Empirical Comparison of Different Methods of Estimation of Heritability of Stayability in Dairy Cattle

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SUMMARY

Stayability being an threshold character in dairy cattle breeding needs detailed genetic analysis. Herdlife, a measure of stayability depends on many characters of interest. In order to arrive at a true measure, this has been adjusted for various production and reproductive traits. The adjusted herdlife for production is further converted to binary trait using threshold probability and the resultant trait is used for estimation of heritability of stayability. The procedure of beta-binomial was modified to incorporate the adjustment of herdlife. Dempster-Lerner method was also used to estimate this parameter and compared it empirically with the beta-binomial method. It is seen that even small adjustment on account of production has a great effect on estimates of heritability of stayability. Relative root mean square errors were also obtained and found that precision and accuracy of estimates were affected by adjustment of production. From this study, it is concluded that beta-binomial method gives improved estimates than other methods.

Key words : Stayability, Heritability, Beta-binomial, Root mean square error.

1. Introduction

There are many characters of economic importance in animal and plant breeding whose inheritance is polygenic but their phenotypic expressions show discontinuities. The characters are expressed in "all or none" fashion. Although lacking a continuous distribution, such characters are known to be multifactorial in their inheritance. The relationship between polygenes and expression of such characters comes about through the establishment of 'threshold'. Thus there are two separate scales for the description of the phenotypic values. The underlying polygenic distribution which is continuous and the visible phenotypic distribution which is discontinuous and the two scales are connected by the 'threshold-a point of discontinuity'. Heritabilities of these important traits are thus to be obtained by technique other than classical methods employed for continuous traits. Dempster and Lerner [3] and Bhatia *et al.* [1] developed an

algorithm for calculating the heritability of such binary traits and further Gianola [4] generalized it. Van Vleck [6] used the algorithm in a simulation study of sib and parent offspring analysis of binary trait. Magnussen and Kremer [5] considered the beta-binomial model for estimating heritability of binary trait in plant breeding using the concept of selection response and realized heritability. In beta-binomial model, in which the residual variance is binomial with probability parameter varying according to the beta distribution. However the methodologies mentioned above can be examined further for stayability trait adjusted for production. The present investigation takes this problem empirically by incorporating the effect of auxiliary traits on the main characteristics of stayability.

2. Data Model

Consider a half sib analysis of an intrinsically mixed process under independent polygenic and environment influences in a randomized herd design. In a given population the process is explained by a standardized normal variable (Z) with a mean zero and variance one. Whenever Z exceeds a certain threshold value, say Z', an outwardly observation character (δ) is expressed. This character is dichotomous on a binary scale, and has a value of 1 for presence and 0 for absence.

The linear model for the intrinsic variable Z is

$$Z_{ijk} = \mu + S_i + e_{ijk} \tag{1}$$

where Z_{ijk} is the observation on k^{th} individual in i^{th} family of jth herd

μ is overall mean

S_i is i^{th} family effect

e_{ijk} is the residual effect containing error effects

$$S_i \sim N(0, \sigma_f^2) \text{ and } e_{ijk} \sim N(0, \sigma_e^2)$$

Transformation of the intrinsic variable Z to a binary trait (δ) on the outward scale is done as follows :

$$\delta_{ijk} = 0 \text{ for } Z_{ijk} \leq Z' \text{ or } \Phi(Z_{ijk}) \leq P$$
$$= 1 \text{ for } Z_{ijk} > Z' \text{ or } \Phi(Z_{ijk}) > P \tag{2}$$

where Φ denotes the cumulative probability function of a normal distribution and P denotes the population probability of observing the dichotomous character (δ). Data are simulated by using the above half sib model so that variance

of Z is 1. Sire's values (S_j) are simulated as normal variate with mean zero and variance of 0.0125, 0.0375 and 0.0625. Environmental values (e_{ijk}) *i.e.* errors are simulated as a normal variate with mean zero and variance of $(1 - \sigma_s^2)$. The thresholds used are $P = 0.05, 0.10, 0.15, 0.20, 0.25$ which were the probabilities of observing the binary trait. The threshold probabilities were restricted to 0.25 because in real life situations, probability of occurrence of fitness character is generally low. Simulations are generated for experimental designs with number of sires as 50 and 100 and number of herds as 3 and 5 and of five daughters.

