Breeding and Genetics: Current Issues in Dairy Cattle Breeding

8 Improved accuracy of computer programs that optimize breeding and replacement decisions for dairy cattle. A. De Vries*, *University of Florida, Gainesville.*

Objective was to improve the accuracy of computer programs that optimize breeding and replacement decisions for individual cows to support economic decision making. Most recently published optimization programs characterize cows by a limited number of discrete states, a combination of (at least) parity, level of milk production, stage of lactation, and pregnancy status. The number of states is necessarily limited to make computations feasible. Consequently, cows may not be well represented by a state and the program's decisions may be significantly different from optimal. For example, a small number of lactation curves (for example Wood's curves) are typically used depending on parity and level of milk production. In practice, every cow has a unique lactation curve. A significant improvement in accuracy of prediction of cow performance can be obtained when the states for the current lactations of the cows currently in the herd are separated from the states for their next lactation and replacement heifers. The states for cows currently in the herd can then be dramatically increased with few extra computations. These adjustments allow for much more accurate predictions of individual cow performance in the current lactation than previously available. Predicted cow performance for the remainder of the lactation can be updated daily. Consequently, optimized breeding and culling decisions are more accurate. To illustrate, 400 cows from the University of Florida dairy research herd were used. Individual lactation curves were predicted by Best Prediction. The resulting 400 lactation curves predicted milk yields in the remainder of the lactation better than the few standard Wood's curves in traditional programs. Optimal breeding and culling decisions were frequently different. The program currently runs as an add-on to existing dairy herd information systems using automated data exchange. The proposed improvement in accuracy is an important step towards more realistic computerized decision support on dairy farms.

Key Words: Optimization, Breeding, Replacement

9 Genetic analysis of profitability of Canadian Holstein cows. J. Bohmanova*[1], J. Jamrozik[1], K. Hand[2], D. Lazenby[2], and F. Miglior[3,4], [1]*CGIL, University of Guelph, Guelph, ON, Canada*, [2]*CanWest DHI, Guelph, ON, Canada*, [3]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [4]*Canadian Dairy Network, Guelph, ON, Canada.*

Profitability functions, developed by Dairy Herd Improvement (DHI) in Canada, are widely used by Canadian farmers to evaluate profitability of their cows. Profit of a cow is defined as the difference between revenues and expenses. Revenues are functions of total amount of fat, protein and other solids, adjusted for amount of fluid in milk. Expenses are calculated as sum of overhead, maintenance feed, marginal feed and quota opportunity costs. Costs associated with fertility and health are not considered due to unavailability of data. The aim of this study was to estimate variance components and breeding values (EBV) for profit in the first 3 lactations and to calculate correlations between EBV for profit and other traits currently evaluated in Canada. Multi-trait (MT) and random regression models (RRM) were applied. The four traits estimated in MT were rearing costs and daily profits in first, second and third lactation. In the RRM analysis, profit was assumed to be a continuous trait, defined as function of age. The rearing cost was evaluated as a correlated trait with the same effects as in MT. Variance components were estimated by Gibbs sampling using a sub-sample of data consisting of records from 68,434 cows. Breeding values were estimated for 3,329,689 animals. In MT, heritability of rearing cost and daily profit in first, second and third lactation were 0.22, 0.28, 0.28 and 0.43, respectively. Rearing cost was lowly and negatively correlated (-0.18) with daily profit in first and uncorrelated with profit in later parities. In RRM, heritability of rearing cost was 0.36. Heritability of profit increased with age and ranged between 0.32 and 0.45. Medium and negative correlations were found between rearing cost and profit across all three lactations. Profit EBV were highly correlated with EBV for production traits (0.85), moderately with Lifetime Profit Index and negatively correlated with fertility, longevity and daughter calf survival. No correlations were found between EBV for conformation traits and profit, except for angularity and bone quality.

