Understanding Cow Evaluations in Univariate and Multivariate Animal and Random Regression Models

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ABSTRACT

The relationship between cow evaluations from a 305-d lactation yield animal model [i.e., lactation model (LM)] and a random regression model (RRM) were studied using the first-lactation milk yield of 2,477,807 Holstein heifers. In the LM analysis, 2 values of heritability were used, 0.35 (LM1-H) or 0.57 (LM2-H), the latter being equal to that used in the random regression model for the analysis of the Holstein test-day records (RRM-H). The relative weights on parent average (PA) and yield deviations (YD) were computed and studied to understand factors contributing to reranking of cows' predicted transmitting abilities (PTA) from the various models. The degree of relatedness and inbreeding were calculated for the top 2,000 cows from the various models. Analyses of Jersey milk yield in the first 3 parities was implemented using 305-d lactation yield multivariate animal (MLM-J) and random regression models (MRRM-J). The ability of both models using only first-parity yield records to predict evaluations in second and third parities when records for these later parities were excluded was studied in a sample of cows. The correlations of cow PTA between LM1-H or LM2-H and RRM-H were 0.91 and 0.92, respectively, in the Holstein data. The data sets used were identical in this case for all models in terms of number of cows and yield records. The correlations were slightly lower at 0.89, 0.87, and 0.88 for parities 1, 2, and 3 in the Jersey analyses, where the data sets were not identical. The relative weights on PA and YD were 0.28 (0.11) and 0.72 (0.89), respectively, from the LM2-H (RRM-H). The RRM-H placed more emphasis on YD and therefore on Mendelian sampling deviations. Thus, the top 2,000 cows from the RRM-H were less related and inbred. The average additive genetic relationship was 22% greater in the LM2-H and average inbreeding coefficients were 0.68 and 0.43% for the LM2-H and RRM-H, respectively. When records were initially available in the first parity,

the MRRM-J predicted PTA in parities 2 and 3 with about 2 to 7% greater accuracy compared with the MLM-J.

Key words: random regression, animal model, inbreeding, yield deviation

INTRODUCTION

One of the criteria examined by countries updating their genetic evaluations from a 305-d lactation yield animal model (LM) to a random regression model (RRM) is the correlations between evaluations from both models. The correlations tend to be high for bulls and usually vary from 0.90 to 0.98. However, the correlations between cow evaluations are usually lower varying from 0.80 to 0.88 (Reents et al., 1998; Van Doormaal and Kistemaker, 1999; Lidauer et al., 2000), which is indicative of high reranking that may manifest itself especially in top cow lists. This could have implications in terms of selection of bull dams and dams to breed cows and therefore, the efficiency of national breeding programs. Understanding of the factors contributing to this high degree of reranking and its implications are therefore important. Intuitively, a possible explanation is that cow evaluations are based on more limited information relative to bull evaluations and are, therefore, affected more by differences in the models in terms of effects fitted and genetic parameters. However, in a preliminary study, Mrode et al. (2000) suggested that, compared with LM evaluations, RRM places greater emphasis on animal performance relative to pedigree information. The greater emphasis on yield may imply that top lists of cows could include individuals with greater Mendelian sampling effects, cows that are likely to be less related and thus have lower levels of inbreeding.

Second, many countries implement multilactation RRM, and the single published cow evaluations are breeding values averaged across several parities. In the case of young cows, yield information will initially be available in the first parity; therefore, cow evaluations could change over time as additional yield information becomes available in later lactations. Differences in the predictive ability of evaluations in later parities of the

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LM compared with the RRM when yield data are only initially available in the first parity could be important in terms of the overall ranking of cow evaluations from both models.

This study was carried out to examine the relationship between cow evaluations in the top cow lists from the analysis of first-lactation Holstein milk yield fitting an LM with 2 levels of heritability and a RRM. Relative weights on pedigree, yield information, and Mendelian sampling effects were examined to better understand cow evaluations from these models. In addition, relative weights on parent and yield information in a multitrait situation using LM or RRM with milk yield in the first 3 lactations treated as different traits were computed. The predictive abilities of LM and RRM using the first 3 lactations of the Jersey breed when yield information was available only in first parity or in the first 2 lactations were examined. The degree of relatedness and levels of inbreeding were studied in the top 2,000 cows using results from the LM and RRM of the first-lactation analyses of the Holstein.

