

Breeding and Genetics: Applications and Methods in Animal Breeding—Dairy II

307 Genetic correlations between feed intake and type traits in dairy cattle. G. Bilal^{*1,2}, R. I. Cue², and J. F. Hayes², ¹*Department of Livestock Production and Management, Faculty of Veterinary and Animal Sciences, Arid Agriculture University, Rawalpindi, Punjab, Pakistan*, ²*Department of Animal Science, McGill University, Ste-Anne-de-Bellevue, Quebec, Canada.*

The objective of the present study was to estimate genetic correlations between feed intake and type traits with a view to considering the potential of indirect genetic selection for feed intake using type traits in dairy cattle. Feed intake data on 119,388 first lactation Holstein cows were obtained from Dairy Production Centre of Expertise, Valacta. Type trait records on 93,619 cows were obtained from Holstein Canada and were recorded during 1 to 365 d of first lactation. Feed traits included 305-d dry matter intake (DMI), 305-d net energy of lactation intake (NELI) and 305-d crude protein intake (CPI). Type traits included dairy strength, angularity, body depth, stature and final score. The statistical model of analysis for feed intake traits included age at first calving and herd-year-season of calving as fixed effects and random effects of animal and residual. The statistical model for type traits included fixed effects of age at first calving, days in milk and herd-round-classifier and random effects of animal and residual. Additionally, 13 (8 male and 5 female) phantom parent groups were fitted as covariates for all traits. Pedigree of animals with data was traced back 5 generations on both the male and female side to account for relationships among animals. Genetic parameters were estimated by fitting 5-trait animal models under restricted maximum likelihood using Wombat program. Estimates of heritabilities for DMI, NELI and CPI were 0.12, 0.13 and 0.13, respectively. Estimates of heritabilities of dairy strength, angularity, body depth, stature and final score were 0.31, 0.24, 0.30, 0.50 and 0.22, respectively. All phenotypic and genetic correlations between feed intake and type traits were positive. Genetic correlations between angularity and feed intake traits were strong and positive (0.60 to 0.65). Dairy strength showed strong positive genetic correlations (0.48 to 0.54) with feed intake traits. Both stature and body depth showed moderate positive genetic correlations (0.29 to 0.36) with feed intake traits. Angularity, dairy strength, stature and body depth may be useful for indirect selection of feed intake traits in dairy cattle.

Key Words: dairy cattle, feed, type

308 Genetic parameters for methane emissions predicted from milk mid-infrared spectra in dairy cows. P. B. Kandel^{*1}, M. L. Vanrobays¹, A. Vanlierde², F. Dehareng², E. Froidmont², P. Dardenne², E. Lewis³, F. Buckley³, M. Deighton³, S. McParland³, N. Gengler¹, and H. Soyeurt¹, ¹*University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium*, ²*Walloon Agricultural Research Center, Gembloux, Belgium*, ³*Teagasc, Animal & Grassland Research and Innovation Center, Moorepark, Ireland.*

Genetic selection of low methane (CH₄) emitting animals is additive and permanent but the difficulties associated with individual CH₄ measurement result in a paucity of records required to estimate genetic variability of CH₄ traits. Recently, it was shown that direct quantification of CH₄ emissions by mid-infrared spectroscopy (MIR) from milk. The CH₄ prediction equation was developed using 452 SF₆ CH₄ measurements with associated milk spectra and the calibration equation was developed using PLS regression. The obtained SD of predicted CH₄

was 126.39 g/day with standard error of cross validation 68.68 g/day and a cross-validation coefficient of determination equal to 70%. The equation was applied on a total of 338,917 spectra obtained from milk samples collected between January 2007 and August 2012 during the Walloon milk recording for first parity Holstein cows. The prediction of MIR CH₄ was 547 ± 111 g/d and MIR CH₄ g/kg of fat and protein corrected milk (FPCM) was 23.66 ± 8.21. Multi-trait random regression test-day models were used to estimate the genetic variability of MIR predicted CH₄ and milk production traits. The heritability, phenotypic and genetic correlations between MIR predicted CH₄ traits and milk traits are presented in Table 1. Estimated heritability for CH₄ g/day and CH₄ g/kg of FPCM were lower than common production traits but would still be useful in breeding programs. While selection for cows emitting lower amounts of MIR predicted CH₄ (g/d) would have little effect on milk production traits, selection on MIR predicted CH₄ (g/kg of FPCM) would decrease FPCM, fat and protein yields. These genetic parameters of CH₄ indicator traits might be entry point for selection that accounts mitigation of CH₄ from dairy farming.

