Breeding and Genetics: Milk and Carcass Composition

784   Feasibility of a genetic evaluation for milk fatty acids in dairy cattle.   H. Soyeurt*[1,2], V. M.-R. Arnould[1], S. Vanderick[1], and N. Gengler[1,2], [1]*University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Namur, Belgium*, [2]*National Fund for Scientific Research, Brussels, Brussels, Belgium*.

Recent development of equations based on mid-infrared (MIR) spectrometry for the prediction of milk fatty acid (FA) contents allows their measurement on a large scale during performance recording. The objective was to show that a genetic evaluation for milk FA in dairy cattle is feasible in the Walloon region of Belgium and to report first results. Estimated breeding values (EBV) and associated reliabilities (REL) were computed using a multi-trait test-day animal model similar to the one used for the routine genetic evaluation for yield traits. Studied traits were first lactation test-day milk, fat and protein yields, fat (FAT) and protein contents, and content of saturated fatty acids in milk (g/100g of milk, SAT). More than 6,700,000 records were available for common production and content traits and 194,000 records were used for SAT. Used variance components were estimated using REML. The average SAT content was 2.79% with a standard deviation (SD) of 0.50%. A total of 1,707 Holstein bulls used in Walloon Region had REL superior to 0.49 for all studied traits. REL for SAT ranged from 0.53 to 0.99. A total of 1,217 bulls had REL superior to 0.74. SD of EBV for SAT was 0.20%. The maximum and minimum SAT EBV values were 0.89% and −0.69%, respectively. To have a direct measure of the part of FAT that is not due to SAT, a new trait (dSAT) was post-evaluated and defined as difference between expected SAT EBV for a given FAT EBV and the estimated EBV for SAT. This new trait can be assumed to be a direct predictor of the content of unsaturated fatty acids in fat. The interest is that this trait cannot be accurately predicted directly by MIR. The maximum and minimum EBV for dSAT for the 1,707 bulls were −0.28% and 0.24%, respectively. Based on these results, a genetic evaluation for milk fatty acids is feasible. In the bull population used recently, a genetic variability for dSAT exists and could be used to improve the milk fat composition.

Key Words: genetic parameter, milk, fatty acid

785   Heterogeneity of residuals variances of milk fatty acids in dairy cattle.   V. M.-R. Arnould*[1], H. Soyeurt[1,2], S. Vanderick[1], and N. Gengler[1,2], [1]*University of Liège, Gembloux Agro-Bio Tech, Gembloux, Belgium*, [2]*National Fund for Scientific Research, Brussels, Belgium*.

Routine genetic evaluation for milk fatty acids is under development in the Walloon Region of Belgium. The objective of this study was to test the heterogeneity of residual variances and therefore indirectly the potential need to adjust for this heterogeneity if it exists. The residuals were computed as the difference between the observed and the estimated values using a multi-trait random regression test-day model, similar to the Walloon routine model, used for first lactation only milk yield, quantities and percentages of protein (PROT) and fat (FAT), content of saturated fatty acids in milk (g/100g of milk, SAT) and, content of mono-unsaturated fatty acids in milk (g/100g of milk, MONO). Residuals were considered homogeneous inside strata defined, among others, by weeks of lactation, by days in milk and by calendar months of test date. About 6,687,000 records were available for milk yield and for FAT and PROT parameters. For SAT and for MONO, about 184,000 records were available in this database. Means of residuals were stable and close to zero for all traits. Variances were more variable for MONO and SAT than for milk yield, for example. Daily and weekly variances tended to decrease at the end of the lactation (50%). When the variances were computed by month of test date, some variations were observed and some periods of year were more marked. In conclusion, the observed residual variances were less stable for MONO and SAT. We can conclude that introduction for heterogeneous residual variance is more important for the new traits (MONO, SAT) than it was for the old, traditional ones.

Key Words: routine genetic evaluation, heterogeneity of residual variances, milk fatty acids

786   Relationships between feedlot growth and carcass traits in Angus: Tri-County Steer Carcass Futurity.   L. D. Leachman*, D. R. Notter, S. P. Greiner, and R. M. Lewis, *Virginia Tech, Blacksburg*.

