

Breeding and Genetics: Dairy Cattle Breeding I

469 Assessing accuracy of heat detection in dairy herds. H. Seegers*¹, D. Billon¹, E. Bossard-Apper², C. Ponsart³, B. Grimard⁴, and N. Bareille¹, ¹Research Group Epidemiology and Risk Analysis Oniris-INRA, Nantes, France, ²Agriculture School, Angers, France, ³UNCEIA, Maisons-Alfort, France, ⁴Veterinary School, Maisons-Alfort, France.

Herd reproductive performance depends on accuracy of heat detection and conception rate. Assessing the accuracy of the detection practices on a farm is a quite difficult exercise. Therefore, the objective was to provide a method to estimate the accuracy of heat detection in dairy herds, using quite only data available in fertility reports (mainly information about calving and insemination dates). A first step relied on the development of a simulation model to represent the biological processes (cyclicality resumption, detectability of ovulation, conception rate, embryonic and fetal deaths) and managerial processes (detection, submission rules, culling decisions) involved. This simulation tool was then used to generate fertility reports for 384 scenarios with known levels in sensitivity and specificity of heat detection, in combination with different levels for other parameters (especially herd size, milk yield, conception rate and managerial rules). At second step, the simulation outcomes were analyzed with stepwise multiple regression models to obtain prediction equations for the accuracy criteria, using as predictors the criteria present in a classical fertility report. Accuracy criteria were the % detected within detectable heats (separating 2 periods: until 1st AI and After 1st AI) and the % of AIs outside an ovulation period. At third step, these prediction equations were applied to a data set of 40,000 yearly fertility reports to obtain the distribution of estimated accuracy criteria in a population of 10,000 French farms with Holstein herds. Raw estimates calculated from the data set were almost considered plausible by authors and external experts. The % of detection averaged 55.3% (Q1 = 40.1; Q2 = 58.2; Q3 = 73.7) until the 1st AI and 50.1% (Q1 = 38.2; Q2 = 50.1; Q3 = 63.4) later. The % of AIs done outside an ovulation period averaged 6.3% (Q1 = 2.9; Q2 = 5.7; Q3 = 9.1). A test of the method is ongoing, based on confrontation with AI technicians guesses for a sub-sample of farms. If consistency reached is deemed sufficient, a use on a semiquantitative scale (very good, good, intermediate, low and very low) seems to be an acceptable way to express the results for farmers and advisors.

Key words: dairy cow, estrus, detection

470 Heritability and repeatability estimates for twinning rate in the Irish dairy and beef cattle. A. M. Doyle¹, R. D. Evans², and A. G. Fahey*¹, ¹University College Dublin, Belfield, Dublin 4, Ireland, ²Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland.

Twinning rate is a complex threshold trait with a binary phenotype (1 = single, 2 = twin) and a quantitative phenotype. Increasing the twinning rate in beef cattle and decreasing twinning rate in dairy cattle could have positive economic effects for both industries. In beef cattle twinning can increase the rate of production if problems associated with twinning such as dystocia, longer rebreeding and retained placentas can be overcome. Decreasing twinning in dairy cattle would be beneficial as although twinning can increase milk production, fertility problems and the occurrence of freemartins make it disadvantageous. The objective of this study was to estimate the heritability and repeatability for twinning rate in 6 dairy (n = 1,070,457) and 10 beef (n = 83,476) breeds in Ireland using SAS 9.1 Software and DMU Animal Breeding Software. Heritability and repeatability estimates were analyzed using

a linear animal model with fixed effects for herd-year-season, parity, age, heterosis and recombination; while sire and dam were included as random effects. Heritability was estimated to be between 0.002 and 4.0% and 0.0–4.1% for dairy and beef breeds respectively, and repeatability was estimated to be between 0.002 and 6.1% and 0.002–8.1% for dairy and beef breeds respectively. Twinning rate increased as parity increased. A comparison of gestation length between single and twin births found gestation length of twins to be significantly ($P < 0.05$) shorter than single births. The analysis suggests that there is a genetic component to twinning rate in dairy and beef breeds and this trait could be included in national selection index to reduce the incidence of twinning in dairy cattle and increase the rate of twinning in beef cattle due to a cumulative effect over time.

Key words: twinning, repeatability, heritability

471 Genetic analysis of ovulatory disorders in Austrian Fleckvieh cows: A comparison between linear models and survival analysis. A. Koeck*^{1,2}, B. Fuerst-Waltl², J. Sölkner², C. Egger-Danner³, and G. Meszaros², ¹Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, ²Division of Livestock Sciences, University of Natural Resources and Life Sciences, Vienna, Austria, ³ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria.