Table 1. Heritability (diagonal), phenotypic (below the diagonal) and genetic (above the diagonal) correlations between MIR CH₄ and production traits

| Trait | MIR CH ₄ | | FPCM | Fat yield | Protein yield |
|------------------------------------|---------------------------|----------------|-------|-----------|---------------|
| | MIR CH ₄ (g/d) | (g/kg of FPCM) | | | |
| MIR CH ₄ (g/d) | 0.11 | 0.42 | 0.03 | 0.19 | 0.04 |
| MIR CH ₄ (g/kg of FPCM) | 0.59 | 0.18 | -0.83 | -0.63 | -0.78 |
| FPCM | -0.01 | -0.74 | 0.23 | 0.87 | 0.93 |
| Fat yield | 0.03 | -0.68 | 0.95 | 0.24 | 0.70 |
| Protein yield | 0.02 | -0.70 | 0.94 | 0.82 | 0.22 |

Key Words: methane emissions, heritability, dairy

309 Genetics of body energy status of Holstein cows predicted by mid-infrared spectrometry. C. Bastin^{*1}, D. P. Berry², N. Gengler¹, and S. McParland², ¹*University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium*, ²*Teagasc Moorepark Dairy Production Research Center, Fermoy, Co. Cork, Ireland.*

Energy balance (EB) status has been demonstrated to affect health and fertility in dairy cows. Recent research proposed mid-infrared (MIR) analysis of milk, potentially routinely available within milk recording schemes, to predict body energy status of dairy cows. Hence MIR prediction of body energy status is easy, quick and inexpensive and could warrant the inclusion of EB in breeding programs. The objective of this study was to estimate genetic parameters of body energy status traits predicted by MIR spectrometry for Walloon Holstein cows and to investigate their relationships with fertility. Three body energy status traits were considered: direct EB (dEB; MJ/d), body energy content (EC; MJ), and effective energy intake per day (EEI; MJ/d). Only dEB, EC, and EEI MIR predictions that encompassed the variability represented in the prediction equations calibration data set were considered. Genetic parameters were estimated using single-trait 3-lactation random regression models. Data included 336,142 dEB records from 36,694 cows in 580 herds and 354,900 EC and EEI records from 38,531 cows in 607 herds. For all traits, heritability estimates were the highest in mid to late lactation and ranged across lactation from 0.15 to 0.55 for dEB, from

0.10 to 0.30 for EC, and from 0.10 to 0.25 for EEI. Genetic correlations within trait across lactation were stronger than 0.85. Genetic correlations between the body energy status traits and fertility (number of days from calving to conception or days open; DO) were estimated in first-parity cows using bivariate models that included a random regression for body energy status traits. Data included 125,921 dEB, EEI and EC records and 24,419 DO records from 24,419 cows in 361 herds. The genetic correlation with DO ranged from -0.22 to -0.17 for dEB, from -0.30 in early lactation to 0.00 in mid-lactation for EEI, and from -0.05 at 5 d in milk to -0.30 at 305 d in milk for EC. Results from this study indicated that body energy status traits predicted by mid-infrared are heritable but lowly to moderately correlated with DO.

Key Words: energy balance, mid infrared, genetic correlation

310 Heterogeneity across research stations in genetic variation and energy sink relationships for feed efficiency in lactating dairy cattle. R. J. Tempelman^{*1}, D. M. Spurlock², M. Coffey³, R. F. Veerkamp⁴, L. E. Armentano⁵, K. A. Weigel⁵, Y. deHaas⁴, C. R. Staples⁶, M. D. Hanigan⁷, and M. J. Vandehaar¹, ¹Michigan State University, East Lansing, ²Iowa State University, Ames, ³Scottish Agricultural College, Midlothian, UK, ⁴Wageningen UR, Lelystad, the Netherlands, ⁵University of Wisconsin, Madison, ⁶University of Florida, Gainesville, ⁷Virginia Tech, Blacksburg.

