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Heritability and Repeatability for Milk Production Traits of Japanese Holsteins from an Animal Model¹

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ABSTRACT

Records of the first three lactations of cows were obtained from the file of the Dairy Herd Testing Association in Hokkaido. The data were divided into 10 files containing approximately 24,000 cows each. The derivative-free REML method was used to estimate variances with a repeatability model. The model contained herd-year, calving month, and the linear and quadratic effects of age at calving as fixed effects; additive genetic, permanent environmental, and temporary environmental effects were the random effects. Estimates from the 10 data files were pooled into a simple arithmetic mean. Empirical standard errors were calculated from the samples. Average estimates of heritability were the same for milk and fat yields ($h^2 = .30$). Heritabilities for protein ($h^2 = .26$) and SNF yields ($h^2 = .27$) are slightly lower than those for milk and fat yields. Estimates of repeatabilities, .52 to .54, are considerably different from those now used for genetic evaluations in Japan.

(Key words: Japanese Holstein, milk production, heritability, repeatability)

Abbreviation key: DF = derivative-free.

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INTRODUCTION

For dairy cattle improvement, prediction of breeding values with an animal model instead of computation of separate genetic evaluations for cows and bulls is becoming common. Some countries implemented national animal model evaluations in the late 1980s [e.g., (3, 5, 7, 14)]. In Japan in 1992, the maternal grand-sire model evaluation was replaced by the animal model. Evaluation is with a repeatability model, which includes the first five lactation records of cows. Good estimates of variances for milk yield traits in Japan are not available. To estimate variance components, use of the model for prediction, or of a similar model as used for the prediction of breeding values, seems desirable. The estimation of variance components, however, is more difficult than computation of genetic evaluations. Smith and Graser (8) and Graser et al. (4) presented a derivative-free (DF) REML algorithm for animal models that does not require direct inversion. Their procedure is applicable to relatively large data files. The procedure also can be extended to models with more than one random effect (1, 6).

The objective of this study was to estimate heritabilities and repeatabilities for milk, fat, protein, and SNF yields of Holsteins in Japan by the DF REML algorithm using the animal model with repeated records, which is similar to the model used for predicting breeding values in Japan.

MATERIALS AND METHODS

Yield records of the first three lactations were extracted from the file of the Dairy Herd Testing Association in Hokkaido. Because testing for milk protein and SNF began only re-

cently and cows were required to have a first lactation record and all four yield traits, the period of calving varied between 1985 and 1991 and differed by region. The data were divided into 10 files by herd within region, each with about 24,000 cows (Table 1). Two-generation pedigrees for dams and three-generation pedigrees for sires were used in calculating the inverse of the numerator relationship matrix. To estimate variances with the repeatability model, REML, with a DF algorithm using SPARSPAK (1), was used. The primary differences between animal model evaluations for Japan and the US are that, in Japan, records are not preadjusted for age, and herd-year is used rather than herd-year means for contemporary grouping so that the model contains effects for calving age, month of calving, and herd-year. The univariate model for estimating variance components was

$$Y_{ijkl} = HY_i + M_j + a_k + p_k + b_1 x_{ijkl} + b_2 (x_{ijkl})^2 + e_{ijkl}$$

where Y_{ijkl} is milk, fat, protein, or SNF yield with twice daily milking and complete records of length 240 to 305 d for cow k in herd-year i , calving month j , and lactation l ; HY_i is effect of herd-year i ; M_j is effect of calving month j ; x_{ijkl} is the cow age at calving; a_k is additive genetic effect of cow k ; p_k is the permanent environmental effect of cow k ; b_1 and b_2 are the partial regression coefficients for linear and quadratic effects of age at calving; and e_{ijkl} is

random residual associated with each record. All numerator relationships within a data file and the two- and three-generation pedigrees were utilized. Covariances of additive genetic and permanent environmental effects were assumed to be zero. Second lactation records of cows were included in the analyses only if the cow had a first lactation record in the data. Similarly, third lactation records were included only if the cow had both preceding records in the data. Estimates from the 10 data files were pooled as the simple arithmetic mean. Yerex (15) showed that the mean provided nearly the same estimates as analysis of all data in a single analysis if the samples were about the same size. In addition, estimates from several samples provide empirical estimates of variability of estimated components for genetic and environmental terms, although such standard errors also may be influenced by the structure of genetic relationships that would seem to be similar across data files based on number of animals with records and order of numerator relationship matrix.

