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Simulation, prediction, and genetic analyses of daily methane emissions in dairy cattle

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ABSTRACT

This study presents an approach combining phenotypes from novel traits, deterministic equations from cattle nutrition, and stochastic simulation techniques from animal breeding to generate test-day methane emissions (MEm) of dairy cows. Data included test-day production traits (milk yield, fat percentage, protein percentage, milk urea nitrogen), conformation traits (wither height, hip width, body condition score), female fertility traits (days open, calving interval, stillbirth), and health traits (clinical mastitis) from 961 first lactation Brown Swiss cows kept on 41 low-input farms in Switzerland. Test-day MEm were predicted based on the traits from the current data set and 2 deterministic prediction equations, resulting in the traits labeled MEm1 and MEm2. Stochastic simulations were used to assign individual concentrate intake in dependency of farm-type specifications (requirement when calculating MEm2). Genetic parameters for MEm1 and MEm2 were estimated using random regression models. Predicted MEm had moderate heritabilities over lactation and ranged from 0.15 to 0.37, with highest heritabilities around DIM 100. Genetic correlations between MEm1 and MEm2 ranged between 0.91 and 0.94. Antagonistic genetic correlations in the range from 0.70 to 0.92 were found for the associations between MEm2 and milk yield. Genetic correlations between MEm with days open and with calving interval increased from 0.10 at the beginning to 0.90 at the end of lactation. Genetic relationships between MEm2 and stillbirth were negative (0 to −0.24) from the beginning to the peak phase of lactation. Positive genetic relationships in the range from 0.02 to 0.49 were found between MEm2 with clinical mastitis. Interpretation of genetic (co)variance components should also consider the limitations when using data generated by prediction equations. Prediction functions only describe that part of MEm which is dependent on the factors and effects included in the function. With high probability, there are more important effects contributing to variations of MEm that are not explained or are independent from these functions. Furthermore, autocorrelations exist between indicator traits and predicted MEm. Nevertheless, this integrative approach, combining information from dairy cattle nutrition with dairy cattle genetics, generated novel traits which are difficult to record on a large scale. The simulated data basis for MEm was used to determine the size of a cow calibration group for genomic selection. A calibration group including 2,581 cows with MEm phenotypes was competitive with conventional breeding strategies.

Key words: predicted methane emissions, genetic parameters, random regression models

INTRODUCTION

Modern dairy cattle breeding goals incorporate a variety of traits representing the overall categories of productivity and functionality. Breeding goals will continue to be extended by the direct inclusion of additional functional traits mainly reflecting health and product quality (Boichard and Brochard, 2012). In addition, and especially when following the consumers' perspective, dairy cattle's environmental impact or resource efficiency will play a major role in future breeding strategies (König et al., 2013).

As a by-product of bacterial fermentation in ruminants, greenhouse gas (**GHG**) emissions, mainly including CH_4, contribute to global climate change and an inefficient use of dietary energy. The dairy cattle sector accounts for 4% of the total global anthropogenic GHG emissions, with a 52% contribution from methane (FAO, 2010). Controlling and mitigating of methane emissions (**MEm**) is imperative because the expected global warming potential for MEm is 25 times larger than for CO_2 (Forster et al., 2007). Several methods to measure enteric MEm from ruminants can be applied, whereas the most traditional and accurate method is

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the use of respiration chambers (Muñoz et al., 2012). This expensive method requires tremendous logistical efforts, and can only be applied to a limited number of individuals. The sulfur hexafluoride tracer technique (Johnson et al., 1994) was used to measure MEm from individuals kept under grazing conditions. However, when using this tracer technique, a permeation tube containing sulfur hexafluoride has to be placed into the cow's rumen and a sampling apparatus must be attached to the cow. Moreover, this method does not allow measuring the small amount of MEm produced in the large intestine (Murray et al., 1976). A further indicator used for the prediction of individual MEm is based on samples from milk (i.e., FA compositions measured by GC; e.g., Chilliard et al., 2009) or based on milk mid-infrared spectral data (Dehareng et al., 2012). This method requires access to milk laboratories with capacities for analyzing and saving spectral data as well as the development and validation of prediction equations. Utilization of a mobile laser methane detector allows direct on-farm measurements of breath MEm without disturbing the natural behavior of cows (Chagunda et al., 2009). However, high costs for the mobile equipment including technician input, hamper commercial application. The same applies to measurements of breath MEm of individual cows by using the Fourier transform infrared method (Lassen et al., 2012).

