

Sampling Distributions of Heritability

P. Sandhya Kiran, V.K. Bhatia and A.R. Rao

Indian Agricultural Statistics Research Institute, New Delhi-110012

(Received : July, 2003)

SUMMARY

Heritability is one of the most important genetic parameter widely used in plant and animal breeding genetic improvement studies. Traditionally the estimates used most often are based on analysis of variance (ANOVA) techniques and there has been no information on the distributions of the estimates of heritability. This paper presents empirical distributions of the estimates of heritability obtained from half-sib and full-sib data using analysis of variance estimates of variance components.

Key words : Heritability, Sampling distributions, Half-sibs, Full-sibs.

1. Introduction

The components of variance derived from the relationships among relatives are used in estimating the important parameter heritability. Traditionally the estimates used most often are based on analysis of variance (ANOVA) technique and the estimate of heritability may assume negative values because of the occurrence of negative estimates of variance components, other than the error variance. Gill and Jensen [1] derived the probability of getting negative estimates of heritability under balanced situation and Singh [3] under unbalanced random model. Harville and Finech [2] obtained exact confidence interval for heritability. Singh [4] gave the density function of heritability in case of half-sibs. Though there are empirical studies on the sampling distribution of variance components there has been no information on the distribution of estimates of heritability. The present investigation is concerned with some properties of heritability estimates in half-sib and full-sib analysis in normal population.

2. Methodology

Consider the half-sib model

$$y_{ij} = \mu + s_i + e_{ij}, \quad i = 1, 2, \dots, s; \quad j = 1, 2, \dots, n$$

where

y_{ij} = the phenotypic performance of the progeny of the j -th dam mated to the i -th sire

μ = overall mean

s_i = the effect of i -th sire, and

e_{ij} = the residual effect

s_i and e_{ij} are random and independent variables with zero means and variances σ_s^2 and σ_e^2 respectively.

The narrow sense heritability from the above model is
$$\hat{h}^2 = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_e^2}$$

In case of full-sib analysis, the model is

$$y_{ijk} = \mu + s_i + d_{ij} + e_{ijk}, i = 1, 2, \dots, s; j = 1, 2, \dots, d; k = 1, 2, \dots, n$$

where

y_{ijk} = measurement on k -th offspring of j -th dam mated to i -th sire

μ = the general mean

s_i = the effect of i -th sire

d_{ij} = the effect of j -th dam mated to the i -th sire, and

e_{ij} = the random error effect

$$s_i \sim N(0, \sigma_s^2), d_{ij} \sim N(0, \sigma_d^2), e_{ijk} \sim N(0, \sigma_e^2)$$

The sire component of heritability is
$$h_s^2 = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_d^2 + \hat{\sigma}_e^2}$$
 and (sire + dam)

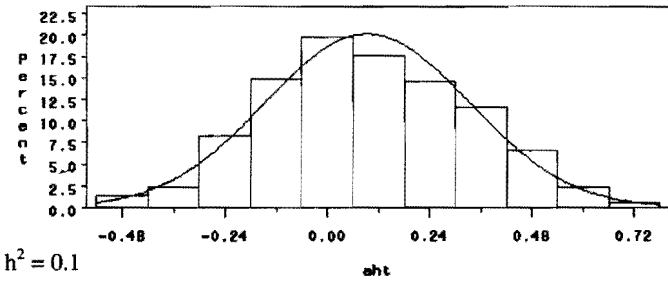
component of heritability is
$$h_{s+d}^2 = \frac{2(\hat{\sigma}_s^2 + \hat{\sigma}_d^2)}{\hat{\sigma}_s^2 + \hat{\sigma}_d^2 + \hat{\sigma}_e^2}$$

