ARTICLE IN PRESS



J. Dairy Sci. 101:1–8

https://doi.org/10.3168/jds.2017-13402

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Genetic correlations between methane production and fertility, health, and body type traits in Danish Holstein cows

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ABSTRACT

Our aim was to investigate the genetic correlations between CH₄ production and body conformation, fertility, and health traits in dairy cows. Data were collected from 10 commercial Holstein herds in Denmark, including 5,758 cows with records for body conformation traits, 7,390 for fertility traits, 7,439 for health traits, and 1,397 with individual CH₄ measurements. Methane production was measured during milking in automatic milking systems, using a sniffer approach. Correlations between CH_4 and several different traits were estimated. These traits were interval between calving and first insemination, interval between first and last insemination, number of inseminations, udder diseases, other diseases, height, body depth, chest width, dairy character, top line, and body condition score. Bivariate linear models were used to estimate the genetic parameters within and between CH_4 and the other traits. In general, the genetic correlations between CH_4 and the traits investigated were low. The heritability of CH_4 was 0.25, and ranged from 0.02 to 0.07 for fertility and health traits, and from 0.17 to 0.74for body conformation traits. Further research with a larger data set should be performed to more accurately establish how CH_4 relates to fertility, health, and body conformation traits in dairy cattle. This will be useful in the design of future breeding goals that consider the production of CH_4 .

Key words: methane, functional trait, body conformation

INTRODUCTION

Farming has had a major effect on CH_4 emissions, with the ruminant population being accountable for 2

billion metric tonnes of CO_2 -equivalents per year. This makes cattle the largest contributors to the increase in global greenhouse gasses (O'Mara, 2011). Ruminants produce CH_4 during digesting high-fiber feeds, and 95% of the CH₄ produced is eructed through cows' breath (Murray et al., 1976). Several animal factors are assumed to cause differences in individual CH₄ production, such as the passage rate of digesta, microbial activity, fermentation conditions, anatomical and physiological differences in the gastrointestinal tract, and grazing behavior (Iqbal et al., 2008; Hegarty et al., 2010). Also, the genetic make-up of the animal affects its rumen microbe population (Guan et al., 2008), digestive function (Hegarty, 2004), feed intake, and feed efficiency (Arthur et al., 1996, 2001; Herd et al., 1997). Therefore, some of the factors assumed responsible for differences in CH₄ production among animals have been found. However, little is known about the role genetics has in explaining those differences, or how to select for lower emitting cows.

Breeding has been practiced through the use of selection indices, with breeding goals focusing mainly on production traits, without much consideration given to the effects of it in the overall production system. However, decades of intensive selection for productive traits only has been shown to compromise cows' health and fertility status (Veerkamp et al., 2001; Walsh et al., 2011). Over the last 15 yr, national selection indices across the globe have been putting more emphasis on health and fertility traits, to try and minimize the negative effects of intensive selection on production traits only (Miglior et al., 2005). Therefore, it is of great importance to understand the direct and indirect consequences of selection for the traits included in dairy cattle breeding programs, and what potential effects, if any, mitigation strategies could have in future breeding goals.

The last decade has brought an increasing interest in understanding the relationship between CH_4 production and traits of economic interest in dairy cattle, such as milk yield (**MY**) and DMI. However, little is

Received June 27, 2017.

Accepted November 26, 2017.

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known about its relationships to functional traits and body conformation. Garnsworthy (2004) showed that restoring dairy cows' fertility status to 1995 levels would cause a reduction of 10% in CH₄ production over their productive lifetime, due to a decrease in involuntary culling due to reproductive issues. Sick, unfertile cows have their productive levels, such as MY or estrus expression, compromised while generating extra costs. Fertility issues are one of the major causes for involuntary culling, which leads to animal waste and a higher number of replacements heifers needed to maintain production levels (Hegarty and McEwan, 2010). An improvement in a herd's reproductive status could help by decreasing involuntary culling and improving fertility traits, such as calving intervals, shortening unproductive periods and, therefore, lowering unnecessary costs along with CH_4 production. However, the way CH₄ production correlates to fertility, health, and body conformation traits is unknown. This information is important to know the effects of incorporating CH_4 into selection indexes. Hence, the objective of this study was to estimate genetic parameters for CH₄ production, measured by a sniffer approach in commercial Danish Holstein herds, and the genetic correlations between CH_4 and a group of health, fertility, and body conformation traits.

MATERIALS AND METHODS

CH₄ Data

Data were collected in 10 commercial Holstein herds from all over Denmark, from December 2011 until July 2013. A total of 1,397 individual CH_4 measurements were recorded, by using a portable FTIR gas analyzer (GASMET 4300; Gasmet Technologies Oy, Helsinki, Finland). The FTIR technique uses an infrared transmission spectrum of an air sample, and it measures the concentration of CH_4 and CO_2 in the cows' breath, through an air inlet placed inside automatic milking systems (AMS). The air inlet was placed in the frontal part of the AMS, close to the animals' heads, and it recorded every 5 s, for 7 d in each farm. Cows in all herds were fed ad libitum mixed rations, and concentrate supplement was offered inside the AMS as a way to attract the cows to milking. All herds had Lely A3 AMS (Lely International N. V., Maassluis, the Netherlands), equipped with scales to collect individual live weight (LW) measurements. Records on LW and MY for each milking were collected within the same period, and they were merged with the CH_4 measurements for each cow. The CH_4 phenotype was obtained by using information on LW, fat- and protein-corrected milk (FPCM), and days carried calf (**DCC**) to predict CO_2 production (Madsen et al., 2010), based on heat-producing units (**HPU**):

HPU =
$$5.6 \times LW^{0.75} + 22 \times FPCM$$

+ $1.6 \times 10^{-5} \times DCC.$

The ratio between CH_4 and CO_2 is measured, in ppm, by the FTIR unit, and combined with the HPU estimated for each cow. The final CH_4 phenotype is expressed in liters per day. Pedersen et al. (2008) recommend a CO_2 production of 180 l per HPU per hour for individual dairy cows; therefore,

$$CH_4 (L/d) = CH_4/CO_2 \times 180 \times 24 \times HPU.$$

Milk yield records were available for all cows, and average daily milk production from the week the CH_4 records were collected was used to estimate FPCM, which was calculated as

$$FPCM = MY \times (0.25 + 0.122 \times fat \% + 0.077 \times protein \%).$$

Fat and protein percentage were provided by the Danish Cattle Database (SEGES, Skejby, Denmark), from milk recordings that were the closest to when CH_4 production was recorded in each farm, meaning maximum of 30-d interval before or after CH_4 recording. The traits LW, FPCM, and CH_4 were based on weekly averages. Cows which were above 500 DIM and cows without DIM information were excluded from the analysis. To keep as many CH_4 records as possible, no animals were discarded due to a high lactation number. However, 35% of the CH_4 records were from first lactation cows and 89% from cows in first, second, or third lactation, with the remainder being between 4th and 7th lactation.

Body Conformation, Fertility, and Health Data

Data on conformation, fertility and health were extracted from the Danish Cattle Database (SEGES). For body conformation, the traits analyzed were BCS, body depth, back line (**BL**), chest width, height, and dairy character (**DC**). Fertility traits analyzed were interval between calving and first insemination (**CF**), interval between first and last insemination (**FL**), and number of inseminations. Health traits were udder health (**UH**) and other diseases (**OD**). Information on all lactations available was considered for cows with both CH_4 and fertility, or health, or conformation traits. For the herd mates without CH_4 measurements, only cows with seDownload English Version:

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