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Empirical comparison of different estimate of heritability of herd life using related auxiliary traits in case of non-normal situations

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ABSTRACT

Survivability of a dairy animal is an important character in dairy cattle breeding which is influenced by production and auxiliary traits. After adjusting by production the true estimate of heritability of herd life (stayability) was obtained by different authors. Here production, i.e. auxiliary trait has significant effect on the estimates and their standard errors. There is more scope of obtaining true estimate by adjusting for production as well as other related auxiliary traits. The methods were studied for normal, lognormal and gamma distributions. Empirical comparisons are done among the estimates of different procedures and among the above said distributions.

Key words: Auxiliary traits, Beta-binomial, Heritability, Relative root mean square error, Unbalancedness

Herd life is an important character in animal breeding, both from economic point of view and making room for heifer replacement. The improvements in estimation of heritability of stayability or herd life can be brought about by using information on secondary traits in case of normal situation Paul and Bhatia (2002 a, b).

Magnussen and Kremer (1995) suggested the beta-binomial estimate of heritability of all or none trait. Paul and Bhatia (2003) studied the effect of production on the estimate of heritability of stayability. In the study, an attempt has been made to observe the effect of more than one related auxiliary traits using beta-binomial method and Dempster-Lerner method for normal, lognormal and gamma distributions.

MATERIALS AND METHODS

The data structure for the stayability is that in a given population the process is explained by a standardized Gaussion variable (Z) with mean zero and variance one. Whenever the Z exceeds certain threshold value, say Z' which is known, the observation character (δ) is expressed. This character is dichotomous on a binary scale, has a value of 1 for presence and 0 for absence. The linear model used for the observable variable (Z) and transformation of the intrinsic variable (Z) to a binary trait (δ) was used as discussed by Paul and Bhatia (2002b).

In beta-binomial model approach, following Magnussen and Kremer (1995) 3 sets of beta parameters: one for phenotypic family probabilities, one for the family probabilities and finally one of the additive genetic probability, are assumed for obtaining the heritability estimates based on the model of a binary traits. Paul and Bhatia (2002a) discussed the details of these procedures.

Simulation

Data on half sibs using related auxiliary characters are simulated following the procedure Paul and Bhatia (2003). Following Paul and Bhatia (2000, 2003) adjustment of herd life for related auxiliary traits are processed.

Simulation for non-normal situation: to observe the effect of non normality in different method of estimation we consider here two cases – (i) log normal distribution, and (ii) gamma distribution.

For this purpose all the methods of estimation are same as in normal distribution. Only difference is that we have to generate data following the above defined distributions. The algorithms for generation of data set following different non-normal distribution are given as follows:

Log normal distribution: (a) Generate Y normally distributed with mean μ and variance σ^2. (b) Output $X = e^Y$.

Gamma distribution – (a) Generate uniform variate over (0,1).

(b) Set Set $X = \frac{1}{a} \log U_i$ where U_i's uniform variates are

(c) Output $Y = \sum_{i=1}^{k} X_i$ is a gamma variate with parameters a and k.

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It is the case when k is an integer. But when k is not an integer then the following algorithm we have to follow.

(a) Set $m=[k]$ and $q=k-m$,

(b) Generate m uniform variate over (0, 1) and

set $Z=-\log\left(\prod_{i=1}^{m} U_i\right)$ where U_i's are uniform variate.

(c) Generate a beta variate say W with parameter q and (1–q).

(d) Generate another uniform variate U over (0, 1) and set Y= log U.

(e) Return $X=(Z+WY)/a$ is a gamma variate with parameter a and k.

Estimates of the heritability on data not transformed to binary

The individual narrow sense heritabilities and family mean heritabilities were calculated according to Paul and Bhatia (2002a).

The true heritability or heritability on raw data is heritability, which is computed using the original half sib simulated data (Z_{ij}) without changing to a binary data or threshold character.

