J. Dairy Sci. 87:2277–2284

Use of Early Lactation Days Open Records for Genetic Evaluation of Cow Fertility

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ABSTRACT

National genetic evaluations for cow fertility were introduced by the USDA in February, 2003. These evaluations, reported as daughter pregnancy rate, are based on days open. One requirement of the evaluation system is that lactations be at least 250 d in milk (DIM) to be included for analysis. The objective of this research was to develop a predictor of days open, usable in genetic evaluation, to allow for earlier predicted transmitting abilities (PTA), especially for young bulls. The final prediction equation included an overall intercept, the effects of lactation and calving ease score, the linear and quadratic effects of age at calving, and a regression on days open based on last breeding. Data used for estimation were breeding records from 4 dairy records processing centers for the years 1995 through 1998. Genetic correlations were ≥0.91 by d 130, and phenotypic means of predicted days open were in agreement with means for final days open, indicating that the predictions were phenotypically unbiased. Comparison of mean PTA based on actual and predicted days open indicated no bias in PTA, and correlations between PTA were ≥0.92 by d 130. The earlier use of data increased reliability by about 5% for sires between the ages of 4 and 5 yr. The USDA began using predicted days open for records that are at least 130 DIM in national evaluations starting November, 2003.
(**Keywords:** fertility, genetic evaluation, prediction)

Abbreviation key: DO = days open, **DPR** = daughter pregnancy rate, **DO_LB** = days open based on last breeding.

INTRODUCTION

The USDA introduced a new genetic evaluation for cow fertility in February, 2003, for US dairy cattle (VanRaden et al., 2004). These evaluations are reported as daughter pregnancy rate (**DPR**) but are based on days open (**DO**). The DPR is just a linear transformation of DO [DPR = 0.25 (233 − days open)], done primarily to enhance ease of interpretation of PTA. One requirement of the evaluation system was that records be at least 250 DIM to be included for analysis. This was done to avoid a potential bias that could be created by using only cows that were bred early in lactation. One implication of this 250-d requirement, though, is a longer waiting period for DPR evaluations based on daughter fertility information, which is particularly consequential for early progeny test results. A young sire can get an evaluation for production, based on daughter performance, as early as 40 d after his first daughters initiate their first lactation. It would then be another 210 d before he could get a PTA for DPR that is based on breedings of milking daughters (heifer breedings were not previously reported to Animal Improvement Programs Laboratory). The objectives of this research were 1) to develop a predictor of DO, usable in the single trait national genetic evaluations for DPR, 2) to determine how early in lactation the predictor can be used, and 3) to compute expansion and weighting factors to correct for differences in genetic and error variances between actual and predicted records.

Prediction of DO requires knowledge of factors affecting DO. Numerous studies have found effects of both parity and age on DO (Seykora and McDaniel, 1983; Taylor et al., 1985; Marti and Funk, 1994; Dematawewa and Berger, 1998). Virtually all research on DO has indicated differences in herds and/or regions, years, and seasons (Seykora and McDaniel, 1983; Taylor et al., 1985; Marti and Funk, 1994; Dematawewa and Berger, 1998). The effect of milk yield on DO has also been well established, although estimates of the magnitude of the association have varied. Most estimates of genetic correlation between milk yield and DO have been around 0.3 to 0.35 (Hansen et al., 1983; Seykora and McDaniel, 1983; VanRaden et al., 2004), although Dematawewa and Berger (1998) reported correlations around 0.55. Calving ease is another factor affecting DO, with more difficult calving resulting in more DO

Received November 18, 2003.
Accepted January 20, 2004.
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(Dematawewa and Berger, 1997). Days open is a function of days to first breeding, number of services to conception, and intervals between services. Raheja et al. (1989) reported genetic correlations between days to first breeding and DO in the range of 0.28 to 0.12 for lactations 1 through 3. Estimates from Hansen et al. (1983), however, were considerably higher, ranging from 0.8 to 1.0. Heritability estimates for DO have generally been in the range of 0.03 to 0.05 (Seykora and McDaniel, 1983; Marti and Funk, 1994; Dematawewa and Berger, 1998; VanRaden et al., 2004).