The aim was to compare linear models and survival analysis for genetic analysis of ovulatory disorders, which included veterinary treatments of silent heat/anestrus and cystic ovaries. Data of 23,450 daughters of 274 Austrian Fleckvieh sires were analyzed. For linear model analyses, ovulatory disorders were defined as a binary response (presence or absence) in the time periods from calving to 150 d after calving and from calving to 300 d after calving. For survival analysis, ovulatory disorders were defined either as the number of days from calving to the day of the first treatment for an ovulatory disorder (uncensored record) or from calving to the day of culling, or the last day of the period under investigation (until 150 or 300 d after calving; censored record). Estimates of heritability were very similar (0.016 to 0.020) across methods and periods. Correlations between sire EBV from linear model and survival analysis were 0.98; whereas correlations from different time periods were slightly lower (0.95 and 0.96).

Key words: ovulatory disorder, linear model, survival analysis

472 Montbeliarde-sired crossbred cows compared to pure Holstein cows for production, SCS, days open, and survival during their first three lactations. A. R. Hazel*, L. B. Hansen, B. J. Heins, and J. G. Linn, University of Minnesota, St. Paul.

Montbeliarde × Holstein crossbred cows (MH, n = 58) and Montbeliarde × Jersey/Holstein crossbred cows (MJH, n = 78) were compared with pure Holstein cows (HO, n = 122) for 305-d milk, fat, and protein production, SCS, days open (DO), and survival during the first 3 lactations. Cows were in 2 research herds of the University of Minnesota and calved from October 2005 to June 2010. Best Prediction was used to calculate production for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. Cows were required to have at least 250 DIM for DO, and cows with DO greater than 250 d were truncated to 250 d. For production, SCS, and DO, independent variables for statistical analysis were the fixed effects of herd, parity group (primiparous or multiparous), breed, interaction

of herd and parity group, lactation number (2 or 3) nested within multiparous parity group, herd-year of calving nested within interaction of herd and parity group, interaction of herd and breed, interaction of lactation number nested within parity group and breed, interaction of herd, lactation nested within parity group, and breed, and random cow nested within breed. The MH, MJH, and HO, respectively, were not significantly different ($P > 0.05$) for fat plus protein production during first lactation (503 kg, 496 kg, 514 kg), second lactation (605 kg, 604 kg, 605 kg), or third lactation (675 kg, 645 kg, 656 kg). The MH (2.11) had lower SCS ($P < 0.05$) than MJH (2.57) and HO (2.70) during second lactation, and MH (2.67) had lower SCS ($P < 0.05$) than HO (3.39) during third lactation. The MH (133 d) and MJH (122 d) had fewer DO ($P < 0.01$) in first lactation than HO (170 d). During second lactation, MH (141 d) and MJH (140 d) had fewer DO ($P < 0.05$) than HO (179 d). The MH had higher survival rates ($P < 0.01$) than HO to third (62% vs. 39%), fourth (44% vs. 16%), and fifth (32% vs. 8%) calving. The MH (4%) and MJH (4%) had lower mortality rates ($P < 0.05$) than HO (17%) within 3 years of first calving.

Key words: crossbreeding, heterosis, Montbeliarde

473 Joint estimation of genetic parameters for test day somatic cell count and mastitis using a random regression model in the United Kingdom. R. Mrode*, T. Pritchard, M. Coffey, and E. Wall, *Scottish Agricultural College, Penicuik, Midlothian, UK.*

Genetic parameters were estimated in a joint analysis of log-transformed somatic cell count (SCC) and mastitis (MAS) in Holstein/Friesian cows for the first 3 parities using a random regression model. There were 67175, 30,617 and 16,366 cows with records for SCC in parities 1, 2 and 3 respectively. Corresponding numbers for MAS were 9070, 6009 and 4012 respectively. The percentage incidence for MAS was 14, 20 and 25% in parities 1, 2 and 3 respectively. The model for SCC included herd-test-day, fixed lactation curves nested with calving year-groups, age and month at calving, random regressions with Legendre-polynomials of order 2 for animal and permanent environmental (PE) effects. The model for MAS included fixed herd-year-season, age and month of calving, random animal and PE effects. Two separate analyses were implemented with MAS analyzed as binary trait or as number of infections in the lactation. The analyses were carried out using Gibbs sampling with a chain length of 120,000, of which the first 40,000 were discarded as burn-in period. Estimates of heritability were 0.11, 0.14 and 0.15 for SCC in parities 1, 2 and 3 respectively. Corresponding estimates for MAS were 0.05, 0.07 and 0.09 as a binary trait. Estimates for MAS using number of infections were similar at 0.06, 0.07 and 0.12. Posterior standard deviations were about 0.01 for all estimates. The genetic correlation of 0.75 estimated between parities 1 and 2 for SCC was lower than the 0.92 between parities 2 and 3. The corresponding estimates for MAS were 0.54 and 0.89 respectively from the binary analysis. SCC in the first 3 parities had genetic correlations of about 0.55 with MAS in the first parity but this increased to about 0.63 with MAS in parity 2. However, the genetic correlations between SCC in parities 1 and 2 with MAS in parity 3 were about 0.48 while it was 0.68 between SCC and MAS in the third parity. It is intended that the new parameters will be used in setting up a national evaluation system for the joint analysis of SCC and MAS.