The individual narrow sense heritability

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

the estimated components are derived from an analysis of variance (Pal and Bhatia 2000b) applied to the above model.

True family mean heritability is

$$\hat{h}^2_{(z)} = \frac{\hat{\sigma}^2_f(Z)}{\hat{\sigma}^2_f(Z)+\dfrac{\hat{\sigma}^2_e(Z)}{\text{observation}}}$$

RESULTS AND DISCUSSION

To get the true picture of the inheritance of the stayability measure in terms of herd life, both raw data, i.e. without transforming to binary data and data adjusted for different traits are used. For the comparison purpose, the different methods discussed above are used. For carrying out the comparative studies extending for different values of heritabilities of various traits, the analyses are subjected to Monte Carlo simulation techniques. This is especially done so as to study the performance of various methods under different parametric values, which is not possible for the given set of real data.

Family values (S_i) are simulated as a normal variate with mean zero and variance of 0.0152 and 0.0695. Errors, i.e. environmental values (e_{ijk}) are simulated as a single Gaussian variable with mean of zero and variance of $1-\sigma^2_f$.

To compare empirically performance of modified beta-binomial approach and other methods, the estimates of narrow sense heritability and family mean heritability are calculated as per Paul and Bhatia (2002a). The relative root mean square error (RMSE) and degree of unbalancedness of different estimates is also obtained to compare the procedures among themselves following Paul and Bhatia (2002b). All the comparisons are done by considering 2 unbalanced situation having different degree unbalancedness of which one having 0.0 (zero) unbalancedness.

For all the comparisons, we have taken the no. of sire 5 having 2 different combinations of offspring which is shown in the tabular form below.

Cases	Observations on offsprings					Unbalancedness
I	20	20	20	20	20	0.0000
II	16	23	19	22	20	7.5001

From these 2 different combinations we can also compare the effect of unbalanceness on different estimates.

Though there are numerous combinations of the parametric values of different parameters but using the past experience of different studies the prior information about the parameters have been taken into consideration and selected parametric values accounted for the present study. The input parameter combinations were taken from Dekkers (1993) and Paul and Bhatia (2002a, 2003).

Unadjusted for two characters (related)

For these situation 2 characters, i.e. production and other related character say, udder depth are considered. Data are simulated on the basis of some prior knowledge about the parametric value of h^2_x (heritability of other related character say, udder depth) = 0.26, $r_{X,HI}$ (phenotypic correlation between herd life and other related character say, udder depth) = 0.15, r_{a1} (genetic correlation between production and other related character say, udder depth) = –0.40, r_{a2} (genetic correlation between herd life and stayability) = 0.20, r_{a3} (genetic correlation between production and stayability) = –0.20, m_x (standardized partial regression coefficient of herd life on other related character say, udder depth) = 0.20. For 2 character case we are considering r_{pl} (phenotypic correlation between production and other related character say, udder depth)= 0.35.

Taking averages over the threshold probabilities all the estimates are tabulated in Table 1 and 2. Individual narrow sense heritability using raw data (h^2_z) (without transformed with the help of threshold probability) provides best estimate than the beta-binomial estimate ($h^2_{(real)b}$) and Dempster-Lerner (h^2_{DL}) estimate. When we make comparison among beta-binomial ($h^2_{(real)b}$) and Dempster-Lerner (h^2_{DL}) estimate we can observe that Dempster-Lerner (h^2_{DL}) estimate provides better estimate but standard error and RMSE value in Dempster-Lerner estimate is more in some situations. In family mean heritability the beta-binomial estimate ($h^2_{f(beta)}$) and realized heritability ($h^2_{f(\Delta P/beta)b}$) estimate provide similar

Table 1. Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h^2_f) of herd-life for various values of h^2_s (heritability for stayability) for normal, lognormal (Lnormal) and gamma distribution in balanced situation