MATERIALS AND METHODS

Data

Data available for estimation and testing of proposed prediction models were breeding records from 4 dairy record processing centers: Dairy Records Management Systems, Ag Source Cooperative, Agri Tech Analytics, and Pennsylvania DHIA. These records included breeding date and service sire for each breeding in a lactation. Calving dates spanned 1995 through 1999, but data were restricted to calvings through 1998 to ensure completed records. Initially, about 4.5 million records were available and included primarily Holsteins but also a small number of records on Jerseys. After additional edits such as requiring Holsteins, AI matings, and only fifth and earlier lactations, along with a number of other edits to ensure validity of data (e.g., require 1.8 yr ≤ age at calving ≤ 12 yr), about 3.5 million records were available, overall, for analysis. Days open were calculated as differences between breeding dates and calving dates. To be consistent with the USDA's definition of final or actual DO (VanRaden et al., 2004), DO greater than 250 were set to 250 d and those lower than 50 were set to 50 d.

Prediction Models

The two basic prediction equations considered were

$$\hat{y} = \text{Intercept} + \text{Lactation} + \text{CE} + \beta_1{*}\text{Age} + \beta_2{*}\text{Age}^2 + \beta_3{*}\text{DO\_LB} \quad [1]$$

$$\hat{y} = \text{Intercept} + \text{Lactation} + \text{CE} + \beta_1{*}\text{Age} + \beta_2{*}\text{Age}^2 + \beta_3{*}\text{DO\_LB} + \beta_4{*}\text{Milk} + \beta_5{*}\text{Milk}^2 \quad [2]$$

where $\hat{y}$ is the predicted DO, CE is calving ease score (scores of 1 through 5), age is age at calving in years (e.g., 2.5 yr), **DO_LB** is DO based on last breeding, milk is the average of first 3 test-day milk yields, and β_1 through β_5 are regression coefficients for corresponding effects. The prediction models were fit separately for each of 9 DIM groups: 70, 90, ..., 230. Nesting within DIM was done to allow for determination of minimum DIM required before using records in progress and to provide for more accurate predictions, especially for cows not yet bred. Separate solutions for different DIM groups allows higher predicted DO for cows later in lactation and known to be not yet bred. Separate sets of solutions were also computed for cows that did not have calving ease scores and cows that did not have a breeding. There were a total 9 (DIM groups) ×2 (with/without calving ease scores) ×2 (with/without a breeding) = 36 sets of solutions for each prediction model.

Inclusion of DO_LB in the model reflects the uncertainty in pregnancy status associated with a last reported breeding. If it were known with certainty that the last breeding resulted in a pregnancy, then the record would be excluded from prediction.

Inclusion of milk yield in the predictor was tested as an option because of the known phenotypic and genetic correlation of milk yield with DO (VanRaden et al., 2004). However, with milk yield in the predictor, early lactation predictions could be affected more by milk yield than by fertility differences, which could result in a genetic correlation between predicted DO and milk yield that was higher than the genetic correlation between actual DO and milk yield. This, in turn, could reduce early DPR PTA for high-milk sires more than is appropriate. Genetic correlations between predicted DO and milk yield were estimated for both models to assess this concern.

Calculation of DO_LB. The DO_LB was calculated for each DIM group as the difference between breeding date and calving date, using the last breeding prior to the cutoff point for the given DIM group. Thus, if a cow had breedings at 85, 115, and 135 d, her DO_LB was 85 for the first 2 DIM groups (70, 90), 115 for the third DIM group (110), and 135 for each DIM group thereafter. If a cow did not have a breeding by the upper end of the DIM group, then for estimation of effects in [1] and [2] she contributed to the "without breeding" subset rather than the "with breeding" subset of solutions for both models.

Other alternatives. Numerous preliminary models were tested prior to the final selection of [1] and [2]. One preliminary model used days to first breeding instead of DO_LB, but use of DO_LB provided a higher correlation with final DO, so it was included in the final models. To improve phenotypic correlations, attempts were also made to include environmental effects such as herd, year, and season, but these all resulted in predictors with severe phenotypic bias and were thus excluded. For second and later lactations, consideration was also given to using an animal's previous DO and previous number of services to conception. This increased both the phenotypic and genetic correlations with final DO, without the consequence of creating a difference between mean predicted DO and final DO (i.e., phenotypic bias). However, previous DO and previous number of services were not included in the final predictor because of concern about correlated errors between records in genetic evaluation.