MATERIALS AND METHODS

Univariate Analysis of First-Lactation Holstein Data

The 305-d first-parity milk yield of 2,477,807 Holstein cows from 21,157 herds was analyzed with an LM equivalent to that used in the United Kingdom before the adoption of the RRM (Interbull, 2000). The fixed effects consisted of herd-year-season, age at calving by season of calving, heterosis, and recombination loss. There were 285,488 herd-year-season subclasses present in the data set and a heritability of 0.35 (used in the national LM evaluation) was used (**LM1-H**). The analysis was repeated using a heritability of 0.57 (**LM2-H**) computed for 305-d yield from the RRM genetic parameters. The random regression model (**RRM-H**) used to analyze 23,615,532 test-day records (**TD**) for the same set of cows with 1,914,963 herd-test-date subclasses represented, was:

$$y_{ijklmt} = htd_i(DIM_t) + hd_j(DIM_t) + Fix_{kt} + \sum_{l=0}^4 \phi_{lmt}\beta_l + \sum_{l=0}^2 \phi_{lmt}\mathbf{u}_{lm} + \sum_{l=0}^2 \phi_{lmt}\mathbf{p}_{lm} + e_{ijklmt}, \quad [1]$$

where y_{ijklmt} is the TD of cow m made on day t within herd-test-date (**htd**) subclass i in the j th herd (**hd**); **htd** (random) and **hd** (fixed) effects depended linearly on DIM, with an intercept and a slope; Fix_{kt} are other fixed effects in the model consisting of heterosis, recombination loss calculated from percentage North American Holstein genes and days pregnant by stage of lactation; β_l are fixed regression coefficients nested within age-

season subclasses; $\mathbf{u}_{lm}$ and $\mathbf{p}_{lm}$ are vectors of the l th random regression for animal and permanent environmental effects respectively for animal m ; ϕ_{lmt} is the vector of the l th Legendre polynomial for the test-day record of cow m made on day t , and e_{ijklmt} is the random residual. It is assumed that $\text{var}(\mathbf{u}) = \mathbf{A} \otimes \mathbf{G}$, $\text{var}(\mathbf{p}) = \mathbf{I} \otimes \mathbf{P}$ and $\text{var}(\mathbf{e}) = \mathbf{R}$ and $\text{cov}(\mathbf{u}, \mathbf{p}) = \text{cov}(\mathbf{u}, \mathbf{e}) = \text{cov}(\mathbf{p}, \mathbf{e}) = 0$, where $\mathbf{A}$ is the relationship matrix, $\mathbf{G}$ and $\mathbf{P}$ are the variance and covariance matrices for the random animal and permanent environmental regression effects, respectively, and $\mathbf{R}$ is the diagonal matrix of residual effects. There were 4 classes of residual variances fitted in the RRM-H and these were: 7.86kg², 4.38kg², 3.28kg², and 2.89kg², for d 4 to 24, 25 to 49, 50 to 249, and 250 to 305 in milk, respectively.

All data sets were preadjusted for heterogeneity of variance using the method described by Reents et al. (1998) before analyses using the above models. For the RRM-H, this briefly involved correcting all TD for the stage of lactation, age, and season effects using fixed lactation curves estimated from a fixed effect model. A weighted standard deviation was then calculated for each htd based on an observed standard deviation, expected standard deviation according to the production level to which the htd was assigned, and the herd size. The weighted standard deviation was then used to calculate the standardization factor for each htd. The same procedure was used in the LM except that 305-d milk yield was corrected for age and season effects and herd-year-season subclasses were used instead of htd.

On convergence, 305-d PTA for RRM-H were computed from the regression coefficients for each animal. The PTA were computed from the breeding values from LM1-H and LM2-H. Correlations between cow evaluations from the 3 analyses were computed using all cows with yield information. All PTA were adjusted to the mean of cows born in the base year of 2000.

