.1514	0.1205
	max	0.6413	0.4410	0.4312	0.3761	0.3277
	sd	0.1412	0.0775	0.0618	0.0470	0.0409
50	mean	0.2011	0.2219	0.2273	0.2386	0.2220
	min	0.0471	0.1127	0.1220	0.1625	0.1532
	max	0.4426	0.4283	0.3327	0.2955	0.2787
	sd	0.0797	0.0612	0.0477	0.0357	0.0284
70	mean	0.1930	0.2153	0.2236	0.2301	0.2247
	min	0.0281	0.1497	0.1437	0.1672	0.1620
	max	0.3773	0.3250	0.3122	0.2956	0.2888
	sd	0.0736	0.0432	0.0372	0.0333	0.0347
100	mean	0.2111	0.2219	0.2362	0.2223	0.2294
	min	0.0649	0.1192	0.1476	0.1721	0.1644
	max	0.3717	0.3241	0.2888	0.2872	0.2809
	sd	0.0715	0.0486	0.0326	0.0240	0.0248

Table A.2.39 The mean, minimum, maximum and standard deviation of REML heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD5.

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.2607	0.2176	0.2259	0.2336	0.2213
		min	0.0000	0.0718	0.1294	0.1537	0.1221
		max	0.6779	0.4524	0.4368	0.3795	0.3301
		sd	0.1470	0.0786	0.0623	0.0472	0.0411
	50	mean	0.2148	0.2276	0.2302	0.2406	0.2234
		min	0.0537	0.1165	0.1240	0.1640	0.1543
		max	0.4663	0.4374	0.3364	0.2978	0.2804
		sd	0.0833	0.0622	0.0481	0.0359	0.0285
	70	mean	0.2053	0.2205	0.2263	0.2318	0.2260
		min	0.0325	0.1537	0.1456	0.1686	0.1631
		max	0.3977	0.3320	0.3156	0.2977	0.2904
		sd	0.0769	0.0439	0.0375	0.0335	0.0349
	100	mean	0.2234	0.2269	0.2388	0.2240	0.2307
		min	0.0704	0.1224	0.1494	0.1735	0.1654
		max	0.3911	0.3309	0.2919	0.2892	0.2824
		sd	0.0748	0.0495	0.0329	0.0242	0.0249

Table A.2.40 The mean, minimum, maximum and standard deviation of HM heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD5.

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.1378	0.0795	0.0569	0.0472	0.0398
		min	0.0655	0.0553	0.0456	0.0398	0.0315
		max	0.2320	0.1159	0.0801	0.0604	0.0490
		sd	0.0370	0.0128	0.0071	0.0044	0.0034
	50	mean	0.0896	0.0580	0.0414	0.0348	0.0286
		min	0.0429	0.0385	0.0280	0.0269	0.0225
		max	0.1573	0.0926	0.0548	0.0407	0.0332
		sd	0.0231	0.0107	0.0060	0.0036	0.0024
	70	mean	0.0801	0.0528	0.0378	0.0313	0.0266
		min	0.0289	0.0408	0.0278	0.0249	0.0210
		max	0.1318	0.0724	0.0489	0.0379	0.0323
		sd	0.0218	0.0077	0.0047	0.0033	0.0030
	100	mean	0.0800	0.0506	0.0371	0.0288	0.0255
		min	0.0349	0.0316	0.0258	0.0235	0.0196
		max	0.1259	0.0684	0.0437	0.0354	0.0299
		sd	0.0211	0.0088	0.0041	0.0025	0.0022

Table A.2.41 The mean, minimum, maximum and standard deviation of ML heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.1297	0.0779	0.0566	0.0471	0.0399
	min	0.0631	0.0526	0.0450	0.0394	0.0313
	max	0.2223	0.1142	0.0797	0.0604	0.0486
	sd	0.0360	0.0128	0.0072	0.0045	0.0034
50	mean	0.0837	0.0567	0.0408	0.0344	0.0284
	min	0.0398	0.0375	0.0277	0.0268	0.0224
	max	0.1461	0.0903	0.0533	0.0400	0.0332
	sd	0.0217	0.0105	0.0058	0.0035	0.0024
70	mean	0.0746	0.0513	0.0373	0.0311	0.0265
	min	0.0268	0.0397	0.0273	0.0248	0.0210
	max	0.1238	0.0699	0.0479	0.0376	0.0320
	sd	0.0204	0.0075	0.0046	0.0033	0.0030
100	mean	0.0746	0.0492	0.0366	0.0285	0.0253
	min	0.0326	0.0308	0.0255	0.0234	0.0195
	max	0.1176	0.0667	0.0430	0.0349	0.0297
	sd	0.0198	0.0085	0.0040	0.0024	0.0022

Table A.2.42 The mean, minimum, maximum and standard deviation of REML heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.1440	0.0796	0.0573	0.0476	0.0400
	min	0.0664	0.0544	0.0463	0.0405	0.0318
	max	0.6762	0.1170	0.0806	0.0605	0.0481
	sd	0.0651	0.0127	0.0074	0.0044	0.0035
50	mean	0.0896	0.0583	0.0413	0.0347	0.0286
	min	0.0430	0.0386	0.0282	0.0272	0.0226
	max	0.1550	0.0925	0.0536	0.0402	0.0335
	sd	0.0231	0.0107	0.0058	0.0035	0.0025
70	mean	0.0799	0.0526	0.0378	0.0314	0.0267
	min	0.0290	0.0409	0.0276	0.0250	0.0212
	max	0.1322	0.0716	0.0485	0.0379	0.0322
	sd	0.0217	0.0076	0.0046	0.0034	0.0030
100	mean	0.0799	0.0506	0.0371	0.0288	0.0255
	min	0.0354	0.0318	0.0259	0.0236	0.0197
	max	0.1256	0.0685	0.0436	0.0352	0.0299
	sd	0.0211	0.0087	0.0041	0.0024	0.0022

Table A.2.43 The mean, minimum, maximum and standard deviation of HM sire variance estimates from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7814	0.6389	0.6597	0.6866	0.6449
	min	−0.0117	0.2109	0.3570	0.4668	0.3441
	max	2.3204	1.4018	1.3601	1.1590	1.0173
	sd	0.4646	0.2425	0.1918	0.1491	0.1297
50	mean	0.6352	0.6606	0.6787	0.7079	0.6540
	min	0.1490	0.3321	0.3469	0.4813	0.4500
	max	1.4819	1.3532	1.0039	0.9154	0.8136
	sd	0.2627	0.1910	0.1520	0.1151	0.0847
70	mean	0.6031	0.6434	0.6638	0.6785	0.6619
	min	0.0952	0.4520	0.4189	0.4912	0.4687
	max	1.1740	0.9472	0.9245	0.8756	0.8513
	sd	0.2344	0.1339	0.1125	0.1005	0.1070
100	mean	0.6561	0.6666	0.7008	0.6545	0.6752
	min	0.1892	0.3415	0.4224	0.5006	0.4714
	max	1.1885	0.9856	0.8632	0.8738	0.8297
	sd	0.2340	0.1526	0.1009	0.0760	0.0791

Table A.2.44 The mean, minimum, maximum and standard deviation of ML sire variance estimates from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7113	0.6129	0.6477	0.6772	0.6388
	min	0.0000	0.1900	0.3464	0.4519	0.3397
	max	2.0384	1.3231	1.3335	1.1431	0.9859
	sd	0.4377	0.2356	0.1909	0.1467	0.1274
50	mean	0.5913	0.6448	0.6668	0.6997	0.6498
	min	0.1303	0.3211	0.3424	0.4791	0.4476
	max	1.3986	1.3178	0.9659	0.8947	0.8159
	sd	0.2485	0.1877	0.1468	0.1126	0.0850
70	mean	0.5638	0.6250	0.6545	0.6735	0.6574
	min	0.0818	0.4394	0.4104	0.4875	0.4679
	max	1.1116	0.9137	0.9055	0.8682	0.8515
	sd	0.2216	0.1300	0.1103	0.1003	0.1062
100	mean	0.6167	0.6501	0.6919	0.6486	0.6710
	min	0.1759	0.3346	0.4183	0.4968	0.4694
	max	1.1209	0.9642	0.8555	0.8614	0.8271
	sd	0.2220	0.1485	0.0997	0.0752	0.0785

Table A.2.45 The mean, minimum, maximum and standard deviation of REML sire variance estimates from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7779	0.6369	0.6600	0.6856	0.6449
	min	0.0000	0.2075	0.3557	0.4592	0.3443
	max	2.1714	1.3605	1.3528	1.1545	0.9935
	sd	0.4608	0.2402	0.1929	0.1476	0.1281
50	mean	0.6341	0.6625	0.6758	0.7059	0.6542
	min	0.1489	0.3323	0.3481	0.4837	0.4510
	max	1.4846	1.3492	0.9776	0.9022	0.8211
	sd	0.2616	0.1915	0.1483	0.1134	0.0854
70	mean	0.6018	0.6409	0.6628	0.6791	0.6615
	min	0.0949	0.4517	0.4162	0.4918	0.4711
	max	1.1782	0.9355	0.9162	0.8751	0.8566
	sd	0.2332	0.1326	0.1114	0.1009	0.1068
100	mean	0.6550	0.6656	0.7000	0.6537	0.6750
	min	0.1910	0.3438	0.4236	0.5009	0.4723
	max	1.1857	0.9861	0.8653	0.8679	0.8318
	sd	0.2337	0.1516	0.1007	0.0757	0.0789