Finally, for cows that had at least one breeding, an attempt was made to utilize number of days since last breeding. If 2 cows are both at 150 DIM, for example, and one was last bred at 80 d and the other at 149 d, it was conceivable that the regression on DO_LB could dominate the predictor more so for the cow that had gone over for 70 d than for the cow that had gone over for only 1 d. Thus, records were classified according to both DIM and days since last breeding, and the prediction model fit separately for each subclass. Use of days since last breeding, however, did not improve accuracy of prediction, primarily because there was little variation in DO_LB within subclass, when records were classified according to both DIM and days since last breeding. Days since last breeding added little information beyond DIM and DO_LB, so days since last breeding was not used as part of the final predictor.

Evaluation of Predictors

Phenotypic bias, phenotypic and genetic correlations, and PTA based on final versus predicted DO were used as criteria to evaluate the predictors. Means of predicted and actual DO were used to evaluate phenotypic bias within each DIM group.

The primary criteria for choice of model and DIM to begin predictions were genetic, rather than phenotypic, correlations because the objective was to develop a prediction of DO suitable for genetic evaluation. Inclusion of environmental factors such as season or region-season was not given priority consideration because, while they would increase the phenotypic correlations between predicted and final DO, they would have no impact on genetic correlations. The predictor could put them in only to have the genetic evaluation model remove them. Furthermore, season effects vary by year, and it would not be appropriate to estimate year-season effects from the incomplete data (records in progress) available for genetic evaluation because that could introduce the very bias that use of predicted records is intended to avoid. Thus, extensive attempts to include environmental effects such as season were considered a nonproductive complication and were not extensively pursued.

Phenotypic and genetic correlations. Phenotypic and genetic correlations were estimated for each DIM group. A multiple-trait sire model was used for REML estimation of genetic correlations. The model included, in addition to the random effect of sire, only the fixed effect of herd-year-season-parity of calving. Eleven traits were included: final DO, 9 predicted DO corresponding to the 9 DIM groups, and milk yield, which was the average of the first 3 test days.

Each lactation for each cow included in the analysis had a record for each trait. Although a cow-lactation could contribute to only one set of solutions (e.g., with or without a breeding) for estimation of effects in [1] and [2], each cow-lactation had a predicted DO for each DIM group. If the cow did not have a breeding by the end of the upper limit for the DIM group, she was simply predicted using the “without a breeding” set of solutions for [1] or [2]. Approximately 670,000 records were used for estimation of correlations and calculation of phenotypic means for evaluating bias. Calving years for data included in estimation of correlations were 1995 through 1998, inclusive. In contrast, only years 1995 through 1997 were used to estimate the effects in the prediction models. Therefore, there was one additional year of data used for prediction that was not used in estimation of effects in the prediction models. A data set completely independent of that used for estimation of effects would have been desirable, but that alternative was not practical given a limited amount of data.

Comparison of PTA based on actual and predicted DO. Two data sets, PTAy and PTA$\hat{y}$, were formed to evaluate PTA computed using predicted DO. The 2 data sets contained the same cow-lactations, roughly 374,000 records that included calvings from 1995 through 1998. For computation of PTA, cows were required to have first lactation. In national DPR evaluations, most records would be completed, while projected DO would be mainly for current records in progress. To make the comparison between PTA based on actual vs. predicted DO as realistic as possible, PTA$\hat{y}$ contained predicted records only for the last year of data included (1998), while all previous years in PTA$\hat{y}$ (1995 through 1997) contained actual DO. There were about 127,000 predicted records in PTA$\hat{y}$, which was roughly 34% of all records. The 1998 records accounted for more than 25% of the data, expected given 4 yr of data, partly because there were more records in the later years and partly because edits for this comparison, in particular the one requiring cows to have a first lactation, removed more cow-records from the earlier years than from the later years.

In contrast to PTA$\hat{y}$, PTAy contained only actual DO for all years. Days open breeding values for this comparison were computed from an animal model that included the fixed effect of herd-year-season-parity and the random effects of animal and permanent environment. Criteria to compare the 2 sets of PTA were mean differences and correlations, computed separately for cows and sires. This PTA comparison was done only for DIM groups 110, 130, and 150.

