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Genetic parameters for methane production, intensity, and yield predicted from milk mid-infrared spectra throughout the lactation in Montbéliarde cows

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Genetic selection of dairy cows against methane (CH4) emissions requires estimating genetic parameters and correlations with milk traits. Predicting CH4 from mid-infrared (MIR) milk spectra provides sufficient data for genomic predictions. In this study, we used 608,072 MIR milk spectra collected from 92,500 first and second parity Montbéliarde cows from 70 to 200 days in milk to predict CH4 emissions expressed as direct CH4 production (MeP_direct) in g/d, CH4 intensity (MeI) in g/kg of fat- and protein corrected milk (FPCM), and as CH4 yield (MeY) in g/kg of dry matter intake. An indirect CH4 production (MeP_indirect) in g/d was also obtained by multiplying MeI by the observed FPCM. Bivariate random regression models were performed between first and second parity data for a given CH4 trait or between CH4 traits and milk traits (milk yield [MY], fat [FY] and protein [PY] yields). Methane traits were stable both within and across lactations, with average genetic correlations greater than 0.93. Average heritability estimates ranged from 0.27 to 0.44. The four CH4 traits were genetically distinct, as their average correlations were lower than 0.41 except for the correlations of 0.74 between MeP and MeY, and the correlation of 0.53 between MeI and MeP_indirect. All three MeP_direct, MeI and MeY presented weak correlations with MY (<0.27 in average), FY (from -0.16 to 0.04 in average), and PY (from -0.07 to 0.32 in average). On the contrary, MeP_indirect was highly correlated with the three milk traits, with average correlations greater than 0.73. We recommend selecting on a combination of CH4 traits, to avoid any strong opposition between CH4 and milk traits.

Sequence-based GWAS of heat tolerance traits in Holstein and Montbeliarde cattle

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Global warming will affect European cattle production systems, decreasing overall performance and welfare. In such a context, it is thus relevant to identify genomic regions involved in heat tolerance for production and functional traits. By combining the French bovine genetic database (focusing on French Holstein and Montbéliarde dairy cattle) with weather conditions (Safran database, Meteo-France), we estimated breeding values (BV) of animals along a temperature-humidity index (THI) gradient with a reaction-norm model. Heat tolerance traits were defined as the slope of BV at THI 70 for three traits: test-day milk yield, conception rate at first insemination, and somatic cell score. 50K SNPs from 4564 Holstein and 1737 Montbéliarde bulls were imputed to whole genome sequence using the run9 of the 1000 bull genomes project, resulting in ~13 million SNPs (R2 Minimac ≥ 0.2 and MAF ≥ 0.01) to perform within-breed GWAS of heat tolerance for the three traits. Few genomic regions were significantly associated with heat tolerance, however these regions differed between breeds and traits. Beyond revealing novel regions associated to heat tolerance, our study also identified some regions already reported in previous studies, emphasizing their relevance. Finally, given the genetic background of heat tolerance in both production and functional traits, selection for heat tolerance should be considered. This study received funding from the European Union's Horizon 2020 research and innovation program under grant number 101000226 (Rumigen) and from APIS-GENE (CAICalor). The authors thank Meteo-France for the Safran database.