Key Words: Profitability, Rearing Cost, Random Regression Model

10 Alternatives for evaluating daughter performance of progeny-test bulls between official evaluations. H. D. Norman*[1], J. R. Wright[1], and K. A. Weigel[2], [1]*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*, [2]*University of Wisconsin, Madison.*

In August 2007, USDA changed from calculating official genetic evaluations quarterly to triannually to coincide with the schedule for international evaluations. Industry cooperators requested that unofficial interim evaluations be initiated between official evaluations for progeny-test (PT) bulls to offset part of the delay in receiving information due to the schedule change. To determine whether interim evaluations could provide accurate information for semen collection and storage (banking) for bulls of potentially superior genetic merit, interim evaluations were calculated with the current USDA animal model system and 4 data subsets of milk yield records from daughters of Holstein PT bulls with official August 2006 evaluations: 1) most recent 12 mo of calvings from cooperator herds with ≥1 PT daughter, 2) most recent 18 mo of calvings from herds with ≥1 PT daughter, 3) most recent 12 mo of calvings from herds with ≥5 PT daughters, and 4) most recent 18 mo of calvings from herds with ≥5 PT daughters. Interim evaluations from each data subset were compared with previous and subsequent official USDA evaluations. Correlations between interim and official evaluations were high (0.95 to 0.98 for bulls of interest) for all 4 subsets, which indicated that interim evaluations could provide valuable information between official evaluations. Correlations were highest when data were included from the most recent 18 mo of calvings from herds with ≥1 PT daughter. Interim evaluations had a higher reliability than that of previous official evaluations for almost all PT bulls that added daughters and had a lower reliability for almost all non-PT bulls. The Council on Dairy Cattle Breeding and dairy records processing centers supported June, September, and November interim evaluation with release limited to PT bulls with ≥10 daughters and an increase in reliability since the most recent official sire evaluation.

Key Words: Interim Evaluation, Genetic Evaluation, Progeny Test

11 Comparison of herds that currently supply young bulls to progeny testing programs with large commercial herds that could serve as dedicated suppliers. A. D. Coburn[*][1,2], K. A. Weigel[1], S. A. Schnell[2], and G. Abdel-Azim[2], [1]*University of Wisconsin, Madison*, [2]*Genex Cooperative Inc, Shawano, WI*.

Young dairy bulls for artificial insemination (AI) programs have traditionally been provided by seed stock producers. However, the number of seed stock herds has decreased due to changing dynamics of the dairy industry, including increases in average herd size, changes in business priorities, and attrition of stereotypical registered Holstein herds. Our objective was to compare the genetic profiles of herds that supply young AI sires at present with those of large commercial herds that might serve as dedicated suppliers of young sires to specific AI organizations in the future. A total of 693 current supplier herds were identified; these were the herd of record for the dam of a Holstein bull sampled by a major AI stud from 2005 to 2007. In addition, 976 large commercial herds were identified; these had more than 300 Holstein cows that contributed to the most recent routine national genetic evaluation. Frequency of 3X milking was greater in large commercial herds (55%) than in current supplier herds (19%). Among testing plans, DHIR was most common in current supplier herds (73%), whereas DHI-AP was most common among large commercial herds (71%). Mean lactation yield was higher in large commercial herds than in current supplier herds for milk (11,408 kg vs. 11,012 kg), fat (416 kg vs. 414 kg), and protein (348 kg vs. 339 kg), whereas mean lactation somatic cell score (SCS) was lower (2.69 vs. 2.74). Among large commercial herds, 208 herds had mean milk yield > 12,273 kg; 173 herds had mean fat yield > 455 kg; 273 herds had mean protein yield > 364 kg; 207 herds had mean SCS < 2.40; 238 had data collection rating (DCR) for milk > 90%, and 492 had DCR for components > 90%. Mean predicted transmitting abilities (PTA) were similar for current supplier herds and large commercial herds, although the range was less for commercial herds. Current supplier herds had a greater percentage of cows designated with elite status, but the total number of cows with elite status was similar for both groups of herds.

Key Words: Progeny Testing, Dairy, Artificial Insemination

12 Genetic analysis of Canadian dairy cows milked by an automatic milking system. M. Nixon[*][1], J. Bohmanova[1], J. Jamrozik[1], L. R. Schaeffer[1], G. Mason[1], J. Rodenburg[2], F. Miglior[3,4], and K. Hand[5], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Ontario Ministry of Food, Agriculture and Rural Affairs, Woodstock, ON, Canada*, [3]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [4]*Canadian Dairy Network, Guelph, ON, Canada*, [5]*CanWest DHI, Guelph, ON, Canada*.