Expansion and Weighting Factors

The USDA routinely uses projected records in the single-trait national genetic evaluations for production traits, SCS, and productive life (VanRaden et al., 1991; VanRaden and Klaaskate, 1993). Expansion and weighting factors are applied because variances for predicted and actual records are generally not equal (VanRaden et al., 1991).

"Expansion factors" equalize genetic variances for predicted and actual records (VanRaden et al., 1991; VanRaden and Klaaskate, 1993). These expansion factors are computed simply as the ratio of additive genetic standard deviation for actual records to additive genetic standard deviation for predicted records. Genetic variances are equalized, then, by multiplying deviations of predicted records from their management group mean by the appropriate expansion factor. Expansion factors for predicted DO records were estimated for each of the 9 DIM groups.

"Weighting factors" refer to the diagonal elements of $\mathbf{R}^{-1}$, the inverse of the error variance-covariance matrix for genetic evaluation. These are computed as the ratio of error variance for actual records to error variance for predicted records. Although USDA utilizes a diagonal error variance-covariance matrix for national evaluations, the diagonal elements are not required to be equal. Thus, in contrast to the expansion factors which are used as a prior adjustment, the weighting factors are used directly in the mixed-model equations. After expansion, predicted records generally have larger error variances than actual records and get less weight than actual records, which is intuitively appealing. Weighting factors were computed for each of the 9 DIM groups.

Effects on DPR Evaluations

Although collection of more complete breeding information has been initiated by the USDA in the form of the new "format 5" [Format 5 will include information on each breeding: service sire, service number, date of service, type of mating (AI or natural service). Additionally, observed heats, synchronizations, embryo transfers, results of pregnancy exams and "do not breed designations" can also be reported.] record (VanRaden et al., 2004), the historical USDA database, which is what the national DPR evaluations are based on, contains only final DO as opposed to information on each individual breeding. For records in progress, "final" DO, in the USDA database, is DO based on last breeding. Thus, implementation cannot be tested, for example, by using actual vs. predicted DO, since only final DO is known. Nonetheless, properties of evaluations using predicted DO can still be compared to evaluations using only final DO.

The DPR evaluations using predicted DO were computed using data available at the time of the August, 2003 run. Mean sire PTA and reliabilities by birth year were compared to those for the August, 2003 run which used only final DO. Only sires designated with sampling status S (S = semen distributed to at least 40 herds with records qualifying for use in USDA genetic evaluations.) by the National Association of Animal Breeders were included in this comparison.

RESULTS AND DISCUSSION

Table 1 has mean squares, computed from SAS type III sum of squares (SAS Institute, 1999), for effects in the prediction models for DIM groups 110, 130, and 150. The DO_LB was, by far, the main factor in the prediction equations, with lactation effects generally accounting for the second largest amount of variation.

Given the importance of availability of at least one breeding in predicting DO, percentage of cows with a breeding by given DIM is summarized in Table 2. At 90 d, over 60% of cows already had at least one breeding, and by 130 d, 86% of cows had at least one breeding. About 2% of cows did not have their first breeding until after d 250.

Phenotypic means and correlations for predicted and final DO are in Table 3. Estimates in Table 3 are only for the case in which milk was included in the predictor, but there was little difference between the two models for these parameters. Mean of predicted DO agreed quite well with actual mean DO, indicating little or no phenotypic bias. Phenotypic correlations between predicted and actual DO increased from 0.28 at 70 DIM to 0.88 at 230 DIM. The increase in correlation with increasing DIM was primarily due to more cows having at least one breeding as DIM increased. Dematawewa and Berger (1998) reported a mean DO of 169 d. Mean DO was somewhat lower in this study because of the restriction to a 250-d maximum.

Genetic correlations between predicted and actual DO are in Table 4 for both prediction models. Genetic correlations also increased as DIM increased, again because of increasing number of cows with at least one breeding as DIM increased. There was no loss in genetic correlation when milk yield was excluded from the predictor. By 130 DIM, genetic correlations were 0.90 and higher. It should be emphasized that the correct inter-

Table 1. Mean squares for effects in prediction models without milk [1] and with milk [2] by DIM group.

