Effect of more than one related auxiliary trait on estimation of heritability of herd life

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ABSTRACT

Culling of a dairy animal is an important character in dairy cattle breeding, which is influenced by production as well as auxiliary traits. One approach to get true estimate of heritability of herd life (stayability) by adjusting production was reported in literature. Here it is seen that though they observed significant effect of production 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. It is seen that this technique also improves the standard errors.

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

In animal breeding, stayability or herd life is an important character both from economic point of view as well as making room for heifer replacement. The improvements in longevity or stay of dairy animal in herd can be brought about by using information on secondary traits. This aptitude has been called by animal breeders either stayability, survivability or wearability.

Magnussen and Kremer (1995) suggested the beta-binomial estimate of heritability of all or none trait. Paul and Bhatia (2002) studied the effect of production on the estimate of heritability of stayability. In the present 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.

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 0 and variance 1. Whenever the Z' exceeds certain threshold value, say 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 () discussed by Paul and Bhatia (2002).

In beta-binomial model approach, following Magnussen and Kremer (1995) three sets of beta parameters: one for phenotypic family probilities, one for the family

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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 (2002) discussed the details of these procedures.

Simulation

To study the applicability and efficiency of various procedures the empirical comparison is done on simulated data. The data on half sibs can be generated by assuming the usual half sib model as

$$Y_{ij} = \mu + S_i + e_{ij}$$

where Y_{ij}, record of j th offspring of i th sire, μ, general mean; S_i, i th sire effect, $S_i \sim N(0, \sigma_s^2)$; e_{ij}, error component, $e_{ij} \sim N(0, \sigma_e^2)$.

The simulation in this case will be carried out in the following

$$P_{ij} = \mu + s_s \times a_i + \sigma_e \times a_{ij}$$

where a_i, a_{ij} are random standard normal values. With known values of the σ_s and σ_e one can obtain the phenotypic value of P_{ij} of the character under study for the jth half sib of ith sire. Here these characters such as production, other auxiliary trait say, udder depth and stayability which are inter correlated among themselves can be generated.

The first character (X) is generated using simple half sib model.

$$P_{x(i,j)} = \mu_x + \sigma_{sx} \times b_x + \sigma_{ex} \times e_x$$

Here b_x and e_x are random standard normal value. The second character (Y) is generated by following Ronningen (1974) by retaining the relationship between Y and X as:

Here r_{ai} and r_{ei} are the genetic and environmental correlation between Y and X respectively. b_x, b_y, e_x, e_y are the random standard normal value.

$$P_{Y(ij)} = \mu_Y + \left(r_{a_1} \times \sigma_{SY}\right) b_X + \sqrt{1 - r_{a_1}^2}\,\sigma_{SY} b_Y + r_{e_1}\sigma_{eY}e_X + \sqrt{1 - r_{e_1}^2}\,\sigma_{eY}e_Y$$

The third character (Z) is generated by where

$$P_{Z(i,j)} = \mu_Z + r_{a_2}\sigma_{SZ}b_X + \left\{ \frac{\left(r_{a_3} - r_{a_1}r_{a_2}\right)}{\sqrt{1 - r_{a_1}^2}} \right\}\sigma_{SZ}b_Y +$$

$$\sqrt{\frac{\left(1 - r_{a_1}^2 - r_{a_2}^2 - r_{a_3}^2 + 2r_{a_1}r_{a_2}r_{a_3}\right)}{\left(1 - r_{a_1}^2\right)}}\,\sigma_{SZ}b_Z + r_{e_2}\sigma_{eZ}e_X$$

$$+ \left\{ \frac{\left(r_{e_3} - r_{e_1}r_{e_2}\right)}{\sqrt{1 - r_{e_1}^2}} \right\}\sigma_{eZ}e_Y + \sqrt{\frac{\left(1 - r_{e_1}^2 - r_{e_2}^2 - r_{e_3}^2 + 2r_{e_1}r_{e_2}r_{e_3}\right)}{\left(1 - r_{e_1}^2\right)}}\,\sigma_{eZ}e_Z$$

where b_x, b_y, b_z, e_x, e_y, e_z are random standard normal value r_1, r_2, r_3 are the genetic correlation between X and Y, X and Z and Y and Z respectively, r_{e1}, r_{e2}, r_{e3} are the environmental correlation between X and Y, X and Z and Y and Z respectively.