The purpose of this paper is to present the empirical results relating to the distribution of heritability estimates for normal population. Data were simulated by using the above half-sib and full-sib models. In case of half-sibs, sire values (s_i) were simulated as normal variates with mean zero and variances 0.02564, 0.0526, 0.1111, 0.1763 and 0.25, errors were simulated as normal variates with mean zero and variance 1 for heritabilities 0.1, 0.2, 0.4, 0.6 and 0.8 respectively. Four sires were taken each with 50 offspring. In case of full-sibs,

sire values (s_i) and dam values within sires (d_{ij}) were simulated as normal variates with mean zero and same variances 0.0215, 0.0555, 0.125, 0.2143 and 0.3333, errors were simulated as normal variates with mean zero and variance one for heritabilities 0.1, 0.2, 0.4, 0.6 and 0.8 respectively. Simulations were generated with number of sires as 20 and number of dams as 4 with 3 offsprings per mating. The sampling was repeated 500 times and for each of the simulated data sets ANOVA and subsequently estimates of heritability was obtained. Various goodness of fit tests were applied to examine statistical distribution of the 500 values of the estimates of heritability. Probability-probability plots, quantile plots and frequency distribution of the estimates were obtained, for different population heritability values, for better assessment and visualization of the sampling distribution. Also, to support the simulation results, estimates of variance components from real data of sample size 120 (12 sires with 10 offsprings per each sire) observations were considered from half-sib mating design and the same was used to study the empirical distribution of heritability estimates. This data was pertained to the breeding experiment on Holstein-Friesian x Haryana half breeds, conducted at the Cattle and Buffalo farm of the Indian Veterinary Research Institute, Izatnagar. The character under study was the milk yield of first lactation. Further, full-sib data related to the egg weight (in grams) of poultry birds of sample size 60 (5 sires, 4 dams per sire, 3 offsprings per sire-dam combination) was extracted from Narain *et al.* [3] to study the empirical distribution of sire-component of heritability estimates.

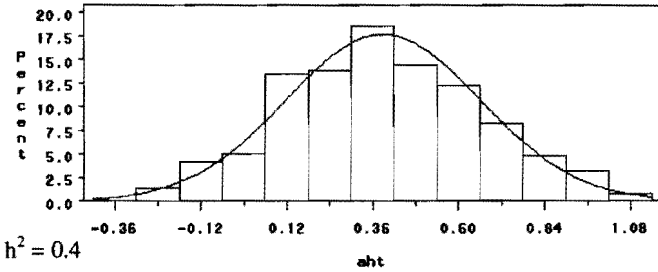
3. Results and Discussion

As per the methodology discussed above, samples were generated for both half-sib and full-sib family structures. These were further analyzed by the theory of ANOVA technique for obtaining estimates of heritability. The estimates so obtained were used to construct standard histograms. The standardized histograms with superimposed normal density curve for the estimates of heritability (from population heritability levels 0.1, 0.4 and 0.6) obtained from half-sib data are shown in Figure 1. From these histograms, it is visualized that normal curve might be a suitable approximation. Various goodness of fit tests for normal distribution indicated the normality of estimates in case of half-sib data. The histograms and goodness of fit tests of the estimates of (sire+dam) component of heritability (from population heritability levels 0.1, 0.4 and 0.6) in case of full-sibs were also obtained and are shown in Figure 2 whereas for sire component of heritability are shown in Figure 3. The estimates of (sire + dam) component exhibited normality whereas the estimates of sire component of heritability at lower parametric values ($h^2 = 0.1$ and 0.2) indicate the possible departure from normality. In the latter case, the histograms displayed that a gamma curve might be a suitable approximation. On examining the histograms with superimposed gamma curves and goodness of fit tests it was confirmed that



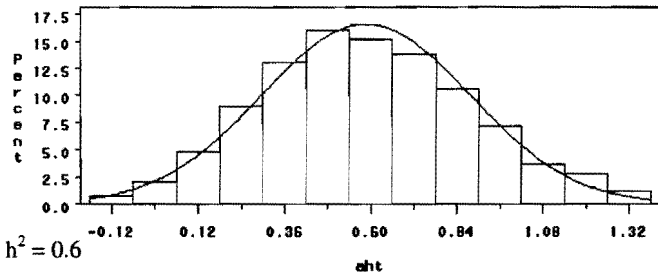
— Normal Curve			
Kolmogorov (D)	0.047534	Pr > D	< 0.0100
C-von M (W-Square)	0.15524	Pr > W-Square	0.0213
A-D (A-Square)	0.896339	Pr > A-Square	0.0227