The importance of dairy cattle feed efficiency will further intensify with human population and land constraint pressures. It seems imperative then to coordinate extensive collaboration between research stations in different countries to facilitate large enough databases for genetic improvement while recognizing that potential heterogeneities will exist in the way traits are recorded and related with each other across research stations. Milk, fat, protein, and lactose production, converted to net energy units (Milke), dry matter intakes (DMI), body weights (BW), and body condition scores (BCS) were collected on 6,061 lactations from 4,341 Holstein cows from research stations in Scotland, the Netherlands, and the United States. Weekly DMI was fitted as a function of Milke, BW^{0.75}, BCS, and change in BW (Δ BW), parity, and its interaction with parity with a 5th order polynomial on days in milk (DIM) ranging from 50 to 200d. The residuals from this analysis were considered to be a measure of feed efficiency; i.e., residual feed intake (RFI). Partial regression coefficients of DMI on Milke and on BW^{0.75} were always important ($P < 0.0001$). These coefficients were generally consistent (0.40–0.45 kg/Mcal) for Milke, whereas partial regression coefficients on BW^{0.75} uniformly ranged from 0.06 to 0.16 kg/kg^{0.75}. Significant ($P < 0.05$) partial regression coefficients on Δ BW ranged up to 0.120 kg/kg across stations. Heritabilities for country-specific RFI were based on fitting random regression models and ranged from 0.08 to 0.22 depending on DIM; residual variances were particularly heterogeneous across research stations likely due in part to differences in data recording protocols. The overall heritability from 60 to 90 DIM across all research stations was 0.14 ± 0.03 . Hence future genomic selection programs on feed efficiency appear to be promising, provided that care is taken to allow for heterogeneous variance components and relationships across environments between DMI and other energy sink traits as used to determine RFI.

Key Words: residual feed intake, heritability

311 Repeatability and genetic correlations of residual feed intake across stages of lactation in dairy cattle. G. Manafiazar^{*}, T. McFadden, E. Okine, L. Goonewardene, and Z. Wang, University of Alberta, Edmonton, Alberta, Canada,

Residual feed intake (RFI) is a measure of net feed efficiency. Animals with low RFI eat less feed than expected on the basis of its maintenance and production levels. To the best of our knowledge, there is no published report on repeatability and genetic correlation among RFI prediction across stages of lactation, which is ultimately essential for wide-scale adaptation of RFI by producers. Individual daily actual energy intake (AEI), monthly body weight, and monthly milk yield and composition data of 200 first lactation cows from 5 to 305 d in milk (DIM) were acquired at the University of Alberta. 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 DIM using random regression Legendre polynomial. Individual RFI value was estimated from the regression of total AEI on total estimated MPER, EBWC, and MBW for the same animal in 4 periods: 5 to 305 DIM (RFI_{lact}), 5 to 105 DIM (RFI_{early}), 106 to 205 DIM (RFI_{mid}), and 206 to 305 DIM (RFI_{late}). A bivariate animal model was used to estimate genetic and phenotypic parameters among the RFIs. Daily RFI_{lact}, RFI_{early}, RFI_{mid}, and RFI_{late} averaged zero, with SD 2.29, 3.41, 3.38, and 3.03 NE_L Mcal/d, respectively. Phenotypic and genetic correlations were significant between RFI_{lact} and RFI_{early} (0.64 ± 0.04 and 0.93 ± 0.42 , respectively), RFI_{lact} and RFI_{mid} (0.78 ± 0.03 and 0.96 ± 0.4), RFI_{lact} and RFI_{late} (0.59 ± 0.05 and 0.83 ± 0.22), RFI_{early} and RFI_{mid} (0.26 ± 0.07 and 0.85 ± 0.73), RFI_{early} and RFI_{lact} (0.04 ± 0.07 and 0.49 ± 0.72), and RFI_{mid} and RFI_{late} (0.41 ± 0.06 and 0.98 ± 0.65). Estimated repeatability for RFI was 0.42 ± 0.04 . The results showed that RFI was moderately repeatable across stages of lactation, and RFI_{lact} and RFI_{mid} had higher genetic and phenotypic correlations. Therefore, results indicate that dairy industry may select animals based on RFI estimation in the mid stage of lactation.

Key Words: dairy cattle, residual feed intake, repeatability

312 Individual and maternal heterosis in performance traits of Holstein and Jersey crosses with Sahiwal cattle. M. S. Khan^{*1}, F. Hassan¹, and S. A. Bhatti², ¹Department of Animal Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan, ²Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Pakistan.

