

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.** C. Bastin<sup>\*1</sup>, D. P. Berry<sup>2</sup>, H. Soyeurt<sup>1,3</sup>, and N. Gengler<sup>1</sup>, <sup>1</sup>University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, <sup>2</sup>Teagasc Moorepark Dairy Production Research Center, Fermoy, Co. Cork, Ireland, <sup>3</sup>National Fund for Scientific Research (F.R.S.-FNRS), Brussels, Belgium.

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.** C. Bastin<sup>\*1</sup>, G. Leclercq<sup>1</sup>, H. Soyeurt<sup>1,2</sup>, and N. Gengler<sup>1</sup>, <sup>1</sup>University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, <sup>2</sup>National Fund for Scientific Research (F.R.S.-FNRS), Brussels, Belgium.

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.** 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<sub>6</sub>) 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,