Breeding and Genetics: Dairy Cattle Breeding III–Genetic Evaluation

707 Extension of Bayesian procedures to integrate and to blend multiple external information into genetic evaluations. J. Vandenplas*[1,2] and N. Gengler[1], [1]*University of Liege - Gembloux Agro-Bio Tech, Gembloux, Belgium,* [2]*National Fund for Scientific Research, Brussels, Belgium.*

Current genetic evaluations are mostly based on local data, potentially followed by an international second step, as it is performed by Interbull (Uppsala, Sweden) for dairy breeds. However, reliability of estimated breeding values (EBV) for animals with few local data may be limited. Furthermore, the current development of genomic selection makes this issue more important and the blending of those multiple sources more necessary. Current methods are based on selection index and Bayesian procedures were proposed for a single external source. The aim of this research was to extend these methods to integrate information from multiple sources outside a given evaluation system, i.e., external information, into this genetic evaluation, i.e., internal evaluation, and to assess its potential to blend multiple sources of information when only external information is available. To allow simplifications of the computational burden and the propagation of all external information through the whole pedigree, all animals were considered as animals associated to external information thanks to the prediction of external information from available one for internal animals, i.e., animals with no external information. Multiple considerations of contributions due to relationships among animals were also taken into account. Two dairy cattle populations were simulated across 5 generations. Internal females were randomly mated with internal and 50 external males. Milk production for the first lactation for each female was simulated in both populations. Results for 100 replicates showed that average rank correlations among Bayesian EBV and EBV based on the joint use of external and internal data were close to 1 for both external and internal animals. The respective correlations for the internal evaluation were equal to 0.54 and 0.95. Mean squared error, expressed as a percentage of the internal mean squared error, was close to 0% for both external and internal animals. Thereby, the Bayesian procedure has the potential to integrate and to blend multiple sources of external information to evaluate animals more reliably.

Key Words: Bayesian, integration, multiple

708 Are in-line measurements of somatic cell counts equally or more useful for genetic evaluations as those from DHI? L. P. Sørensen* and P. Løvendahl, *Department of Molecular Biology and Genetics, Center for Quantitative Genetics and Genomics, Aarhus University, Tjele, Denmark.*

The aim was to estimate and compare genetic parameters for log-transformed somatic cell counts (SCC) based on in-line measurements (OCC, DeLaval) in automatic milking systems with monthly test-day SCC from traditional herd testing schemes. Data was collected during a 29-mo interval from 6 herds and 1294 first parity cows (5 to 305 d in milk). Cell counts were analyzed using a 2-trait linear animal model. There were a total of 298,988 records for OCC and 7779 for test-day SCC. The fixed part of the model included lactation curves fitted as a Wilmink function, and the random parts included animal and herd-test-day effects. Age at calving and days in milk was included as covariates. Estimates of heritability were similar for the 2 traits, $h^2 = 0.26$ and 0.25 for OCC and SCC, respectively, and the genetic correlation between the 2 traits was close to unity ($r_g = 0.98$). The results suggest that somatic cell counts based on in-line measurements are similar but not preferable to traditionally obtained SCC despite several OCC measurements per cow per day.

Key Words: dairy cattle, somatic cell count, genetic parameters

709 Prediction of residual feed intake for first and second lactation dairy cows. G. H. Manafiazar,* T. McFadden, E. Okine, L. Goonewardene, and Z. Wang, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada.*

Individual daily feed intake of 77 heifers from calving to the end of their second lactation was recorded at the Dairy Research and Technology Centre of the University of Alberta. Individual milk yields, and milk composition data of these cows were obtained from Dairy Herd Improvement (DHI) program and their body weights were recorded on the same days as the DHI milk sampled. Daily animal solutions for metabolic body weight (MBW), milk production energy requirements (MPER), and empty body weight changes (EBWC) were predicted from 5 to 305 d in milk using random regression Legendre polynomial. Total MBW, MPER, and EBWC over 301 d were predicted as the summation of their respective daily solutions. The total actual energy intake (AEI) over 301 d was linearly regressed on total 301-d predicted MBW, MPER, and EBWC to develop expected energy intake (EEI) prediction equation. The EEI prediction equation for the first and second lactation had R^2 of 0.82 and 0.81, respectively. Individual RFI over 301 d was calculated as the difference between total AEI and EEI over 301-d. The averaged daily RFI value ranged from −3.95 to 5.11 MJ NE_L d^{-1} and −4.86 to 4.34 MJ NE_L d^{-1} for the first and second lactation period, respectively. The animals were grouped into 3 classes of Low (<0.5 SD), medium (±0.5 SD), or high (>0.5 SD) from the mean (0) based on SD of RFI within lactation. The results showed that 30% of animals remained their respective RFI group between lactations, 54% of animals changed their RFI by less than 0.5 SD, and 15% of animals changed their RFI group by 1 SD. The results indicate that the developed RFI prediction equations could be used to calculate RFI in the first and second lactation; however, reranking exists between animals in the first and second lactation.

