Estimates of Genetic Parameters for the Canadian Test Day Model with Legendre Polynomials for Holsteins Based on More Recent Data

Bethany Muir, Gerrit Kistemaker and Brian Van Doormaal
Canadian Dairy Network

INTRODUCTION

The current implementation of the Canadian Test Day Model (CTDM) for production traits in Holsteins includes Legendre polynomials of order four (five coefficients) for fixed, random animal and permanent environmental regressions (Jamrozik and Schaeffer, 2000, 2003). Implementation of the same model for the remaining 6 coloured breeds commenced in February 2004 using recently calculated genetic parameters (Muir et al, 2003). Parameters for Holsteins were estimated using test day records on approximately 3,500 cows from lactations with calving dates up to 1996 (Jamrozik et al., 1998; Jamrozik and Schaeffer, 2003). The GEB requested that NEW genetic parameters also be estimated for Holsteins (as was done for the coloured breeds) based on more cows and more recent data such that more generations of dam-daughter pairs with test day records are included. Including more recent data to estimate parameters in the Ayrshire and Brown Swiss breeds increased genetic correlations across lactations in yield traits (Muir et al., 2003) but no obvious trends were found in Jerseys.

DATA AND METHODS

Data Data were a random sample of test day records extracted for the official genetic evaluations released in November 2003 (calving dates 1988 to 2003). Table 1 shows the number of animals and number of test day records randomly sampled in each analysis (previous estimation and current estimation). Days in milk on test day ranged from 5 to 305. In the current estimation, herds were required to have a minimum of 50 cows in the data set to be randomly selected. In the previous estimation, herds were required to have a minimum of 300 test day records in order to be randomly selected. Both estimations required that all four traits (milk, fat, protein, somatic cell score) were recorded on a test day to be included in the analysis.

Model The model a multiple trait random regression test day animal model, as reported by Schaeffer et al. (2000) (with Legendre polynomials as random regressions instead of the Wilmink function). The model for trait i in lactation j was:

$$\mathbf{y}_{ijtlmno} = \mathbf{HTD}_{ijl} + \Sigma \mathbf{b}_{ijnp}\mathbf{z}_{tp} + \Sigma a_{ijmp}\mathbf{z}_{tp} + \Sigma \mathbf{p}_{ijnp}\mathbf{z}_{tp} + \mathbf{e}_{ijtlmno}$$

where **y** was the record o on cow m made on day t within herd-test day effect l, for a cow in the subclass n for season-age of calving, **HTD** was fixed herd-test day effect, **b** were fixed regression coefficients specific to subclass n, **a** were random regression coefficients specific to cow m, **p** were random permanent environmental coefficients specific for cow m, **e** was the residual effect for each observation, and **z** were covariates assumed to be the same for both fixed and random coefficients. Shapes of lactation curves were modeled using Legendre polynomial curve of order 4 (5 covariates). The same function was used for all regressions. Residual variances were assumed the same within four intervals: DIM 5 to 45, DIM 46 to 115, DIM 116 – 265, DIM 266 – 305.

Bayesian methods with Gibbs Sampling were used to generate posterior distributions as described by Jamrozik et al. (1998). Posterior means of (co)variance components were estimated using 45,000 samples after a burn-in of 5000 iterations. Variances for 305d milk, fat, and protein yield and average daily SCS were calculated as described by Jamrozik and Schaeffer (2003). Daily heritability was defined as a ratio of genetic variance to the sum of genetic, permanent environmental (PE) and residual variances for each day in milk from 5 to 305 days, and averaged across the entire lactation for each of the first three lactations. The results of the current parameter estimation were then compared to the previous estimates using the same model (Jamrozik and Schaeffer, 2000, 2003), with an older data set (Jamrozik et al., 1998).

RESULTS AND DISCUSSION

Genetic and PE variances for cumulative 305d milk, fat and protein yield, and average daily SCS are shown in Table 2. As hypothesized, all variances were higher than previous estimates using older data (Jamrozik and Schaeffer, 2003). Average daily heritabilities, genetic and PE correlations for 305d yields of milk, fat and protein yield, and average daily SCS in the first three lactations are shown in Table 3 for the current study. Differences between the current and previous estimates are shown in Table 4.

Average daily heritabilites for milk, fat and protein yield from the current parameter estimation ranged from .33 to .39, and were highest for milk yield (Table 3). Heritability for SCS was generally lower (.25 to .32). New estimates of heritability for milk yield tended to be higher (.01 - .05) than previous estimates (Table 4). Heritability of fat and protein yield tended to be the same, and heritability of SCS was lower (.03 - .05), in the current estimates compared to the previous estimates.

Differences between genetic correlations across parameter estimations were variable. Genetic correlations within trait across lactations increased for milk, fat and protein yield (.04 - .07), and for SCS (.08 - .14) (Table 4). Genetic correlations within lactation between fat yield and other yield traits decreased significantly, specifically correlations between fat and milk yield decreased by .17 - .20 and correlations between fat and protein yield decreased by .12 - .13. It is interesting to note that while the genetic correlations among yield traits involving fat decreased, no change was observed in the genetic correlations between milk and protein yields. Genetic correlations between SCS and yield traits in first lactation increased by .05 - .11.