Multivariate Analyses of Jersey First Three Lactation Milk Yield

The first 3 lactation TD milk yields were extracted from the data used for the official genetic evaluation of the Jersey breed in May 2007, and were analyzed using a multivariate random regression model (**MRRM-J**), regarding milk yield in each lactation as a different trait. The data consisted of 155,137 cows born between 1975 and 2005 with 3,282,323 test-day milk records in the first 3 lactations. The test-day records were from 2,474 herds with 262,585 herd-test-date subclasses represented. The mean number of records per herd-test-date subclass was 22, with a minimum of 2 and a maximum of 305. The distribution of records per lactation

Table 1. Summary of test day and 305 d yields for the Jersey breed in the first three lactations

Lactation number	Test-day yields		305-d yields
	Cows, n	Test days, n	Cows, n
1	155,137	1,326,371	129,538
2	116,640	1,085,483	90,185
3	93,825	870,469	66,130

is given in Table 1. The model used was a multivariate extension of model described in equation [1] and it was:

$$y_{ijklmqt} = htd_i(DIM_t) + hd_j(DIM_t) + Fix_{kqt} + \sum_{l=0}^4 \phi_{lmqt} \beta_{lq} + \sum_{l=0}^2 \phi_{lmqt} \mathbf{u}_{lmq} + \sum_{l=0}^2 \phi_{lmqt} \mathbf{p}_{lmq} + e_{ijklmqt} \quad [2]$$

where $y_{ijklmqt}$ is the TD of cow m for trait q made on day t within htd subclass i in the j th herd. The htd and hd effects were as defined in [1] and were fitted across the 3 traits, but Fix_{kqt} is now the fixed effect of days pregnant by stage of lactation for the q th trait. All other effects in [2] for the q th trait were as defined in model [1]. The variance and covariance structure assumed was as defined in [1] but were now for 3 traits. There were 4 classes of residual variances fitted for each parity as described for model [1]. After convergence, PTA for 305-d yield in each lactation were computed from the regression coefficients for each animal.

The data were reanalyzed with test-day records omitted in later parities for all cows born after December 31, 2000. In the first analysis, TD records were omitted from both the second and third parities for these cows (**MRRM1-J**); then, in a second analysis, TD records were only omitted from the third parity (**MRRM2-J**). The ability of the MRRM-J to predict PTA in the second and third parities when TD records were excluded was studied in a random sample of 1,300 cows that had their second and third or only third lactation TD records deleted. For this sample of cows, their progeny were also excluded from the data. This was to ensure that PTA values predicted for the later parities of these cows when observations were excluded did not contain contributions from progeny. The PTA from MRRM1-J and MRRM2-J for this sample of cows were correlated with and regressed on PTA from MRRM-J after all PTA had been adjusted to the same base.

Corresponding multivariate animal model evaluations were implemented on the same data using 129,538 cows that had completed 305-d yield records. The 305-d records were from 1,738 herds with 38,040 herd-year-season subclasses represented. The mean number of records per herd-year-season subclass was 7, with a minimum of 2 and a maximum of 165. The multivariate

Table 2. Genetic parameters for 305-d milk yield in the first 3 lactations showing heritabilities along the diagonal (in boldface) and genetic and phenotypic correlations below and above the diagonal, respectively

Parity	1	2	3
1	0.57	0.54	0.49
2	0.76	0.56	0.63
3	0.69	0.95	0.60

lactation animal model (**MLM-J**) used for the analyses consisted of herd-year season, month of calving, and age effects as fixed effects, and random effects were animal and permanent environmental effects. The permanent environmental effects were equivalent to those fitted for the MRRM-J and this implies that residual variances in all 3 parities were uncorrelated. The genetic parameters used for the analyses were computed from the random regression parameters (Thompson et al., 2005) and are shown in Table 2. Multivariate lactation animal models with 305-d yields omitted in parities 2 and 3 (**MLM1-J**) or in only parity 3 (**MLM2-J**) for cows born after December 31, 2000, were also implemented. Again, the sample of 1,300 cows that had both their second and third or only third lactations deleted and with their progeny excluded from the data sets was also studied. The PTA in the 3 parities from MLM-J were averaged and correlated with equivalent ones from MRRM-J. The PTA from MLM1-J and MLM2-J were correlated with, and regressed on, those from MLM-J in the sample of 1,300 cows. A summary of the various data analyses implemented, models and abbreviations are shown in Table 3.

