

Breeding and Genetics: Dairy Cattle Breeding II

707 Methods for the assessment of milk coagulation properties: A genetic analysis. A. Cecchinato*, M. Penasa, M. De Marchi, C. Cipolat Gotet, I. Bazzoli, N. Cologna, and G. Bittante, *Department of Animal Science, University of Padova, Viale dell'Università, Legnaro, Padova, Italy.*

Milk coagulation properties (MCP: clotting time, curd firmness) are of great importance because they influence cheese processing, yield and quality. Assessment of MCP can be performed through Formagraph (FMG), which is an instrument based on the tiny forces exerted by pendulums when samples of coagulating milk are exposed to linear oscillations, or Optigraph (OPT), which is based on an optical signal in the near-infrared reflectance spectroscopy. The FMG provides measures of milk clotting time (RCT, min), defined as the time from the addition of rennet to milk until the beginning of coagulation (within a 90-min testing time), and curd firmness (in mm) measured at different time: 30 (a30), 60 (a60), 75 (a75) and 90 (a90) min from the beginning of the test. The OPT provides same measures of MCP by means of particular feature points extracted from optical information acquired in real time. The aim of this study was to estimate heritabilities of and genetic correlations between MCP obtained from FMG and OPT. A total of 1,014 Brown Swiss cows were sampled once in 68 herds from January 2010 to February 2011. Individual milk samples were collected during the evening milking and analyzed for MCP by using FMG and OPT. A Bayesian standard linear model was implemented via Gibbs Sampling. The model included the non genetic effects of days in milk, parity, herd and the additive genetic effect of animals. For RCT measured by FMG, marginal posterior mean (SD) of heritability was 0.30 (0.09). Estimates of heritability for a30, a60, a75 and a90 averaged 0.14 (0.06) and ranged from 0.13 (0.06) to 0.16 (0.07). For OPT, corresponding estimates were slightly lower. Genetic correlations between MCP from FMG and OPT approached 0.90 (0.06). On the basis of the genetic parameters obtained in this study, the improvement of MCP through selection is possible, regardless the method used.

Key words: milk coagulation properties, near-infrared spectroscopy, genetic parameters

708 Genetic relationships between fertility and content of major fatty acids in milk for first-parity Walloon Holstein cows. C. Bastin*¹, N. Gengler^{1,2}, and H. Soyeurt^{1,2}, ¹*University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium,* ²*National Fund for Scientific Research, Brussels, Belgium.*

Fertility traits are difficult to measure and have low heritabilities. Consequently, indicators traits are of interest for breeding value estimation for fertility especially if these traits are easier to measure, have higher heritabilities and are well correlated with fertility. Furthermore, some traits of the milk fatty acid (FA) profile could be considered because they can be related to the energy balance status. Therefore the objective of this study was to estimate genetic correlations between days open (DO) and the contents of 19 individual and groups of milk FA. Fatty acids contents (in g/dl of milk) were estimated by MIR and were: saturated, unsaturated, monounsaturated, polyunsaturated, long chain, short chain, medium chain, C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C17:0, C18:0, C18:1, C18:1 cis, and C18:1 cis-9. Data included 143,332 FA and 29,792 DO records collected from 29,792 Holstein cows in first parity. Co(variances) were estimated using 19 2-trait models that included random regression for FA traits. Overall, genetic correlations between DO and FA contents in milk changed sig-

nificantly over the lactation. For unsaturated, monounsaturated, long chain, C18:0, C18:1, C18:1 cis, and C18:1 cis-9, genetic correlations with DO were positive in early lactation and became negative after 100 d in milk. For the other fatty acids, genetic correlations with DO were negative along the whole lactation. At 5 d in milk, genetic correlation between DO and C18:1 cis-9 was 0.40 and genetic correlations between DO and C6:0 to C16:0 ranged between -0.55 and -0.20. These results emphasized the relationship between fertility and energy balance status and could be explained by the release of long chain fatty acids in early lactation due to the mobilization of body fat reserves and the consequent inhibition of de novo FA synthesis in the mammary gland. At 200 d in milk, correlations between DO and fatty acid contents ranged between -0.40 for C18:1 cis-9 to -0.10 for C6:0. This research suggested the interest of using FA contents in milk in indirect selection for better fertility in dairy cows.