RECOMMENDATION

The new estimates of (co)variance components for Holsteins were estimated on a larger and more recent dataset compared to the previous estimates. Therefore, these estimates are expected to be more accurate and should be implemented for the next round of genetic evaluations in May 2004. To achieve this objective, a parallel run to the February 2004 official release will be done using the new genetic parameters and resulting bull proofs will be submitted to the Interbull test run scheduled for March 2004.

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Table 1: Number of test day records and animals used for the previous (Jamrozik and Schaeffer, 2003) and current parameter estimations.

	Previous Estimation	Current Estimation
Cows with records	3,696	12,411
Pedigree animals	11,050	28,822
Test Day records	60,811	176,381
HTD classes	9,694	15,853

Table 2: Genetic and permanent environmental variances for the previous (Jamrozik and Schaeffer, 2003) and current parameter estimations.

		Previous Estimation			Current Estimation		
		Lactation 1	Lactation 2	Lactation 3	Lactation 1	Lactation 2	Lactation 3
Genetic	Milk	399,079	666,927	749,871	602,060	886,426	996,560
	Fat	551	1094	1224	785	1472	1746
	Protein	339	577	630	455	715	802
	SCS	0.38	0.41	0.67	0.41	0.49	0.705
PE	Milk	564,222	847,658	876,283	589,530	932,318	1,086,734
	Fat	707	1045	1247	826	1290	1538
	Protein	465	751	835	508	810	949
	SCS	0.79	1.03	1.04	1.26	1.34	1.42

Table 3: Average daily heritabilities (diagonal), 305d PE correlations (above diagonal) and 305d genetic correlations (below diagonal) for the **NEW** estimated genetic parameters.

	M 1	F 1	P 1	S 1	M 2	F 2	P 2	S 2	M 3	F 3	P 3	S 3
M 1	**.41**	.79	.95	-.20	.46	.32	.46	-.09	.39	.26	.37	.02
F 1	.49	**.33**	.84	-.14	.35	.52	.42	-.06	.30	.42	.34	.01
P 1	.88	.61	**.37**	-.16	.45	.39	.50	-.09	.38	.32	.41	.01
S 1	.21	.07	.19	**.19**	-.08	-.04	-.08	.38	-.11	-.05	-.09	.24
M 2	.81	.39	.69	.14	**.40**	.81	.96	-.31	.46	.36	.47	-.06
F 2	.30	.82	.40	.00	.53	**.36**	.85	-.28	.35	.51	.43	-.06
P 2	.69	.53	.78	.14	.89	.68	**.37**	-.29	.47	.43	.53	-.05
S 2	.18	.07	.17	.52	-.01	-.11	-.01	**.23**	-.20	-.17	-.20	.48
M 3	.73	.32	.62	.16	.88	.43	.77	.02	**.40**	.84	.96	-.26
F 3	.24	.75	.34	.03	.40	.85	.53	-.06	.53	**.36**	.88	-.25
P 3	.57	.45	.67	.15	.75	.57	.85	.01	.88	.68	**.38**	-.23
S 3	.09	-.02	.07	.44	-.09	-.17	-.11	.61	-.13	-.21	-.14	**.28**

Table 4: **Differences** between average daily heritabilities (diagonal), 305d PE correlations (above diagonal) and 305d genetic correlations (below diagonal) between the previously estimated (Jamrozik and Schaeffer, 2003) and NEW estimated genetic parameters.

	M 1	F 1	P 1	S 1	M 2	F 2	P 2	S 2	M 3	F 3	P 3	S 3
M 1	**.05**	-.04	.01	.02	-.11	-.07	-.09	-.07	-.09	-.03	-.08	-.03
F 1	-.17	**.00**	-.07	.01	-.06	.00	-.08	-.04	-.06	-.03	-.09	-.04
P 1	-.02	-.13	**.02**	.00	-.10	-.10	-.11	-.07	-.09	-.07	-.10	-.04
S 1	.09	.05	.11	**-.05**	.03	.00	.01	-.06	-.03	-.04	-.03	-.09
M 2	.04	-.11	.03	.13	**.03**	-.04	.00	-.05	-.08	-.02	-.04	.01
F 2	-.20	.04	-.14	.04	-.20	**-.01**	-.06	.02	-.07	-.01	-.07	.03
P 2	.00	-.05	.04	.12	-.02	-.13	**.01**	-.04	-.07	-.04	-.05	.01
S 2	.05	.00	.01	.11	.05	-.04	-.01	**-.03**	-.04	.00	-.05	-.13
M 3	.05	-.10	.04	.08	.05	-.15	.03	.02	**.01**	-.01	.01	-.01
F 3	-.17	.07	-.12	.00	-.14	.06	-.07	-.06	-.20	**.00**	-.04	.02
P 3	-.01	-.03	.04	.07	.03	-.05	.06	-.06	-.03	-.12	**.01**	.00
S 3	.11	.03	.07	.08	.07	-.02	.03	.14	.07	-.01	.00	**-.04**

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