Curve: — Normal(Mu=0.0934 Sigma=0.2377)



— Normal Curve			
Kolmogorov (D)	0.042968	Pr > D	0.0237
C-von M (W-Square)	0.080404	Pr > W-Square	0.2119
A-D (A-Square)	0.53747	Pr > A-Square	0.1750

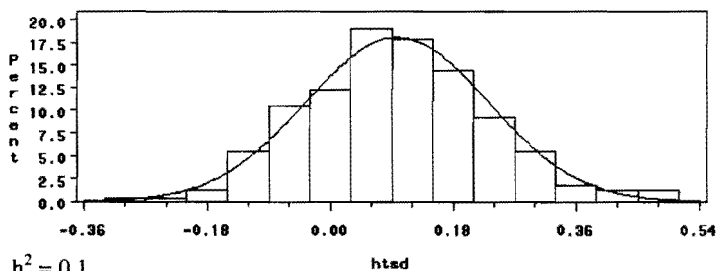
Curve: — Normal(Mu=0.389 Sigma=0.2717)



— Normal Curve			
Kolmogorov (D)	0.02859	Pr > D	> 0.1500
C-von M (W-Square)	0.046996	Pr > W-Square	> 0.2500
A-D (A-Square)	0.342809	Pr > A-Square	> 0.2500

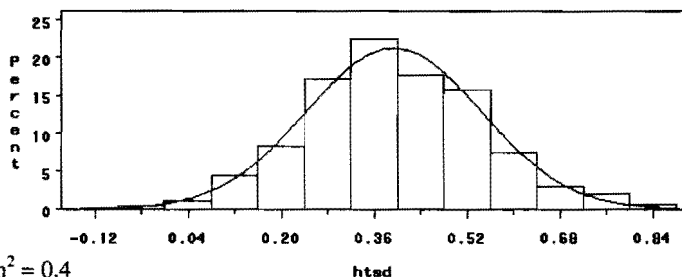
Curve: — Normal(Mu=0.586 Sigma=0.2887)

Figure 1. Empirical distributions of heritability estimates in the case of half-sib data



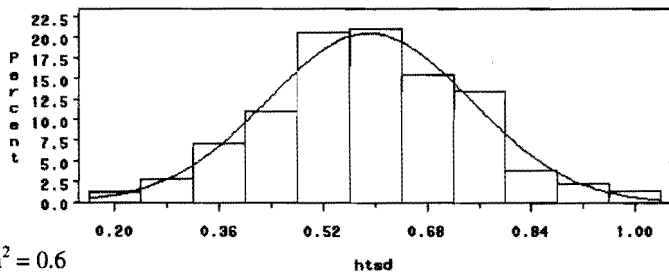
Normal Curve			
Kolmogorov (D)	0.026058	Pr > D	> 0.1500
C-von M (M-Square)	0.046648	Pr > M-Square	> 0.2500
A-D (A-Square)	0.394318	Pr > A-Square	> 0.2500

Curve: — Normal(Mu=0.0976 Sigma=0.1328)



Normal Curve			
Kolmogorov (D)	0.032884	Pr > D	> 0.1500
C-von M (M-Square)	0.065572	Pr > M-Square	> 0.2500
A-D (A-Square)	0.426867	Pr > A-Square	> 0.2500