RESULTS AND DISCUSSION

Means for milk, fat, protein, and SNF yields for the 10 data files are shown in Table 2. The results for milk, fat, protein, and SNF yields, respectively, are presented in Tables 3 to 6. Convergence occurred within 100 rounds by the criterion that the variance of the log likelihoods in the simplex [see, e.g., (1)] was less than 10^{-7} in all data files and for all traits. Mean heritabilities were .30, .30, .26, and .27 for milk, fat, protein, and SNF yields, respectively. These values are almost the same or slightly higher than those estimated by Henderson's method 3 using similar data with a sire model (9) and are within the range of reported values with an animal model (10, 11, 13). Average repeatability was .54 for milk yield and was .52 for fat, protein, and SNF yields. These estimates are comparable with estimates of .53 to .56 obtained by Visscher and Thompson (13). Estimates of heritabilities and repeatabilities are not greatly different across data files compared with those of Van Vleck and Dong (10), but variance components from the additive genetic effects varied considerably. For example, the minimum estimate for additive variance of genetic effects for fat

TABLE 1. Number of records by lactation and order of the numerator relationship matrix A and mixed model equations (MME) for 10 data files.

Subset	Lactation			Order of	
	First	Second	Third	A	MME
1	24,731	15,278	8572	30,037	58,199
2	24,697	16,319	9948	29,317	57,928
3	23,289	15,265	9258	28,083	55,306
4	24,803	14,815	7621	30,125	57,616
5	24,733	14,429	7284	30,086	57,671
6	23,614	13,837	6831	28,839	55,517
7	24,793	15,694	9148	30,191	58,104
8	23,141	14,542	8277	27,642	53,622
9	24,858	15,184	8310	29,529	56,740
10	24,780	14,694	7400	29,299	56,659

TABLE 2. Means and standard deviations of milk (M), fat (F), protein (P), and SNF (S) yields for 10 data files by lactation.

Data subset	First lactation				Second lactation				Third lactation			
	M	F	P	S	M	F	P	S	M	F	P	S
(kg)												
1												
\bar{X}	6627	248	210	587	7840	293	247	685	8425	314	262	729
SD	1360	52	42	119	1605	62	49	139	1676	66	51	144
2												
\bar{X}	6307	236	199	557	7538	280	237	658	8097	300	253	701
SD	1318	51	42	116	1583	60	49	137	1647	63	51	142
3												
\bar{X}	6265	233	197	551	7379	275	232	642	7949	294	247	686
SD	1271	50	40	111	1488	58	46	128	1539	61	47	132
4												
\bar{X}	6781	253	215	600	8067	299	256	704	8605	318	270	744
SD	1326	51	42	117	1571	60	48	136	1606	62	49	139
5												
\bar{X}	6837	254	217	605	8027	297	255	701	8567	315	268	740
SD	1347	51	43	119	1606	61	50	139	1679	63	51	144
6												
\bar{X}	6674	250	211	589	7845	291	248	683	8361	308	261	721
SD	1292	49	41	114	1540	58	47	132	1573	59	48	135
7												
\bar{X}	6118	227	191	536	7359	272	231	639	7979	293	248	687
SD	1200	46	38	105	1440	54	44	124	1508	57	46	129
8												
\bar{X}	5984	225	186	523	7210	270	225	623	7784	290	241	667
SD	1182	46	37	103	1424	55	43	121	1495	57	45	127
9												
\bar{X}	6029	229	189	527	7360	279	231	637	7990	302	249	685
SD	1226	48	38	107	1453	56	44	124	1519	59	46	129
10												
\bar{X}	6027	229	189	527	7248	275	228	627	7815	296	244	671
SD	1204	47	37	105	1413	55	43	121	1501	60	45	128

TABLE 3. Estimated variance components,¹ heritabilities, and repeatabilities (R) of milk yield for 10 data files with means and empirical standard errors.

Subsets	$\hat{\sigma}_a^2$	$\hat{\sigma}_p^2$	$\hat{\sigma}_e^2$	h^2	R
1	428,434	342,251	705,362	.29	.52
2	392,230	308,267	652,472	.29	.52
3	376,293	261,408	608,725	.30	.51
4	378,277	305,932	703,141	.27	.49
5	452,460	291,879	708,161	.31	.51
6	376,338	292,226	666,288	.28	.50
7	489,450	345,570	597,150	.34	.58
8	435,667	411,703	545,908	.34	.61
9	288,459	288,008	543,053	.26	.51
10	480,144	444,486	522,103	.33	.64
\bar{X}	409,775	329,173	625,236	.30	.54
SE	17,999	17,484	21,573	.01	.01

¹ $\hat{\sigma}_a^2$ = Estimated variance component for additive genetic effects (kilograms squared), $\hat{\sigma}_p^2$ = estimated variance component for permanent environmental effects (kilograms squared), and $\hat{\sigma}_e^2$ = estimated error variance (kilograms squared).

TABLE 4. Estimated variance components,¹ heritabilities, and repeatabilities (R) of fat yield for 10 data files with means and empirical standard errors.