Table A.2.46 The mean, minimum, maximum and standard deviation of HM sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.4385	0.2442	0.1743	0.1456	0.1215
	min	0.1879	0.1556	0.1281	0.1179	0.0906
	max	0.9567	0.4012	0.2764	0.2015	0.1600
	sd	0.1531	0.0501	0.0279	0.0177	0.0134
50	mean	0.2789	0.1783	0.1283	0.1079	0.0880
	min	0.1200	0.1122	0.0806	0.0825	0.0678
	max	0.5594	0.3191	0.1735	0.1327	0.1039
	sd	0.0857	0.0387	0.0217	0.0135	0.0085
70	mean	0.2475	0.1620	0.1170	0.0971	0.0823
	min	0.0849	0.1241	0.0819	0.0755	0.0632
	max	0.4312	0.2229	0.1533	0.1196	0.1015
	sd	0.0758	0.0270	0.0159	0.0116	0.0107
100	mean	0.2488	0.1571	0.1154	0.0887	0.0788
	min	0.0959	0.0911	0.0755	0.0707	0.0583
	max	0.4214	0.2216	0.1389	0.1145	0.0943
	sd	0.0761	0.0308	0.0144	0.0088	0.0080

Table A.2.47 The mean, minimum, maximum and standard deviation of ML sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.4034	0.2360	0.1716	0.1439	0.1205
	min	0.1783	0.1523	0.1257	0.1166	0.0894
	max	0.8345	0.3792	0.2700	0.1982	0.1559
	sd	0.1398	0.0480	0.0276	0.0173	0.0131
50	mean	0.2576	0.1731	0.1258	0.1064	0.0873
	min	0.1109	0.1091	0.0794	0.0812	0.0671
	max	0.5177	0.3079	0.1670	0.1296	0.1034
	sd	0.0788	0.0375	0.0208	0.0130	0.0084
70	mean	0.2286	0.1565	0.1150	0.0961	0.0816
	min	0.0781	0.1204	0.0806	0.0748	0.0624
	max	0.4000	0.2140	0.1497	0.1183	0.1010
	sd	0.0697	0.0259	0.0155	0.0115	0.0106
100	mean	0.2299	0.1522	0.1135	0.0877	0.0782
	min	0.0894	0.0889	0.0748	0.0700	0.0583
	max	0.3891	0.2147	0.1371	0.1122	0.0938
	sd	0.0703	0.0297	0.0141	0.0087	0.0078

Table A.2.48 The mean, minimum, maximum and standard deviation of ML sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.4519	0.2422	0.1742	0.1455	0.1211
	min	0.1882	0.1529	0.1295	0.1196	0.0911
	max	1.9414	0.3840	0.2739	0.1990	0.1546
	sd	0.2107	0.0483	0.0282	0.0171	0.0133
50	mean	0.2781	0.1786	0.1276	0.1074	0.0879
	min	0.1201	0.1123	0.0809	0.0814	0.0680
	max	0.5588	0.3171	0.1685	0.1303	0.1046
	sd	0.0850	0.0387	0.0210	0.0132	0.0085
70	mean	0.2467	0.1611	0.1167	0.0970	0.0822
	min	0.0848	0.1240	0.0814	0.0756	0.0633
	max	0.4321	0.2203	0.1518	0.1197	0.1018
	sd	0.0753	0.0267	0.0157	0.0116	0.0107
100	mean	0.2482	0.1568	0.1152	0.0885	0.0787
	min	0.0975	0.0917	0.0758	0.0708	0.0584
	max	0.4202	0.2214	0.1392	0.1134	0.0944
	sd	0.0760	0.0306	0.0143	0.0088	0.0079

Table A.2.49 The mean, minimum, maximum and standard deviation of HM error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	10.9886	11.0259	10.9844	11.0289	10.9890
	min	9.5006	9.6016	10.1758	10.3958	10.5097
	max	13.1055	12.3727	11.7018	11.5324	11.4315
	sd	0.7882	0.5861	0.3582	0.2701	0.2500
50	mean	11.0843	10.9375	11.0404	11.0131	11.0544
	min	10.1692	10.3340	10.6468	10.7141	10.6018
	max	12.1384	11.6797	11.7891	11.5889	11.3645
	sd	0.4351	0.3066	0.2313	0.2037	0.1733
70	mean	11.0819	10.9719	11.0488	11.0301	11.0318
	min	10.1626	10.3173	10.6697	10.7090	10.8019
	max	12.3338	11.5962	11.6686	11.4502	11.3088
	sd	0.4349	0.2525	0.1928	0.1686	0.1177
100	mean	10.9918	11.0410	11.0141	11.0100	11.0174
	min	10.3275	10.6399	10.6836	10.7182	10.7531
	max	11.8549	11.8504	11.4192	11.2723	11.2909
	sd	0.3033	0.2253	0.1712	0.1341	0.0886

Table A.2.50 The mean, minimum, maximum and standard deviation of ML error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	10.9858	11.0228	10.9841	11.0294	10.9873
	min	9.5047	9.6178	10.1729	10.4034	10.5115
	max	13.1175	12.3548	11.6917	11.5342	11.4308
	sd	0.7863	0.5862	0.3559	0.2709	0.2485
50	mean	11.0841	10.9377	11.0402	11.0129	11.0544
	min	10.1685	10.3333	10.6455	10.7139	10.6025
	max	12.1393	11.6797	11.7879	11.5886	11.3655
	sd	0.4350	0.3068	0.2313	0.2037	0.1733
70	mean	11.0818	10.9717	11.0487	11.0301	11.0318
	min	10.1620	10.3169	10.6698	10.7089	10.8019
	max	12.3342	11.5962	11.6685	11.4499	11.3089
	sd	0.4349	0.2524	0.1928	0.1686	0.1177
100	mean	10.9917	11.0409	11.0141	11.0100	11.0174
	min	10.3271	10.6397	10.6836	10.7182	10.7531
	max	11.8550	11.8501	11.4192	11.2724	11.2909
	sd	0.3032	0.2253	0.1712	0.1341	0.0886

Table A.2.51 The mean, minimum, maximum and standard deviation of REML error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD5.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	10.9862	11.0228	10.9841	11.0293	10.9873
		min	9.5042	9.6171	10.1730	10.4033	10.5115
		max	13.1155	12.3553	11.6919	11.5342	11.4308
		sd	0.7866	0.5862	0.3559	0.2709	0.2485
	50	mean	11.0841	10.9377	11.0402	11.0129	11.0544
		min	10.1686	10.3334	10.6455	10.7139	10.6025
		max	12.1392	11.6797	11.7879	11.5886	11.3655
		sd	0.4350	0.3068	0.2313	0.2037	0.1733
	70	mean	11.0818	10.9717	11.0487	11.0301	11.0318
		min	10.1620	10.3169	10.6698	10.7089	10.8019
		max	12.3342	11.5962	11.6685	11.4500	11.3089
		sd	0.4349	0.2524	0.1928	0.1686	0.1177
	100	mean	10.9917	11.0409	11.0141	11.0100	11.0174
		min	10.3272	10.6397	10.6836	10.7182	10.7531
		max	11.8550	11.8501	11.4192	11.2724	11.2909
		sd	0.3032	0.2253	0.1712	0.1341	0.0886

Table A.2.52 The mean, minimum, maximum and standard deviation of HM error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD5.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean	0.7972	0.5059	0.3564	0.2922	0.2521
		min	0.6893	0.4406	0.3302	0.2753	0.2410
		max	0.9508	0.5677	0.3796	0.3055	0.2623
		sd	0.0572	0.0269	0.0116	0.0072	0.0057
	50	mean	0.5007	0.3125	0.2230	0.1816	0.1579
		min	0.4593	0.2953	0.2152	0.1766	0.1513
		max	0.5484	0.3338	0.2381	0.1910	0.1625
		sd	0.0197	0.0088	0.0047	0.0034	0.0025
	70	mean	0.4219	0.2642	0.1881	0.1533	0.1328
		min	0.3869	0.2484	0.1817	0.1490	0.1300
		max	0.4696	0.2793	0.1987	0.1591	0.1360
		sd	0.0166	0.0061	0.0033	0.0024	0.0014
	100	mean	0.3493	0.2219	0.1566	0.1278	0.1108
		min	0.3282	0.2138	0.1520	0.1245	0.1082
		max	0.3768	0.2381	0.1622	0.1308	0.1136
		sd	0.0096	0.0045	0.0024	0.0015	0.0009

Table A.2.53 The mean, minimum, maximum and standard deviation of ML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.7967	0.5055	0.3562	0.2921	0.2520
	min	0.6894	0.4410	0.3300	0.2755	0.2410
	max	0.9510	0.5667	0.3791	0.3055	0.2621
	sd	0.0570	0.0269	0.0115	0.0072	0.0057
50	mean	0.5007	0.3125	0.2230	0.1817	0.1579
	min	0.4593	0.2953	0.2152	0.1766	0.1513
	max	0.5484	0.3338	0.2381	0.1910	0.1625
	sd	0.0197	0.0088	0.0047	0.0034	0.0025
70	mean	0.4219	0.2642	0.1881	0.1533	0.1328
	min	0.3869	0.2484	0.1817	0.1490	0.1300
	max	0.4696	0.2793	0.1987	0.1591	0.1360
	sd	0.0166	0.0061	0.0033	0.0024	0.0014
100	mean	0.3493	0.2219	0.1566	0.1278	0.1108
	min	0.3282	0.2138	0.1520	0.1245	0.1082
	max	0.3768	0.2381	0.1622	0.1308	0.1136
	sd	0.0096	0.0045	0.0024	0.0015	0.0009

Table A.2.54 The mean, minimum, maximum and standard deviation of REML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD5.

