

Effect of Auxiliary Traits on Estimation of Heritability of Stayability

Amrit Kumar Paul and V.K. Bhatia

Indian Agricultural Statistics Research Institute, New Delhi-110 012

(Received : May, 2000)

SUMMARY

Stayability being a binary trait in animal breeding needs thorough genetic analysis. For a true measure of stayability this need to be adjusted for various production and reproductive traits. For estimation of heritability of stayability this adjusted herd life for production is converted to binary trait using threshold probability. The exhaustive methodology for threshold characters has been outlined by Falconer and Mackey [3]. The procedure of beta-binomial Paul and Bhatia [6] and Dempster-Lerner [2] methods have been used to estimate the heritability of stayability in unbalanced data sets. It is seen that even small adjustment on account of production has a great effect on estimates of heritability of stayability. The unbalancedness led to estimates with large standard error. Further relative root mean square errors are also obtained and found that precision as well as accuracy of estimates are affected by adjustment of production. The results of modified beta-binomial method of estimation show some what consistency whereas for other procedures, no specific trend is seen for adjustment of data for production.

Key words : Stayability, Heritability, Modified beta-binomial, Unbalancedness, Root mean square error.

1. Introduction

Binary traits in animal breeding are often important determinants of production efficiency and are indicators of underlying factors that are difficult or costly to measure. In the case of characters whose phenotype is expressed in all or none type, the classical usual methods do not directly apply. One such character in dairy cattle which is classified as threshold is the stayability of a cow in the herd. If the cow is retained then it is interpreted as if it is stayed in the herd, otherwise it is categorised as culled. There are different methods to estimate the heritability of threshold characters, however not all the methods are directly applicable for unbalanced data set. Further since the measure of stayability is influenced by production and reproduction traits. So there is a need to incorporate its effects on the estimation procedures of heritability of

stayability. For this point of view, an attempt has been made to study the comparative performance of the two modified Beta-binomial and Dempster-Lerner methods in the case of unbalanced data.

2. Data Model

The data structure for the stayability is that, in a given population the process is explained by a standardized Gaussian variable (Z) with mean zero and variance one. Whenever Z exceeds a certain threshold value, say Z' which is known, an outwardly observation character (δ) is expressed. This character is dichotomous on a binary scale, the character has a value of 1 for presence and 0 for absence.

In the beta-binomial model approach, following Magnussen and Kremer [5] three sets of beta parameters: one for phenotypic family probabilities, one for the family probabilities and one for the additive genetic probability are assumed for obtaining heritability estimates based on the model of a binary trait. The details of these procedures are discussed by Paul and Bhatia [6].

3. Adjustment of Stayability for Auxiliary Traits

As the character stayability is affected significantly by the auxiliary characters like production and other type characters, so for getting the true picture of the inheritance of stayability it is advisable to eliminate the effect of auxiliary character. For example, the dairy cattle herd life consists of survival and production trait, which governs by the equation

$$P_{HL} = m_Y P_Y + m_S P_S \quad (1)$$

where P_{HL} , P_Y , P_S are the phenotypic value of herd life, production and survival respectively. m_Y , m_S are standardized partial regression coefficients of P_{HL} on P_Y and P_S respectively.

A new phenotypic variable of herd life adjusted for production can easily be obtained as

$$\begin{aligned} P_{HL/Y} &= P_{HL} - r_{Y,HL} P_Y \\ &= m_S (P_S - r_P P_Y) \end{aligned} \quad (2)$$

Now treating $P_{HL/Y}$ as original variable, transforming this new variate to a binomial variate with the help of different points of truncation for given probability of success, estimate of heritability of herd life adjusted for production can easily be obtained. The estimation of heritability of adjusted character will now reflect the true picture of its inheritance whereas the original value of herd life (main trait) may be significantly influenced by auxiliary character (production).

4. Relative Root Mean Square Error

The comparison of different methods is done on the basis of some measure of its precision. As all the estimates are not unbiased so the estimate of variance may not give a clear picture. In order to account the magnitude of the bias as well as some measure of precision, a measure called relative root mean square error is defined as

$$\text{RMSE}\% = \frac{[E(\text{estimate} - \text{'true value'})^2]^{0.5}}{\text{'true value'}} \times 100 \quad (3)$$

The unequal number of observations i.e. the degree of unbalancedness is defined as $\Delta = N(n - \lambda)$, with all the symbols carry their usual meaning.

5. Estimates of the Heritability on Raw Data

The data is generated by Monte Carlo Simulation, for the following half sib model

$$Z_{ijk} = \mu + S_i + e_{ijk}$$

The true heritability or heritability on raw data is heritability which is computed using the original half sib simulated data without changing to a binary data or threshold character.

The individual narrow sense heritability is

$$\hat{h}_{(z)}^2 = \frac{4\hat{\sigma}_f^2(z)}{\hat{\sigma}_f^2(z) + \hat{\sigma}_e^2(z)} \quad (4)$$

the estimated components are derived from an analysis of variance (Henderson's Method III, Searle *et al.* [7]) applied to the above model.