	Unadjusted						Adjusted for production						Adjusted for production and udder depth					
Distribution	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma
Estimates	0.06	0.06	0.06	0.26	0.26	0.26	0.06	0.06	0.06	0.26	0.26	0.26	0.06	0.06	0.06	0.26	0.26	0.26
h^2_i	0.07	0.08	0.09	0.26	0.29	0.32	0.08	0.09	0.10	0.25	0.30	0.33	0.06	0.06	0.07	0.24	0.26	0.29
	0.08	**0.10**	**0.12**	**0.11**	**0.13**	**0.17**	**0.06**	**0.08**	**0.09**	**0.13**	**0.16**	**0.19**	**0.06**	**0.07**	**0.09**	**0.12**	**0.15**	**0.19**
	114.69	262.12	453.09	80.44	183.85	317.78	103.79	237.21	410.03	66.90	152.89	264.28	86.78	198.32	342.81	68.22	155.92	269.51
$h^2_{(real)b}$	0.08	0.07	0.08	0.28	0.27	0.31	0.09	0.08	0.10	0.27	0.28	0.32	0.06	0.06	0.07	0.25	0.24	0.28
	0.09	**0.11**	**0.15**	**0.12**	**0.15**	**0.21**	**0.07**	**0.08**	**0.12**	**0.14**	**0.18**	**0.24**	**0.06**	**0.08**	**0.11**	**0.14**	**0.17**	**0.23**
	154.50	353.11	610.36	108.37	247.66	428.09	139.82	319.55	552.35	90.12	205.96	356.01	116.90	267.16	461.79	91.90	210.04	363.06
h^2_{Dt}	0.07	0.08	0.08	0.27	0.28	0.30	0.08	0.09	0.09	0.26	0.29	0.31	0.06	0.06	0.07	0.24	0.25	0.27
	0.10	**0.12**	**0.14**	**0.14**	**0.17**	**0.19**	**0.08**	**0.10**	**0.11**	**0.16**	**0.20**	**0.22**	**0.07**	**0.09**	**0.10**	**0.15**	**0.19**	**0.21**
	188.37	430.51	744.15	132.12	301.95	521.93	170.47	389.60	673.43	109.88	251.11	434.05	142.52	325.72	563.02	112.05	256.08	442.65
$h^2_{f(z)}$	0.19	0.20	0.22	0.71	0.73	0.81	0.22	0.23	0.25	0.68	0.75	0.84	0.16	0.16	0.18	0.64	0.65	0.73
	0.15	**0.19**	**0.23**	**0.21**	**0.26**	**0.32**	**0.12**	**0.15**	**0.18**	**0.25**	**0.30**	**0.38**	**0.11**	**0.14**	**0.17**	**0.24**	**0.29**	**0.36**
	363.58	830.94	1436.31	255.01	582.79	1007.38	329.03	751.97	1299.80	212.07	484.67	837.77	275.09	628.68	1086.70	216.27	494.27	854.36
$h^2_{f(beta)}$	0.09	0.09	0.10	0.32	0.33	0.37	0.10	0.10	0.12	0.31	0.34	0.38	0.07	0.07	0.08	0.29	0.30	0.33
	0.13	**0.16**	**0.20**	**0.18**	**0.23**	**0.28**	**0.10**	**0.13**	**0.16**	**0.21**	**0.26**	**0.33**	**0.10**	**0.12**	**0.15**	**0.20**	**0.25**	**0.31**
	273.55	625.19	1080.66	191.86	438.49	757.94	247.56	565.77	977.96	159.56	364.66	630.33	206.97	473.01	817.62	162.72	371.88	642.81
$h^2_{(\Delta P/beta)}$	0.09	0.09	0.10	0.32	0.33	0.37	0.10	0.10	0.12	0.31	0.35	0.38	0.07	0.07	0.08	0.29	0.30	0.33
	0.13	**0.17**	**0.21**	**0.19**	**0.23**	**0.28**	**0.10**	**0.13**	**0.16**	**0.22**	**0.27**	**0.33**	**0.10**	**0.12**	**0.15**	**0.21**	**0.26**	**0.32**
	312.80	714.88	1235.70	219.39	501.40	866.69	283.08	646.94	1118.26	182.45	416.98	720.76	236.67	540.88	934.93	186.07	425.23	735.03

– Figures in bold are standard errors – figures in italics are root mean squares error.