Adjustment of stayability for auxiliary traits

For dairy cows, length of productive life or herd life is a trait of major economic importance. Herd life is determined by culling decisions of individual producers. Herd life can be separated into production and other important traits like udder characteristics, leg characteristics, workability character, milking speed, reproductive performance and other conformation traits. Some characters are inter related but some are not. Here we considered the characters which are intercorrelated among themselves.

Herd life adjusted for production *(HL/Y)* can be obtained by regression procedure

$$P_{HL/Y} = P_{HL} - r_{Y,HL}P_Y \quad \left[r_{Y,HL} = m_Y + m_S r_p\right]$$
$$= m_S \left(P_S - r_p P_Y\right)$$

This is the case when herd life consists of production and survival only. Paul and Bhatia (2003) showed, that stayability is affected significantly by the auxiliary trait e.g. production.

In general, it can be extended to 2 characters by assuming that a cow's phenotypic value of herd life (P_{HL}) is to be a linear function of production (P_Y), stayability (P_S) and say, udder depth (P_X).

$$P_{HL} = m_X P_X + m_Y P_Y + m_S P_S$$

Here survivalability includes all factors affecting herd life except production and udder depth. Variables considered here are assumed to be standardized normal.

Following the path diagram given in Paul and Bhatia (2003) we can write,

$$r_{p1} = r(P_x, P_y) = h_x r_{a1} h_y + e_x r_{e1} e_y$$
$$r_{p2} = r(P_x, P_z) = h_x r_{a2} h_z + e_x r_{e2} e_z$$
$$r_{p3} = r(P_y, P_z) = h_y r_{a3} h_z + e_y r_{e3} e_z$$

Here $e_i = \sqrt{1 - h_i^2}$

$$r_{x1}\,HL = m_x + m_y r_{p1} + m_s r_{p2}$$
$$r_{y1}\,HL = m_y + m_x r_{p1} + m_s r_{p3}$$
$$V(P_{HL}) = m_x^2 + m_y^2 = m_s^2 + 2m_x^2 x\,m y r_{p1} + 2m y\,m_s r_{p3} + 2m_x\,m_s r_{p2} = 1$$

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 (2002).

The data generated by Monte Carlo Simulation, follows the half sib model

$$Z_{ij} = \mu + S_i + e_{ij}$$
$$S_i \sim N\,(0, \sigma_f^2) \quad \text{and}\ e_{ij} \sim N(0, \sigma_e^2)$$

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.

In individual narrow sense heritability

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

the estimated components are derived from an analysis of variance (Henderson's Method III, Searle *et al.* 1992) applied to the above model.

True family mean heritability is

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

Relative root mean square error

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

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

Measure of unbalanced ness

We also compare the effect of unbalanced ness in the different estimates. The degree of unbalanced can be defined as $\Delta = N\,(n - \lambda)$,

where $\qquad n = N/S,\ \displaystyle\sum_{i=1}^{s} n_i = N$

$$\lambda = \frac{1}{S-1}\left[\sum_i n_i - \frac{\displaystyle\sum_i n_i^2}{N}\right]$$

Here S, number of sire, n_i , number of daughter of ith sire; and N, total number of daughters.

RESULTS AND DISCUSSION

To visualize the true nature 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 comparison purpose, the different methods discussed above are used. For carrying out 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, 0.0283 0.0417, 0.055 and 0.0695. Errors i.e. environmental values (e_{ijk}) are simulated as a single Gaussian variable with mean of zero and variance of $1-\sigma_f^2$.