Twice a day milking is currently the most often used milking schedule in Canadian dairy cattle. However, with the use of an automatic milking system (AMS), dairy cows can be milked more frequently. One of the major drawbacks of an AMS are cows that attend the milking system less than twice a day, and therefore have to be manually brought (or fetched) to the AMS by the farmer. The objective of this study was to examine milking intervals of the fetched dairy cow and to estimate genetic parameters for milking frequency of dairy cows milked in an AMS. The data collected was 166,712 daily records of 1,786 primiparous cows from 14 farms in Ontario and Quebec. Majority of cows visited milking robot 2 (47%) or 3 (37%) times a day. A two-trait random regression model was used for estimation of (co)variance components for 24-h milk yield and milking frequency. The model included fixed effect of herd x test-date, fixed regression on days in milk nested within season and random regression for additive genetic and permanent environmental effects. Both fixed and random regressions were fitted by Legendre polynomials of order four. The variance components were estimated using restricted maximum likelihood. Heritabilities for the daily milking frequency and daily milk yield ranged between 0.06 and 0.19 and 0.20 and 0.39, respectively. Genetic correlations between daily milk yield and daily milking frequency were highest at the peak of lactation (0.86) and lowest in mid-lactation (0.45). Further investigation is needed into later parities and estimating breeding values for milking frequency.

Key Words: Dairy Cattle, Automatic Milking System, Heritability

13 Impact of selection for decreased somatic cell score on productive life and culling for mastitis. H. D. Norman[*], R. H. Miller, and J. R. Wright, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Impact of continued selection for decreased somatic cell score (SCS) was examined to determine if such selection produced cows with difficulty responding to bacteria within the mammary gland as expressed by greater mastitis susceptibility and shorter productive life (PL). Holstein artificial-insemination bulls with a predicted transmitting ability (PTA) for SCS based on ≥35 daughters were grouped by quintile based on PTA SCS. Then 25 cow groups were formed based on sire and maternal grandsire (MGS) quintiles. Cows had birth dates from 1993 through 1999 and calving dates from 1995 through 2005. Cows that changed herds or had unreported lactations for their first 5 parities were excluded as were herds with <5 cows. Data were available from 2,556,402 cows in 27,167 herds. Mean cow PL was 27.1 mo; time opportunity was a restricting factor. Mean PTA SCS was 3.26 for sires and 3.25 for MGS for the cow group with highest sire and MGS quintiles and 2.77 and 2.76 for the group with lowest sire and MGS quintiles. Least squares difference in PL was examined on a within-herd basis with cow birth year in the model. Cows from the lowest sire-MGS quintile group had 3.2 mo longer PL than those from the highest sire-MGS quintile group and were less likely to be culled for mastitis (9 versus 13%) based on reported reason for record termination. Advantage for cows with a sire or MGS with lower PTA SCS was nearly linear across groups within MGS or sire quintile, respectively. Difference in PL between cow groups with highest and lowest sire quintiles for PTA SCS ranged from 2.0 to 2.4 mo; corresponding difference for MGS quintiles ranged from 0.8 to 1.2 mo. Because each month of additional PTA PL is valued at $29 in the current USDA lifetime net merit index, a 200-cow herd from the lowest sire-MGS group for PTA SCS would be worth nearly $6,000 more annually than a 200-cow herd from the highest sire-MGS group without considering any additional income or expense associated directly with SCS. Selection for decreased SCS across generations is expected to produce cows that are less likely to be culled for mastitis.

Key Words: Somatic Cell Score, Productive Life, Mastitis

14 Derivation of factors to estimate daily yield from single milkings for Holsteins milked two or three times daily. M. M. Schutz[*][1], J. M. Bewley[1], and H. D. Norman[2], [1]*Purdue University, West Lafayette, IN*, [2]*USDA-ARS, Beltsville, MD*.

The objective was to derive factors to predict daily yield when milk weights are recorded once when cows are milked twice (2x) or once or