	DIM 110		DIM 130		DIM 150	
Source	[1]	[2]	[1]	[2]	[1]	[2]
Lactation	1,100,261	1,336,358	1,103,481	1,346,478	885,726	1,089,532
Calving ease	193,602	198,901	152,534	156,097	107,392	110,844
Age	111,039	105,518	152,251	148,268	123,868	120,600
Age^2	118,110	145,173	81,788	101,421	64,193	79,935
DO_LB[1]	88,639,160	86,930,369	203,318,080	200,620,882	344,109,737	340,395,792
Milk		250,017		222,574		134,457
Milk^2		27,699		23,704		6902
Error	3273	3256	2857	2843	2397	2387
R^2 (%)	11.8	12.3	23.3	23.7	36.3	36.6

[1] DO_LB = Days open based on last breeding.

pretation of this correlation is that if all cows were 130 DIM, the genetic correlation between final and predicted DO would be 0.90 or 0.91. Thus, if cows were required to be at least 130 DIM before having their record predicted and included in genetic evaluation, the absolute minimum “overall” genetic correlation between predicted and final records would be 0.90. Since some cows will be more than 130 DIM, the overall genetic correlation between actual and predicted records would be higher than 0.90.

Genetic correlations between milk yield and predicted DO at each DIM are in Table 5. These can be compared to the estimated genetic correlation between final DO and milk yield of 0.31, which is consistent with estimates from Hansen et al. (1983), Seykora and McDaniel (1983), Raheja et al. (1989), and VanRaden et al. (2004). With milk yield in the predictor, genetic correlation of milk with predicted DO was generally higher than the correlation between milk and actual DO. Conversely, without milk in the predictor, genetic correlations of milk with predicted DO were similar to that between milk and final DO. Within model, the genetic correlations in Table 5 show a slight pattern of decreasing, with increasing DIM after d 130. This simply reflects the increasing correlation between predicted and final DO as DIM increases; as DIM approaches 250, the genetic correlation between predicted DO and milk yield approaches the genetic correlation between final DO and milk yield.

Expansion and weighting factors are in Table 6. Weights for this trait were peculiar relative to other traits such as production because the weights were not only higher at earlier stages of lactation but also greater than one, indicating that more “weight” should be given to early predictions than even to final DO. Although inclusion of milk yield may have exacerbated this peculiarity, it was not the main cause, as the same pattern existed when milk yield was excluded from the predictor. The higher weights for early DIM might be expected given the heritabilities for early-lactation predictions vs. heritability of actual DO (Table 6). The higher heritabilities in early lactation reflected less error variance for predicted DO ($\sigma^2_{e\hat{y}}$) than for actual DO (σ^2_{ey}), in which case the ratio of error variances ($\sigma^2_{ey}/\sigma^2_{e\hat{y}}$) is necessarily greater than one. In turn, the higher heritabilities for predictions in the earlier stages of lactation were likely reflecting the fact that the heritability of days to first breeding is higher than the heritability of final DO. VanRaden et al. (2004) estimated heritability for days to first breeding at 0.07, which was consistent with the 0.06 estimate of Weigel and Rekaya (2000).

Table 2. Percentage of cows with first breeding by DIM.

DIM	Percent	Cumulative Percent
70	36.2	36.2
90	25.4	61.6
110	15.5	77.1
130	8.8	85.9
150	5.1	91.0
170	3.1	94.1
190	1.9	96.0
210	1.2	97.2
230	0.8	98.0
>250	2.0	100.0

Table 3. Phenotypic means and correlations for actual days open (DO) and predicted DO for the prediction model where milk was included.

DIM	Mean	Correlation
Actual	138.8	1.0
70	138.7	0.29
90	138.1	0.38
110	137.8	0.46
130	137.9	0.55
150	138.1	0.63
170	138.3	0.71
190	138.4	0.78
210	138.5	0.84
230	138.5	0.88

Table 4. Genetic correlations of predicted days open (DO) with actual DO for the prediction model without milk ([1]) and with milk ([2]) by DIM group.