Key words: somatic cell count, mastitis, genetic parameters

474 Estimation of genetic parameters for health and survival in Canadian Holstein calves. C. E. McCorquodale*¹, F. Miglior^{2,3},

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The objective of this study was to estimate the genetic parameters of calf survival and health in a population of Ontario Holsteins. Heifer calves on 16 south-western Ontario dairy farms were followed from time of birth to approximately 4 mo of age. Visits were made at 1–8 (T1), 14–22 (T2), 35–43 (T3) and 90–120 (T4) days of age. At each visit, the height, weight, temperature, and a health score were collected. A blood sample was taken at T1 to measure serum total protein using refractometry. Details of birth events and colostrum feeding information were recorded on individual birth records. Information on treatment for illness events and death information was collected for the duration of the study. In total 1,462 calves, sired by 246 different bulls were included in the study. Two linear animal models were used to analyze survival and treatment separately. Survival of calves was measured as a binary trait (0 = survived to T4; 1 = dead before T4) and treatment of calves at T1, T2 and T3 was recorded as a binary trait (0 = not treated; 1 = treated). Both models included the fixed effects of herd, season of birth with 4 classes, calving ease score with 4 classes, type of birth with 2 classes (1 = single birth and 2 = twin), and weight group with 5 classes. Fixed regressions included the total volume of colostrum consumed during the first 24 h and the serum total protein score. The random effects of the models included animal and residual. Estimates of heritability for treatment during T1, T2 and T3 were 0.11, 0.05 and 0.09, respectively. The heritability estimate for survival was 0.05. Similar to recently published data from Norway and New York State, heritability estimates for calf survival and health in Ontario calves give additional reason to consider routine genetic evaluation for these traits.

Key words: Canadian Holstein, calf health and survival, genetic parameters

475 Genetic parameters of lactation yield in the tropical carora breed with random regression test-day models. E. Tullo*¹, S. Biffani², C. Maltecca³, and R. Rizzi¹, ¹*University of Milan, Faculty of Veterinary Medicine, Department of Veterinary Science and Technology for Food Safety, Milan, Italy,* ²*Parco Tecnologico Padano, Lodi, Italy,* ³*Department of Animal Science, North Carolina State University, Raleigh, NC, USA.*

In tropical environments, lactation curves with lower peaks and higher persistencies might be desirable from both an economical and a physiological standpoint. The objective of this study was to obtain genetic parameters for test day yields (TD), and persistencies (P) for the tropical breed Carora and to compare these with results from a standard 305-yield animal model. A random regression animal model (RR-AM) was employed for the analysis of 181,810 test day records collected in the west-central part of Venezuela from 1992 to 2009, and belonging to 7,075 Carora cows, daughters of 436 sires. Milk TD yields (kg), comprised between 5 and 305 DIM, were analyzed with a model that included fixed effects of class of age, year and month of calving, herd and third order Legendre polynomials of days in milk. Random effects were fitted for the interaction herd-year-month-of-test and for the additive genetic and permanent environmental effects. Third order Legendre polynomials were applied as random regression covariates for both additive genetic and permanent environmental effects. Estimated daily

heritabilities for milk yields ranged from 0.15 to 0.25, with the lowest values around the peak of the lactation. Within lactation repeatabilities ranged from 0.39 to 0.48. Genetic correlations among test days within lactation ranged from -0.20 to 0.99. To investigate differences among models, the re-ranking between EBVs for 305d yield, obtained with Lactation Animal Model (L-AM) and RR-AM was investigated. For the top 100 sires a rank correlation of 0.54 was found. The average re-ranking among sires was of 21.9 ± 16.93 . Correlations between persistency and 305d milk yield EBV ranged from 0.06 (P as a deviation

from the peak) to 0.32 (P as production difference between the first and the second stage of lactation). Understanding persistency trends with respect to milk yield, in tropical environment should allow selecting individuals able to express their potential genetic values without incurring in excessive heat stress losses.

Key words: random regression test-day model, tropical dairy cattle, persistency