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 fair idea of the inheritance of stayability it is desirable to eliminate the effect of auxiliary character. For example, in dairy cattle, herdlife consists of survival and production trait, which is expressed by some function of P_Y and P_S

$$P_{HL} = f (P_Y, P_S) \tag{3}$$

where P_{HL}, P_Y, P_S are the phenotypic value of herdlife, production and survival respectively. In case of linear association between P_{HL} and P_Y, a new phenotypic variable of herdlife adjusted for production can thus easily be obtained as

$$P_{HL/Y} = P_{HL} - r_{Y, HL} P_Y \tag{4}$$

$r_{Y, HL} = $ phenotypic correlation between production and herdlife

The correlation coefficients are not estimated from the same data but they are known in advance. Further transforming this new $P_{HL/Y}$ variate to a binomial variate with the help of different points of truncation for given probability of occurrence, estimate of heritability of herdlife adjusted for production can easily be obtained. The estimate of heritability obtained from adjusted character reflects the true picture of its inheritance.

4. Estimation of Heritability

Dempster-Lerner Method

Following Dempster and Lerner [3] the estimate of individual narrow sense heritability designated by h_{DL}^2 is obtained by the following expression

$$\hat{h}^2_{DL} = 4\hat{\sigma}^2_f(\delta) \times [\, \phi\,(Z')\,]^{-2} \tag{5}$$

where ϕ denotes the normal probability density function evaluated at the threshold Z' for expression at the binary scale $[\, Z' = \Phi^{-1}(P)\,]$ and $\sigma^2_f(\delta)$ is the estimate of the family variance component obtained from analysis of variance (ANOVA) method applied to binary trait.

Raw Data-Individual

Further Z_{ijk} generated by above procedure follows the half sib model

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

The heritability on this raw data is heritability obtained by using the original half sib simulated data without changing to a binary data.

The individual narrow sense heritability is

$$\hat{h}^2_{(Z)} = \frac{4\hat{\sigma}^2_{f(Z)}}{\hat{\sigma}^2_{f(Z)} + \hat{\sigma}^2_{e(Z)}} \tag{6}$$

The estimated components are obtained from an analysis of variance.

Raw Data-Family Mean Heritability

The family mean heritability is

$$\hat{h}^2_{f(Z)} = \frac{\hat{\sigma}^2_{f(Z)}}{\hat{\sigma}^2_{f(Z)} + \dfrac{\hat{\sigma}^2_{e(Z)}}{n_{daughter} \times n_{herd}}} \tag{7}$$

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 finally one of additive genetic probability are considered for obtaining beta binomial based heritability estimates. These will give the estimates of heritability as :

The realized individual narrow sense beta-binomial heritability estimate is

$$\hat{h}^2_{(beta)} = \frac{[\,\Phi^{-1}(\hat{P}_{a/\delta}) - \Phi^{-1}(\bar{P})\,]}{\hat{i}} \tag{8}$$

The family mean beta-binomial heritability estimate is

$$h^2_{f\,(beta)} = \frac{\hat{\alpha}_f \times \hat{\beta}_f \times (\hat{\alpha}_{pf} + \hat{\beta}_{pf})^2 \times (\hat{\alpha}_{pf} + \hat{\beta}_{pf} + 1)}{\hat{\alpha}_{pf} \times \hat{\beta}_{pf} \times (\hat{\alpha}_f + \hat{\beta}_f)^2 \times (\hat{\alpha}_f + \hat{\beta}_f + 1)} \tag{9}$$

The realized family mean beta-binomial heritability is

$$h^2_{f\,(\Delta P\,/beta)} = \frac{\Phi^{-1}(\overline{P}_{f/\delta\,=\,1}) - \Phi^{-1}(\overline{P})}{\Phi^{-1}(\overline{P}_{pf/\delta\,=\,1}) - \Phi^{-1}(\overline{P})} \tag{10}$$

where the symbols have their usual meaning and are described in detail by Magnusssen and Kremer [5].

The estimates of heritability were also obtained by each of the methods for stayability by adjusting for production.

