

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. Arnould¹, S. Vanderick¹, and N. Gengler^{1,2}, ¹University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Namur, Belgium, ²National 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. Vanderick¹, and N. Gengler^{1,2}, ¹University of Liège, Gembloux Agro-Bio Tech, Gembloux, Belgium, ²National 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) cm²; 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 correlations¹

	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

¹Heritabilities 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. Weaber¹, T. M. Taxis^{*1}, W. R. Shafer², L. L. Berger³, D. B. Faulkner⁴, M. M. Rolff¹, D. L. Dow¹, J. F. Taylor¹, and C. L. Lorenzen¹, ¹University of Missouri, Columbia, ²American Simmental Association, Bozeman, MT, ³University of Nebraska, Lincoln, ⁴University of Illinois, Urbana.