

... were estimated using a single-trait random regression model. 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

**713 Genetic parameters for methane indicator traits based on milk fatty acids in cows.** P. B. Kandel\*<sup>1</sup>, A. Vanlierde<sup>2</sup>, F. Dehareng<sup>2</sup>, E. Froidmont<sup>2</sup>, N. Gengler<sup>1</sup>, and H. Soyeurt<sup>1,3</sup>, <sup>1</sup>*Animal Science Unit, Gembloux Agro Biotech, University of Liège, Passage des Deportes, Gembloux, Belgium*, <sup>2</sup>*Valorisation of Agricultural Products Department, Walloon Agricultural Research Centre, Gembloux, Belgium*, <sup>3</sup>*National Fund for Scientific Research (FNRS), Brussels, Belgium*.

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  $0.35 \pm 0.01$ ,  $0.35 \pm 0.02$  and  $0.32 \pm 0.02$  for the first 3 lactations, respectively. Similarly, the lactation heritability was  $0.67 \pm 0.02$ ,  $0.72 \pm 0.03$  and  $0.62 \pm 0.03$ . 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<sup>2</sup>. 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.** H. D. Norman\*<sup>1</sup>, J. R. Wright<sup>1</sup>, R. L. Powell<sup>1</sup>, T. J. Lawlor<sup>2</sup>, and C. W. Wolfe<sup>3</sup>, <sup>1</sup>*Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD*, <sup>2</sup>*Holstein Association USA Inc., Brattleboro, VT*, <sup>3</sup>*American Jersey Cattle Association, Reynoldsville, OH.*

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