106

J. Anim. Sci. Vol. 86, E-Suppl. 2/J. Dairy Sci. Vol. 91, E-Suppl. 1

twice when cows are milked thrice (3x) per d. Data were from herds enrolled in Dairy Herd Improvement and automatically recording milking weights and times. Following edits, 83,690 daily records of 1842 first lactation cows and 143,670 records of 2957 later lactation cows in 5 2x herds and 41,657 records of 779 first lactation cows and 84,131 records of 1999 later lactation cows in 4 3x herds remained. Factors currently in use to adjust single milking yields for milking interval (MINT) were applied. Also, 3 methods were compared to estimate factors or equations to predict daily yield. Factors were estimated as the ratio of the sum of daily milk to the sum of partial milk within a parity-MINT class (24 intervals in 2 parities) [Method 1] or as the sum of the ratios of daily milk to partial daily yield for each cow-day divided by the number of cow-days within parity-MINT class [Method 2]. Resulting factors from both methods were smoothed, applied to data, and residuals were regressed on days in milk (DIM). Regression equations (n=168) were also developed within parity-MINT-DIM classes (2x7x12) [Method 3] to simultaneously account for MINT and DIM. Separate factors and equations were derived for each milking in 2x or 3x herds. Method 3 resulted in consistently stronger correlations between estimated and actual yields and smallest root mean squared error (rMSE) for all milkings and parities. For 2x herds, Method 3 resulted in rMSE of 2.3, 3.0, 2.6, and 3.4 kg for AM milkings for Parity 1 and 2 and PM milkings for parity 1 and 2, respectively; compared to rMSE of 2.6, 3.2, 4.1, and 4.8 kg from current factors for the same milkings and parities. Likewise for 3x herds, Method 3 had smallest rMSE, while Method 1 had rMSE similar to those from current factors. Work is ongoing to determine whether equations from Method 3 will allow accurate estimation of daily yield when applied to other herds and traits fat, protein, and somatic cell score.

Key Words: Milking Interval, Adjustment Factor, Milking Frequency

15   Genetic correlation of live weight with price and calves' commercial values. R. Dal Zotto*, M. Cassandro, M. Penasa, M. De Marchi, and G. Bittante, *University of Padova, Legnaro, Padova, Italy.*

Aim of this study was to estimates heritabilities and genetic correlation of live weight and commercial values of Brown Swiss calves. A total of 23,911 individual live weight (kg) and commercial value (Euro/kg and Euro/calf) of Brown Swiss calves were recorded by Kovieh, the wholesale cattle organization of Bolzano province (Italy), from January 2003 to December 2007. Data were derived by 239 weekly auctions of calves sold at age from 7 to 50 days, with a live weight from 30 to 110 kg, and with a commercial value from 1.0 to 5.0 Euro/kg. Only calves with registered breed of sire and dam have been considered. Age at auction (24 ± 8 d) has been classified into three classes, (young, intermediate and old). (Co)variance components were estimated with a multiple-trait animal model based on Restricted Maximum Likelihood (REML) procedure using VCE package (Groeneveld, 1998). The pedigree file included all animals with at least a phenotypic record on one trait and all known ancestors of animals with phenotypic record. For all traits a linear model was used considering the following fixed effects: herd of birth (3116 levels), auction test-day (239 levels), age (3 levels). Animal and residual effects were considered as random and assumed to be independents. Heritabilities were 0.364 ± 0.015 for live weight (kg), 0.112 ± 0.036 for price commercial value (Euro/kg) and 0.175 ± 0.023 for calves commercial value (Euro/calf). Genetic correlations between live weight and price and between liveweight and calf commercial value were 0.046 ± 0.096 and 0.707 ± 0.047, respectively. Genetic correlation between price and calves commercial values was, as expected, high and equal to 0.734 ± 0.041.

These estimates of (co)variance components should provide the parameters for breeding value estimation of Brown Swiss bulls for these beef traits useful as additional information to increase the breed profit.

Key Words: Genetic Parameters, Commercial Values, Dairy Calves

16   Relationship between milk production and female fertility traits in Holsteins. A. Sewalem*[1,2], G. Kistemaker[2], and F. Miglior[1,2], [1]*Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, Quebec, Canada,* [2]*Canadian Dairy Network, Guelph, ON, Canada.*

Milk production and reproductive traits are major factors with respect to overall efficiency and profitability of the dairy industry. Various reports indicated that breeding for increased production in dairy cattle has negative side effects on health and fertility traits. The aim of this study was to assess the relationship between production trait and selected female fertility traits. Data consisted of Canadian test day and breeding records of the Holstein breed with first calving occurring between 1997 and 2007. A total of 15,000 records randomly selected herd were used for genetic parameter estimations Traits studied were calving to first service (CTFS), first service to conception (FSTC) and test day milk yield close to 90 DIM (TD90M). The data included only records of first parity cows. The mean CTFS, FSTC and TD90M were 89.35 ± 33.86, 31.39 ± 44.78 and 30.24 ± 61.73, respectively. The genetic correlation between CTFS and TD90M was 0.29 and between FSTC and TD90M was 0.12, showing that cows with high milk production at time of first insemination tended to have longer intervals of CTFS and FSTC.