Number of Sires

Mean Number of Progeny Per Sire		20	50	100	150	200
20	mean	0.8077	0.5055	0.3562	0.2921	0.2519
	min	0.6897	0.4417	0.3299	0.2757	0.2411
	max	1.9414	0.5661	0.3789	0.3055	0.2622
	sd	0.1279	0.0269	0.0115	0.0072	0.0057
50	mean	0.5007	0.3125	0.2230	0.1817	0.1579
	min	0.4593	0.2952	0.2150	0.1767	0.1515
	max	0.5484	0.3337	0.2381	0.1912	0.1624
	sd	0.0196	0.0088	0.0047	0.0034	0.0025
70	mean	0.4219	0.2642	0.1881	0.1533	0.1328
	min	0.3868	0.2484	0.1817	0.1489	0.1300
	max	0.4696	0.2792	0.1987	0.1592	0.1361
	sd	0.0166	0.0061	0.0033	0.0023	0.0014
100	mean	0.3493	0.2219	0.1565	0.1278	0.1107
	min	0.3282	0.2139	0.1518	0.1244	0.1081
	max	0.3768	0.2382	0.1623	0.1308	0.1135
	sd	0.0096	0.0045	0.0024	0.0015	0.0009

Table A.2.55 The mean, minimum, maximum and standard deviation of HM heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.2157	0.2226	0.2196	0.2305
		min		0.0391	0.1297	0.1480	0.1232
		max		0.5528	0.3361	0.3900	0.3144
		sd		0.0791	0.0566	0.0507	0.0380
	50	mean		0.2130	0.2449	0.2282	0.2267
		min		0.1325	0.1423	0.1776	0.1671
		max		0.3242	0.3345	0.3114	0.3091
		sd		0.0537	0.0401	0.0375	0.0343
	70	mean		0.2322	0.2332	0.2377	0.2344
		min		0.0993	0.1390	0.1442	0.1964
		max		0.3472	0.3182	0.3454	0.2751
		sd		0.0526	0.0456	0.0370	0.0191
	100	mean		0.2294	0.2226	0.2281	0.2231
		min		0.1276	0.1514	0.1720	0.1700
		max		0.3482	0.3132	0.2756	0.3053
		sd		0.0454	0.0383	0.0269	0.0239

Table A.2.56 The mean, minimum, maximum and standard deviation of ML heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.2091	0.2181	0.2162	0.2288
		min		0.0387	0.1278	0.1412	0.1259
		max		0.5240	0.3288	0.3866	0.3155
		sd		0.0761	0.0568	0.0506	0.0375
	50	mean		0.2065	0.2409	0.2262	0.2255
		min		0.1282	0.1406	0.1761	0.1660
		max		0.3148	0.3306	0.3125	0.3086
		sd		0.0525	0.0394	0.0373	0.0345
	70	mean		0.2261	0.2303	0.2351	0.2331
		min		0.0961	0.1387	0.1431	0.1941
		max		0.3440	0.3127	0.3380	0.2738
		sd		0.0512	0.0443	0.0360	0.0194
	100	mean		0.2241	0.2197	0.2266	0.2211[1]
		min		0.1249	0.1509	0.1717	0.1710
		max		0.3430	0.3102	0.2713	0.3032
		sd		0.0452	0.0379	0.0266	0.0232

1 = 98 replicates

Table A.2.57 The mean, minimum, maximum and standard deviation of REML heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD7.

Mean Number of Progeny Per Sire		Number of Sires				
		20	50	100	150	200
20	mean		0.2169	0.2221	0.2188	0.2308
	min		0.0433	0.1310	0.1436	0.1274
	max		0.5364	0.3338	0.3901	0.3179
	sd		0.0773	0.0572	0.0509	0.0376
50	mean		0.2119	0.2439	0.2282	0.2269
	min		0.1321	0.1427	0.1777	0.1672
	max		0.3222	0.3344	0.3149	0.3104
	sd		0.0534	0.0397	0.0375	0.0347
70	mean		0.2315	0.2330	0.2370	0.2345
	min		0.0991	0.1406	0.1444	0.1953
	max		0.3514	0.3161	0.3404	0.2753
	sd		0.0521	0.0447	0.0362	0.0194
100	mean		0.2291	0.2222	0.2283	0.2233
	min		0.1281	0.1527	0.1730	0.1720
	max		0.3501	0.3134	0.2733	0.3048
	sd		0.0460	0.0382	0.0267	0.0239

Table A.2.58 The mean, minimum, maximum and standard deviation of HM heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD7.

Mean Number of Progeny Per Sire		Number of Sires				
		20	50	100	150	200
20	mean		0.0792	0.0566	0.0458	0.0406
	min		0.0487	0.0456	0.0390	0.0316
	max		0.1295	0.0694	0.0612	0.0473
	sd		0.0129	0.0065	0.0047	0.0031
50	mean		0.0556	0.0431	0.0335	0.0288
	min		0.0414	0.0304	0.0284	0.0237
	max		0.0746	0.0537	0.0416	0.0358
	sd		0.0094	0.0048	0.0037	0.0029
70	mean		0.0547	0.0386	0.0319	0.0274
	min		0.0308	0.0268	0.0224	0.0241
	max		0.0742	0.0489	0.0424	0.0309
	sd		0.0091	0.0056	0.0037	0.0017
100	mean		0.0510	0.0351	0.0292	0.0248
	min		0.0327	0.0261	0.0234	0.0201
	max		0.0713	0.0461	0.0339	0.0319
	sd		0.0080	0.0047	0.0027	0.0021

Table A.2.59 The mean, minimum, maximum and standard deviation of ML heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.0782	0.0565	0.0460	0.0409
		min		0.0469	0.0453	0.0384	0.0319
		max		0.1269	0.0696	0.0620	0.0481
		sd		0.0129	0.0069	0.0050	0.0032
	50	mean		0.0541	0.0425	0.0333	0.0287
		min		0.0403	0.0301	0.0283	0.0236
		max		0.0725	0.0531	0.0416	0.0357
		sd		0.0091	0.0047	0.0037	0.0030
	70	mean		0.0532	0.0381	0.0316	0.0272
		min		0.0299	0.0267	0.0223	0.0238
		max		0.0730	0.0480	0.0416	0.0307
		sd		0.0089	0.0054	0.0036	0.0017
	100	mean		0.0496	0.0346	0.0289	0.0246[1]
		min		0.0319	0.0259	0.0233	0.0202
		max		0.0698	0.0455	0.0334	0.0316
		sd		0.0079	0.0047	0.0027	0.0020

1 = 98 replicates

Table A.2.60 The mean, minimum, maximum and standard deviation of REML heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.0798	0.0572	0.0464	0.0412
		min		0.0469	0.0459	0.0387	0.0313
		max		0.1285	0.0709	0.0619	0.0488
		sd		0.0134	0.0069	0.0049	0.0033
	50	mean		0.0555	0.0430	0.0336	0.0289
		min		0.0408	0.0306	0.0285	0.0238
		max		0.0747	0.0537	0.0421	0.0361
		sd		0.0093	0.0048	0.0037	0.0030
	70	mean		0.0546	0.0386	0.0319	0.0274
		min		0.0307	0.0271	0.0225	0.0240
		max		0.0751	0.0486	0.0419	0.0309
		sd		0.0091	0.0054	0.0036	0.0017
	100	mean		0.0510	0.0350	0.0292	0.0248
		min		0.0329	0.0263	0.0236	0.0203
		max		0.0717	0.0461	0.0337	0.0318
		sd		0.0081	0.0047	0.0027	0.0021

Table A.2.61 The mean, minimum, maximum and standard deviation of HM sire variance estimates from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.6375	0.6514	0.6397	0.6765
		min		0.1128	0.3472	0.4196	0.3605
		max		1.7636	1.0042	1.2008	0.9323
		sd		0.2541	0.1797	0.1577	0.1167
	50	mean		0.6185	0.7196	0.6695	0.6646
		min		0.3691	0.4096	0.4976	0.4823
		max		0.9887	1.0025	0.9252	0.9406
		sd		0.1641	0.1256	0.1173	0.1090
	70	mean	—	0.6862	0.6839	0.6970	0.6874
		min		0.2807	0.3928	0.4210	0.5634
		max		1.0680	0.9648	1.0210	0.8137
		sd		0.1713	0.1405	0.1123	0.0599
	100	mean		0.6741	0.6528	0.6664	0.6514
		min		0.3630	0.4364	0.4927	0.4923
		max		1.0308	0.9171	0.8163	0.9225
		sd		0.1347	0.1196	0.0834	0.0737

Table A.2.62 The mean, minimum, maximum and standard deviation of ML sire variance estimates from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.6162	0.6374	0.6291	0.6710
		min		0.1115	0.3417	0.3997	0.3680
		max		1.6569	0.9913	1.1881	0.9359
		sd		0.2435	0.1797	0.1566	0.1153
	50	mean		0.5984	0.7070	0.6634	0.6608
		min		0.3599	0.4046	0.4931	0.4790
		max		0.9663	0.9899	0.9287	0.9392
		sd		0.1595	0.1231	0.1165	0.1097
	70	mean		0.6671	0.6748	0.6891	0.6835
		min		0.2716	0.3891	0.4177	0.5574
		max		1.0259	0.9433	0.9970	0.8095
		sd		0.1664	0.1363	0.1091	0.0605
	100	mean		0.6576	0.6438	0.6618	0.6450[1]
		min		0.3551	0.4347	0.4915	0.4954
		max		1.0139	0.9077	0.8091	0.9156
		sd		0.1336	0.1181	0.0822	0.0712

1 = 98 replicates

Table A.2.63 The mean, minimum, maximum and standard deviation of REML sire variance estimates from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD7.