Computing Relative Weights for Parent Average and Yield Deviation

For a cow with no progeny, the equation of VanRaden and Wiggans (1991) was used to compute the relative weight on pedigree and yield information in LM1-H and LM2-H:

$$PTA_{\text{cow}} = W_1 (\text{PA}) + W_2 (\text{YD}/2) \quad [3]$$

where **PA** is the parent average PTA, **YD** is the yield deviation that represents the yield of the animal adjusted for all effects in the model other than the genetic merit and error, and W_1 and W_2 are relative weights for PA and YD, respectively, that sum to unity. The numerators of W_1 and W_2 are αu_{par} and n respectively, with $\alpha = \sigma_e^2 / \sigma_a^2$, $u_{\text{par}} = 2, 4/3$, or 1 when both, 1, or neither parents are known, and n is the number of records. The denominator of either W_1 or W_2 is the sum of the 2 numerators. The relative weight for Mendelian sam-

Table 3. Summary of data, models and abbreviations for various analyses implemented

Abbreviation	Analyses
Analyses on Holstein data	
LM1-H	Animal model for Holstein first-lactation milk yield, heritability of 0.35
LM2-H	Animal model for Holstein first-lactation milk yield, heritability of 0.57
RRM-H	Random regression model for Holstein first-lactation milk yield
Analyses on Jersey data set	
MLM-J	Multivariate animal model for Jersey first 3 lactation milk yield
MLM1-J	Multivariate animal model for Jersey first 3 lactation milk yield with records for second and third parities deleted for cows born after the year 2000
MLM2-J	Multivariate animal model for Jersey first 3 lactation milk yield with records for third parities deleted for cows born after the year 2000
MRRM-J	Multivariate random regression model for Jersey first 3 lactation milk yield
MRRM1-J	Multivariate random regression model for Jersey first 3 lactation milk yield with records for second and third parities deleted for cows born after the year 2000
MRRM2-J	Multivariate random regression model for Jersey first 3 lactation milk yield with records for third parities deleted for cows born after the year 2000

pling (**MS**) was calculated by expressing [3] (Mrode, 2005) as:

$$PTA_{\text{cow}} = PA + W_2 (MS). \quad [4]$$

Equivalent equations to [3] and [4] (Mrode and Swanson, 2004) were used to calculate relative weights for PA and YD or MS for the RRM-H. Similar to the definition in [3], YD in the RRM-H case is a vector of the weighted average of a cow's TD corrected for all fixed and permanent environmental effects. The weighting is based on the inverse of the residual variance relevant to the TD in the different stages of the lactation. However, these relative weights are matrices of order 3. The use of Legendre polynomials in [1] implies that the majority of the information for 305-d evaluations computed from the random regression coefficients for animals would be coming from the relative weights on the intercept for PA and YD. Thus, the relative weights on the intercept were used as approximate weights on PA and YD. This is equivalent to solving the multivariate equations equivalent to [3] (Mrode and Swanson, 2004) by assigning the same value of [1 0 0] to **PA'** and **YD'**. The summation of the actual information contributed by PA and YD as a ratio of overall PTA over a large number of cows should approximate W_1 and W_2 calculated using equations [3] and [4]. This was done for LM1-H, LM2-H, and RRM-H, and the summation was over 1,434,516 Holstein cows with no progeny.

On the basis of the models used for the multivariate analyses of Jersey milk yield in the first 3 lactations as different traits, equivalent equations to [3] (Mrode and Swanson, 2004) were set up to compute relative weights on PA and YD for MLM-J and MRRM-J. From [2], Legendre polynomials of order 2 were used for each lactation; therefore, the genetic covariance for random regression coefficients for animal effects was of order 9 for the 3 lactations. Similarly, the weights on PA (W_1)

and YD (W_2) for the MRRM-J were matrices of order 9 but for MLM-J, these matrices were of order 3. In the case of MLM-J, the relative weights for PA and YD in each lactation were obtained by solving the multivariate equations equivalent to [3] by assigning the same values to PA and YD. In the case of the MRRM-J, the approximate relative weights based mainly on the intercept were computed by assigning the same value of [1 0 0 1 0 0 1 0 0] to **PA'** and **YD'**.

Relative Contribution of PA and YD

Using [3] and [4], the relative contributions from PA, YD, and MS were computed and studied in a random sample of 7,500 Holstein cows in the evaluations from LM2-H and RRM-H. The influence of these relative contributions on the reranking of cow evaluations was examined in this sample of cows.

Degree of Relatedness

A 4-generation pedigree was extracted for the top 2,000 cows in each of the 3 models (RRM-H, LM1-H, and LM2-H) used to analyze the first-lactation yield of the Holstein data, and the degree of relatedness and inbreeding were computed for the cows in these datasets.