Key words: fatty acid, fertility, genetic correlation

709 Relationships between mortality and 305-d milk yield of Holstein cows in three regions in US. K. Tokuhisa*, S. Tsuruta, and I. Misztal, *University of Georgia, Athens.*

Several recent research reports have indicated increasing dairy cow mortality over the years; however, the reasons for the increase are unclear. This study aimed to investigate the relationship between mortality and 305-d milk yield. DHI data contained 3 regions: Southeast (SE), Southwest (SW), and Northeast (NE). A total of 3,522,824 records for 3 parities were used: 732,009 (SE), 656,768 (SW), 2,134,047 (NE) from 1999 to 2008. Termination code "6" was regarded as "death" and used for mortality calculation. A 2-trait (305-d milk yield, mortality) animal model fitting fixed effects of herd year, age, DIM, month-of-termination, and random animal genetic effect was used to compute correlations and heritability, separately for each region and parity. Mortality was the highest in August for any parity, and the lowest in spring (i.e., the largest difference between the highest and the lowest mortality in SE was 0.63% in 3rd parity). The highest mortality was observed in SE, and mortality in NE and SW were similar. Mortality increased with parity in all regions. Mortalities in first 3 parities across regions were 3.3%, 4.8%, 7.2% (SE), 2.4%, 3.3%, 5.0% (SW), and 2.2%, 3.7%, 5.4% (NE). The span of mortality between 1st and 3rd parity was the largest in SE (3.9%) and the smallest in SW (2.6%). Genetic correlations between the 2 traits were 0.09, 0.09, 0.17 (SE), -0.03, -0.05, 0.17 (SW), and 0.19, 0.19, 0.00 (NE). The environmental correlations were 0.03, 0.05, 0.06 (SE), 0.03, 0.05, 0.05 (SW), and 0.01, 0.05, 0.06 (NE). Heritability estimates of milk yields were 0.28, 0.19, 0.13 (SE), 0.32, 0.19, 0.16 (SW), and 0.35, 0.24, 0.19 (NE). Heritability estimates of mortality were 0.01 for all 3 parities and all 3 regions. The mortality is the highest in SE and is influenced by season and by parity. Environmentally, high milk producing cows tend to have high mortality. Genetically, effects of high milk production on mortality are less clear. Results may have been influenced by special veterinary care to superior cows.

Key words: US Holsteins, cow mortality, regions

710 Genetic parameters of body condition score and other type traits in Canadian Holsteins. S. Loker*¹, C. Bastin², F. Miglior^{3,4}, A. Sewalem^{3,4}, L. R. Schaeffer¹, J. Jamrozik¹, and V. Osborne⁵, ¹*CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph,*

ON, Canada, ²University of Liège, Gembloux Agro-Bio Tech, Gembloux, Belgium, ³Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada, ⁴Canadian Dairy Network, Guelph, ON, Canada, ⁵Centre for Nutrition Modelling, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.

The objective of this research was to estimate the genetic parameters of body condition score (BCS) and other type traits. The data analyzed in this study was from Holstein Canada's new classification system and included BCS, angularity (ANG), chest width (CW), height at front end (HFE), body depth (BD), pin width (PW), and stature (STA), recorded between rounds 72 to 79 (year 2006 to 2010). The model included the fixed effects age of calving × stage of lactation, and herd × round × classifier, and a random additive genetic animal effect. All 7 traits were analyzed together. In general, it was found that larger cows (taller, wider, less angular cows) were genetically inclined to have higher than average BCS, which other studies have linked to better health and fertility. The 2 traits with the strongest genetic correlation with BCS were ANG (-0.70) and CW (0.72). Heritabilities were 0.21, 0.18, and 0.19 for BCS, ANG, and CW, respectively. Genetically, ANG was strongly negatively correlated with BCS (-0.70), whereas CW was strongly positively correlated with BCS (0.72), but ANG and CW were not strongly correlated with each other (-0.16), and so both could be useful as additional information in a genetic evaluation of body condition score. All 3 traits would be useful in conjunction with Valacta's BCS (Sainte-Anne-de-Bellevue, QC, Canada) (collected several times per cow throughout lactation for Québec herds) for a first lactation longitudinal genetic analysis of BCS. A genetic evaluation of BCS would inevitably lead to selection for cattle with improved health and fertility.

Key words: body condition score, type traits, genetic correlation

711 Relationship between body condition score, locomotion and dairy strength with functional longevity in Canadian Holsteins. A. Sewalem^{*1,2}, F. Miglior^{1,2}, and G. Kistemaker², ¹Agriculture and Agri-Food Canada, Guelph, Ontario, Canada, ²Canadian Dairy Network, Guelph, Ontario, Canada.