To compare empirically performance modified beta-binomial approach and other methods, the estimates of narrow sense heritability and family mean heritability are calculated as per Paul and Bhatia (2002, 2003). The relative root mean square error of different estimates is also obtained to compare the procedures among themselves. All the comparisons are done by considering 3 unbalanced situation having different degree unbalanced ness of which one having 0.0 (zero) unbalancedness.

For all the comparisons, we have taken the no. of sire 5 having 3 different combinations of offspring, which is shown in the Table 1. From these 3 different combinations we can also compare the effect of unbalance ness on different estimates.

Table 1. Three different combinations of offsprings

Cases	Observations on offsprings					Unbalancedness
I	20	20	20	20	20	0.0000
II	18	21	23	17	21	5.9999
III	16	23	19	22	20	7.5001

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 (2000, 2002, 2003).

One character without adjustment

From the prior knowledge of parameters, the data sets are generated on the basis of the parameters $h_s^2 = 0.25$ (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), (standardized partial regression coefficient of herd life on production). Five different values of heritability are used $h_s^2 = 0.06, 0.11, 0.16, 0.21, 0.26$ (heritability of stayability). Once the data are simulated then 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 estimates of narrow sense heritability (h_t^2) is obtained from original simulated data values, beta-binomial estimates of individual narrow sense heritability $h_{t(real)b}^2$ and Demster-Lerner estimate of individual narrow sense heritability (h_{DL}^2) are also obtained for different threshold values. True estimates of family mean heritability $(h_{f,a}^2)$, beta-binomial estimate of family mean heritability $h_{f(beta)}^2$ and beta binomial estimate of realized family mean heritability $h_{f(real-beta)}^2$ are obtained using the formulae as defined in the estimation. Taking average over the all threshold probabilities average estimated values are tabulated. From the Table 2 it is seen that in all the parametric value of heritability the true heritability based on the original data is more close to the parametric values. The standard errors are also less as compared to the other estimates. Both narrow sense beta-binomial and Demster Lerner estimates have found to be close to the true heritability. Though the Demster Lerner estimates are somewhat more closer to the true value as compared to the beta estimates but the standard errors are less for beta estimates in almost all the situations. This implies that beta-binomial estimates are estimated with some better precision as compared to Demster Lerner method. For the family mean heritability the estimate of beta-binomial heritability $h_{f(beta)}^2$ and realized family mean heritability $h_{f(real-beta)}^2$ both are better than the family mean heritability of true sense h_{f2}^2 Beta-binomial family mean heritability is estimated almost twice than that of the true parametric value of heritability, but family mean heritability of original data set is more than twice as compared to the parametric values. All the estimates of heritability are over estimated the parametric values. Standard errors for family mean heritability also increases with increase in parametric values but the RMSE value decreases in all the estimates with increase in the parametric values. In unbalanced data the result shows somewhat inconsistency, the standard error as well as RMSE both are higher than that of balanced case.

Adjusted for production

True estimate of narrow sense heritability h_2^2, beta-binomial estimate in narrow sense $h_{t(real)b}^2$, Dempster-Lerner estimate in narrow sense heritability $h_{DL,p}^2$, true estimate of family mean heritability h_{f2r}^2, beta-binomial estimate of family mean heritability $h_{f(AP-beta)}^2$ and family mean realized heritability have been computed using the methodology discussed earlier. Taking average over the threshold

Table 2. Average estimates of individual narrow-Sense heritability (h^2) and family mean Heritability (h^2) of herd-life without adjustment for various values of h^2 (heritability forsStayability) for normal distribution