Crossbreeding of indigenous Sahiwal (S) cattle with Holstein (H) and Jersey (J) started in Pakistan in mid 1970s to see if it could be adopted as a general strategy for upgrading local cattle. Farmers generally rear cattle in a low to medium input system under climatic conditions (-2°C to 52°C). Present study reports preliminary estimates for breed group differences, individual and maternal additive and heterotic effects for some economic traits using data on 178 cows (740 lactations) in a university herd. The 305-d milk yield (305MY, liters) (\pm SD), total lactation milk yield (TMY, liters) and lactation length (LL, days) averaged 2668 ± 952.9 , 3217 ± 1480.4 and 384 ± 40.6 , respectively. Age at first calving (AFC, months), calving interval (CI, days) and productive life (PL, months) averaged 49 ± 26.2 , 491 ± 155.2 and 41 ± 24.8 , respectively. The AFC was minimum in F1 J (40 ± 13.7). The H F1 crossbreds performed better than any other genetic group for milk yield traits. Period and seasons of calving, parity and genetic groups were used as fixed effects. Parity groups were excluded for analyzing AFC while model for PL had period of birth and genetic groups as only fixed effects. Least squares means for 305MY was 3167 ± 1210.2 and 2333 ± 1028.3 for F1 H and F1 J, respectively and lowest (1323 ± 1020.8) for $>75\%$ S. The CI did not differ among genetic groups while PL was maximum in F1 H (43 ± 30.7) and minimum (6 ± 28.2) for $>75\%$ S. The $>75\%$ S group had highest AFC (62 ± 14.2), longest CI (512 ± 165.3) and shortest LL (277 ± 166.8). Individual additive breed effect (*Bos taurus* – *Bos indicus*)

was 904.8, 1296.2, 75.3 and 13.7 for 305MY, TMY, LL and PL, respectively. Maternal additive genetic effects were significant ($P < 0.01$) for 305MY (-250), TMY (-396) against *Bos taurus* inheritance. Individual heterosis was also significant ($P < 0.01$) for AFC, 305MY, TMY and PL. *Bos taurus* inheritance improved performance but going beyond 75% deteriorated traits, especially the PL. Lifetime performance studies are needed to suggest upgradation policy for local cattle of Pakistan.

Key Words: heterosis, Sahiwal, crossbred

313 Effect of timed AI use on reproductive performance and culling rate in Wisconsin dairy herds. A. H. Souza^{*1,2}, P. A. Carvalho¹, R. D. Shaver¹, M. C. Wiltbank¹, and V. Cabrera¹, ¹*Department of Dairy Science, University of Wisconsin, Madison*, ²*Ceva Sante Animale, Libourne, France*.

We examined the use and effect of synchronization programs on reproductive performance and culling rates in dairy herds in WI. Backups ($n = 200$) from herds using DC305 were collected from 2009 to 2012. Average lactating cows per herd was 660 (51–7,273) and 305ME production was 12,427kg (9,476–16,112). Service rate (SR) and pregnancy rate (PR) calculations used either the actual voluntary waiting period (VWP) in the herd or were set at 50DIM. Culling rate was defined as the number of culled cows (sold plus dead) over 12 mo divided by the average number of mature cows in the herd. Percentage of breedings done with timed

AI was assessed by recorded breeding codes in DC305. Overall, 91% of the herds reported more than 10% of their breeding codes associated with a timed AI protocol, and 52% of all breedings happened following a synchronization program. Herds were divided in quartiles in terms of percentage of breedings by timed AI (Q1 = 0–36%; Q2 = 37–55%; Q3 = 56–69%; Q4 = 67–99%). Average VWP was 57.4d and % pregnant to 1st AI (P/1stAI) was 36.6%. As expected, herds using more timed AI delayed 1st postpartum AI (VWP: Q1 = 49.6 d vs. Q4 = 67.5 d; $P < 0.01$) but had improved P/1st AI (Q1 = 34.9% vs. Q4 = 39.9%; $P < 0.01$). In addition, PR increased from 15.8% to 20.0%, for Q1 and Q4 respectively ($P < 0.01$) with a greater proportion of herds having outstanding reproductive performance (PR >20%; Q1 = 12.3% vs. Q4 = 55.7% of herds; $P < 0.01$). Increased milk production was associated with increased use of timed AI ($r = 0.39$, $P < 0.01$), increased SR ($r = 0.36$, $P < 0.01$), no change in P/AI ($r = -0.04$, $P = 0.53$), increased PR ($r = 0.24$, $P < 0.01$), and lower early cullings ($r = -0.24$, $P < 0.01$). Regardless of the proportion of breedings performed with timed AI, PR was not associated with overall culling rate ($r = 0.008$, $P = 0.91$), but was negatively correlated with later (>300 DIM) cullings ($r = -0.32$, $P < 0.01$). Younger age at first calving in heifers was associated with greater culling rates in the lactating herd ($P < 0.01$). Thus, timed AI appears to be a critical part of reproductive management programs in WI dairies, particularly in high-producing herds.

Key Words: dairy farm, synchronization program, Ovsynch