Key Words: dairy, residual feed intake, random regression

710 Random forest approach for SNP effects of residual feed intake in dairy cattle. C. Yao*[1], D. M. Spurlock[2], K. A. Weigel[1], L. E. Armentano[1], C. D. Page[1], and M. J. VandeHaar[3], [1]*University of Wisconsin, Madison,* [2]*Iowa State University, Ames,* [3]*Michigan State University, East Lansing.*

The objective of this study was to identify significant associations between single nucleotide polymorphisms (SNP) markers and residual feed intake (RFI) in dairy cattle using a random forest (RF) algorithm. Genomic data included 54,609 SNP genotypes for 395 Holstein cows, whereas phenotypic data included RFI measurements from 50 to 150 d postpartum. Residual feed intake was defined as the difference between observed dry matter intake (DMI) and predicted DMI after accounting for year and season of calving, year and season of measurement, age at calving nested within parity, days in milk (DIM), milk yield, body weight (BW), and body weight change (ΔBW). Measurements of BW were smoothed by using the fitted value of a quadratic function of weekly weights regressed on DIM, whereas ΔBW was calculated as the difference between fitted values for BW on adjacent days. Random Forest is an ensemble-based machine learning algorithm that uses a collection of tree predictors and can be adapted to classification and regression problems. Variable importance scores of RF, which were based on increases in mean squared error after permutation, were used to rank individual SNPs with large effects. Important combinations of SNPs, which may indicate the presence of epistasis even in the absence of significant main effects, were identified by examining the structure of trees. A 2-step RF algorithm was implemented, and parameters were tuned through 5-fold cross validation. A total of 4411 SNPs were selected at the first step based on importance scores; in the second step, individual SNPs with the largest importance scores and pairs of SNPs that appeared most repeatedly in combination within decision trees were evaluated relative to previously published studies of RFI in livestock. Among the 15 SNPs that were identified in our study, 7 are located within reported quantitative trait locus intervals for RFI in beef cattle, 6 are associated with annotated genes, and 5 are located in the introns of known genes. Based on these results, RF algorithms may be an effective method for identifying individual SNPs with large additive effects and combinations of SNPs with epistatic effects for quantitative traits.

Key Words: feed intake, random forest, SNP

711 Use of milk fatty acids to substitute for body condition score in breeding purposes.

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The general objective of this research was to investigate whether fatty acids (FA) profile in milk could substitute for body condition score (BCS) as an indicator of energy balance status in genetic evaluations. First, genetic correlations between BCS and the content in milk of 10 major FA predicted by mid-infrared spectrometry (C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C17:0, C18:0, and C18:1 *cis-9*; in g/dL of milk) were estimated using 10 2-trait random regression models. Data included from 36,964 to 37,239 FA records depending on the trait and 30,500 BCS records collected in 85 herds from 7,623 first-parity Holstein cows. Genetic correlations among BCS and FA were at the highest in early lactation. At 5 d in milk, genetic correlations with BCS ranged from 0.26 to 0.32 for C4:0 to C14:0 and were 0.15 for C16:0, −0.01 for C17:0, 0.05 for C18:0, and −0.15 for C18:1 *cis-9*. These results could be explained by the release of long chain FA in milk in early lactation due to the body fat mobilization and the consequent inhibition of de novo FA synthesis in the mammary gland. Also, results indicated that FA contents in milk in early lactation would impact BCS during the whole subsequent lactation: genetic correlation between C18:1 *cis-9* at 20 d in milk was −0.14 with BCS at 20 d in milk and −0.25 with BCS at 305 d in milk. Second, the part of the genetic variance in BCS explained by FA contents in milk along the lactation was calculated using selection index theory. Results indicated that the part of genetic variance in BCS explained by FA was 38% at 5 d in milk, was at the highest (56%) at 150 d in milk, and then decreased to 44% at 305 d in milk. Future studies will aim at estimating the part of the genetic variance in fertility explained either by BCS or FA contents in milk or both and will further investigate if FA contents in milk could substitute for body condition score.