Estimates	UB*=0.00					UB=5.9999					UB=7.5001				
	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26
h^2_z	0.0912	0.1391	0.1738	0.2317	0.2633	0.0951	0.1431	0.2015	0.2552	0.2761	0.0937	0.1556	0.2072	0.2487	0.2834
	0.0807	**0.1059**	**0.0937**	**0.1036**	**0.1143**	**0.0831**	**0.1090**	**0.0965**	**0.1067**	**0.1177**	**0.0866**	**0.1136**	**0.1006**	**0.1112**	**0.1227**
	120.5869	*107.9209*	*95.0689*	*102.7061*	*93.7026*	*123.8307*	*110.8240*	*97.6263*	*105.4689*	*96.2232*	*128.6477*	*115.1350*	*101.4239*	*109.5716*	*99.9662*
h^2_{health}	0.0976	0.1488	0.1859	0.2479	0.2817	0.1017	0.1531	0.2156	0.2730	0.2954	0.1002	0.1665	0.2217	0.2661	0.3032
	0.0904	**0.1186**	**0.1050**	**0.1161**	**0.1281**	**0.0931**	**0.1222**	**0.1081**	**0.1195**	**0.1319**	**0.0970**	**0.1273**	**0.1127**	**0.1246**	**0.1374**
	162.4426	*145.3802*	*128.0674*	*138.3554*	*126.2267*	*166.8123*	*149.2910*	*131.5124*	*142.0771*	*129.6222*	*173.3013*	*155.0984*	*136.6282*	*147.6039*	*134.6645*
h^2_{DL}	0.0937	0.1429	0.1785	0.2381	0.2705	0.0977	0.1470	0.2070	0.2622	0.2837	0.0962	0.1599	0.2129	0.2555	0.2912
	0.1012	**0.1329**	**0.1176**	**0.1300**	**0.1435**	**0.1043**	**0.1369**	**0.1211**	**0.1339**	**0.1478**	**0.1087**	**0.1426**	**0.1262**	**0.1396**	**0.1540**
	198.0516	*177.2490*	*156.1410*	*168.6843*	*153.8969*	*203.3792*	*182.0170*	*160.3412*	*173.2219*	*158.0367*	*211.2907*	*189.0975*	*166.5785*	*179.9602*	*164.1843*
h^2_{TA}	0.2461	0.3752	0.4687	0.6251	0.7103	0.2564	0.3860	0.5436	0.6884	0.7448	0.2527	0.4198	0.5590	0.6710	0.7645
	0.1566	**0.2056**	**0.1820**	**0.2012**	**0.2220**	**0.1613**	**0.2117**	**0.1874**	**0.2072**	**0.2286**	**0.1681**	**0.2206**	**0.1953**	**0.2159**	**0.2382**
	382.2636	*342.1121*	*301.3710*	*325.5810*	*297.0396*	*392.5465*	*351.3149*	*309.4779*	*334.3392*	*305.0300*	*407.8166*	*364.9811*	*321.5166*	*347.3450*	*316.8956*
$h^2_{f(beta)}$	0.1126	0.1717	0.2145	0.2860	0.3250	0.1173	0.1766	0.2487	0.3149	0.3408	0.1156	0.1921	0.2558	0.3070	0.3498
	0.1357	**0.1780**	**0.1576**	**0.1742**	**0.1922**	**0.1397**	**0.1834**	**0.1623**	**0.1795**	**0.1980**	**0.1456**	**0.1911**	**0.1691**	**0.1870**	**0.2063**
	287.6106	*257.4011*	*226.7480*	*244.9633*	*223.4891*	*295.3473*	*264.3252*	*232.8475*	*251.5528*	*229.5009*	*306.8363*	*274.6074*	*241.9052*	*261.3382*	*238.4285*
$h^2_{f(AP\,beta)}$	0.1127	0.1719	0.2147	0.2864	0.3254	0.1175	0.1769	0.2491	0.3154	0.3412	0.1157	0.1923	0.2561	0.3074	0.3502
	0.1373	**0.1802**	**0.1595**	**0.1763**	**0.1945**	**0.1414**	**0.1856**	**0.1643**	**0.1816**	**0.2004**	**0.1474**	**0.1934**	**0.1712**	**0.1892**	**0.2088**
	328.8743	*294.3307*	*259.2797*	*280.1084*	*255.5533*	*337.7211*	*302.2482*	*266.2543*	*287.6433*	*262.4276*	*350.8584*	*314.0056*	*276.6116*	*298.8327*	*272.6361*