A variety of animal-associated and environmental effects contribute to variations of daily MEm. Cow-specific effects include milk productivity (Garnsworthy, et al., 2012a), parity, BW, and stage of lactation (Bell, et al., 2011; Garnsworthy, et al., 2012b). Major environmental factors reflect influences of feeding systems and of feeding strategies (Vlaming et al., 2005). Feeding components include variations of MEm due to diet compositions (Yan et al., 2006) and due to the amount of fluids in diets and further nutritional factors (Hegarty and McEwan, 2010). Also, the recording technique used affects the accuracy of MEm measurements (Muñoz et al., 2012). Direct MEm measurements are associated with technical challenges and high costs, implying the development of MEm prediction equations. Available prediction equations are based on information from a limited number of cows kept in experimental herds and on data from feed rations combined with physiological parameters (e.g., Kirchgessner et al., 1995; Haas et al., 2011; Garnsworthy et al., 2012b). Furthermore, prediction equations build upon different assumptions (e.g., with regard to predefined levels of energy required for maintenance and for productivity). Nevertheless, considerable MEm variation was detected also for dairy cows fed the same diet (Grainger et al., 2007) and housed under identical commercial conditions (Garnsworthy et al., 2012b). Substantial MEm variation in spite of identical environmental conditions indicates differences on the genetic scale. A heritable component for MEm is a prerequisite for implementing sustainable breeding strategies to reduce GHG and to improve resource efficiency of dairy cattle farming.

Moderate heritabilities in the range of 0.30 to 0.35 for predicted and real measurements of MEm were reported for dairy cows and sheep (Haas et al., 2011; Pinares-Patiño et al., 2011). Positive genetic correlations were found between predicted MEm and fat- and protein-corrected milk yield (0.31), as well as between MEm and residual feed intake (0.31; Haas et al., 2011). Such moderate genetic relationships suggest the use of MEm as an indicator for feed efficiency. Inclusion of MEm into overall breeding goals requires additional genetic covariances and genetic correlations between MEm with fertility and with health traits. Consequently, the objectives of the present study were (1) to develop a strategy which combines deterministic equations and stochastic simulations to predict daily MEm based on routinely recorded on-farm data; (2) to estimate daily heritabilities and genetic variances for predicted longitudinal MEm with random regression models; (3) to estimate genetic correlations between predicted longitudinal MEm with test-day production traits [milk yield (**MY**), fat percentage (**Fat%**), protein percentage (**Pro%**) and MUN], fertility traits [calving interval (**CI**), days open (**DO**), and stillbirth (**SB**)], and with the binary health trait clinical mastitis (**CM**); and (4) to evaluate a variety of direct and indirect MEm breeding strategies with and without genomic information.

MATERIALS AND METHODS

Data

Basis for data generation and data analyses were 916 first parity Brown Swiss cows born between 2000 and 2007. The cows were kept on 41 low-input farms located in mountainous regions of Switzerland. Herd size ranged from 9 to 49 cows, with an average of 22.34 cows per herd. The average number of observations per contemporary group (herd × test-year-season) included 7.05 cows. A total of 911 cows were daughters of 274 sires (5 cows had unknown parents), indicating an average of 3.32 daughters per sire. The genetic structure was as follows: 138 sires had only 1 daughter, 105 sires had 2 to 5 daughters, 13 sires had 6 to 10 daughters, 10 sires had 11 to 20 daughters, 6 sires had 21 to 30 daughters, and 3 sires had 31 to 50 daughters. The largest progeny include 47 daughters per sire.