Relative Root Mean Square Error

The comparison of different methods is required to be 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 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

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

5. Results and Discussion

To compare empirically the performance of beta-binomial approach and other methods, the estimates of heritability of stayability along with relative root mean squares were obtained. For assessing the usefulness and performance of these methods in a general sense, varying family size and different herd sizes were considered. Data were generated using different parameters of heritability of stayability (h^2_s = 0.05, 0.15, 0.25). For these parametric values, samples were generated for 100 sires with 5 daughters per sire arranged in 5 herds. Once the data were simulated then it was transferred to categorical data with the help of five threshold probabilities, (P = 0.05, 0.10, 0.15, 0.20, 0.25). The estimate of heritability was obtained from original simulated data. Taking average over the threshold probabilities, the average estimated values are tabulated in Table 1. From Table 1 it is seen that in all parametric value of heritability, the estimate of heritability based on original data h^2_z is close to the parametric value. The standard error obtained

Table 1 : Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h_f^2) of herdlife for various values of given h_s^2 (heritability of stayability).

Parameter		$h_s^2 = 0.05$		$h_s^2 = 0.15$		$h_s^2 = 0.25$	
		$n_{herd} = 5$	$n_{herd} = 3$	$n_{herd} = 5$	$n_{herd} = 3$	$n_{herd} = 5$	$n_{herd} = 3$
h_Z^2	$n_{fam} = 100$	0.0511	0.0487	0.1525	0.1487	0.2531	0.2488
		(0.0290)	(0.0483)	(0.0436)	(0.0588)	(0.0573)	(0.0698)
		0.0486	**0.0452**	**0.1445**	**0.1412**	**0.2417**	**0.2389**
		(0.0280)	(0.0442)	(0.0339)	(0.0542)	(0.0525)	0.0640
	$n_{fam} = 50$	0.0516	0.0477	0.1548	0.1485	0.2569	0.2490
		(0.0412)	(0.0661)	(0.0608)	(0.0836)	(0.0792)	(0.0994)
		0.0497	**0.0449**	**0.1446**	**0.1403**	**0.2408**	**0.2378**
		(0.0397)	(0.0633)	(0.0569)	(0.0770)	(0.0739)	(0.0993)
$h_{rea(b)}^2$	$n_{fam} = 100$	0.0566	0.0567	0.1666	0.1651	0.2793	0.2822
		(0.0703)	(0.1221)	(0.0907)	(0.1477)	(0.1109)	(0.1773)
		0.0500	**0.0489**	**0.1516**	**0.1498**	**0.2607**	**0.2605**
		(0.0663)	(0.1187)	(0.0844)	(0.1390)	(0.1032)	(0.1622)
	$n_{fam} = 50$	0.0572	0.0533	0.1694	0.1639	0.2836	0.2804
		(0.1016)	(0.1721)	(0.1297)	(0.2083)	(0.2459)	(0.2426)
		0.0541	**0.0518**	**0.1547**	**0.1522**	**0.2645**	**0.2560**
		(0.1002)	(0.1652)	(0.1254)	(0.1926)	(0.1527)	(0.2291)
h_{DL}^2	$n_{fam} = 100$	0.0552	0.0537	0.1634	0.1591	0.2705	0.2702
		(0.0781)	(0.1189)	(0.0887)	(0.1389)	(0.1082)	(0.1570)
		0.0493	**0.0469**	**0.1491**	**0.1462**	**0.2537**	**0.2510**
		(0.0651)	(0.1167)	(0.0830)	(0.1334)	(0.1037)	(0.1536)
	$n_{fam} = 50$	0.0547	0.0491	0.1658	0.1562	0.2752	0.2683
		(0.0999)	(0.1530)	(0.1262)	(0.1927)	(0.1516)	(0.2230)
		0.0543	**0.0470**	**0.1530**	**0.1456**	**0.2568**	**0.2479**
		(0.0990)	(0.1628)	(0.1255)	(0.1867)	(0.1538)	(0.2169)
$h_{f(Z)}^2$	$n_{fam} = 100$	0.2303	0.1370	0.4875	0.3538	0.6209	0.4892
		(0.1087)	(0.1339)	(0.0757)	(0.0972)	(0.0575)	(0.0756)
		0.2200	**0.1291**	**0.4741**	**0.3424**	**0.6097**	**0.4789**
		(0.1120)	(0.1299)	(0.0756)	(0.0951)	(0.0557)	(0.0747)
	$n_{fam} = 50$	0.2168	0.1168	0.4820	0.3403	0.6175	0.4791
		(0.1607)	(0.1304)	(0.1079)	(0.1400)	(0.0797)	(0.1038)
		0.2121	**0.1068**	**0.4649**	**0.3275**	**0.6014**	**0.4677**
		(0.1522)	(0.1993)	(0.1066)	(0.1475)	(0.0809)	(0.1126)