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.6405	0.6499	0.6373	0.6774
		min		0.1248	0.3507	0.4065	0.3727
		max		1.7022	1.0076	1.2000	0.9437
		sd		0.2488	0.1816	0.1576	0.1159
	50	mean		0.6151	0.7164	0.6694	0.6653
		min		0.3718	0.4110	0.4979	0.4826
		max		0.9908	1.0021	0.9364	0.9451
		sd		0.1627	0.1244	0.1172	0.1103
	70	mean		0.6840	0.6832	0.6948	0.6877
		min		0.2803	0.3946	0.4216	0.5610
		max		1.0501	0.9544	1.0047	0.8143
		sd		0.1698	0.1377	0.1098	0.0608
	100	mean		0.6733	0.6514	0.6670	0.6518
		min		0.3647	0.4403	0.4956	0.4984
		max		1.0368	0.9180	0.8153	0.9207
		sd		0.1363	0.1192	0.0828	0.0739

Table A.2.64 The mean, minimum, maximum and standard deviation of HM sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD7.

			Number of Sires				
			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		0.2462	0.1748	0.1409	0.1261
		min		0.1411	0.1253	0.1140	0.0949
		max		0.4831	0.2267	0.2095	0.1523
		sd		0.0543	0.0274	0.0191	0.0122
	50	mean		0.1702	0.1344	0.1038	0.0894
		min		0.1187	0.0900	0.0831	0.0707
		max		0.2480	0.1749	0.1334	0.1175
		sd		0.0334	0.0181	0.0137	0.0111
	70	mean		0.1712	0.1201	0.0993	0.0850
		min		0.0889	0.0781	0.0678	0.0721
		max		0.2494	0.1603	0.1367	0.0975
		sd		0.0351	0.0200	0.0130	0.0060
	100	mean		0.1589	0.1087	0.0901	0.0765
		min		0.0959	0.0781	0.0700	0.0608
		max		0.2304	0.1459	0.1077	0.1039
		sd		0.0270	0.0171	0.0097	0.0074

Table A.2.65 The mean, minimum, maximum and standard deviation of ML sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD7.

Mean Number of Progeny Per Sire			Number of Sires			
		20	50	100	150	200
20	mean		0.2384	0.1714	0.1389	0.1250
	min		0.1353	0.1233	0.1109	0.0949
	max		0.4508	0.2236	0.2062	0.1517
	sd		0.0516	0.0272	0.0188	0.0120
50	mean		0.1642	0.1316	0.1025	0.0885
	min		0.1158	0.0889	0.0819	0.0700
	max		0.2402	0.1715	0.1330	0.1166
	sd		0.0319	0.0175	0.0135	0.0111
70	mean		0.1653	0.1179	0.0979	0.0843
	min		0.0860	0.0768	0.0671	0.0714
	max		0.2366	0.1562	0.1330	0.0970
	sd		0.0336	0.0193	0.0126	0.0061
100	mean		0.1538	0.1068	0.0892	0.0756[1]
	min		0.0933	0.0775	0.0693	0.0608
	max		0.2245	0.1439	0.1063	0.1030
	sd		0.0265	0.0167	0.0095	0.0071

1 = 98 replicates

Table A.2.66 The mean, minimum, maximum and standard deviation of REML sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data type SD7.

Mean Number of Progeny Per Sire			Number of Sires			
		20	50	100	150	200
20	mean		0.2443	0.1739	0.1404	0.1259
	min		0.1355	0.1249	0.1113	0.0932
	max		0.4602	0.2286	0.2065	0.1540
	sd		0.0536	0.0276	0.0185	0.0123
50	mean		0.1688	0.1334	0.1035	0.0892
	min		0.1198	0.0906	0.0828	0.0709
	max		0.2476	0.1739	0.1346	0.1179
	sd		0.0328	0.0177	0.0137	0.0112
70	mean		0.1703	0.1197	0.0988	0.0849
	min		0.0885	0.0784	0.0677	0.0719
	max		0.2444	0.1582	0.1341	0.0976
	sd		0.0346	0.0194	0.0126	0.0062
100	mean		0.1585	0.1083	0.0901	0.0765
	min		0.0962	0.0786	0.0703	0.0610
	max		0.2315	0.1459	0.1074	0.1035
	sd		0.0274	0.0170	0.0096	0.0074

Table A.2.67 The mean, minimum, maximum and standard deviation of HM error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		11.0764	10.9989	10.9800	11.0505
		min		10.2017	10.1412	10.4589	10.4612
		max		11.9485	11.8649	11.5688	11.6721
		sd		0.4485	0.3835	0.2687	0.2640
	50	mean		10.9692	11.0141	11.0481	11.0449
		min		10.4029	10.5965	10.6833	10.6880
		max		11.8268	11.8157	11.5423	11.4155
		sd		0.3389	0.2272	0.2032	0.1728
	70	mean		11.0777	11.0275	11.0258	11.0402
		min		10.5386	10.6673	10.6802	10.8121
		max		11.6066	11.6666	11.4288	11.2935
		sd		0.2552	0.2018	0.1659	0.1112
	100	mean		11.0843	11.0554	11.0108	11.0200
		min		10.6283	10.6854	10.7388	10.7518
		max		11.9101	11.3579	11.2830	11.1900
		sd		0.2793	0.1726	0.1237	0.0934

Table A.2.68 The mean, minimum, maximum and standard deviation of ML error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny Per Sire	20	mean		11.0688	10.9981	10.9809	11.0492
		min		10.2119	10.1469	10.4662	10.4601
		max		11.9352	11.8587	11.5529	11.6712
		sd		0.4485	0.3841	0.2673	0.2612
	50	mean		10.9686	11.0138	11.0480	11.0449
		min		10.4030	10.5970	10.6831	10.6889
		max		11.8253	11.8140	11.5408	11.4164
		sd		0.3382	0.2273	0.2032	0.1730
	70	mean		11.0776	11.0275	11.0257	11.0402
		min		10.5392	10.6672	10.6803	10.8123
		max		11.6054	11.6661	11.4290	11.2940
		sd		0.2552	0.2017	0.1660	0.1112
	100	mean		11.0842	11.0554	11.0108	11.0187[1]
		min		10.6283	10.6859	10.7387	10.7519
		max		11.9095	11.3579	11.2831	11.1899
		sd		0.2791	0.1726	0.1238	0.0939

1 = 98 replicates

Table A.2.69 The mean, minimum, maximum and standard deviation of REML error variance estimates from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD7.

			Number of Sires				
Mean Number of Progeny Per Sire			20	50	100	150	200
	20	mean		11.0690	10.9981	10.9809	11.0492
		min		10.2116	10.1469	10.4662	10.4600
		max		11.9355	11.8588	11.5530	11.6711
		sd		0.4485	0.3840	0.2673	0.2612
	50	mean		10.9687	11.0138	11.0480	11.0449
		min		10.4030	10.5969	10.6831	10.6888
		max		11.8253	11.8140	11.5408	11.4164
		sd		0.3382	0.2273	0.2032	0.1730
	70	mean		11.0776	11.0275	11.0258	11.0402
		min		10.5391	10.6672	10.6803	10.8123
		max		11.6054	11.6661	11.4290	11.2940
		sd		0.2552	0.2017	0.1660	0.1112
	100	mean		11.0843	11.0554	11.0108	11.0200
		min		10.6284	10.6858	10.7387	10.7519
		max		11.9095	11.3579	11.2831	11.1899
		sd		0.2791	0.1726	0.1238	0.0934

Table A.2.70 The mean, minimum, maximum and standard deviation of HM error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD7.

			Number of Sires				
Mean Number of Progeny Per Sire			20	50	100	150	200
	20	mean		0.5082	0.3568	0.2909	0.2535
		min		0.4681	0.3291	0.2771	0.2400
		max		0.5483	0.3850	0.3064	0.2678
		sd		0.0206	0.0124	0.0071	0.0060
	50	mean		0.3134	0.2225	0.1823	0.1578
		min		0.2972	0.2140	0.1764	0.1526
		max		0.3379	0.2387	0.1905	0.1631
		sd		0.0097	0.0046	0.0033	0.0025
	70	mean		0.2667	0.1877	0.1533	0.1329
		min		0.2538	0.1817	0.1483	0.1300
		max		0.2795	0.1987	0.1587	0.1360
		sd		0.0061	0.0034	0.0023	0.0013
	100	mean		0.2228	0.1571	0.1278	0.1108
		min		0.2135	0.1520	0.1245	0.1082
		max		0.2394	0.1616	0.1308	0.1122
		sd		0.0056	0.0025	0.0014	0.0009

Table A.2.71 The mean, minimum, maximum and standard deviation of ML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD7.