Table 2. Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h^2_f) of herd-life for various values of h^2_s (heritability for stayability) for normal, log normal (Lnormal) and gamma distribution in unbalanced situation

	Unadjusted						Adjusted for production						Adjusted for production and udder depth					
Distribution	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma	Normal	Lnormal	Gamma
Estimates	0.06	0.06	0.06	0.26	0.26	0.26	0.06	0.06	0.06	0.26	0.26	0.26	0.06	0.06	0.06	0.26	0.26	0.26
h^2_Z	0.07	0.08	0.09	0.27	0.30	0.34	0.09	0.10	0.11	0.30	0.33	0.37	0.06	0.07	0.07	0.24	0.27	0.30
	0.08	**0.10**	**0.13**	**0.12**	**0.14**	**0.18**	**0.07**	**0.08**	**0.10**	**0.14**	**0.17**	**0.21**	**0.06**	**0.08**	**0.10**	**0.13**	**0.16**	**0.20**
	122.36	279.64	483.38	85.82	196.13	339.03	110.73	253.07	437.44	71.37	163.11	281.95	92.58	211.58	365.72	72.78	166.34	287.53
$h^2_{(mal)b}$	0.08	0.08	0.09	0.29	0.28	0.32	0.09	0.09	0.10	0.32	0.31	0.36	0.06	0.06	0.07	0.26	0.25	0.29
	0.10	**0.12**	**0.16**	**0.13**	**0.16**	**0.22**	**0.07**	**0.09**	**0.13**	**0.15**	**0.19**	**0.26**	**0.07**	**0.09**	**0.12**	**0.15**	**0.18**	**0.25**
	164.83	376.71	651.16	115.61	264.21	456.70	149.17	340.91	589.27	96.14	219.73	379.81	124.71	285.02	492.66	98.05	224.08	387.33
h^2_{Dl}	0.08	0.08	0.08	0.28	0.29	0.31	0.09	0.09	0.10	0.31	0.32	0.35	0.06	0.06	0.07	0.25	0.26	0.28
	0.11	**0.13**	**0.15**	**0.15**	**0.18**	**0.20**	**0.08**	**0.10**	**0.11**	**0.17**	**0.21**	**0.23**	**0.08**	**0.10**	**0.11**	**0.16**	**0.20**	**0.22**
	200.97	459.29	793.90	140.95	322.13	556.82	181.87	415.64	718.45	117.22	267.89	463.07	152.05	347.49	600.66	119.54	273.20	472.23
$h^2_{f(z)}$	0.20	0.20	0.23	0.74	0.76	0.85	0.24	0.24	0.27	0.82	0.84	0.93	0.16	0.17	0.18	0.66	0.68	0.75
	0.16	**0.20**	**0.25**	**0.23**	**0.28**	**0.35**	**0.13**	**0.16**	**0.20**	**0.26**	**0.33**	**0.40**	**0.12**	**0.15**	**0.18**	**0.25**	**0.31**	**0.39**
	387.89	886.48	1532.32	272.05	621.75	1074.72	351.02	802.23	1386.69	226.25	517.07	893.77	293.47	670.71	1159.34	230.73	527.31	911.47
$h^2_{f(beta)}$	0.09	0.09	0.10	0.34	0.35	0.39	0.11	0.11	0.12	0.37	0.39	0.43	0.07	0.08	0.08	0.30	0.31	0.34
	0.14	**0.18**	**0.22**	**0.20**	**0.24**	**0.30**	**0.11**	**0.14**	**0.17**	**0.23**	**0.28**	**0.35**	**0.10**	**0.13**	**0.16**	**0.22**	**0.27**	**0.33**
	291.84	666.98	1152.90	204.69	467.80	808.61	264.11	603.59	1043.33	170.23	389.04	672.46	220.81	504.63	872.28	173.60	396.74	685.78
$h^2_{(\Delta P/beta)}$	0.09	0.09	0.10	0.34	0.35	0.39	0.11	0.11	0.12	0.38	0.39	0.43	0.07	0.08	0.08	0.30	0.31	0.34
	0.14	**0.18**	**0.22**	**0.20**	**0.25**	**0.30**	**0.11**	**0.14**	**0.17**	**0.23**	**0.29**	**0.35**	**0.11**	**0.13**	**0.16**	**0.22**	**0.27**	**0.34**
	333.71	762.67	1318.30	234.06	534.91	924.62	302.00	690.19	1193.02	194.65	444.85	768.94	252.49	577.03	997.42	198.50	453.66	784.17