The objective was to characterize growth and carcass traits and associated genetic parameters in 2,199 steers and 424 heifers sired by registered Angus bulls and evaluated under feedlot conditions in the 2002–2006 Iowa Tri-County Steer Carcass Futurity Program. Traits evaluated were initial (IBW) and slaughter BW (SBW; kg), and carcass backfat thickness (CFAT), marbling score (CMAR) and ribeye area (CREA). Univariate and bivariate sire models were fitted with ASReml3. Fixed effects included contemporary group (CG) and linear and quadratic effects of age at IBW nested within season and year of feedlot delivery. Random effects were sire and residual. The CG consisted of sex, pen, dam breed-type, owner, and feedlot. Delivery seasons were January–April, May–August and September–December. Data were edited to CG and sire families with at least 5 animals. Trait sample means (SD) for steers were: IBW, 289 (40.3) kg; SBW, 543 (46.4) kg; CFAT, 1.21 (0.33) cm; CREA, 79 (7.2) cm^2; and, CMAR 1057 (89.0). Heifers weighed less, had smaller CREA, and more fat. Phenotypic variances, heritabilities and correlations are shown in Table 1. All traits were moderately to highly heritable. Cattle with heavier IBW had heavier SBW and larger CREA at harvest. Heavier SBW was strongly associated with larger CREA and with a tendency for less CMAR. More CFAT was related moderately to smaller CREA. Given their heritabilities, and the size and direction of most correlations, feedlot traits are clearly amenable to selection.

Table 1. Phenotypic variances (P-var), heritabilities, and genetic and phenotypic correlations[1]

	IBW	SBW	CFAT	CREA	CMAR
P-var	711	1933	0.0918	50	6751
IBW	0.50±0.11	0.69±0.09	0.03±0.19	0.35±0.15	−0.07±0.16
SBW	0.58±0.02	0.45±0.10	0.04±0.20	0.63±0.12	0.25±0.17
CFAT	0.06±0.03	0.13±0.02	0.27±0.08	−0.34±0.18	−0.11±0.19
CREA	0.26±0.02	0.41±0.02	−0.12±0.02	0.39±0.09	0.23±0.18
CMAR	−0.09±0.03	0.07±0.03	0.12±0.02	−0.03±0.03	0.46±0.10

[1]Heritabilities in bold on diagonal; genetic and phenotypic correlations above and below the diagonal.

Key Words: feedlot, performance, cattle

787   Heritabilities, genetic and phenotypic correlations among Warner-Bratzler shear force and repeated objective measurements of temperament in fed cattle.   R. L. Weaber[1], T. M. Taxis*[1], W. R. Shafer[2], L. L. Berger[3], D. B. Faulkner[4], M. M. Rolf[1], D. L. Dow[1], J. F. Taylor[1], and C. L. Lorenzen[1], [1]*University of Missouri, Columbia*, [2]*American Simmental Association, Bozeman, MT*, [3]*University of Nebraska, Lincoln*, [4]*University of Illinois, Urbana*.

Tenderness is a primary meat palatability attribute affecting consumer satisfaction of beef. Beef cattle temperament has been associated with a variety of performance measures. Performance data and pedigree records were provided by the American Simmental Association (ASA) to elucidate the relationship between temperament and tenderness in *Bos taurus* breeds. Data included WBSF records from ASA's carcass-merit program and a subset collected at the University of Illinois (UI). Exit velocities were recorded when cattle went on trial (EV1) and 42 d later (EV2). Single animal and single sire contemporary groups (CG) were removed from the data set leaving 2,819 WBSF, 917 EV1 and 976 EV2 phenotypes in 176 CG for evaluation. A pedigree was formed with 13,418 animals including 2,488 sires. Phenotypic means (SD) were 36.65 N (10.56 N) for WBSF, 1.74 m/s (0.76 m/s) for EV1 and 1.65 m/s (0.79 m/s) for EV2. A tri-variate animal model with CG, sire and dam breed composition as fixed effects and animal as random effect was fit to estimate variance components. Phenotypic correlations (SE) estimated between WBSF with EV1 and EV2 were −0.05 (0.05) and −0.03 (0.04), respectively, and between EV1 and EV2 was 0.59 (0.02). Heritabilities (SE) for WBSF, EV1 and EV2 were 0.19 (0.06), 0.30 (0.11) and 0.25 (0.10) respectively. Genetic correlations estimated between WBSF with EV1 and EV2 were 0.02 (0.38) and −0.30 (0.36) respectively. Given the high genetic correlation between EV1 and EV2 of 0.99 (0.07) a repeated records analysis was conducted for EV with an uncorrelated random effect for animal using the same fixed effects as before. A likelihood ratio test was used to determine that the repeated records model implemented provided a better fit ($P < 0.0001$) to the data than did the tri-variate model. Heritabilities were 0.19 (0.06) and 0.39 (0.08) for WBSF and EV, respectively, with a genetic correlation of −0.10 (0.20). The near zero genetic correlation and moderate heritabilities suggest producers can select to improve temperament and/or WBSF without substantial correlated response.