Key Words: fatty acid, body condition score, genetic correlation

712 Genetics of the mid-infrared prediction of lactoferrin content in milk for Holstein first-parity cows.

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Lactoferrin is an iron-binding protein present in bovine milk. Interests taken to this protein are related to its therapeutic properties. Lactoferrin can be isolated from whey and used as a specialty food ingredient or as an antimicrobial agent. Furthermore, lactoferrin content in milk has been demonstrated to be higher in (sub)clinical mastitic cows. The objective of this study was to assess the genetic variability of the mid-infrared prediction of lactoferrin content in milk (MIRLf) and to estimate its genetic correlations with milk, fat, and protein yields, somatic cell count (SCS), and contents in milk (g/dL) of 7 groups of fatty acids (FA) predicted by mid-infrared spectrometry (saturated, monounsaturated, polyunsaturated, unsaturated, short chain, medium chain, and long chain). Data included more than 88,000 milk, fat, and protein records, 85,000 SCS records, and 61,000 FA and MIRLf records from 9878 first-parity Holstein cows. Co(variances) were estimated using 11 2-trait random regression models. Heritability for MIRLf increased from 0.20 at 5 d in milk to 0.40 at 250 d in milk. Genetic correlations of MIRLf with milk, fat, and protein yields decreased along the lactation; from 0.50 to −0.50 for milk, from 0.40 to −0.10 for fat yield, and from 0.55 to −0.25 for protein yield. Genetic correlation between MIRLf and SCS increased along the lactation from 0.10 at 5 d in milk to 0.30 at 305 d in milk. This positive correlation substantiated the potential interest of MIRLf as an indicator of udder health. Finally, for all FA groups, genetic correlation with MIRLf increased along the lactation. Average daily genetic correlations between MIRLf and FA ranged from 0.25 to 0.40 and were higher for unsaturated FA, indicating that selection for higher MIRLf would increase the content of unsaturated FA in milk to a larger extent than saturated FA. Concomitant selection of MIRLf and unsaturated FA is therefore feasible and this could be considered as beneficial for the genetic improvement of nutraceutical properties of milk.

Key Words: lactoferrin, mid-infrared prediction, genetic correlation

713 Genetic parameters for methane indicator traits based on milk fatty acids in cows.

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Dairy production is pointed out for its large methane emission. Therefore, currently studies of factors affecting emission and methods to abate methane emission are numerous. However, an important issue is the development of easily obtainable indicators, because they would also allow estimating animal genetic variability of methane emission. Recently methane indicators were proposed using gas chromatography based milk fatty acid composition. We derived these published methane indicators using 1100 calibration samples directly from mid-infrared (MIR). For the published indicator showing the highest relationship ($R^2 = 0.88$) with sulfur hexafluoride (SF_6) methane emission data, genetic parameters for this MIR based indicator were estimated by single trait random regression test-day models from 619,272 records collected from 2007 to 2011 on 71,188 Holstein cows in their first 3 lactations at Walloon region of Belgium. The average daily heritability was 0.35 ± 0.01, 0.35 ± 0.02 and 0.32 ± 0.02 for the first 3 lactations, respectively. Similarly, the lactation heritability was 0.67 ± 0.02, 0.72 ± 0.03 and 0.62 ± 0.03. As expected, methane production was higher during the peak milk production depicting the normal lactation curve. The largest differences between estimated breeding values (EBV) of sires having cows in production eructing the highest and the lowest methane content was 21.80, 22.75 and 24.89 kg per lactation for the first 3 parities, the variances of the EBV of the sires with daughters were 10.67, 12.46, 12.18 kg^2. Results were similar for other indicators. This study suggested that methane indicator traits can be predicted by MIR. Genetic parameters also indicated a rather high heritability and genetic variability exist for these published indicators and consequently a potential high genetic variability of methane eructation by dairy cows. Therefore, these first finding might open new opportunities for animal selection programs that include the reduction of methane emission.