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

Table 3: Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h^2_f) of herd-life adjusted for production for various values of h^2 (heritability for stayability) for normal distribution

Estimates	UB=0.00					UB=5.9999					UB=7.5001				
	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26
h^2_z	0.0821	0.1222	0.1719	0.2218	0.2530	0.0832	0.1235	0.1732	0.2041	0.2816	0.0879	0.1350	0.1914	0.2483	0.3035
	0.0613	**0.0847**	**0.0792**	**0.0947**	**0.1267**	**0.0632**	**0.0872**	**0.0816**	**0.0975**	**0.1305**	**0.0658**	**0.0909**	**0.0850**	**0.1016**	**0.1359**
	103.7942	*83.3766*	*74.9858*	*70.1750*	*66.8992*	*106.5863*	*85.6195*	*77.0029*	*72.0627*	*68.6988*	*110.7325*	*88.9501*	*79.9983*	*74.8659*	*71.3712*
$h^2_{(culth)}$	0.0878	0.1307	0.1839	0.2373	0.2707	0.0890	0.1322	0.1853	0.2183	0.3012	0.0940	0.1444	0.2047	0.2656	0.3247
	0.0687	**0.0949**	**0.0888**	**0.1061**	**0.1419**	**0.0708**	**0.0977**	**0.0914**	**0.1093**	**0.1462**	**0.0737**	**0.1018**	**0.0953**	**0.1139**	**0.1523**
	139.8212	*112.3167*	*101.0133*	*94.5327*	*90.1200*	*143.5823*	*115.3380*	*103.7306*	*97.0756*	*92.5442*	*149.1677*	*119.8246*	*107.7657*	*100.8518*	*96.1442*
h^2_{DL}	0.0843	0.1255	0.1766	0.2279	0.2600	0.0854	0.1269	0.1779	0.2097	0.2893	0.0903	0.1387	0.1966	0.2551	0.3118
	0.0770	**0.1063**	**0.0994**	**0.1189**	**0.1590**	**0.0793**	**0.1095**	**0.1024**	**0.1224**	**0.1637**	**0.0826**	**0.1140**	**0.1067**	**0.1276**	**0.1706**
	170.4713	*136.9376*	*123.1564*	*115.2552*	*109.8752*	*175.0570*	*140.6212*	*126.4694*	*118.3555*	*112.8308*	*181.8667*	*146.0914*	*131.3890*	*122.9596*	*117.2199*
$h^2_{f(A)}$	0.2214	0.3295	0.4636	0.5983	0.6826	0.2243	0.3333	0.4672	0.5505	0.7595	0.2370	0.3641	0.5163	0.6698	0.8186
	0.1191	**0.1644**	**0.1539**	**0.1839**	**0.2460**	**0.1227**	**0.1693**	**0.1585**	**0.1894**	**0.2533**	**0.1278**	**0.1765**	**0.1651**	**0.1974**	**0.2640**
	329.0303	*264.3062*	*237.7068*	*222.4564*	*212.0724*	*337.8812*	*271.4160*	*244.1012*	*228.4405*	*217.7771*	*351.0248*	*281.9741*	*253.5967*	*237.3269*	*226.2486*
$h^2_{f(beta)}$	0.1013	0.1508	0.2121	0.2737	0.3123	0.1026	0.1525	0.2137	0.2519	0.3475	0.1085	0.1666	0.2362	0.3064	0.3745
	0.1032	**0.1424**	**0.1333**	**0.1593**	**0.2130**	**0.1063**	**0.1467**	**0.1373**	**0.1640**	**0.2194**	**0.1107**	**0.1528**	**0.1430**	**0.1709**	**0.2286**
	247.5585	*198.8608*	*178.8478*	*167.3736*	*159.5607*	*254.2178*	*204.2102*	*183.6588*	*171.8759*	*163.8529*	*264.1069*	*212.1539*	*190.8031*	*178.5619*	*170.2268*
$h^2_{f(\Delta P\,beta)}$	0.1014	0.1510	0.2124	0.2741	0.3127	0.1028	0.1527	0.2140	0.2522	0.3479	0.1086	0.1668	0.2365	0.3069	0.3750
	0.1044	**0.1441**	**0.1349**	**0.1612**	**0.2156**	**0.1075**	**0.1484**	**0.1389**	**0.1660**	**0.2221**	**0.1120**	**0.1547**	**0.1447**	**0.1730**	**0.2314**
	283.0760	*227.3916*	*204.5073*	*191.3868*	*182.4530*	*290.6907*	*233.5084*	*210.0085*	*196.5351*	*187.3610*	*301.9986*	*242.5919*	*218.1778*	*204.1804*	*194.6494*