Key Words: heritability, beef temperament, tenderness

788   Development and validation of an Angus-specific IGENITY profile for marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate based on a whole genome scan.   B. W. Woodward*[1], D. J. Garrick[2], R. L. Fernando[2], S. Northcutt[3], B. Bowman[3], S. W. Bauck[1], R. D. Schnabel[4], and J. F. Taylor[4], [1]*Merial Limited*, *Duluth, GA*, [2]*Iowa State University*, *Ames*, [3]*American Angus Association*, *St. Joseph, MO*, [4]*University of Missouri*, *Columbia*.

Genomic markers are now being widely used in the selection of beef and dairy breeding animals via various commercial products with a wide range in price. The objective of this study was to develop a cost effective, yet informative low-density panel of SNPs derived from the Illumina Bovine SNP50 specifically for Angus cattle. Target traits were marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate. Multiple methods were initially evaluated for SNP selection and the method of choice involved a 2-stage process combining Bayesian model averaging and semi-parametric models. There were 41,028 SNP genotypes for 1,710 bulls born between 1955 and 2003. Predictability was assessed as the correlation between genomic predictions and EPD in training and cross-validation sets of animals, and by validating on a new set of 275 younger bulls. EPD were from the American Angus Association. Correlations between molecular breeding values and EPD for marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate in cross-validation bulls were 0.71, 0.68, 0.73, 0.68, 0.71, and 0.32, respectively. Corresponding correlations in the group of 275 bulls were 0.66, 0.38, 0.73, 0.68, 0.76, and 0.20. Therefore, correlations for both groups of validation bulls indicate this SNP panel derived from the SNP50 could provide a powerful tool for genomic selection.

Key Words: SNP, whole genome, selection

789   The economics of using DNA markers for beef bull selection in the seedstock sector.   A. L. Van Eenennaam*[1], J. H. van der Werf[2], and M. E. Goddard[3,4], [1]*University of California, Davis,* [2]*University of New England, Armidale, NSW, Australia,* [3]*Victorian Department of Primary Industries, Bundoora, VIC, Australia,* [4]*University of Melbourne, Parkville, VIC, Australia*.

The objective of this study was to estimate the value derived from using DNA test information to increase the accuracy of beef sire selection in a closed seedstock nucleus herd. Breeding objectives for commercial production systems targeting 2 diverse markets, a domestic market where steers are finished on pasture, or a high value export market where steers are finished on concentrate rations and marbling has a high value, were examined considering both maternal (self-replacing) and terminal herds. Selection index theory was used to predict the response to conventional selection based on phenotypic performance records, and this was compared with including information from 2 hypothetical marker panels. In one case the marker panel explained a percentage of additive genetic variance equal to the heritability for all traits in the breeding objective, and in the other case to half this amount. Discounted gene flow methodology was used to calculate the value of DNA test information over that derived from conventional selection for the modeled seedstock herd. Results were ultimately calculated as discounted returns per DNA test purchased by the seedstock operator. DNA testing using these hypothetical marker panels increased the selection response between 33 and 171%. The value of this improvement relative to that obtained using traditional performance recording ranged from AU$156–681 per commercial bull, and AU$9,203–35,823 per stud bull. If the entire bull calf crop was tested to achieve these gains, the value of genetic gain derived from DNA testing ranged from AU$367–1,386 per test. These values assumed commercial producers were willing to pay a price premium for genetically superior bulls and some level of industry vertical integration such that market signals from the processor and feedlot were transferred up the chain to commercial and seedstock producers. All values were sensitive to index accuracy in the absence of DNA information. The development of selection indexes including DNA-based predictions of economically relevant traits not currently included in genetic evaluations will be required to assess the value of DNA information for the beef industry.

Key Words: DNA marker, beef bull, accuracy