True family mean heritability is

$$\hat{h}_{f(z)}^2 = \frac{\hat{\sigma}_f^2(z)}{\hat{\sigma}_f^2(z) + \hat{\sigma}_e^2(z) / n_{\text{herd}} \times n_{\text{offspring}}} \quad (5)$$

6. Results and Discussion

In order to compare the two methods of estimation of heritability of stayability, different data sets with varying degree of unbalancedness have been simulated on computer for different parameters of heritability.

Data on Z_{ijk} are generated according to the linear model $Z_{ijk} = \mu + S_i + e_{ijk}$ for a normally distributed observable variable Z with total variance of 1.0 in the series of half sib herd.

Family values (S_i) are simulated as a normal variate with mean zero and variance of 0.0125, 0.025, 0.0375, 0.05 and 0.0625. Errors i.e. environmental values (e_{ijk}) are simulated as a single Gaussian variable with mean zero and variance $1 - \sigma_f^2$. Five points of truncation or threshold levels (P) are used to convert intrinsic to binary data. The thresholds used are $P = 0.05, 0.10, 0.15, 0.20, 0.25$ which are the probabilities of observing the binary trait. Data are generated using different parameters of heritability of stayability ($h_S^2 = 0.05, 0.10, 0.15, 0.20, 0.25$). For the parametric value the samples are generated for 20 sires with number of daughters ranging from 5 to 24. The simulated data thus generated were subjected to different estimation procedures of heritability of stayability and results thus obtained are presented in Table 1. It is noticed from Table 1 that narrow sense beta binomial realized heritability ($h_{\text{rea}(b)}^2$) give nice results than any other estimates. Dempster-Lerner estimates are more or less equally efficient. But family mean heritability estimates are highly biased. One interesting point to notice is that due to unbalancedness the standard errors are considerably high.

Table 1. Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h_f^2) of herd life for various values of given h_S^2 (heritability of stayability) in case of unequal family size

Estimates	$h_S^2 = .05$	$h_S^2 = .10$	$h_S^2 = .15$	$h_S^2 = .20$	$h_S^2 = .25$
$h_{\frac{1}{2}}^2$	0.0502 (0.0354)	0.1001 (0.0525)	0.1503 (0.0702)	0.2001 (0.0848)	0.2450 (0.0598)
$h_{\text{rea}(b)}^2$	0.0465 (0.0671)	0.0987 (0.0879)	0.1521 (0.0879)	0.2092 (0.1344)	0.2675 (0.1600)
h_{DL}^2	0.0460 (0.0660)	0.0977 (0.0870)	0.1493 (0.0961)	0.2045 (0.1323)	0.2598 (0.1570)
$h_{f(Z)}^2$	0.4105 (0.2292)	0.6032 (0.1560)	0.7031 (0.1145)	0.7649 (0.0905)	0.8086 (0.0786)
$h_{f(\text{beta})}^2$	0.1546 (0.3098)	0.3310 (0.2490)	0.4465 (0.2085)	0.5306 (0.1786)	0.5539 (0.1554)
$h_{f(\Delta P/\text{beta})}^2$	0.1540 (0.3084)	0.3295 (0.2478)	0.4449 (0.2056)	0.5206 (0.2128)	0.5907 (0.1547)

In parentheses are the average standard deviation. Degree of unbalancedness = 35.0001

7. Adjustment for Production

Data for stayability using the parametric value h_Y^2 (heritability of production) = 0.25, m_Y (standardized regression coefficient of herd life on production) = 0.4, $r_{Y,HL}$ (phenotypic correlation of herd life and production) = 0.25. The idea about these parametric values have been taken from Dekkers [1] along with different heritabilities of stayability ($h_S^2 = 0.05, 0.10, 0.15, 0.20, 0.25$). The adjusted data thus obtained are further converted to binary scale. Results for adjusted stayability data are shown in Table 2. Improved results are seen in case of Dempster-Lerner and narrow sense beta-binomial heritability estimates. For other procedures results are heavily biased. It is interesting to notice that due to adjustment not only the estimates are very close to population parameters but errors are also reduced considerably and thus add to precision of the estimators.

Table 2. Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h_f^2) of herd life adjusted for production for various values of given h_S^2 (heritability of stayability) in case of unequal family size

Estimates	$h_S^2 = .05$	$h_S^2 = .10$	$h_S^2 = .15$	$h_S^2 = .20$	$h_S^2 = .25$
h_z^2	0.0503 (0.0334)	0.0977 (0.0484)	0.1457 (0.0615)	0.1937 (0.0751)	0.2420 (0.0884)
$h_{rea(b)}^2$	0.0524 (0.0679)	0.1027 (0.0872)	0.1536 (0.1050)	0.2079 (0.1278)	0.2628 (0.1503)
h_{DL}^2	0.0534 (0.0681)	0.1027 (0.0868)	0.1529 (0.1075)	0.2058 (0.1320)	0.2586 (0.1563)
$h_{f(z)}^2$	0.5113 (0.2951)	0.7056 (0.1451)	0.7912 (0.0929)	0.8393 (0.0676)	0.8702 (0.0528)
$h_{f(beta)}^2$	0.1866 (0.3015)	0.3488 (0.2449)	0.4550 (0.2041)	0.5338 (0.1745)	0.5926 (0.1541)
$h_{f(AP/beta)}^2$	0.1857 (0.3002)	0.3457 (0.2482)	0.4529 (0.2031)	0.5313 (0.1733)	0.5899 (0.1544)

In parentheses are the average standard deviation.