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

Table 4. Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h^2) of herd-life without adjusted production and other related trait for various values of h^2 (heritability for stayability) for normal distribution $r_{pi}=0.35$

Estimates	UB=0.00					UB=5.9999					UB=7.5001				
	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26
h^2_z	0.0713	0.1144	0.1599	0.2093	0.2622	0.0724	0.1182	0.1692	0.2156	0.2704	0.0733	0.1202	0.1674	0.2203	0.2748
	0.0790	**0.0770**	**0.0830**	**0.0919**	**0.1089**	**0.0814**	**0.0793**	**0.0855**	**0.0947**	**0.1122**	**0.0848**	**0.0826**	**0.0891**	**0.0987**	**0.1169**
	114.6944	*99.4050*	*86.9354*	*83.9189*	*80.4434*	*117.7797*	*102.0790*	*89.2740*	*86.1764*	*82.6073*	*122.3613*	*106.0499*	*92.7467*	*89.5286*	*85.8207*
$h^2_{croⁿⁱˢ}$	0.0763	0.1224	0.1711	0.2239	0.2805	0.0774	0.1265	0.1810	0.2307	0.2892	0.0784	0.1285	0.1791	0.2356	0.2940
	0.0885	**0.0862**	**0.0930**	**0.1030**	**0.1220**	**0.0912**	**0.0888**	**0.0958**	**0.1061**	**0.1257**	**0.0950**	**0.0925**	**0.0998**	**0.1105**	**0.1310**
	154.5049	*133.9085*	*117.1107*	*113.0472*	*108.3652*	*158.6611*	*137.5106*	*120.2609*	*116.0882*	*111.2803*	*164.8330*	*142.8598*	*124.9391*	*120.6040*	*115.6091*
h^2_{DL}	0.0732	0.1175	0.1643	0.2150	0.2694	0.0743	0.1214	0.1738	0.2215	0.2778	0.0753	0.1234	0.1720	0.2263	0.2823
	0.0991	**0.0966**	**0.1042**	**0.1154**	**0.1367**	**0.1021**	**0.0995**	**0.1073**	**0.1188**	**0.1408**	**0.1064**	**0.1037**	**0.1118**	**0.1238**	**0.1467**
	188.3739	*163.2625*	*142.7825*	*137.8283*	*132.1200*	*193.4411*	*167.6543*	*146.6233*	*141.5359*	*135.6740*	*200.9660*	*174.1760*	*152.3270*	*147.0416*	*140.9517*
$h^2_{f(Z)}$	0.1923	0.3086	0.4313	0.5646	0.7073	0.1952	0.3189	0.4564	0.5817	0.7293	0.1978	0.3241	0.4515	0.5941	0.7412
	0.1534	**0.1495**	**0.1612**	**0.1785**	**0.2115**	**0.1580**	**0.1539**	**0.1660**	**0.1839**	**0.2179**	**0.1646**	**0.1604**	**0.1730**	**0.1916**	**0.2270**
	363.5844	*315.1164*	*275.5875*	*266.0253*	*255.0076*	*373.3648*	*323.5931*	*283.0008*	*273.1814*	*261.8673*	*387.8887*	*336.1808*	*294.0095*	*283.8081*	*272.0539*
$h^2_{f(beta)}$	0.0880	0.1412	0.1973	0.2583	0.3236	0.0893	0.1459	0.2088	0.2661	0.3337	0.0905	0.1483	0.2066	0.2718	0.3391
	0.1329	**0.1294**	**0.1396**	**0.1546**	**0.1832**	**0.1368**	**0.1333**	**0.1438**	**0.1592**	**0.1887**	**0.1426**	**0.1389**	**0.1498**	**0.1659**	**0.1966**
	273.5566	*237.0898*	*207.3487*	*200.1542*	*191.8646*	*280.9152*	*243.4676*	*212.9264*	*205.5384*	*197.0258*	*291.8428*	*252.9385*	*221.2093*	*213.5338*	*204.6901*
$h^2_{f(ΔP/beta)}$	0.0881	0.1414	0.1976	0.2586	0.3240	0.0894	0.1461	0.2091	0.2665	0.3341	0.0906	0.1485	0.2069	0.2722	0.3396
	0.1345	0.1310	0.1413	0.1565	0.1854	0.1385	0.1349	0.1455	0.1612	0.1910	0.1443	0.1406	0.1516	0.1679	0.1990
	312.8040	*271.1054*	*237.0973*	*228.8706*	*219.3917*	*321.2184*	*278.3981*	*243.4752*	*235.0272*	*225.2933*	*333.7138*	*289.2278*	*252.9464*	*244.1698*	*234.0572*