RESULTS AND DISCUSSION

Correlations Between Cow Evaluations

The correlation between evaluations for Holstein cows from LM1-H and LM2-H with RRM-H were 0.91 and 0.92, respectively. These are slightly greater than the estimates of Reents et al. (1998), Van Doormaal and Kistemaker (1999), and Lidauer et al. (2000). This could be due to the fact that both models were applied to identical data sets. This would not be the case in

Table 4. The relative weights on parents' average (PA¹) in different lactations from multitrait equations for 305-d lactation-yield animal model (MLM-J) or random regression model (MRRM-J)

Parity no.	Test days, ² n	MRRM-J			MLM-J		
		PA ₁	PA ₂	PA ₃	PA ₁	PA ₂	PA ₃
1	3	0.39	0.49	0.45			
1	6	0.22	0.31	0.26			
1	8	0.16	0.24	0.20			
1	10	0.11	0.19	0.15	0.28	0.33	0.29
2	10	0.09	0.03	0.03	0.20	0.06	0.06
3	10	0.09	0.04	0.01	0.20	0.06	0.01

¹Parent average in the *i*th parity.²Number of test day records in each lactation.

national evaluation schemes, because the RRM may include cows with TD records from uncompleted lactations, which would not be in the LM analysis. On the other hand, cows with only 305-d yield records and no TD records would only be included in the LM evaluations and not in the RRM evaluations. Thus, parent and progeny contributions to the evaluations of the same cows in both models will be different for some animals. The correlations of Jersey cow PTA from the multivariate analysis, MLM-J, which used data in all lactations with those from the MRRM-J, were 0.89, 0.87, and 0.88, respectively, for the first, second, and third parities. The correlation was 0.88 for a PTA averaged across the 3 parities. These are more similar to estimates reported in the literature because data sets were not identical for both models. The MRRM-J included TD records from part-lactation yields, whereas these cows were not in the data set for MLM-J. These correlations confirm substantial reranking among cows across all 3 parities between both models.

Computing Relative Weights for PA and YD

The relative weights from the univariate analysis on PA and YD from [3] were 0.74 and 0.26 for LM1-H. Corresponding estimates were 0.28 and 0.72 for LM2-H. The information contributed by PA or YD as a ratio of overall PTA summed over the 1.4 million cows was 0.68 or 0.22, respectively, for LM1-H. Similar estimates for PA and YD were 0.31 and 0.69 for LM2-H, and these are not very different from the relative weights calculated using equation [3]. For the RRM-H, the relative weights for a cow with 10 test-day records approximated by the weights on the intercept were 0.11 for PA and 0.89 for YD. The ratio of the actual contribution from PA or YD to 305-d PTA summed over the 1.4 million cows was 0.14 or 0.86, respectively. These are not significantly different from the relative weights based on the intercept. The relative weights on PA and YD obtained using [3] for LM1-H, LM2-H, and equivalent equations for RRM-H were based on a situation in

which no inbreeding was assumed in calculating $\mathbf{A}^{-1}$. If inbreeding was accounted in $\mathbf{A}^{-1}$ and an inbreeding coefficient of 0.125, for instance, was assumed for an animal, the relative weights obtained using [3] were similar to the situation with no inbreeding. The relative weights on PA increased to 0.75 for LM1-H and 0.30 for LM2-H, but remained unchanged at 0.11 for RRM-H.

Thus, as expected, as heritability increased (LM1-H vs. LM2-H), the relative weight on pedigree information decreased in the LM analyses. However, a greater reduction on the relative weight on PA with the RRM-H, indicates that at the same level of heritability, RRM-H placed more emphasis on YD and, therefore, on MS. In fact, the relative weight on PA for a cow with 4 TD records in the RRM-H is equivalent to that in LM2-H in which a whole lactation has been used. Thus, at the same level of heritability, the emphasis placed on pedigree and yield in the LM2-H was similar to that in the RRM-H for a cow with just 4 TD records. The use of individual TD records in the RRM-H represents better use of information compared with one record in the LM2-H, thus evaluations are less regressed to the parent average in the RRM-H (Lidauer, 2002). This explains why the standard deviations of evaluations for the RRM are usually larger than those from the LM, even at the same level of heritability (Lidauer, 2002). The standard deviation of cow evaluations in the RRM-H in this study was about 20% greater than in the LM2-H. This is comparable to the increase of about 15 to 20% reported by Lidauer (2002).