Figures in bold are standard errors; figures in italics are root mean squares error.

estimate but raw data ($h^2_{f(z)}$) (without transformed with the help of threshold probability) gives higher value estimate with less degree of precision. The estimates show different picture for gamma distribution that of normal and lognormal distribution. The standard error as well as root mean square values are higher in gamma than that in normal lognormal.

Adjusted for production

From the prior knowledge of parameters, the data sets are generated on the basis of the parameters $h^2_y = 0.25$ (heritability of production), $r_a = -0.2$ (genetic correlation between production and stayability), $r_{Y, Hl} = 0.25$ (phenotypic correlation between production and herd life), $m_Y = 0.4$ (standardized partial regression coefficient of herd life on production). Two different values of heritability are used $h_s^2 = 0.06, 0.26$ (heritability of stayability). Once the data are simulated than it is transformed to the categorical data with the help of 5 threshold probabilities (P= 0.05, 0.10, 0.15, 0.20, 0.25) having threshold values as 1.645, 1.282, 1.036, 0.842, and 0.674. True estimate of narrow sense heritability (h_z^2), beta-binomial estimate in narrow sense ($h^2_{(real)h}$), Dempster-Lerner estimate in narrow sense heritability $h^2_{f(beta)}$ and family mean heritability $h^2_{f(z)}$, beta-binomial estimate of family mean heritability ($h^2_{f(beta)}$ and family mean realized heritability ($h^2_{f(\Delta P/beta)}$) have been computed using the methodology discussed earlier. Taking average over the threshold probabilities, the average estimated values are tabulated in Tables 1 and 2. One point is noticed that in adjustment all the estimated heritability values are more nearer to the parametric values than to without adjustment. Standard error (SE) and root mean square (RMSE) values also decreases with adjustment. From these tables it is concluded that adjustment seems to be correction on the estimates of heritability of herd life. The estimates for normal and lognormal distributions are almost same but for gamma distribution it is highly biased. The standard error and root mean square values are higher for gamma distribution than that in normal and lognormal distributions.

Adjustment for two related characters

The simulation is carried out for adjusted case of 2 related characters using above discussed parameters. Taking averages over the threshold probabilities all the estimates are tabulated in Table 1 and 2. It gives far better estimate as compare to the single character adjustment case. For two character adjustment all the narrow sense heritability estimates are almost closer to the parameteric value. The standard error also reduced as compared to the one character adjustment. $RMSE_e$ value are also following the same trend as standard error but for the family mean heritability estimates for almost all the estimator having larger value than that of individual narrow sense heritability with more standard errored and more RMSE value. In lognormal distribution, the estimates are comparable to normal but in case of gamma distribution it is not comparable. Root mean square values are more higher in case of gamma distribution. In some cases it is noticed that RMSE is extremely large.

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