Mean Number of Progeny Per Sire		Number of Sires: 20	50	100	150	200
20	mean		0.5074	0.3565	0.2906	0.2533
	min		0.4682	0.3289	0.2771	0.2398
	max		0.5473	0.3844	0.3058	0.2676
	sd		0.0206	0.0125	0.0071	0.0060
50	mean		0.3134	0.2225	0.1823	0.1578
	min		0.2972	0.2140	0.1764	0.1526
	max		0.3378	0.2387	0.1903	0.1631
	sd		0.0096	0.0046	0.0033	0.0025
70	mean		0.2667	0.1877	0.1533	0.1329
	min		0.2538	0.1817	0.1483	0.1300
	max		0.2795	0.1985	0.1587	0.1360
	sd		0.0061	0.0034	0.0023	0.0013
100	mean		0.2228	0.1571	0.1278	0.1108[1]
	min		0.2135	0.1520	0.1245	0.1082
	max		0.2394	0.1616	0.1308	0.1122
	sd		0.0056	0.0025	0.0014	0.0009

1 = 98 replicates

Table A.2.72 The mean, minimum, maximum and standard deviation of REML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data type SD7.

Mean Number of Progeny Per Sire		Number of Sires: 20	50	100	150	200
20	mean		0.5073	0.3565	0.2906	0.2533
	min		0.4686	0.3291	0.2771	0.2398
	max		0.5469	0.3843	0.3055	0.2676
	sd		0.0206	0.0125	0.0070	0.0060
50	mean		0.3134	0.2225	0.1822	0.1578
	min		0.2972	0.2141	0.1762	0.1527
	max		0.3378	0.2386	0.1903	0.1631
	sd		0.0096	0.0046	0.0034	0.0025
70	mean		0.2667	0.1877	0.1533	0.1329
	min		0.2538	0.1816	0.1485	0.1302
	max		0.2794	0.1986	0.1589	0.1360
	sd		0.0061	0.0034	0.0023	0.0013
100	mean		0.2228	0.1571	0.1278	0.1108
	min		0.2136	0.1519	0.1246	0.1081
	max		0.2394	0.1614	0.1309	0.1125
	sd		0.0056	0.0025	0.0014	0.0009

Table A.2.73 The mean, minimum, maximum and standard deviation of HM, ML and REML heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for data types SD14, SD25 and SD29.

		HM	ML	REML
SD14	mean	0.2302	0.2270	0.2295
	min	0.1738	0.1704	0.1724
	max	0.3034	0.3016	0.3047
	sd	0.0351	0.0335	0.0338
SD25	mean	0.2221	0.2187	0.2213
	min	0.1269	0.1267	0.1284
	max	0.3033	0.2958	0.2990
	sd	0.0424	0.0407	0.0411
SD29	mean	0.2457	0.2402	0.2429
	min	0.1763	0.1751	0.1772
	max	0.3155	0.3072	0.3104
	sd	0.0394	0.0364	0.0368

Table A.2.74 The mean, minimum, maximum and standard deviation of HM, ML and REML heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for data types SD14, SD25 and SD29.

		HM	ML	REML
SD14	mean	0.0360	0.0355	0.0360
	min	0.0290	0.0285	0.0288
	max	0.0449	0.0446	0.0452
	sd	0.0043	0.0041	0.0041
SD25	mean	0.0350	0.0347	0.0351
	min	0.0229	0.0230	0.0234
	max	0.0449	0.0441	0.0448
	sd	0.0053	0.0051	0.0051
SD29	mean	0.0379	0.0374	0.0379
	min	0.0293	0.0293	0.0298
	max	0.0464	0.0455	0.0462
	sd	0.0048	0.0045	0.0045

Table A.2.75 The mean, minimum, maximum and standard deviation of HM, ML and REML sire variance estimates from data sets, with a population sire variance of 0.6783 with 100 replicates, for data types SD14, SD25 and SD29.

		HM	ML	REML
SD14	mean	0.6752	0.6650	0.6729
	min	0.4976	0.4928	0.4990
	max	0.9157	0.9096	0.9199
	sd	0.1131	0.1077	0.1087
SD25	mean	0.6489	0.6385	0.6461
	min	0.3593	0.3587	0.3636
	max	0.9011	0.8770	0.8870
	sd	0.1299	0.1246	0.1258
SD29	mean	0.7221	0.7049	0.7132
	min	0.5169	0.5111	0.5175
	max	0.9309	0.8928	0.9030
	sd	0.1216	0.1126	0.1137

Table A.2.76 The mean, minimum, maximum and standard deviation of HM, ML and REML sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for data types SD14, SD25 and SD29.

		HM	ML	REML
SD14	mean	0.1125	0.1099	0.1115
	min	0.0866	0.0854	0.0868
	max	0.1473	0.1446	0.1469
	sd	0.0163	0.0153	0.0155
SD25	mean	0.1103	0.1067	0.1082
	min	0.0678	0.0671	0.0683
	max	0.1473	0.1404	0.1422
	sd	0.0190	0.0176	0.0178
SD29	mean	0.1218	0.1164	0.1179
	min	0.0917	0.0889	0.0900
	max	0.1523	0.1425	0.1449
	sd	0.0180	0.0160	0.0161

Table A.2.77 The mean, minimum, maximum and standard deviation of HM, ML and REML error variance estimates from data sets, with a population error variance of 11.0106 with 100 replicates, for data types SD14, SD25 and SD29.

		HM	ML	REML
SD14	mean	11.0313	11.0313	11.0313
	min	10.7366	10.7373	10.7373
	max	11.4039	11.4037	11.4037
	sd	0.1678	0.1677	0.1677
SD25	mean	11.0156	11.0155	11.0155
	min	10.6769	10.6771	10.6771
	max	11.3915	11.3914	11.3914
	sd	0.1687	0.1687	0.1687
SD29	mean	11.0198	11.0195	11.0196
	min	10.6865	10.6873	10.6873
	max	11.4044	11.4048	11.4048
	sd	0.1569	0.1570	0.1570

Table A.2.78 The mean, minimum, maximum and standard deviation of HM, ML and REML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for data types SD14, SD25 and SD29.

		HM	ML	REML
SD14	mean	0.1568	0.1568	0.1568
	min	0.1526	0.1526	0.1526
	max	0.1622	0.1622	0.1621
	sd	0.0024	0.0024	0.0024
SD25	mean	0.1566	0.1566	0.1566
	min	0.1517	0.1517	0.1518
	max	0.1619	0.1619	0.1619
	sd	0.0024	0.0024	0.0024
SD29	mean	0.1566	0.1566	0.1566
	min	0.1520	0.1520	0.1519
	max	0.1622	0.1622	0.1621
	sd	0.0022	0.0022	0.0022

Table A.2.79 The mean, minimum, maximum and standard deviation of HM, ML and REML heritability estimates from data sets, with a population heritability of 0.2321, each with 100 replicates, for flocks A, B, C, D, E and F.

		HM	ML	REML
A	mean	0.2365	0.2326	
	min	0.1721	0.1695	
	max	0.4007	0.3800	
	sd	0.0410	0.0397	
B	mean	0.2405	0.2301	0.2363
	min	0.1076	0.0988	0.1022
	max	0.3666	0.3723	0.3817
	sd	0.0599	0.0558	0.0570
C	mean	0.2294	0.2242	0.2275
	min	0.1267	0.1282	0.1305
	max	0.3484	0.3065	0.3105
	sd	0.0445	0.0384	0.0388
D	mean	0.2302	0.2231	0.2277
	min	0.1306	0.1362	0.1395
	max	0.4140	0.3127	0.3192
	sd	0.0527	0.0428	0.0434
E	mean	0.2432	0.2322	0.2369
	min	0.1058	0.0973	0.0997
	max	0.4047	0.3578	0.3642
	sd	0.0694	0.0615	0.0624
F	mean	0.2354	0.2329	0.2365
	min	0.1540	0.1474	0.1500
	max	0.3121	0.3011	0.3055
	sd	0.0425	0.0389	0.0393

Table A.2.80 The mean, minimum, maximum and standard deviation of HM, ML and REML heritability approximate standard errors from data sets, with a population heritability of 0.2321, each with 100 replicates, for flocks A, B, C, D, E, and F.

		HM	ML	REML
A	mean	0.0388	0.0389	
	min	0.0311	0.0313	
	max	0.0575	0.0558	
	sd	0.0048	0.0047	
B	mean	0.0583	0.0577	0.0593
	min	0.0328	0.0318	0.0323
	max	0.0811	0.0835	0.0875
	sd	0.0111	0.0106	0.0111
C	mean	0.0405	0.0417	0.0422
	min	0.0264	0.0279	0.0285
	max	0.0561	0.0530	0.0539
	sd	0.0060	0.0054	0.0055
D	mean	0.0467	0.0487	0.0499
	min	0.0304	0.0337	0.0345
	max	0.0747	0.0634	0.0680
	sd	0.0083	0.0072	0.0071
E	mean	0.0488	0.0500	0.0509
	min	0.0263	0.0264	0.0262
	max	0.0735	0.0703	0.0710
	sd	0.0110	0.0103	0.0102
F	mean	0.0409	0.0433	0.0442
	min	0.0297	0.0307	0.0311
	max	0.0510	0.0528	0.0547
	sd	0.0057	0.0056	0.0057

Table A.2.81 The mean, minimum, maximum and standard deviation of HM, ML and REML sire variance estimates from data sets, with a population sire variance of 0.6783 with 100 replicates, for flocks A, B, C, D, E, and F.