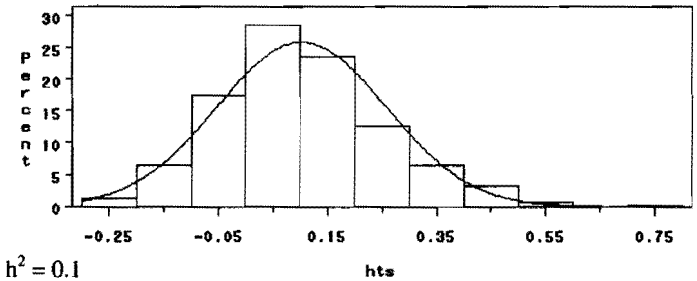
Curve: — Normal(Mu=0.3935 Sigma=0.1503)



Normal Curve			
Kolmogorov (D)	0.02971	Pr > D	> 0.1500
C-von M (M-Square)	0.048105	Pr > M-Square	> 0.2500
A-D (A-Square)	0.287745	Pr > A-Square	> 0.2500

Curve: — Normal(Mu=0.5904 Sigma=0.1556)

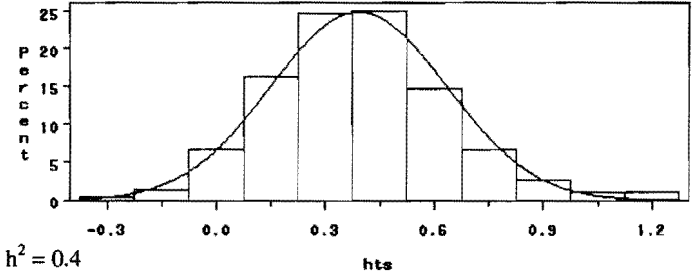
Figure 2. Empirical distributions of (sire+dam) component of heritability estimates in the case of full-sibs



$h^2 = 0.1$

— Normal Curve			
Kolmogorov (D)	0.044568	Pr > D	0.0170
C-von M (W-Square)	0.255028	Pr > W-Square	< 0.0050
A-D (A-Square)	1.518919	Pr > A-Square	< 0.0050

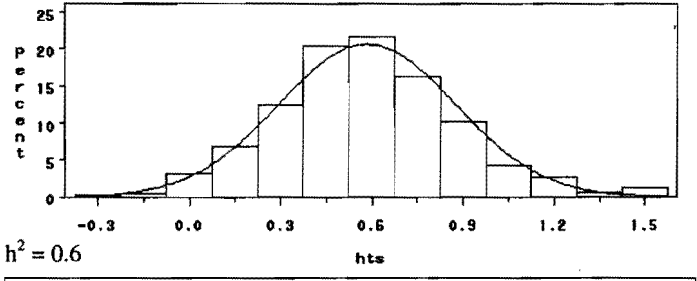
Curve: — Normal($\mu=0.1018$ $\sigma=0.1548$)



$h^2 = 0.4$

— Normal Curve			
Kolmogorov (D)	0.044083	Pr > D	0.0190
C-von M (W-Square)	0.158975	Pr > W-Square	0.0194
A-D (A-Square)	1.09696	Pr > A-Square	0.0074

Curve: — Normal($\mu=0.3921$ $\sigma=0.2409$)

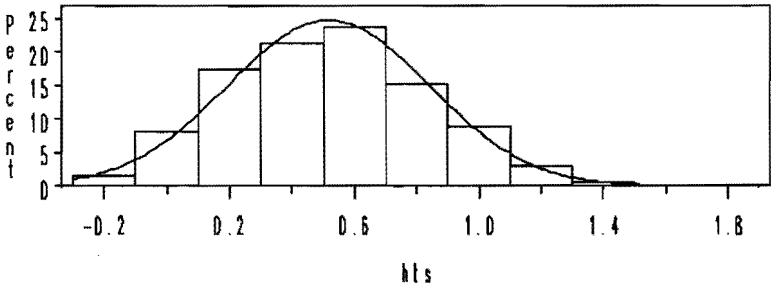


$h^2 = 0.6$

— Normal Curve			
Kolmogorov (D)	0.035317	Pr > D	0.1322
C-von M (W-Square)	0.099655	Pr > W-Square	0.1163
A-D (A-Square)	0.73483	Pr > A-Square	0.0566