Key Words: methane, mid-infrared (MIR), heritability

714 Comparison of daughter performance of New Zealand and North American sires in US herds.

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To improve fertility or other desired traits, some US graziers have chosen bulls from New Zealand (NZ), which relies extensively on seasonal calving and grazing. To compare performance of daughters of NZ and North American (NA; Canadian and US) AI Holstein (HO) and Jersey (JE) bulls, the model included fixed effects for US herd-year-season, parity (≤ 5) and semen source. Cows that calved between January 2000 and July 2010 in all US herds were included as well as in a subset of seasonally calving herds ($\geq 60\%$ of calvings in February through April). First-lactation HO data included records from 438 herds with 1,443 daughters of 54 NZ bulls and 26,444 daughters of 3,055 NA bulls; JE first-lactation data included records from 538 herds with 2,714 daughters of 65 NZ bulls and 76,281 daughters of 1,631 NA bulls. The seasonal calving subset included 22 HO and 26 JE herds. All differences mentioned were significant ($P < 0.05$) unless designated otherwise. Mean milk and protein yields across all parities were higher for NA daughters than for NZ daughters (497 kg milk and 6 kg protein for HO; 264 kg milk and 3 kg protein for JE); mean fat yield was nearly equal for HO but lower (2 kg) for NA JE daughters. Mean somatic cell scores were higher for NZ than NA daughters (0.15 for HO; 0.08 for JE). Mean days open were fewer for HO (9.9 d) and JE (1.3 d, nonsignificant) NZ daughters. Difference between NZ and NA HO daughters for calving ease and stillbirth rate was small and nonsignificant. Results for seasonally calving herds were similar. For 17 HO type appraisal traits, NA daughters scored higher for stature, fore udder attachment, rear udder height, and udder depth. For 13 JE type appraisal traits, NA daughters scored higher for stature, dairy form, fore udder attachment, rear udder height and width, and udder depth but lower for strength and thurl width. Overall, NA HO bull daughters produced more milk and protein but were less fertile than NZ bull daughters. For JE, fertility was not different between NA and NZ daughters. Overall merit of various selection alternatives should be judged on performance of all traits with economic value considered.

Key Words: daughter performance, New Zealand, seasonal calving

715 Genotype environment interaction of Holstein-Friesian dairy cattle in eastern Libya.

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Breeding values (BV) for some productive and reproductive traits of Holstein Friesian sires (6 North American, 57 European and 7 Libyan) under eastern Libyan conditions were estimated and compared with those estimated under, European, and North American conditions in an attempt to assess the genotype environment interaction. To investigate the effect of managerial conditions on the same traits, the heritability coefficients were also estimated under Libyan and Dutch managements. The trait's variance and covariance components and the breeding values of animal were computed using mixed model containing the fixed effects of month of calving, year of calving, management and generation and animal as random effect. The lactation period and age at calving were used as covariates. Genetic correlation values of sires BV for the milk yield under Libyan and European and North American conditions was less than 1. Differences in heritability estimates due to the management system and or to environmental factors reflect genotype × environment interaction. Milk yield traits except dry period had a higher BV during the Libyan than Dutch management. Reproductive traits except age at first calving also had a higher BV during Dutch than Libyan management. Correlations between BV for milk yield ranged between 0.16 and 0.56 under Libyan, European and North American conditions. Breeding values of both North American and European sires were medium, low and negatively ranked under Libyan environment. Breeding values of milk yield traits showed higher variability under the Libyan environment. Sires with low BV ($\geq$ 500) revealed negative ranking under the Libyan conditions.

Key Words: breeding values, genetic correlations, genotype × environment interaction

716 Casein and fatty acid content in milk of crossbred dairy cows under grazing conditions.

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Nutritional, physical, and flavor properties of milk are influenced by its casein and fatty acid (FA) content and they might have an effect on the consumer acceptance of dairy products. Therefore, the manipulation of their content in milk would have an effect on consumer demands, and on health recommendations [e.g., choosing between milks with greater proportion of conjugated linoleic acid (CLA)]. The objective of this study was to evaluate the casein and FA content of milk on Uruguay Holstein cows (UH; North American genetics), New Zealand Holstein and UH (NZH×UH), Jersey and UH (J×UH), and Swedish Red and UH (SRB×UH) under the same feeding strategies and herbage allowance. Forty primiparous cows were selected from a commercial Uruguayan dairy farm (UH, n = 8; HNZ×UH, n = 10; JXH×UH, n = 10; SRB×UH, n = 12). Milk samples were collected at wk 12 of lactation. Means were considered to differ when $P \leq 0.05$. Milk yield was greater in UH than RBS×UH and J×UH cows, while NZH×UH was greater than J×UH. Milk fat yield was greater in J×UH than the rest of the groups. Although milk protein yields were not affected by genotype, total casein production was greater in J×UH than UH cows and no other differences were found. Casein content was not affected by genotype. Saturated FA was greater and monounsaturated were less in milk fat of J×UH and HNZ×UH than RBS×UH. Polyunsaturated FA tended to have a lower concentration in J×UH than in the other groups ($P = 0.09$). Trans FA in milk fat were greater in RBS×UH, than J×UH. No differences among cows were found in CLA concentrations in milk. The results indicate that differences in genotype have an impact on the total casein production, as well as, saturated, monounsaturated, polyunsaturated and *trans* FA concentrations in milk from dairy cows under grazing conditions.