$h^2_{f \, (beta)}$	$n_{fam} = 100$	0.1059	0.0539	0.2740	0.1730	0.3890	0.2699
		(0.1242)	(0.1448)	(0.1076)	(0.1613)	(0.0920)	(0.1187)
		0.0950	**0.0457**	**0.2571**	**0.1613**	**0.3744**	**0.2576**
		(0.1254)	(0.1451)	(0.1062)	(0.1314)	(0.0944)	(0.1181)
	$n_{fam} = 50$	0.0851	0.0291	0.2608	0.1512	0.3791	0.2510
		(0.1876)	(0.2051)	(0.1536)	(0.1869)	(0.1315)	(0.1689)
		0.0818	**0.0276**	**0.2436**	**0.1439**	**0.3625**	**0.2365**
		(0.1891)	(0.2041)	(0.1611)	(0.1853)	(0.1373)	(0.1713)
$h^2_{f(\Delta P \, / \, beta)}$	$n_{fam} = 100$	0.1047	0.0526	0.2702	0.1692	0.3899	0.2640
		(0.1295)	(0.1446)	(0.1041)	(0.1269)	(0.0905)	(0.1160)
		0.0927	**0.0464**	**0.2288**	**0.1578**	**0.3710**	**0.2520**
		(0.1223)	(0.1417)	(0.1073)	(0.1284)	(0.0909)	(0.1154)
	$n_{fam} = 50$	0.0840	0.0286	0.2573	0.1479	0.3742	0.2455
		(0.1853)	(0.2005)	(0.1515)	(0.1825)	(0.1297)	(0.1650)
		0.0808	**0.0270**	**0.2404**	**0.1407**	**0.3578**	**0.2264**
		(0.1865)	(0.1995)	(0.1589)	(0.1811)	(0.1354)	(0.1673)

Note : The bold faces are for adjusted data and figures in the parentheses indicate average standard deviations.

is also less as compared to the other estimates. Both narrow sense beta-binomial ($h^2_{rea(b)}$) and Dempster-Lerner (h^2_{DL}) estimates have also been found to be close to the true value of heritability. In case of beta-binomial estimates, the standard error for almost all situations particularly in the case of heritability below 0.15, were on the lower side. This is a desirable feature of beta-binomial procedure because generally we came across different characters of fitness having heritability as low as 0.15 or less. In case of family mean heritability, the beta-binomial family mean heritability estimate ($h^2_{f(beta)}$) and realized family mean beta-binomial estimate $h^2_{(\Delta P \, / \, beta)}$ were better than family mean heritability of true value of heritability estimate ($h^2_{f(Z)}$). From Table 1 it is clear that standard errors are decreasing with the increase in heritability in case of family mean heritability. In addition to this, data were simulated by incorporating the adjustment due to production. The parametric values were used as that of Dekkers [2]. After adjustment for production the data was converted to binary data with the help of five threshold probabilities ($P = 0.05, 0.1, 0.15, 0.2, 0.25$). Taking average over the threshold probabilities the average estimated values of heritability are also tabulated in Table 1. It is apparent that the beta binomial estimates obtained for adjusted records for production are very close to true value of heritability for all the parametric values. One interesting point is noticed, that in case of adjusted herdlife, the heritability estimate by all the procedures lead to an under estimate. This, thus, advocates that probably adjustments made, are might be over-corrections. In

case of adjustment, all the estimated heritability values are more near to parametric values than compared to without adjustment. The results for herd size 3 are also shown in Table 1 for both the cases of adjustment and unadjustment. It is clearly seen that except for heritability estimate obtained on raw data *i.e.*, true values, all other estimates are over-estimated. The important feature to be noticed from this table is that the value of standard error are on the lower side for herd size 5. This implies that higher the herd size, the more precise the estimate will be.