Curve: — Normal($\mu=0.5838$ $\sigma=0.2904$)

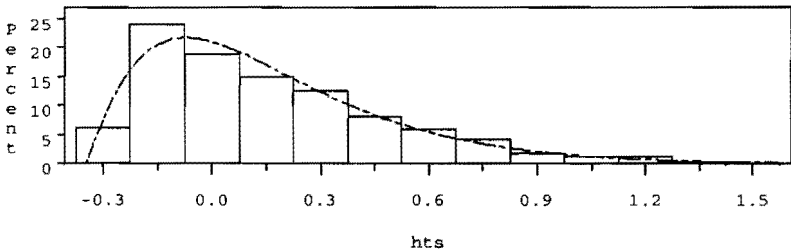
Figure 3. Empirical distributions of sire-component of heritability estimates in the case of full-sibs



— Normal Curve			
Kolmogorov (D)	0.02586	Pr > D	> 0.1500
C-von M (W-Square)	0.059145	Pr > W-Square	> 0.2500
A-D (A-Square)	0.511999	Pr > A-Square	0.2030
Chi-Square	20.87837	Pr > Chi-Square	0.0075

Curve: — Normal($\mu=0.517$ $\sigma=0.323$)

Figure 4. Empirical distribution of half-sib heritability estimates obtained from real data



--- Gamma Curve			
Kolmogorov (D)	0.030122	Pr > D	> 0.2500
C-von M (W-Square)	0.091928	Pr > W-Square	0.1143
A-D (A-Square)	0.536702	Pr > A-Square	0.1412
Chi-Square	10.9553	Pr > Chi-Square	0.3610

Curve: --- Gamma($\theta=-.35$ $\text{Shape}=2.16$ $\text{Scale}=0.24$)

Figure 5: Empirical distribution of sire component of heritability estimates obtained from real data on full-sibs

the estimates follow gamma distribution. It is interesting to observe that for higher population values of heritability, the sire-component estimates of heritability follows normal distribution. The half-sib heritability estimates, obtained from real data, were also observed to follow normal distribution, as per expectation from the simulation results. The histogram with superimposed normal curves along with goodness of fit statistics is given in Figure 4. Figure 5 indicates the empirical distribution of sire-component of heritability estimates obtained through simulation, using the variance component estimates of real data on full-sibs. In this case too, it was confirmed from different test statistics that the estimates follow gamma distribution, as the sample drawn was from a population with low heritability value.

Finally, from the above results, obtained under simulated samples as well as real data, it is concluded that for half-sib mating design, the estimates will always follow normal distribution irrespective of the population parametric values. This is not true for all the situations of full-sib mating design, particularly at low parametric values of heritability. Under sire component estimation of full-sib heritability, the form of distribution will be gamma.

ACKNOWLEDGEMENTS

The authors wish to thank the referee for useful and constructive suggestions in improving the quality and presentation of the paper. Further, authors are thankful to Director, IVRI, Izatnagar for providing the data for illustration purposes.

REFERENCES

- [1] Gill, J.L. and Jensen, E.L. (1968). Probability of obtaining negative estimates of heritability. *Biometrics*, **24**, 517-526.
- [2] Harville, D.A. and Finech, A.P. (1985). Confidence intervals for variance ratio or for heritability in an unbalanced mixed linear model. *Biometrics*, **41**, 137-152.
- [3] Narain, P., Bhatia, V.K., and Malhotra, P.K. (1979). Handbook of Statistical Genetics. IASRI Publication.
- [4] Singh, B. (1991). Probability of negative estimates of heritability in one-way unbalanced random model. *Jour. Ind. Soc. Agril. Stat.*, **43**, 74-80.
- [5] Singh, B. (1993). On the estimation of heritability from unbalanced data. *Biom. J.*, **35**, 823-831.