The aim of this study was to explore the impact of body condition score (BCS), locomotion and dairy strength on the functional survival of Canadian Holstein cows using a Weibull proportional hazard model. The data set consisted of 490,791 cows from 13,786 herds sired by 8,126 sires. Functional survival was defined as the number of days from first calving to culling, death, or censoring. The statistical model included the effects of stage of lactation, season of production, the annual change in herd size, type of milk recording supervision, age at first calving, effects of milk, fat and protein yields calculated within herd-year-parity deviations, herd-year-season of calving, each type trait and the sire. Analysis was done one at a time for each of 3 type traits. The relative culling rate was calculated for animals in each class after accounting for the above-mentioned effects. BCS showed a curvilinear relationship with longevity. Cows with score of 1 (classified as lean) were 35% more likely to be culled compared with the reference class (score = 5). Similarly, cows with score of 9 (classified as fat) were less likely to stay longer in the herd compared with the reference group. This indicates that neither too lean nor fat cows are desired for breeding purposes. The result also showed that lameness and dairy strength had a clear linear relationship with longevity. Cows classified with score 1 (namely cows considered as lame) were more than 34% more likely to be culled than cows classified as intermediate group (score = 5). Additionally, cows with higher score than average were

less likely to be culled than cows from the average group (score = 5). Similarly, for dairy strength cows with poor score were nearly 50% more likely to be culled than the reference group (Good Plus). However, cows with excellent score were found to have longer longevity than the other groups.

Key words: functional survival, body condition score, locomotion

712 Modeling of residual feed intake for primiparous dairy cow using orthogonal polynomial random regression. G. Manafiazar^{*}, T. McFadden, E. Okine, L. Goonewardene, and Z. Wang, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Residual feed intake (RFI) is defined as the difference between an animal's actual energy intake (AEI) and its expected energy intake (EEI) based on its maintenance and various production requirements. Due to the complexities of multifunctional (maintenance, growth, pregnancy, and lactation) energy requirements, there is no method available for evaluating individual RFI in dairy cows currently. The objective of this study is developing a statistical model to evaluate individual RFI for first lactation dairy cow. Two hundred first lactation cows were used in an experiment at the Dairy Research and Technology Center of the University of Alberta. Individual feed intake was measured daily while individual body weight and body condition score of each animal were assessed at the times of calving and each of DHI milk sampling days. Individual milk yield and composition data were obtained from the official DHI data set. The net energy required for maintenance (NE_M), lactation (NE_L), pregnancy (NE_P); energy balance (EB) and 4% fat corrected milk (FCM) traits for each animal were derived from the data. Twenty 5 alternative Legendre polynomial (LP) models were fitted for each trait with fixed (FP) and random (RP) polynomial regressions of orders from 1 to 5. The best model for each trait was selected using multiple statistical criterion. The selected model for NE_M, NE_L, EB and FCM was FP₁RP₄, FP₂RP₂, FP₁LP₄ and FP₂RP₂, respectively, where the subscript numbers stand for order of LP. An individual conversion coefficient of gained or lost energy for each animal was estimated with a simple linear regression of predicted daily FCM on predicted daily EB in the negative period while AEI on predicted daily EB in the positive period. The individual EEI is calculated as a summation of predicted NE_M, NE_L, NE_P and net gained or lost energy from that individual. The model made it feasible to evaluate dairy RFI while accounting for multi-functional energy requirements.

Key words: dairy, feed efficiency, Legendre polynomial

713 Genetic association of days open with feed intake and efficiency. J. E. Vallimont¹, C. D. Dechow^{*1}, J.M. Daubert¹, M. W. Dekleva¹, and J. W. Blum², ¹Pennsylvania State University, University Park, ²University of Bern, Bern, Switzerland.

The objective of this study was to determine the genetic relationship between feed efficiency and days open in dairy cows. Dry matter intake, body weight (BW), and body condition score (BCS) were collected monthly on 970 cows in 11 tie-stall herds for 6 consecutive months and merged with test-day records. Two methods of feed efficiency were considered. Dry matter efficiency (DME) was the ratio of 305-d fat-corrected milk (FCM) to 305-d dry matter intake (DMI). Residual feed intake (RFI) was the difference between DMI and feed intake predicted from National Research Council equations. High values of RFI represent cows with lower feed efficiency. Associations of DMI, DME and RFI with days open were estimated with 5-trait

animal models that included days open, FCM, BW, BCS and either DMI, DME or RFI. Fixed effects were herd-calving-cluster, age at calving and lactation number. Random effects were animal, permanent environment and error. Analyses of DME and RFI were conducted with and without covariables for BCS and change in BCS from day in milk 5 to 60. Heritability estimates were 0.18 for DMI and DME, 0.05 for RFI, and 0.07 for days open. The genetic correlation of DMI with days open was slightly favorable (-0.15), whereas genetic correlations of days open with DME (0.68) and RFI (-1.0) were more unfavorable than the genetic correlation between days open and FCM (0.49). RFI was genetically correlated with higher BCS (0.41), whereas higher

DME was genetically correlated with lower BCS (-0.68). Adjustment of RFI and DME for BCS traits had a modest effect on genetic correlation estimates with days open (-0.85 and 0.58 , respectively). Genetic differences among cows for the RFI measure used in this study were small and appeared to partly reflect BCS differences among cows that were not considered in the predicted DMI equations. There were genetic differences among cows in DME, but cows that were more feed efficient were less efficient reproductively.

Key words: feed efficiency, heritability