DIM	[1]	[2]
70	0.73	0.73
90	0.80	0.80
110	0.86	0.85
130	0.91	0.90
150	0.94	0.94
170	0.97	0.96
190	0.98	0.98
210	0.99	0.99
230	0.99	0.99

Table 6. Expansion and weighting factors for prediction models without milk ([1]) and with milk ([2]).

	Expansion factors		Weighting factors		h^2	
DIM	[1]	[2]	[1]	[2]	[1]	[2]
Actual	1.0	1.0	1.0	1.0	0.041	0.041
70	2.31	2.17	1.77	1.98	0.07	0.078
90	1.93	1.83	1.61	1.79	0.064	0.071
110	1.86	1.75	1.25	1.41	0.05	0.056
130	1.75	1.67	1.02	1.13	0.042	0.046
150	1.63	1.57	0.90	0.96	0.037	0.039
170	1.47	1.43	0.88	0.93	0.036	0.038
190	1.37	1.35	0.85	0.88	0.035	0.036
210	1.26	1.24	0.89	0.91	0.036	0.037
230	1.20	1.19	0.89	0.90	0.036	0.037

In contrast, final DO has a heritability of about 0.04 (VanRaden et al., 2004). The DO_LB would be more akin to days to first breeding in the early predictions than in the predictions later in lactation.

The comparison of PTA based on predicted versus actual records (Table 7) indicated no bias in PTA due to use of predicted records. Correlations between PTA ranged from 0.90 to 0.93 for cows with a predicted record and from 0.93 to 0.95 for sires with at least one daughter that had a predicted record.

Implementation into National DPR Evaluations

The USDA implemented the use of predicted DO in DPR evaluations in November, 2003. Records were used starting at 130 DIM, which is a reduction of 4 months in waiting time for DPR proofs based on daughter performance. By d 130, genetic correlation of predicted with final DO is ≥ 0.90, and overall correlation of sire PTA based on predicted versus final DO was ≥ 0.94. Starting at d 130 also partially circumvents the problem of weighting incomplete records more heavily than complete records, which is counter-intuitive. Weights will be slightly modified from those in Table 6 so as to be more consistent with the amount of information contained in the records, relative to final DO. Weights will be 0.90, 0.91, 0.92, 0.93, 0.94, and 0.95 for records where DIM are ≥ 150, ≥ 170, ≥ 190, ≥ 210, ≥ 230, and ≥ 249, respectively. Records that are complete (DIM ≥ 250) but unconfirmed by a subsequent calving will be given a weight of 0.96. These values are a compromise between the values in Table 6 and the fact that "weights" should reflect the amount of information contained in the predicted value, relative to final DO. The weights in Table 6 are 0.90 for 150 DIM and essentially constant from that point on. Therefore, 0.90 was taken as the initial weight at 130 d and incremented slightly for subsequent DIM groups.

Records will be projected using equation [1], without milk yield in the predictor. Genetic correlations of predicted DO with milk yield were more consistent with the genetic correlation between final DO and milk yield without milk in the predictor than with milk in the predictor. Furthermore, this allows more readily for implementation of approximate multiple trait procedures (VanRaden, 2000), which could combine animals' milk yield and DPR evaluations instead of data.

A record must meet several criteria to be predicted: 1) it must be the cow's last record on file; i.e., either a terminal lactation or a record in progress, 2) 130 ≤ DIM ≤ 249 and 3) calving must have occurred on or after

Table 5. Genetic correlations of predicted days open (DO) with milk yield for the prediction model without milk ([1]) and with milk ([2]) by DIM group.

DIM	[1]	[2]
70	0.29	0.42
90	0.33	0.44
110	0.35	0.45
130	0.36	0.45
150	0.35	0.42
170	0.34	0.39
190	0.33	0.38
210	0.32	0.35
230	0.31	0.34

Table 7. Cow and sire PTA based on actual versus predicted records for the prediction model without milk ([1]) and with milk ([2]) by DIM group.

	Mean Difference[1]		Correlation	
DIM	[1]	[2]	[1]	[2]
Cow PTA				
110	–0.08	–0.05	0.90	0.90
130	–0.03	–0.005	0.91	0.92
150	–0.01	0.008	0.93	0.93
Sire PTA				
110	–0.04	–0.02	0.93	0.93
130	–0.007	0.01	0.94	0.94
150	0.01	0.03	0.95	0.95

[1] Expressed in standard deviation units.