		HM	ML	REML
A	mean	0.6931	0.6804	
	min	0.5066	0.5019	
	max	1.2191	1.1493	
	sd	0.1287	0.1229	
B	mean	0.7062	0.6738	0.6934
	min	0.2980	0.2729	0.2825
	max	1.1247	1.1445	1.1764
	sd	0.1855	0.1732	0.1775
C	mean	0.6726	0.6562	0.6664
	min	0.3695	0.3740	0.3807
	max	1.0629	0.9241	0.9373
	sd	0.1383	0.1192	0.1207
D	mean	0.6760	0.6530	0.6673
	min	0.3805	0.3972	0.4066
	max	1.2700	0.9427	0.9609
	sd	0.1692	0.1348	0.1370
E	mean	0.7174	0.6821	0.6968
	min	0.3038	0.2788	0.2858
	max	1.2773	1.0940	1.1159
	sd	0.2210	0.1933	0.1966
F	mean	0.6914	0.6834	0.6944
	min	0.4302	0.4113	0.4188
	max	0.9564	0.9143	0.9281
	sd	0.1326	0.1199	0.1215

Table A.2.82 The mean, minimum, maximum and standard deviation of HM, ML and REML sire variance large sample standard errors from data sets, with a population sire variance of 0.6783, each with 100 replicates, for flocks A, B, C, D, E and F.

		HM	ML	REML
A	mean	0.1271	0.1201	
	min	0.0990	0.0959	
	max	0.2062	0.1852	
	sd	0.0194	0.0171	
B	mean	0.1944	0.1785	0.1844
	min	0.0975	0.0894	0.0912
	max	0.2939	0.2812	0.2962
	sd	0.0439	0.0380	0.0400
C	mean	0.1379	0.1288	0.1306
	min	0.0849	0.0837	0.0854
	max	0.2071	0.1720	0.1766
	sd	0.0244	0.0192	0.0197
D	mean	0.1674	0.1505	0.1544
	min	0.1025	0.1010	0.1018
	max	0.2988	0.2069	0.2171
	sd	0.0375	0.0261	0.0259
E	mean	0.1739	0.1557	0.1587
	min	0.0849	0.0775	0.0767
	max	0.2958	0.2354	0.2396
	sd	0.0479	0.0373	0.0374
F	mean	0.1415	0.1342	0.1373
	min	0.0943	0.0883	0.0919
	max	0.1895	0.1726	0.1762
	sd	0.0238	0.0198	0.0203

Table A.2.83 The mean, minimum, maximum and standard deviation of HM, ML and REML error variance estimates from data sets, with a population error variance of 11.0106 with 100 replicates, for flocks A, B, C, D, E and F.

		HM	ML	REML
A	mean	11.0094	11.0086	
	min	10.6562	10.6564	
	max	11.7367	11.7311	
	sd	0.2231	0.2222	
B	mean	10.9999	10.9989	10.9989
	min	10.4015	10.4012	10.4012
	max	11.6090	11.6102	11.6102
	sd	0.2653	0.2653	0.2653
C	mean	11.0334	11.0316	11.0316
	min	10.6078	10.6072	10.6072
	max	11.3712	11.3697	11.3697
	sd	0.1854	0.1852	0.1852
D	mean	11.0238	11.0233	11.0233
	min	10.6466	10.6468	10.6468
	max	11.8477	11.8416	11.8417
	sd	0.2539	0.2531	0.2532
E	mean	11.0133	11.0119	11.0120
	min	10.6081	10.6047	10.6048
	max	11.4380	11.4321	11.4320
	sd	0.1964	0.1958	0.1959
F	mean	11.0347	11.0350	11.0350
	min	10.6465	10.6452	10.6452
	max	11.6986	11.6999	11.6999
	sd	0.1922	0.1916	0.1916

Table A.2.84 The mean, minimum, maximum and standard deviation of HM, ML and REML error variance large sample standard errors from data sets, with a population error variance of 11.0106, each with 100 replicates, for flocks A, B, C, D, E and F.

		HM	ML	REML
A	mean	0.1920	0.1920	
	min	0.1857	0.1857	
	max	0.2047	0.2047	
	sd	0.0039	0.0039	
B	mean	0.2612	0.2612	0.2612
	min	0.2470	0.2470	0.2470
	max	0.2757	0.2757	0.2757
	sd	0.0063	0.0063	0.0063
C	mean	0.1897	0.1897	0.1896
	min	0.1825	0.1825	0.1824
	max	0.1954	0.1954	0.1955
	sd	0.0032	0.0032	0.0032
D	mean	0.2033	0.2032	0.2032
	min	0.1962	0.1962	0.1963
	max	0.2184	0.2184	0.2182
	sd	0.0047	0.0047	0.0046
E	mean	0.2046	0.2045	0.2045
	min	0.1970	0.1970	0.1969
	max	0.2124	0.2124	0.2123
	sd	0.0036	0.0036	0.0036
F	mean	0.1831	0.1830	0.1830
	min	0.1766	0.1766	0.1766
	max	0.1942	0.1942	0.1941
	sd	0.0032	0.0032	0.0032

Appendix 3. Data Summaries.

Table A.3.1 Differences between the mean of the heritabilities, estimated using HM, ML and REML, and the population value (0.2321) for data sets from data type SD0.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	0.022	−0.023	−0.006	−0.005	0.006
		ML	0.003	−0.031	−0.010	−0.007	0.004
		REML	0.023	−0.023	−0.006	−0.005	0.006
	50	HM	−0.020	−0.002	0.012	0.003	0.005
		ML	−0.034	−0.008	0.009	0.001	0.004
		REML	−0.020	−0.002	0.012	0.003	0.005
	70	HM	−0.012	−0.003	0.004	0.003	0.005
		ML	−0.025	−0.008	0.001	0.002	0.005
		REML	−0.012	−0.003	0.004	0.003	0.005
	100	HM	0.001	0.012	0.002	0.002	0.004
		ML	−0.012	0.007	0.000	0.000	0.009
		REML	0.001	0.012	0.002	0.002	0.004

Table A.3.2 Differences between the mean of the heritabilities, estimated using HM, ML and REML, and the population value (0.2321) for data sets from data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	−0.008	−0.007	−0.005	0.000	−0.006
		ML	−0.027	−0.015	−0.009	−0.003	−0.008
		REML	−0.008	−0.008	−0.005	0.000	−0.006
	50	HM	−0.001	−0.012	−0.003	−0.008	0.000
		ML	−0.016	−0.018	−0.006	−0.010	−0.002
		REML	−0.001	−0.012	−0.003	−0.008	0.000
	70	HM	−0.017	−0.012	−0.006	0.001	−0.001
		ML	−0.030	−0.017	−0.009	−0.001	−0.002
		REML	−0.017	−0.012	−0.006	0.001	−0.001
	100	HM	−0.005	−0.003	−0.002	0.001	−0.005
		ML	−0.018	−0.008	−0.005	−0.001	−0.006
		REML	−0.006	−0.003	−0.002	0.001	−0.005

Table A.3.3 Differences between the mean of the heritabilities, estimated using HM, ML and REML, and the population value (0.2321) for data sets from data type SD5.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	0.030	−0.014	−0.006	0.002	−0.011
	ML	0.008	−0.022	−0.010	−0.001	−0.013
	REML	0.029	−0.015	−0.006	0.002	−0.011
50	HM	−0.017	−0.005	−0.001	0.009	−0.009
	ML	−0.031	−0.010	−0.005	0.007	−0.010
	REML	−0.017	−0.004	−0.002	0.009	−0.009
70	HM	−0.026	−0.011	−0.006	0.000	−0.006
	ML	−0.039	−0.017	−0.008	−0.002	−0.007
	REML	−0.027	−0.012	−0.006	0.000	−0.006
100	HM	−0.008	−0.005	0.007	−0.008	−0.001
	ML	−0.021	−0.010	0.004	−0.010	−0.003
	REML	−0.009	−0.005	0.007	−0.008	−0.001

Table A.3.4 Differences between the mean of the heritabilities, estimated using HM, ML and REML, and the population value (0.2321) for data sets from data type SD7.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM		−0.016	−0.010	−0.012	−0.002
	ML		−0.023	−0.014	−0.016	−0.003
	REML		−0.015	−0.010	−0.013	−0.001
50	HM		−0.019	0.013	−0.004	−0.005
	ML		−0.026	0.009	−0.006	−0.007
	REML		−0.020	0.012	−0.004	−0.005
70	HM		0.000	0.001	0.006	0.002
	ML		−0.006	−0.002	0.003	0.001
	REML		−0.001	0.001	0.005	0.002
100	HM		−0.003	−0.009	−0.004	−0.009
	ML		−0.008	−0.012	−0.005	−0.011
	REML		−0.003	−0.010	−0.004	−0.009