Key Words: crossbreeding, milk composition, grazing

717 Effect of the milk recording time on the genetic parameters of milk production and mid-infrared milk components in Luxembourg dairy cattle. V. M.-R. Arnould*[1,2], H. Soyeurt[2,3], and N. Gengler[2,3], [1]*CONVIS s.c., Ettelbruck, Luxembourg,* [2]*University of Liège, Gembloux Agro Bio-Tech, Animal Science Unit, Gembloux Belgium,* [3]*National Fund for Scientific Research (F.N.R.S.), Brussels, Belgium.*

Reducing the frequency of official milk recording and the number of recorded samples per test-day (vs. the conventional twice-a-day sampling) would have some advantages for dairy herd management. However, phenotypic variations in milk composition between morning (AM) and evening (PM) milkings are known and documented for major milk components but poor literature exist about genetic differences between AM and PM milkings. Therefore, the objective was to study the effect of milking time (AM or PM) on the estimation of the genetic parameters of milk yield, and mid-infrared milk components such as protein and fat yields and saturated and unsaturated fatty acids groups. A total of 44,833 milk samples were collected between October 2007 and November 2011 (from 9,602 Holstein cows in first lactation belonging to 491 Luxembourg dairy herds): 23,046 records from AM milking and 21,787 from PM milking. All milk samples were analyzed by mid-infrared spectrometry. The model included as fixed effects: herd × date of test, 3 classes of age, 24 classes of days in milk and month of test × year of test. Random effects were permanent environmental, additive genetics, and residual effects. Expect for milk yield ($P = 0.88$), it was observed that the evolution of the daily heritability among the first lactation was different according to the milking time for all studied traits ($P < 0.0001$). Preliminary results based on breeding values of bulls with daughters having records showed a rank correlation of 0.77 (milk yield). Given these results, genetic parameters of milk yield and studied milk components were affected by AM/PM milking.

Key Words: genetic evaluation, alternate milking recording scheme, milk component: heritability

718 Integration of experimental designs and analytical approaches to co-ordinate efficiency of global efforts to optimize environmental and genetic effects on reproductive performance of dairy cattle. E. Block[1], B. Bradford[2], W. M. Chalupa[3], I. J. Lean*[4], S. LeBlanc[5], M. C. Lucy[6], J. McNamara[7], J. Morton[8], A. R. Rabiee[4], J. E. P. Santos[9], W. W. Thatcher[9], M. Van Amburgh[10], and M. J. VandeHaar[11], [1]*Church & Dwight Co, Princeton, NJ,* [2]*Kansas State University, Manhattan,* [3]*University of Pennsylvania, Kennett Square,* [4]*SBScibus, Camden, New South Wales, Australia,* [5]*Population Medicine Ontario Veterinary College University of Guelph, Guelph, ON Canada,* [6]*Division of Animal Sciences, University of Missouri, Columbia,* [7]*Department of Animal Sciences, Washington State University, Pullman,* [8]*Jemora Pty Ltd., Geelong Victoria, Australia,* [9]*Department of Animal Sciences, University of Florida, Gainesville,* [10]*Department of Animal Sciences, Cornell University, Ithaca, NY,* [11]*Department of Animal Sciences, Michigan State University, E. Lansing.*

Our present knowledge of genetic and environmental processes that influence reproductive functions demands a systematic approach to design, conduct and analyze basic and applied studies of dairy cattle reproduction. The effects of genetic selection and population variation, nutritional intake and composition, climate and housing all interact to affect reproductive functions at cellular and molecular levels. Therefore, experiments must be designed to address specific mechanisms within a defined systems framework such that data will be integrated efficiently into knowledge bases, utilizing compilation methods such as meta-analysis and regression. Researchers with interests in reproduction have undertaken a project to produce guidelines to assist in efficient design, conduct, and analysis of experiments. The intent of the guidelines is to provide for design of studies that best fill the most critical knowledge gaps, enhance opportunities for research interaction, and provide new knowledge that can be integrated into our present understanding through appropriate data analyses and pooling methods. Similar guidelines have been developed for randomized controlled clinical studies in medicine, veterinary and animal science using a process of review and consensus. The guidelines will provide 1) clear definitions of experimental conditions, which include dietary, environmental, and reproductive conditions and responses, and 2) appropriate statistical designs and analyses to reduce bias, pseudoreplication, and the risks of Type I and Type II statistical errors. Critical knowledge gaps include the influence on reproductive outcomes of genetic selection and random genetic variation, diet content and intake, reproductive management and environmental conditions. Standardization is being developed for definitions of expression and detection of estrus and ovulation, cyclicity, fertilization, embryonic development, establishment and maintenance of pregnancy, and time to events such as pregnancy and for appropriate minimal sample sizes to detect economically or biologically important outcomes.

Key Words: reproduction, study design, nutrition