In case of adjustment of herdlife for production whose results are tabulated in the same table, it is noticed that heritability estimates are corrected to reduce bias for all the parametric cases. To have comparative picture for different herd size for family size 50, results obtained are tabulated in same table for different parametric value of heritability of stayability. It is clearly seen from this table that as family size reduced to 50, the standard error got increased remarkably. It is noticed that Dempster-Lerner and realized beta binomial estimates give the closer value to the true estimate. In case of herd size 3, it is seen that family mean realized beta binomial estimate gives lower values in all the cases than true value. In the case of adjustment, except beta binomial realized heritability estimates, estimates from other methods are lower than the parametric value which imply some sort of over adjustment. The results for family size 100 with herd size 5 are more accurate as well as efficient for almost all the procedures of estimation and in particular the method of beta binomial realized heritability. It has further been observed that in all situations, the adjustment played a significant role.

Relative Root Mean Square Error

For empirical comparison of different procedures, the average root mean square has been calculated for different heritability and over different threshold probability with different herd sizes and family sizes. This procedure is followed for adjustment as well as for unadjustment case and the results are tabulated in Table 2 and Table 3 respectively. It is seen from Table 2 that the root mean square error are minimum for original data points followed by beta binomial method for all values of heritability of stayability for both family sizes. In Table 3 the results are tabulated for different points of threshold probability. This table clearly shows the role of threshold probability on the root mean square error. With more data points it has found that the relative root mean square error decreases for all the procedures of estimation. These two tables further reveal that in case of lower heritability and lower threshold probability the relative root mean square is highest whereas in higher heritability and higher threshold probability it shows lower values. One interesting point is noticed from both the tables is that relative root mean square errors in case of adjusted for production which are denoted by bold faces are lower in comparison to

Table 2 : Relative root mean square error (RMSE %) of selected estimates of heritability of herdlife of different values of heritability of stayability

Estimates		$h^2_{rea(b)}$		h^2_{DL}		$h^2_{f(beta)}$		$h^2_{f(\Delta P/beta)}$		h^2_Z		$h^2_{f(Z)}$	
	$n_{herd}=$	5	3	5	3	5	3	5	3	5	3	5	3
$h^2_s=0.05$ $n_{fam}=100$		141.24	244.78	156.69	237.94	279.55	291.56	275.55	284.89	58.05	96.56	360.52	319.51
		132.94	**237.85**	**130.35**	**233.62**	**274.23**	**292.51**	**266.73**	**285.99**	**56.79**	**90.02**	**358.00**	**304.15**
$n_{fam}=50$		203.58	344.53	200.22	324.33	387.76	414.01	382.21	404.82	82.65	132.22	463.17	403.70
		200.65	**330.54**	**198.18**	**325.33**	**389.29**	**411.62**	**383.71**	**402.58**	**79.21**	**127.22**	**444.67**	**404.49**
$h^2_s=0.15$ $n_{fam}=100$		61.55	99.13	59.85	85.03	115.57	91.73	111.84	89.35	29.13	39.24	230.58	150.52
		56.34	**92.70**	**55.23**	**89.05**	**107.28**	**92.40**	**94.83**	**90.11**	**26.89**	**36.61**	**221.87**	**143.11**
$n_{fam}=50$		87.52	139.37	84.96	128.74	131.65	127.58	129.22	124.69	40.67	55.73	232.57	157.51
		83.70	**128.40**	**83.71**	**124.52**	**132.01**	**126.76**	**129.67**	**123.99**	**38.16**	**51.77**	**221.65**	**153.07**
$h^2_s=0.25$ $n_{fam}=100$		45.91	72.18	44.05	65.87	71.15	52.65	69.29	51.20	22.94	27.60	149.93	100.32
		40.97	**65.06**	**41.34**	**61.47**	**67.47**	**52.64**	**65.17**	**51.39**	**20.77**	**26.00**	**145.59**	**96.31**
$n_{fam}=50$		64.28	97.88	61.93	89.68	78.42	71.06	76.61	69.48	31.81	39.77	150.41	101.63
		61.40	**91.74**	**61.68**	**86.79**	**77.49**	**70.76**	**75.78**	**71.29**	**29.77**	**36.70**	**144.22**	**87.09**

Note : Bold faces are for adjusted data.