The relative weights on PA and yield information in the first 3 lactations from the multivariate analyses on the Jersey data set are shown in Table 4. Also shown in Table 4 is the relative weight on PA in the first 3 lactations as the number of test-day records increases in the first parity. As more TD records become available in the first lactation, the relative emphasis on PA decreases in all 3 lactations. This is even more so as yield data become available in second and third parities. However, emphasis on PA is still greater by about twice in the MLM-J compared with the MRRM-J. In both

Table 5. Yield deviations, PTA, and proportion contributed by Mendelian sampling (MS) for 3 categories of cows¹

Cows	Yield deviation (kg)		PTA (kg)		MS	
	LM2-H	RRM-H	LM2-H	RRM-H	LM2-H	RRM-H
Category A ²						
Cow 1	945	923	113.3	189.8	0.18	0.41
Cow 2	961	981	178.2	350.3	0.05	0.25
Category B ³						
Cow 1	1,011	1,019	207.0	153.3	0.10	0.09
Cow 2	228	232	-508.9	-601.0	-0.28	-0.58
Category C ⁴						
Cow 1	898	904	65.4	61.8	0.21	0.24
Cow 2	1,199	1,227	369.3	367.0	0.14	0.16

¹See Table 3 for definitions of abbreviations.²PTA values greater in RRM1 than in LM2-H.³PTA values greater in LM2-H than in RRM-H.⁴PTA values very similar in RRM-H and LM2-H.

models, relative weight on PA is lower in parities 2 and 3 compared with first parity. This could be due to the greater heritability in the third parity and the high correlation of 0.95 between second and third parity in this study.

Relative Contribution of PA and YD

For the sample of 7,500 Holstein cows studied, differences in YD were the main factor influencing the relative ranking of cows in the LM2-H and RRM-H. For instance, cows with greater 305-d YD in the RRM-H tended generally to have greater PTA predicted in the RRM-H relative to LM2-H and vice versa. However, for cows with similar YD on a 305-d basis ($\leq 5\%$ different) in the RRM-H and LM2-H, the role of the relative contribution of PA and MS on PTA is shown in some chosen cows (Table 5) that best illustrate the principle. Cows with greater PTA in the RRM-H (>50 kg; category A) had greater (about 30 to 80% greater) positive MS relative contribution in the RRM-H. The relative MS contribution summed over 2,500 sampled cows that fell into this category was 0.14 for LM2-H and 0.22 for RRM-H. For cows with lower PTA in the RRM-H (≤ 50 kg; category B), this was either because of a similar MS

relative contribution in both models, such that a greater emphasis on PA resulted in a greater PTA in the LM2-H or a greater negative MS contribution in the RRM-H. The relative MS contribution summed over 2,500 of the sampled cows that fell into this category was -0.04 for LM2-H and -0.13 for RRM. Category C cows had similar PTA in both models (± 10 kg), and the MS contribution was also very similar. The relative MS contribution summed over 2,500 of the sampled cows in this category was 0.21 for LM2-H and 0.20 for RRM-H.

Predictive Ability

Table 6 shows the mean differences between PTA by parity (MLM1-J - MLM-J and MRRM1-J - MRRM-J) for the sample of 1,300 cows when records were excluded for parities 2 and 3. Also shown in Table 6 are the correlations between PTA from MLM-J and MLM1-J, and MRRM-J and MRRM1-J by parity. The mean differences indicate a slight underprediction in using only first-parity yield data to predict PTA in later lactations. The underprediction varied from 6 to 19 kg of milk for the second parity and about 25 kg for the third parity. However, given the standard deviations of the differences, these mean differences were not significant.

Table 6. Mean differences, correlations, and regressions of PTA from evaluations with yield data omitted from parities 2 and 3 with those from evaluations with no loss of data in a sample of 1,300 cows¹

Item	MLM1-J			MRRM1-J		
	Parity 1	Parity 2	Parity 3	Parity 1	Parity 2	Parity 3
Mean difference	-0.55 (56) ²	-6.40 (176)	-25.44 (222)	-4.79 (62)	-19.68 (151)	-26.88 (177)
Correlation	0.98	0.84	0.78	0.97	0.86	0.85
Regression	1.00	0.96	0.93	1.00	1.00	1.00

¹See Table 3 for definitions of MLM1-J and MRRM1-J.²Standard deviations in parentheses.