Key Words: Reproductive Traits, Production, Canadian Dairy Breeds

17   Genetic correlations between conception rates and test-day milk yields using a threshold-linear random-regression model. S. Tsuruta*[1], I. Misztal[1], C. Huang[1], and T. J. Lawlor[2], [1]*University of Georgia, Athens,* [2]*Holstein Association USA Inc., Brattleboro, VT.*

The objective of this study was to estimate genetic correlations between conception rates (CR) and test-day milk (TDM) yields for different DIM. The data included 245,214 first parity service records of 102,929 first-parity cows born in NY between 1999 and 2003. The CR was defined as the outcome of a single insemination. CR and TDM were analyzed by using a bivariate model with herd-year, age, AI status, service month, cubic regressions on DIM using Legendre polynomials as fixed effects, herd × sire interaction, sire additive genetic and permanent environment with cubic random regressions on DIM, service sire, and residual as random effects. Variance components were estimated using a Bayesian method via Gibbs sampling. Farms were categorized into small (≤ 50 cows) and large operations. Larger herds produced more test-day milk (33.7kg, 30.4kg), have lower CR (31%, 36%), start breeding earlier (77 d, 94 d to first service), and have fewer days open (137 d, 145 d). A more stressful relationship between CR and DIM was observed during the higher production periods of the lactation curve for large herds. For large herds, the genetic correlation between CR and TDM was 0.4 at DIM=50, dropped to 0 at DIM=90, was -0.55 at DIM=155, and rose to 0 at DIM=240. For small herds, the correlation was 0.1 at DIM=50, dropped to 0 at DIM=70, was -0.2 at DIM=120, and rose to 0 at DIM=240. For large (small) herds, the average correlation across

J. Anim. Sci. Vol. 86, E-Suppl. 2/J. Dairy Sci. Vol. 91, E-Suppl. 1

107

DIM between CR and TDM was -0.2 (-0.1). The average heritability estimate for CR was 2.4% (5.3%). The chi-square test showed that the frequencies of service records were significantly different during a week for 60% of large herds and for 11% of small herds, suggesting more timed AI services in large herds. Large herds may be more advantageous for identifying bulls with superior fertility, but small herds may be more advantageous for identifying bulls that sire more fertile daughters.

Key Words: Conception Rate, Test-Day Milk, Threshold-Linear Model

18   Study on genetic parameters of conception rate and heat detection/expression. C. Huang[*1], I. Misztal[1], S. Tsuruta[1], and T. J. Lawlor[2], [1]*University of Georgia, Athens*, [2]*Holstein Association USA Inc., Brattleboro, VT*.

The purpose of this study was to indirectly estimate genetic parameters of heat detection/expression (HDE). Days open (DO) is a composite trait with many components, including conception rate (CR) and HDE. An insemination outcome (IO) is mainly influenced by CR. A genetic correlation between DO and IO contains information about the genetic correlation between the HD/E and CR. Field data were obtained from DRMS, Raleigh, NC, and included milk and service records on 109,278 cows in first lactation from 2,952 herds in NY from 1999 to 2003. A bivariate sire model included DIM, season, milk yield, age, AI status as fixed effects, herd-year, service sire, additive genetic, and permanent environment as random effects. Because of a single record per animal in DO, estimability required that the residual variance for DO be fixed. The data were split by herd size ($\leq$50, $\geq$100); tests indicated that many larger farms use timed AI while few small ones do. The genetic correlation between DO and IO was 0.991 with small herds and 0.996 with large herds. A data set for DO and IO was simulated assuming a range of genetic correlations between CR and HDE. For a range of 0.1-0.9, the genetic correlations between DO and IO were all $\geq$0.99. Subsequent studies looked at correlations of IO and HDE. In simulated data, records analyzed for HDE existed until the insemination resulted in conception. In field data, HDE was estimated as $1/[(DO-df+21)/21 \times ns]$, where df is days at first insemination, and ns is number of services. With the field data set, the genetic correlations between HDE and IO were 0.996 with small herds and 0.994 with large herds. With the simulated data set, these correlations were 0.992, 0.984, and 0.538 when the simulated genetic correlations between HDE and CR were 0.9, 0.5, and 0.1, respectively. Heat detection as present in DO is censored, and very high genetic correlations between DO and IO are estimated even if the true correlations between HDE and CR are low.

Key Words: Conception Rate, Days Open, Heat Detection/Expression

108

J. Anim. Sci. Vol. 86, E-Suppl. 2/J. Dairy Sci. Vol. 91, E-Suppl. 1