Table 8. Mean PTA, reliability, number of daughters, and number of herds for Holstein sires by birth year in the August 2003 run and in a test run using predicted records with data available for the August 2003 run.

		Mean DPR PTA		Mean reliability		Mean number of daughters		Mean number of herds	
Birth year	Number of sires	Aug '03 run	Test run	Aug '03 run	Test run	Aug '03 run	Test run	Aug '03 run	Test run
1986	1218	0.010	0.016	66.0	66.0	412	413	158	158
1987	1279	−0.093	−0.084	64.5	64.5	292	293	120	121
1988	1342	0.036	0.040	63.9	63.9	231	232	100	100
1989	1410	0.148	0.146	64.8	64.8	285	288	114	114
1990	1399	0.033	0.036	65.6	65.6	287	292	116	117
1991	1405	0.021	0.027	65.8	65.9	294	305	116	118
1992	1586	0.012	0.025	64.8	64.9	199	210	88	90
1993	1501	−0.187	−0.176	64.2	64.5	125	137	67	70
1994	1391	−0.201	−0.203	65.2	65.9	116	147	68	79
1995	1362	−0.232	−0.228	64.2	65.0	75	83	51	55
1996	1300	−0.176	−0.169	61.4	62.4	70	71	50	50
1997	1292	0.070	0.106	56.3	58.3	67	70	47	49
1998	1147	−0.032	−0.016	45.9	50.8	31	51	23	37
1999	49	−0.217	−0.192	37.3	41.9	2	16	2	13

January 1, 2000. Records satisfying these criteria can still be excluded from prediction if 1) the herd does not report breedings or 2) the cow was culled for reproductive failure, in which case she is assigned the upper limit of 250 d for that lactation, regardless of DIM, or 3) the cow left the herd without a breeding. Only a cow's last available record will be considered for projection, since DO records for lactations with a subsequent calving can be confirmed by calving interval. Herds that do not report breedings are excluded from prediction because the predictor was not developed to handle such herds. Implementation of the approximate multiple-trait procedure would have the added benefit of bringing these animals into the evaluations as well. Consideration of only calvings on or after January 1, 2000, was introduced as a means to simplify identification of herds not reporting breedings. The effect of this starting point on either PTA or reliabilities will be minimal, since most predicted records will be records in progress.

Changes in mean Holstein sire PTA, reliability, and daughter and herd number, by birth year, are given in Table 8. The predicted DO had little effect on mean sire PTA, which is ideal. An effect on mean PTA would indicate a bias in either the previous or current PTA. Mean reliability increased 4.9% for sires born in 1998 and 4.6% for sires born in 1999, with smaller changes for birth years earlier than 1998. The biggest effect was expected for 1998, since most bulls get first-crop daughters around 5 yr of age. Use of predicted DO made more daughters available earlier for the young bulls, which was the objective. Average number of daughters increased by 20 for bulls born in 1998 and, on average, there were 14 more herds per bull when predicted records were used. For the Holsteins in the August 2003 test run, 92% of predicted records had a breeding. Ten percent of candidate records for prediction were excluded because of herds not reporting breedings.

Future Refinements in Prediction of DO

The USDA began collecting information on the results of pregnancy checks in 2002. This information was not available for this research study but would be valuable in the prediction of DO. If a cow is confirmed pregnant, for example, she might be excluded from prediction and her last reported breeding used as her final DO. Once this information, in conjunction with individual breeding data, has accrued, further research will develop the means to incorporate pregnancy check information into predictions of DO.

CONCLUSIONS

Days open can be adequately predicted for single-trait genetic evaluation at 130 DIM using a predictor, fit within DIM groups, which includes an overall intercept, the effects of lactation and calving ease score, the linear and quadratic effects of age at calving, and regression on DO based on last breeding. Implementation of this predictor, planned for November 2003, is expected to increase reliability by roughly 5% for bulls between the ages of 4 and 5 yr. Future research will focus on incorporating pregnancy confirmation information, which is now being reported to the USDA, into the predictor.

ACKNOWLEDGMENTS

The authors thank John Clay for assembling and providing the data on individual breedings from various processing centers used in this study.

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