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

Table 5. Average estimates of individual narrow-sense heritability (h^2) and family mean heritability (h^2_f) of herd-life adjusted for production and other related trait for various values of h^2_s (heritability for stayability) for normal distribution r_{pj}=0.35

Estimates	UB=0.00					UB=5.9999					UB=7.5001				
	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26	0.06	0.11	0.16	0.21	0.26
h^2_f	0.0586	0.1032	0.1477	0.1918	0.2361	0.0598	0.1040	0.1478	0.1906	0.2335	0.0601	0.1061	0.1521	0.1979	0.2437
	0.0580	**0.0713**	**0.0871**	**0.1086**	**0.1213**	**0.0597**	**0.0734**	**0.0897**	**0.1118**	**0.1249**	**0.0622**	**0.0765**	**0.0935**	**0.1165**	**0.1302**
	86.7773	*84.9231*	*75.2939*	*73.2738*	*68.2238*	*89.1116*	*87.2075*	*77.3193*	*75.2449*	*70.0590*	*92.5780*	*90.5999*	*80.3271*	*78.1719*	*72.7843*
h^2_{health}	0.0627	0.1104	0.1580	0.2052	0.2526	0.0639	0.1113	0.1581	0.2039	0.2498	0.0643	0.1135	0.1627	0.2117	0.2607
	0.0649	**0.0799**	**0.0976**	**0.1216**	**0.1359**	**0.0669**	**0.0823**	**0.1005**	**0.1253**	**0.1399**	**0.0697**	**0.0857**	**0.1048**	**0.1305**	**0.1458**
	116.8976	*114.3999*	*101.4285*	*98.7071*	*91.9043*	*120.0422*	*117.4773*	*104.1569*	*101.3624*	*94.3765*	*124.7118*	*122.0471*	*108.2086*	*105.3054*	*98.0477*
h^2_{bl}	0.0602	0.1060	0.1518	0.1970	0.2425	0.0614	0.1069	0.1518	0.1958	0.2399	0.0617	0.1090	0.1563	0.2033	0.2503
	0.0728	**0.0895**	**0.1093**	**0.1363**	**0.1522**	**0.0749**	**0.0921**	**0.1126**	**0.1404**	**0.1568**	**0.0781**	**0.0960**	**0.1174**	**0.1462**	**0.1634**
	142.5228	*139.4775*	*123.6626*	*120.3447*	*112.0506*	*146.3566*	*143.2295*	*126.9891*	*123.5820*	*115.0648*	*152.0499*	*148.8011*	*131.9290*	*128.3893*	*119.5408*
$h^2_{(t2)}$	0.1580	0.2783	0.3985	0.5174	0.6368	0.1612	0.2806	0.3986	0.5140	0.6299	0.1621	0.2861	0.4103	0.5339	0.6573
	0.1126	**0.1384**	**0.1692**	**0.2108**	**0.2355**	**0.1159**	**0.1426**	**0.1742**	**0.2172**	**0.2426**	**0.1208**	**0.1486**	**0.1816**	**0.2263**	**0.2528**
	275.0862	*269.2085*	*238.6838*	*232.2799*	*216.2712*	*282.4860*	*276.4502*	*245.1044*	*238.5282*	*222.0889*	*293.4747*	*287.2041*	*254.6389*	*247.8070*	*230.7282*
$h^2_{t,h,ml}$	0.0723	0.1273	0.1823	0.2367	0.2914	0.0738	0.1284	0.1824	0.2352	0.2882	0.0742	0.1309	0.1877	0.2443	0.3007
	0.0975	**0.1199**	**0.1465**	**0.1826**	**0.2040**	**0.1004**	**0.1235**	**0.1509**	**0.1881**	**0.2101**	**0.1046**	**0.1287**	**0.1573**	**0.1960**	**0.2189**
	206.9716	*203.5492*	*179.5828*	*174.7646*	*162.7199*	*212.5391*	*207.9978*	*184.4136*	*179.4658*	*167.0971*	*220.8069*	*216.0889*	*191.5873*	*186.4470*	*173.5971*
$h^2_{f,xP,h,ml}$	0.0724	0.1275	0.1826	0.2370	0.2918	0.0739	0.1286	0.1826	0.2355	0.2886	0.0743	0.1311	0.1880	0.2446	0.3011