Subsets	σ_a^2	σ_p^2	σ_e^2	h^2	R
1	662.2	451.3	1077.0	.29	.51
2	576.8	393.5	943.3	.30	.51
3	552.0	339.7	890.3	.31	.50
4	511.2	450.4	973.2	.26	.50
5	678.3	372.1	982.2	.33	.52
6	463.7	446.9	926.9	.25	.50
7	811.9	476.4	833.4	.38	.61
8	633.4	485.7	768.9	.34	.59
9	423.1	394.0	787.6	.26	.51
10	345.3	390.8	786.8	.23	.48
\bar{X}	565.8	420.1	897.0	.30	.52
SE	41.2	14.5	30.5	.01	.01

¹ σ_a^2 = Estimated variance component for additive genetic effects (kilograms squared), σ_p^2 = estimated variance component for permanent environmental effects (kilograms squared), and σ_e^2 = estimated error variance (kilograms squared).

yield occurred in data file 10 and was less than one-half of the maximum estimate from data file 7.

Several factors must be considered for reliable estimation of genetic parameters. Herd yield is one of these factors. Van Vleck et al. (11) reported that heritability for higher yielding herds was larger than for lower yielding herds. There were some differences in mean milk yield among data files. The lowest mean for each trait and in each lactation occurred in

data file 8, and the highest occurred in data file 4 or 5. The difference was 800 kg or more in milk yield. The same tendency was observed for other traits as well (Table 2). The heritability estimates varied from .26 to .34 across data files for milk yield (Table 3), but no obvious relationship existed between the mean yield and the magnitude of heritability.

Dong et al. (2) recognized that ignoring existing relationships resulted in reduced REML estimates of genetic variance. Thus,

TABLE 5. Estimated variance components,¹ heritabilities, and repeatabilities (R) of protein yield for 10 data files with means and empirical standard errors.

Subsets	σ_a^2	σ_p^2	σ_e^2	h^2	R
1	317.0	321.4	616.3	.25	.51
2	298.9	276.2	569.7	.26	.50
3	280.3	237.2	527.3	.27	.50
4	268.3	296.8	604.4	.23	.48
5	354.7	271.5	604.1	.29	.51
6	273.3	277.3	573.1	.24	.49
7	358.5	403.7	496.6	.28	.61
8	427.7	371.6	456.0	.34	.64
9	227.0	241.3	461.8	.24	.50
10	175.6	247.2	451.2	.20	.48
\bar{X}	298.1	294.4	536.1	.26	.52
SE	21.4	16.8	19.7	.01	.02

¹ σ_a^2 = Estimated variance component for additive genetic effects (kilograms squared), σ_p^2 = estimated variance component for permanent environmental effects (kilograms squared), and σ_e^2 = estimated error variance (kilograms squared).

TABLE 6. Estimated variance components,¹ heritabilities, and repeatabilities (R) of SNF yield for 10 data files with means and empirical standard errors.

Subsets	$\hat{\sigma}_a^2$	$\hat{\sigma}_p^2$	$\hat{\sigma}_e^2$	h^2	R
1	2760.8	2594.3	5212.0	.26	.51
2	2541.3	2286.2	4802.3	.26	.50
3	2487.3	1934.4	4423.6	.28	.50
4	2440.8	2296.1	5112.4	.25	.48
5	2982.5	2163.9	5103.5	.29	.50
6	2377.2	2193.0	4819.8	.25	.49
7	3442.5	2448.1	4250.7	.34	.58
8	3427.0	2893.7	3838.7	.34	.62
9	1859.6	2009.1	3853.6	.24	.50
10	1484.0	2066.2	3745.3	.20	.49
\bar{X}	2580.3	2288.5	4516.2	.27	.52
SE	185.7	87.3	171.2	.01	.01

¹ $\hat{\sigma}_a^2$ = Estimated variance component for additive genetic effects (kilograms squared), $\hat{\sigma}_p^2$ = estimated variance component for permanent environmental effects (kilograms squared), and $\hat{\sigma}_e^2$ = estimated error variance (kilograms squared).

higher estimates of heritability might result if more precise pedigree data could be used. For the data in this study, only a small increase would be expected because at least two-generation pedigrees on the dam side and three-generation pedigrees on the sire side were used. Visscher and Thompson (12) suggested that some differences in estimates of genetic variances may be due to types of relatives contributing to parameter estimates.

CONCLUSIONS

With a model similar to the evaluation model used in Japan, estimates of heritability were the same for milk and fat yields ($h^2 = .30$); heritabilities for protein, ($h^2 = .26$) and SNF yields ($h^2 = .27$) were slightly lower than those for milk and fat yields. Estimates of repeatabilities of .52 to .54 are considerably larger than those now used for genetic evaluations in Japan. These results suggest that these estimates should be used as parameters for genetic evaluations in Japan rather than the estimates now used.

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