Table 7. Mean differences (kg), correlations, and regressions of PTA from evaluations with yield data omitted from parity 3 only with those from evaluations with all data in a sample of 1,300 cows

Item	MLM2-J			MRRM2-J		
	Parity 1	Parity 2	Parity 3	Parity 1	Parity 2	Parity 3
Mean difference	-0.32 (35)	-0.31 (99)	-17.27 (155)	2.37 (63)	-7.29 (91)	-12.94 (115)
Correlation	0.99	0.95	0.90	0.99	0.97	0.95
Regression	1.00	0.99	0.98	1.00	0.99	0.99

¹See Table 3 for definitions of MLM2-J and MRRM2-J.

²Standard deviations in parentheses.

The lower standard deviations of the differences for the MRRM-J are, however, indicative of the superior predictive ability of the random regression model. This result is consistent with the greater correlations between PTA MRRM-J and MRRM1-J in parities 2 and 3 compared with equivalent PTA from the multivariate lactation animal model. The regression of PTA from MRRM-J on MRRM1-J gave unity regression coefficients (Table 6), whereas those from the lactation model varied from 0.93 to 0.96. When data were omitted only in the third parity (Table 7), a similar trend was observed with predictions in the third parity for the sample of cows for both models. The correlation was greater in the third parity with the MRRM2-J but the regression was very close to unity. In general, it seems that the MRRM-J model predicted PTA in later parities with an accuracy that was about 2 to 7% greater than with the MLM-J. Thus, differences in the predictive ability of evaluations in later parities when data are not yet available would be contributory factors to the reranking in cow evaluations from both models.

Degree of Relatedness

With less emphasis on parent information, we expected the RRM-H to result in the selection of top cows that were less related and therefore less inbred compared with LM1-H and LM2-H. Summary statistics on the level of relatedness and inbreeding in the top 2,000 cows from the 3 univariate analyses on the Holstein data set are given in Table 8. The RRM-H resulted in

an increase in the number of sires represented in the top 2,000 cows by 78 and 15% compared with LM1-H and LM2-H, respectively, thereby increasing the genetic selection base. However, corresponding increases in the number of dams represented were only 6 and 3% relative to LM1 and LM2-H. The average additive genetic relationships between the cows in LM1-H was twice that in RRM-H but was only 22% greater in LM2-H than RRM-H. The number of related individuals decreased from 1,836 in LM1-H to 1,716 in LM2-H and 1,536 in the RRM-H with corresponding average inbreeding coefficients of 0.72, 0.68, and 0.43%, respectively. The proportion of the top 2,000 cows with greater-than-zero inbreeding coefficients were 0.50, 0.44, and 0.34 for LM1, LM2, and RRM-H, respectively. The distribution of cows by the level of inbreeding coefficient indicated that at each level of inbreeding ranging from 1 to 13%, there were fewer cows from the RRM-H compared with LM1-H and LM2-H. This would imply that progeny bred from the top 2,000 cows, given the same sires, should be less related, have lower inbreeding levels, and therefore less inbreeding depression with the RRM-H compared with LM1-H or LM2-H. However, given the greater emphasis on Mendelian sampling effects by the RRM-H, it is not clear whether estimates of inbreeding depression from including inbreeding in the model as covariate will differ between an LM and RRM, in a given population. This is an area that could be investigated further.

CONCLUSIONS

Factors contributing to the differences in the ranking of top cows between the LM and RRM include the greater emphasis on yield deviation and Mendelian sampling, even at the same level of heritability. In a multivariate situation when data are only initially available in first parity, differences in the predictive ability of evaluations in later parities may be another factor. The greater emphasis on yield deviation in the RRM resulted in the selection of top cows with greater Mendelian sampling and these were less related. This could result in slightly more genetic progress in the

Table 8. Summary of results on the degree of relatedness for the top 2,000 Holstein cows from the lactation models and random regression model¹

Item	LM1-H	LM2-H	RRM-H
No. of sires	249	384	442
No. of dams	1,832	1,886	1,944
No. related	1,836	1,716	1,536
Average relationship (%)	4.4	2.7	2.1
No. inbred	1,005	870	675
Average inbreeding (%)	0.72	0.68	0.43

¹See Table 3 for definition of LM1-H, LM2-H, and RRM-H.

dam pathway to breed bulls and cows, but could also be a problem if there is preferential treatment of bull dams. For countries moving from LM to RRM, the difference in heritability estimates used in both models is another contributing factor to differences in cow ranking.

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