

to reveal the genetic background for the fatty acid variation and to identify quantitative trait loci (QTL) affecting fatty acid composition. The GWAS detected QTLs for milk fatty acids on most chromosomes in the Norwegian Red cattle.

Keywords. Fourier Transform Infrared Spectroscopy, Partial Least Squares Regression, genome-based improvement, milk fat composition.

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GENETIC CORRELATIONS BETWEEN METHANE PRODUCTION AND MILK FATTY ACID CONTENTS OF WALLOON HOLSTEIN CATTLE THROUGHOUT THE LACTATION

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Methane (CH₄) from ruminal fermentation is the major greenhouse gas produced by dairy cattle, which contributes largely to climate change. Production of CH₄ also represents losses of gross energy intake. Therefore, there is a growing interest in mitigating these emissions. Acetate and butyrate have common bio-chemical pathways with CH₄. Because some milk fatty acids (FA) arise from acetate and butyrate, milk FA are often considered as potential predictors of CH₄. However, relationships between these traits remain unclear. Moreover, the evolution of the phenotypic and genetic correlations of CH₄ and milk FA across days in milk (DIM) has not been evaluated. The main goal of

this study was to estimate genetic correlations between CH₄ and milk FA contents throughout the lactation. Calibration equations predicting daily CH₄ production (g·d⁻¹) and milk FA contents (g·100 dl⁻¹ of milk) from milk mid-infrared (MIR) spectra were applied on MIR spectra related to Walloon milk recording. Data included 243,260 test-day records (between 5 and 365 DIM) from 33,850 first-parity Holstein cows collected in 630 herds. Pedigree included 109,975 animals. Bivariate (*i.e.*, CH₄ production and one of the FA traits) random regression test-day models were used to estimate genetic parameters of CH₄ production and seven groups of FA contents in milk. Saturated (SFA), short-chain (SCFA), and medium-chain FA (MCFA) showed positive averaged daily genetic correlations with CH₄ production (from 0.25 to 0.29). Throughout the lactation, genetic correlations between SCFA and CH₄ were low in the beginning of the lactation (0.11 at 5 DIM) and higher at the end of the lactation (0.54 at 365 DIM). Regarding SFA and MCFA, genetic correlations between these groups of FA and CH₄ were more stable during the lactation with a slight increase (from 0.23 to 0.31 for SFA and from 0.23 to 0.29 for MCFA, at 5 and 365 DIM respectively). Furthermore, averaged daily genetic correlations between CH₄ production and monounsaturated (MUFA), polyunsaturated (PUFA), unsaturated (UFA), and long-chain FA (LCFA) were low (from 0.00 to 0.15). However, these genetic correlations varied across DIM. Genetic correlations between CH₄ and MUFA, PUFA, UFA, and LCFA were negative in early lactation (from -0.24 to -0.34 at 5 DIM) and increased afterward to become positive from 15 weeks till the end of the lactation (from 0.14 to 0.25 at 365 DIM). Finally, these results indicate that genetic and, therefore, phenotypic correlations between CH₄ production and milk FA vary following lactation stage of the cow, a fact still often ignored when trying to predict CH₄ production from FA composition.

Keywords. Methane, fatty acid, genetic correlation.

GENETIC AND ENVIRONMENTAL EFFECTS ON INDIVIDUAL WAVENUMBERS OF BOVINE MILK INFRARED SPECTRA

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