Table A.3.5 Differences between the mean of the heritability standard error, estimated using HM, ML and REML, and the standard deviation of the heritability estimates for data sets from data type SD0.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	0.005	0.009	0.004	0.004	−0.007
		ML	0.004	0.008	0.003	0.004	−0.007
		REML	0.006	0.009	0.004	0.004	−0.007
	50	HM	0.011	−0.004	−0.003	−0.005	−0.002
		ML	0.008	−0.005	−0.003	−0.005	−0.002
		REML	0.011	−0.004	−0.003	−0.005	−0.002
	70	HM	0.003	0.005	−0.005	−0.003	−0.005
		ML	0.001	0.004	−0.005	−0.003	−0.005
		REML	0.003	0.005	−0.005	−0.003	−0.005
	100	HM	0.004	0.010	0.003	0.001	−0.003
		ML	0.002	0.009	0.002	0.001	0.000
		REML	0.004	0.010	0.003	0.001	−0.003

Table A.3.6 Differences between the mean of the heritability standard error, estimated using HM, ML and REML, and the standard deviation of the heritability estimates for data sets from data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	0.000	−0.019	0.002	−0.006	0.003
		ML	−0.001	−0.019	0.002	−0.006	0.003
		REML	0.010	−0.019	0.003	−0.006	0.003
	50	HM	−0.005	−0.006	0.002	−0.002	0.003
		ML	−0.007	−0.006	0.002	−0.002	0.003
		REML	−0.005	−0.006	0.002	−0.002	0.003
	70	HM	0.003	0.001	0.000	0.002	0.001
		ML	0.002	0.001	0.000	0.002	0.001
		REML	0.004	0.001	0.000	0.002	0.001
	100	HM	−0.007	0.001	0.004	−0.002	0.001
		ML	−0.008	0.001	0.004	−0.002	0.001
		REML	−0.006	0.001	0.004	−0.002	0.001

Table A.3.7 Differences between the mean of the heritability standard error, estimated using HM, ML and REML, and the standard deviation of the heritability estimates for data sets from data type SD5.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	−0.009	0.000	−0.005	0.000	−0.002
		ML	−0.012	0.000	−0.005	0.000	−0.001
		REML	−0.003	0.001	−0.005	0.000	−0.001
	50	HM	0.006	−0.004	−0.008	−0.002	0.000
		ML	0.004	−0.004	−0.007	−0.001	0.000
		REML	0.006	−0.004	−0.007	−0.001	0.000
	70	HM	0.003	0.008	0.000	−0.002	−0.008
		ML	0.001	0.008	0.000	−0.002	−0.008
		REML	0.003	0.009	0.000	−0.002	−0.008
	100	HM	0.005	0.001	0.004	0.005	0.001
		ML	0.003	0.001	0.004	0.004	0.000
		REML	0.005	0.001	0.004	0.005	0.001

Table A.3.8 Differences between the mean of the heritability standard error, estimated using HM, ML and REML, and the standard deviation of the heritability estimates for data sets from data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM		0.000	0.000	−0.005	0.003
		ML		0.002	0.000	−0.005	0.003
		REML		0.002	0.000	−0.004	0.004
	50	HM		0.002	0.003	−0.004	−0.006
		ML		0.002	0.003	−0.004	−0.006
		REML		0.002	0.003	−0.004	−0.006
	70	HM		0.002	−0.007	−0.005	0.008
		ML		0.002	−0.006	−0.004	0.008
		REML		0.002	−0.006	−0.004	0.008
	100	HM		0.006	−0.003	0.002	0.001
		ML		0.004	−0.003	0.002	0.001
		REML		0.005	−0.003	0.002	0.001

Table A.3.9 Differences between the mean of the sire variances, estimated using HM, ML and REML, and the population value (0.6783) for data sets from data type SD0.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	0.049	−0.070	−0.021	−0.018	0.019
	ML	−0.012	−0.093	−0.033	−0.026	0.013
	REML	0.051	−0.070	−0.021	−0.018	0.019
50	HM	−0.060	−0.005	0.039	0.011	0.017
	ML	−0.102	−0.023	0.029	0.005	0.013
	REML	−0.060	−0.005	0.039	0.011	0.017
70	HM	−0.037	−0.005	0.011	0.015	0.018
	ML	−0.077	−0.022	0.003	0.010	0.016
	REML	−0.037	−0.005	0.011	0.015	0.018
100	HM	0.009	0.037	0.009	0.007	0.015
	ML	−0.031	0.021	0.001	0.001	0.027
	REML	0.009	0.037	0.009	0.007	0.015

Table A.3.10 Differences between the mean of the sire variances, estimated using HM, ML and REML, and the population value (0.6783) for data sets from data type SD2.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	−0.019	−0.020	−0.011	0.001	−0.020
	ML	−0.078	−0.045	−0.023	−0.007	−0.026
	REML	−0.018	−0.021	−0.011	0.001	−0.020
50	HM	0.002	−0.032	−0.011	−0.026	−0.002
	ML	−0.044	−0.050	−0.019	−0.032	−0.007
	REML	0.001	−0.032	−0.011	−0.026	−0.002
70	HM	−0.051	−0.031	−0.016	0.003	−0.002
	ML	−0.092	−0.048	−0.025	−0.003	−0.006
	REML	−0.053	−0.032	−0.017	0.002	−0.002
100	HM	−0.016	−0.006	−0.006	0.003	−0.015
	ML	−0.055	−0.022	−0.014	−0.003	−0.019
	REML	−0.017	−0.007	−0.006	0.003	−0.015

Table A.3.11 Differences between the mean of the sire variances, estimated using HM, ML and REML, and the population value (0.6783) for data sets from data type SD5.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	0.103	−0.039	−0.019	0.008	−0.033
	ML	0.033	−0.065	−0.031	−0.001	−0.039
	REML	0.100	−0.041	−0.018	0.007	−0.033
50	HM	−0.043	−0.018	0.000	0.030	−0.024
	ML	−0.087	−0.034	−0.011	0.021	−0.028
	REML	−0.044	−0.016	−0.002	0.028	−0.024
70	HM	−0.075	−0.035	−0.015	0.000	−0.016
	ML	−0.115	−0.053	−0.024	−0.005	−0.021
	REML	−0.077	−0.037	−0.016	0.001	−0.017
100	HM	−0.022	−0.012	0.022	−0.024	−0.003
	ML	−0.062	−0.028	0.014	−0.030	−0.007
	REML	−0.023	−0.013	0.022	−0.025	−0.003

Table A.3.12 Differences between the mean of the sire variances, estimated using HM, ML and REML, and the population value (0.6783) for data sets from data type SD7.

Number of Sires

Mean Number of Progeny per Sire			50	100	150	200
20	HM		−0.041	−0.027	−0.039	−0.002
	ML		−0.062	−0.041	−0.049	−0.007
	REML		−0.038	−0.028	−0.041	−0.001
50	HM		−0.060	0.041	−0.009	−0.014
	ML		−0.080	0.029	−0.015	−0.017
	REML		−0.063	0.038	−0.009	−0.013
70	HM		0.008	0.006	0.019	0.009
	ML		−0.011	−0.003	0.011	0.005
	REML		0.006	0.005	0.017	0.009
100	HM		−0.004	−0.026	−0.012	−0.027
	ML		−0.021	−0.035	−0.016	−0.033
	REML		−0.005	−0.027	−0.011	−0.026

Table A.3.13 Differences between the mean of the sire variance standard errors, estimated using HM, ML and REML, and the standard deviation of the sire variance estimates for data sets from data type SD0.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	0.031	0.029	0.014	0.016	−0.019
		ML	0.025	0.026	0.013	0.015	−0.020
		REML	0.032	0.029	0.014	0.016	−0.019
	50	HM	0.029	−0.010	−0.011	−0.016	−0.006
		ML	0.021	−0.012	−0.012	−0.016	−0.006
		REML	0.029	−0.010	−0.012	−0.016	−0.006
	70	HM	0.018	0.017	−0.016	−0.011	−0.017
		ML	0.010	0.015	−0.016	−0.012	−0.017
		REML	0.018	0.017	−0.016	−0.012	−0.017
	100	HM	0.006	0.026	0.007	0.006	−0.010
		ML	−0.000	0.024	0.006	0.006	−0.002
		REML	0.006	0.026	0.007	0.006	−0.010

Table A.3.14 Differences between the mean of the sire variance standard errors, estimated using HM, ML and REML, and the standard deviation of the sire variance estimates for data sets from data type SD2.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	0.006	−0.058	0.004	−0.017	0.008
		ML	0.001	−0.059	0.004	−0.017	0.007
		REML	0.034	−0.058	0.005	−0.017	0.007
	50	HM	−0.012	−0.018	0.008	−0.006	0.009
		ML	−0.018	−0.019	0.007	−0.006	0.009
		REML	−0.012	−0.018	0.007	−0.006	0.009
	70	HM	0.011	0.005	0.001	0.005	0.003
		ML	0.005	0.004	−0.000	0.005	0.003
		REML	0.012	0.005	0.000	0.005	0.003
	100	HM	−0.021	0.005	0.011	−0.004	0.002
		ML	−0.025	0.003	0.010	−0.004	0.002
		REML	−0.020	0.005	0.011	−0.004	0.002

Table A.3.15 Differences between the mean of the sire variance standard errors, estimated using HM, ML and REML, and the standard deviation of the sire variance estimates for data sets consisting from data type SD5.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM	−0.026	0.002	−0.018	−0.003	−0.008
		ML	−0.034	0.000	−0.019	−0.003	−0.007
		REML	−0.009	0.002	−0.019	−0.002	−0.007
	50	HM	0.016	−0.013	−0.024	−0.007	0.003
		ML	0.009	−0.015	−0.021	−0.006	0.002
		REML	0.016	−0.013	−0.021	−0.006	0.003
	70	HM	0.013	0.028	0.005	−0.003	−0.025
		ML	0.007	0.027	0.005	−0.004	−0.025
		REML	0.014	0.029	0.005	−0.004	−0.025
	100	HM	0.015	0.005	0.014	0.013	0.000
		ML	0.008	0.004	0.014	0.013	0.000
		REML	0.014	0.005	0.014	0.013	0.000

Table A.3.16 Differences between the mean of the sire variance standard errors, estimated using HM, ML and REML, and the standard deviation of the sire variance estimates for data from data type SD7.