Table 3 : Relative root mean square error (RMSE %) of the estimate of heritability of herdlife for different values of threshold probability

Estimates	$n_{herd} =$	$h^2_{rea(beta)}$ 5	3	h^2_{DL} 5	3	$h^2_{f(beta)}$ 5	3	$h^2_f(\Delta P/beta)$ 5	3
$\bar{p} = 0.05$	$n_{fam} = 100$	124.33 / **110.34**	211.36 / **182.89**	138.98 / **110.99**	199.76 / **179.76**	166.14 / **158.19**	137.88 / **135.88**	163.42 / **145.32**	134.83 / **133.28**
	$n_{fam} = 50$	176.63 / **176.08**	297.09 / **254.08**	170.32 / **179.68**	277.17 / **251.35**	183.29 / **196.20**	197.20 / **191.89**	186.47 / **193.23**	192.72 / **187.71**
$\bar{p} = 0.10$	$n_{fam} = 100$	80.80 / **75.49**	135.39 / **130.62**	78.64 / **63.75**	129.59 / **127.35**	151.89 / **144.99**	130.88 / **132.02**	149.04 / **142.25**	127.26 / **128.26**
	$n_{fam} = 50$	112.80 / **110.12**	192.53 / **177.21**	109.99 / **105.33**	180.02 / **173.98**	181.81 / **188.63**	188.78 / **187.59**	178.79 / **185.26**	184.48 / **183.46**
$\bar{p} = 0.15$	$n_{fam} = 100$	62.74 / **59.66**	105.23 / **102.79**	77.64 / **57.73**	101.21 / **110.58**	137.33 / **127.87**	126.01 / **129.81**	131.36 / **129.03**	122.68 / **126.95**
	$n_{fam} = 50$	93.87 / **88.46**	149.93 / **141.88**	91.16 / **86.02**	143.82 / **139.36**	173.72 / **167.63**	180.64 / **171.86**	170.46 / **171.72**	176.62 / **178.45**
$\bar{p} = 0.20$	$n_{fam} = 100$	56.63 / **54.86**	94.92 / **94.52**	54.47 / **53.12**	89.79 / **91.04**	128.11 / **125.53**	125.53 / **128.14**	125.30 / **118.63**	122.42 / **125.37**
	$n_{fam} = 50$	82.72 / **78.43**	129.20 / **133.13**	80.48 / **76.71**	121.28 / **127.17**	173.54 / **167.63**	170.33 / **171.86**	170.46 / **164.65**	166.50 / **168.06**
$\bar{p} = 0.25$	$n_{fam} = 100$	55.94 / **51.56**	84.19 / **88.27**	55.54 / **50.21**	80.55 / **86.75**	128.07 / **118.66**	124.01 / **120.71**	124.50 / **117.97**	120.82 / **117.95**
	$n_{fam} = 50$	79.16 / **73.82**	113.29 / **125.90**	76.12 / **71.84**	107.57 / **120.24**	170.75 / **164.98**	164.11 / **169.96**	167.98 / **162.98**	160.65 / **166.14**

Note : Bold faces are for adjusted data.

without adjustment root mean square errors. This thus highlights not only the importance of adjustment but also gives a clear picture of the estimate of heritability of stayability. The change in root mean square error due to adjustment has also been noticed. Due to reduction in herd size, the relative root mean square for all the procedures increase tremendously. This means that herd size has a prominent role to play in the estimation of heritability of stayability and its precision. The relative root mean square error for narrow sense beta-binomial realized estimate and Dempster Lerner estimate also show similar results and are significantly less than any other family mean heritability estimates. Due to reduction of family size, the relative root mean square errors are significantly increased. As noticed earlier that herd size is important but from these results it is seen that family size is even more important for reliable estimation of heritability.

Finally from the results it is concluded that family size and herd size have an important role in the estimation of heritability of stayability. The procedure based on real data, narrow sense realized beta-binomial and Dempster Lerner show encouraging results where as procedure based on family mean exhibit very unreliable estimates of heritability. Among the methods which are relatively good, besides the method based on real data, beta binomial is by and large a good procedure of estimation of heritability of stayability for different situations of parametric values of heritability and points of truncation. If prior information on the relationship between stayability and production is available, then it is desired that this may be included for adjustment for arriving the true estimate of heritability obtained from the threshold model based on beta-binomial model approach.

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