	0.0987	**0.1213**	**0.1483**	**0.1848**	**0.2064**	**0.1016**	**0.1250**	**0.1527**	**0.1903**	**0.2126**	**0.1059**	**0.1302**	**0.1591**	**0.1983**	**0.2215**
	236.6660	*231.6092*	*205.3478*	*199.8383*	*186.0655*	*243.0323*	*237.8395*	*210.8716*	*205.2139*	*191.0706*	*252.4862*	*247.0914*	*219.0745*	*213.1967*	*198.5033*

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

probabilities, the average estimated values are tabulated in Table 3. One point is noticed that in case of 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 Table 3 it is concluded that adjustment seems to be correction on the estimates of heritability of herd life.

Unadjusted for two characters (related)

For these situations 2 characters, i.e. production and other related character say, other related character say, udder depth are considered. Data are simulated on the basis of some prior knowledge about the parametric values of (heritability of other related character say, udder depth) = 0.26, $r_{s_{HL}}$ (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 two character case we are considering r_{p1} (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 4. In unadjusted situation when we consider 2 related characters estimates are slightly improved than that of single character unadjusted situation. But the trends are almost same i.e. individual narrow sense heritability using raw data (h^2_r) (without transformed with the help of threshold probability) provides best estimate than the beta-binomial estimate ($h^2_{(beta)}$) and Dempster-Lerner (h^2_{DL}) estimate. When we make comparison among beta-binomial ($h^2_{(beta)}$) 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 are more in some situations. In family mean heritability the beta-binomial estimate ((h^2_{fbeta}) and realized heritability $h^2_{fAP,beta}$ estimate provide similar estimate but raw data ((h^2_{fes}) (without transformed with the help of threshold probability) give higher estimate with lesser degree of precision.

Adjustment for two related characters

Using above discussed all the parameters simulation was carried out for adjusted case of 2 related characters. Taking averages over the threshold probabilities all the estimates are Tabulated in Table 5. It gave far better estimate as compared to the single character adjustment case. For 2 character adjustment all the narrow sense heritability estimates are almost closer to the parametric value. The standard error also reduced as compared to the one character adjustment. RMSE value also follows 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 error and more RMSE value.

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