Number of Sires

			20	50	100	150	200
Mean Number of Progeny per Sire	20	HM		−0.008	−0.005	−0.017	0.009
		ML		−0.005	−0.008	−0.018	0.010
		REML		−0.004	−0.008	−0.017	0.010
	50	HM		0.006	0.009	−0.014	−0.020
		ML		0.005	0.008	−0.014	−0.021
		REML		0.006	0.009	−0.014	−0.021
	70	HM		0.000	−0.020	−0.013	0.025
		ML		−0.001	−0.018	−0.011	0.024
		REML		0.000	−0.018	−0.011	0.024
	100	HM		0.024	−0.011	0.007	0.003
		ML		0.020	−0.011	0.007	0.004
		REML		0.022	−0.011	0.007	0.003

Table A.3.17 Differences between the mean of the error variances, estimated using HM, ML and REML, and the population value (11.0106) for data sets from data type SD0.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	−0.310	−0.010	−0.043	−0.055	−0.003
	ML	−0.313	−0.010	−0.043	−0.055	−0.003
	REML	−0.312	−0.010	−0.043	−0.055	−0.003
50	HM	−0.014	−0.014	0.013	0.034	0.010
	ML	−0.014	−0.014	0.013	0.034	0.010
	REML	−0.014	−0.014	0.013	0.034	0.010
70	HM	−0.043	0.035	−0.022	0.059	0.013
	ML	−0.043	0.035	−0.022	0.059	0.016
	REML	−0.043	0.035	−0.022	0.059	0.013
100	HM	0.010	−0.021	0.027	0.004	0.002
	ML	0.010	−0.021	0.027	0.004	−0.009
	REML	0.010	−0.021	0.027	0.004	0.002

Table A.3.18 Differences between the mean of the error variances, estimated using HM, ML and REML, and the population value (11.0106) for data sets from data type SD2.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	0.023	−0.058	0.025	−0.003	−0.024
	ML	0.020	−0.059	0.024	−0.004	−0.025
	REML	0.021	−0.059	0.024	−0.004	−0.025
50	HM	0.018	0.049	−0.009	−0.022	−0.014
	ML	0.018	0.049	−0.009	−0.022	−0.015
	REML	0.018	0.049	−0.009	−0.022	−0.014
70	HM	−0.043	0.067	0.010	0.000	−0.006
	ML	−0.043	0.067	0.010	0.000	−0.006
	REML	−0.043	0.067	0.010	0.000	−0.006
100	HM	−0.078	0.028	0.000	−0.008	−0.008
	ML	−0.078	0.028	0.000	−0.008	−0.008
	REML	−0.078	0.028	0.000	−0.008	−0.008

Table A.3.19 Differences between the mean of the error variances, estimated using HM, ML and REML, and the population value (11.0106) for data sets from data type SD5.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	−0.022	0.015	−0.026	0.018	−0.022
	ML	−0.025	0.012	−0.027	0.019	−0.023
	REML	−0.024	0.012	−0.027	0.019	−0.023
50	HM	0.074	−0.073	0.030	0.003	0.044
	ML	0.074	−0.073	0.030	0.002	0.044
	REML	0.074	−0.073	0.030	0.002	0.044
70	HM	0.071	−0.039	0.038	0.020	0.021
	ML	0.071	−0.039	0.038	0.020	0.021
	REML	0.071	−0.039	0.038	0.020	0.021
100	HM	−0.019	0.030	0.003	−0.001	0.007
	ML	−0.019	0.030	0.003	−0.001	0.007
	REML	−0.019	0.030	0.003	−0.001	0.007

Table A.3.20 Differences between the mean of the error variances, estimated using HM, ML and REML, and the population value (11.0106) for data sets from data type SD7.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM		0.066	−0.012	−0.031	0.040
	ML		0.058	−0.012	−0.030	0.039
	REML		0.058	−0.012	−0.030	0.039
50	HM		−0.041	0.003	0.037	0.034
	ML		−0.042	0.003	0.037	0.034
	REML		−0.042	0.003	0.037	0.034
70	HM		0.067	0.017	0.015	0.030
	ML		0.067	0.017	0.015	0.030
	REML		0.067	0.017	0.015	0.030
100	HM		0.074	0.045	0.000	0.009
	ML		0.074	0.045	0.000	0.008
	REML		0.074	0.045	0.000	0.009

Table A.3.21 Differences between the mean of the error variance standard errors, estimated using HM, ML and REML, and the standard deviation of the error variance estimates for data sets consisting from data type SD0.

			Number of Sires				
Mean Number of Progeny per Sire			20	50	100	150	200
	20	HM	−0.192	−0.014	0.009	−0.016	0.000
		ML	−0.191	−0.014	0.009	−0.016	0.000
		REML	−0.216	−0.014	0.009	−0.016	0.000
	50	HM	−0.038	0.009	−0.006	−0.015	−0.025
		ML	−0.038	0.009	−0.006	−0.015	−0.025
		REML	−0.038	0.009	−0.006	−0.015	−0.025
	70	HM	−0.040	−0.027	−0.007	−0.017	−0.001
		ML	−0.040	−0.027	−0.007	−0.017	−0.000
		REML	−0.040	−0.027	−0.007	−0.017	−0.001
	100	HM	−0.011	0.030	−0.018	0.010	0.018
		ML	−0.011	0.030	−0.018	0.010	0.018
		REML	−0.011	0.030	−0.018	0.010	0.018

Table A.3.22 Differences between the mean of the error variance standard errors, estimated using HM, ML and REML, and the standard deviation of the error variance estimates for data sets from data type SD2.

			Number of Sires				
Mean Number of Progeny per Sire			20	50	100	150	200
	20	HM	−0.031	0.024	−0.012	0.004	−0.003
		ML	−0.029	0.023	−0.012	0.004	−0.002
		REML	−0.020	0.023	−0.012	0.004	−0.002
	50	HM	−0.028	0.013	0.012	0.012	0.023
		ML	−0.028	0.013	0.012	0.012	0.023
		REML	−0.028	0.013	0.012	0.012	0.023
	70	HM	−0.023	0.019	0.005	0.029	0.003
		ML	−0.023	0.019	0.005	0.029	0.003
		REML	−0.023	0.019	0.005	0.029	0.003
	100	HM	−0.004	0.032	0.000	0.017	0.002
		ML	−0.004	0.032	0.000	0.017	0.002
		REML	−0.004	0.032	0.000	0.017	0.002

Table A.3.23 Differences between the mean of the error variance standard errors, estimated using HM, ML and REML, and the standard deviation of the error variance estimates for data sets from data type SD5.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM	0.009	−0.080	−0.002	0.022	0.002
	ML	0.010	−0.081	0.000	0.021	0.003
	REML	0.021	−0.081	0.000	0.021	0.003
50	HM	0.066	0.006	−0.008	−0.022	−0.015
	ML	0.066	0.006	−0.008	−0.022	−0.015
	REML	0.066	0.006	−0.008	−0.022	−0.015
70	HM	−0.013	0.012	−0.005	−0.015	0.015
	ML	−0.013	0.012	−0.005	−0.015	0.015
	REML	−0.013	0.012	−0.005	−0.015	0.015
100	HM	0.046	−0.003	−0.015	−0.006	0.022
	ML	0.046	−0.003	−0.015	−0.006	0.022
	REML	0.046	−0.003	−0.015	−0.006	0.022

Table A.3.24 Differences between the mean of the error variance standard errors, estimated using HM, ML and REML, and the standard deviation of the error variance estimates for data sets from data type SD7.

Number of Sires

Mean Number of Progeny per Sire		20	50	100	150	200
20	HM		0.060	−0.027	0.022	−0.011
	ML		0.059	−0.028	0.023	−0.008
	REML		0.059	−0.028	0.023	−0.008
50	HM		−0.026	−0.005	−0.021	−0.015
	ML		−0.025	−0.005	−0.021	−0.015
	REML		−0.025	−0.005	−0.021	−0.015
70	HM		0.012	−0.014	−0.013	0.022
	ML		0.012	−0.014	−0.013	0.022
	REML		0.012	−0.014	−0.013	0.022
100	HM		−0.056	−0.015	0.004	0.017
	ML		−0.056	−0.015	0.004	0.017
	REML		−0.056	−0.015	0.004	0.017

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