Degree of unbalancedness = 35.0001

8. Root Mean Square Error

For empirical comparison of different methods the average root mean square error has found to be very handy tool and is calculated for the different values of heritability co-efficient and over different threshold probabilities. The relative root mean square errors averaged over truncation probability for 20 sires with number of daughters ranging from 5 to 24 and from block size 5 are shown in Table 3 and the same averaged over different values of heritability of stayability are shown in Table 4. From Table 3 and Table 4 it is clearly seen that the relative root mean square errors for family mean heritability estimates are numerically significantly higher than any other heritability estimates. From Table 4 it is noticed that the relative root mean square error of family mean heritability of true data points has highest value. In case of adjustment no significant change in root mean square is noticed.

Table 3. Relative root mean square error (RMSE%) of selected estimates of heritability of herd life in case of unequal daughter

Estimate	$h_{ra(b)}^2$	h_{DL}^2	$h_{f(\beta)}^2$	$h_{f(\Delta P/\beta)}^2$	h_z^2	$h_{f(z)}^2$
$h_s^2 = 0.05$	134.80 (131.04)	132.23 (136.60)	670.15 (681.60)	666.94 (678.26)	70.97 (66.69)	854.35 (1055.29)
$h_s^2 = 0.10$	87.98 (86.01)	85.52 (86.95)	351.21 (359.70)	349.30 (310.00)	52.52 (47.59)	526.82 (622.23)
$h_s^2 = 0.15$	72.77 (70.07)	70.77 (71.69)	248.23 (250.65)	206.40 (249.15)	46.82 (41.09)	376.56 (431.90)
$h_s^2 = 0.20$	67.35 (64.05)	66.19 (64.87)	192.44 (191.86)	199.76 (190.56)	42.31 (37.68)	286.05 (321.44)
$h_s^2 = 0.25$	64.40 (60.39)	62.98 (62.63)	154.31 (150.89)	152.61 (150.89)	39.91 (35.52)	224.41 (248.96)

In parentheses are the corresponding root mean square error in the adjusted case.

The relative root mean square errors are found to have inverse relationship with the values of heritability of stayability and the truncation points. The results of true value and beta binomial procedure of estimation show some what consistency whereas for the other procedures no specific trend is seen for adjustment of data on account of production characteristics.

Table 4. Relative root mean square error (RMSE%) of the estimate of herd life in case of unequal daughters

Estimate	$h_{\text{rea}(b)}^2$	h_{DL}^2	$h_{f(\text{beta})}^2$	$h_{f(\Delta P/\text{beta})}^2$
$\bar{p} = 0.05$	118.39 (117.76)	117.73 (125.39)	349.63 (353.46)	348.02 (350.78)
$\bar{p} = 0.10$	91.17 (87.81)	89.43 (91.20)	334.31 (346.21)	332.54 (342.53)
$h_s^2 = 0.15$	72.45 (76.22)	77.36 (75.92)	329.80 (335.36)	328.06 (336.13)
$\bar{p} = 0.20$	71.39 (69.55)	68.19 (67.92)	301.69 (304.36)	299.06 (302.46)
$\bar{p} = 0.25$	67.62 (65.01)	64.99 (62.31)	300.35 (299.29)	298.47 (296.97)

In parentheses are the corresponding root mean square error in the adjusted case.

From these results, it is finally concluded that if one has an access to the assigned data of stayability then estimation of heritability based on this assigned data will yield very efficient and precise estimates and if one has only binary data of stayability then beta-binomial estimates are proved to be very accurate and precise in comparison to other methods of estimation. The unbalancedness however may sometimes lead to estimates with large standard errors.

REFERENCES

- [1] Dekkers Jack, C.M. (1993). Theoretical basis for genetic parameter of herd life and effects on response to selection. *J. Dairy Sci.*, **76**, 1433-1443.
- [2] Dempster, E.R. and Lerner, I.M. (1950). Heritability of threshold characters. *Genet.*, **35**, 212-236.
- [3] Falconer, D.S. and Mackey, T.F.S. (1991). *Introduction to Quantitative Genetics*. 4th edn., Longman, New York.
- [4] Gianola, D. (1979). Heritability of polychotomous characters. *Genet.*, **93**, 1051-1055.
- [5] Magnussen, S. and Kremer, A. (1995). The beta-binomial model for estimating heritability of binary traits. *Theor. Appl. Genet.*, **91**, 544-552.
- [6] Paul, Amrit Kumar and Bhatia, V.K. (2001). Modification of beta-binomial method of estimation of heritability of stayability. *Jour. Ind. Soc. Agril. Stat.*, **54**, 385-395.
- [7] Searle, S.R., Casella, G. and McCullach, C.E. (1992). *Variance Components*. John Wiley and Sons, New York.