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Invited review: Phenotypes to genetically reduce greenhouse gas emissions in dairying

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ABSTRACT

Phenotypes have been reviewed to select for lower-emitting animals in order to decrease the environmental footprint of dairy cattle products. This includes direct selection for breath measurements, as well as indirect selection via indicator traits such as feed intake, milk spectral data, and rumen microbial communities. Many of these traits are expensive or difficult to record, or both, but with genomic selection, inclusion of methane emission as a breeding goal trait is feasible, even with a limited number of registrations. At present, methane emission is not included among breeding goals for dairy cattle worldwide. There is no incentive to include enteric methane in breeding goals, although global warming and the release of greenhouse gases is a much-debated political topic. However, if selection for reduced methane emission became a reality, there would be limited consensus as to which phenotype to select for: methane in liters per day or grams per day, methane in liters per kilogram of energy-corrected milk or dry matter intake, or a residual methane phenotype, where methane production is corrected for milk production and the weight of the cow. We have reviewed the advantages and disadvantages of these traits, and discuss the methods for selection and consequences for these phenotypes.

Key words: environmental phenotypes, greenhouse gases, enteric methane, genomic selection, dairy cattle

INTRODUCTION

Climate change is a growing international concern, and it has been well established that the release of greenhouse gases (**GHG**) is a contributing factor (Gerber et al., 2010). The European Union has committed to reducing its GHG emissions by 20% by 2020 relative to 1990 levels. The global livestock sector, particularly ruminants, contributes about 18% of total anthropogenic GHG emissions (Steinfeld et al., 2006). In the European Union, the livestock sector accounts for about 13% of total GHG emissions (Leip et al., 2010). Of the GHG produced by ruminants, enteric methane (CH_4) is the most important contributor, with a global warming potential 25 times that of carbon dioxide (CO_2).

The rumen is the major site of CH_4 production, in which anaerobic archaeal microorganisms convert hydrogen (H_2) and CO_2 to CH_4. In ruminants, CH_4 is a natural by-product of anaerobic respiration, produced predominantly in the rumen (~90%), and to a small extent in the large intestine (~10%; Ellis et al., 2008). The contribution of CH_4 released by flatulence is only marginal; eructation and air from the lungs accounts for the majority of the total CH_4 produced by a ruminant. Today, CH_4 emission does not have a direct economic value for the farmer, but this could change if a carbon tax was put on CH_4 emissions or in relation to feed efficiency, because approximately 6% of net energy in cow feed is eructed as CH_4 (Johnson et al., 1993). Reductions in CH_4 emissions would not just be beneficial for the environment; it would also result in less energy lost and more efficient animals for the farmer.

Nutritional and microbial manipulation to reduce enteric CH_4 emissions has been and continues to be extensively researched (Cottle et al., 2011). Animal breeding that exploits natural animal variation in CH_4 emissions is an additional mitigation strategy that is inexpensive, permanent, and cumulative (Hayes et al., 2013). Still, within animal production, there has been little or no concerted effort to use long-term breeding strategies to mitigate GHG from ruminants. Several small-scale projects have been undertaken or are currently under way (mainly nationally funded), but they are too small to draw definitive conclusions or make any meaningful contribution to national breeding

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strategies (Chagunda et al., 2009; Garnsworthy et al., 2012; Lassen and Lovendahl, 2016); successful animal breeding strategies require measurements in a large population. With the recent successful incorporation of genomic information into breeding schemes, reliance on very large populations of phenotyped animals has been relaxed. Nevertheless, a reference population of several thousand animals is still needed to accurately estimate the contribution of each genomic region to the expression of the phenotype under investigation (Hayes and Goddard, 2010). Therefore, a data set of several thousand animals with similarly defined records for CH_4 emissions would be sufficient for genetic evaluation of enteric CH_4 emissions. Such data would also be suitable for genome-wide association studies to locate genomic regions that could influence CH_4 emission from dairy cattle (Sahana et al., 2011). The actual size of a reference population for improving methane emission would depend on the desired accuracy and could be calculated using the prediction equations of Daetwyler et al. (2008) or Goddard (2009).

Measuring a trait on several thousand animals requires the trait to be easily recordable, and direct or indirect traits can be used in a selection program. The aim of this review was to provide an overview of phenotypes enabling reduction of GHG emissions in dairying through breeding, and to discuss the methods for selection and consequences for these phenotypes. We have focused on enteric CH_4, as the most important contributor to GHG emissions in dairy cattle.

POSSIBLE DIRECT PHENOTYPES

Precise (and preferably inexpensive) phenotypes are needed to make genetic evaluations appropriate for traits of interest. For CH_4 production, several phenotypes have been suggested (Herd et al., 2013) (Table 1). The first phenotype is methane production defined as liters or grams per day. The obvious problem selecting for this trait is that it is highly correlated with feed intake and the production trait of interest: in dairy, milk production; in sheep or beef, meat production. Another option, then, is to look at methane intensity, defined as liters of CH_4 related to output [e.g., kg milk (for dairy) or meat (for sheep or beef) produced], or at methane yield, defined as liters of CH_4 related to input (e.g., per kg of DMI). Residual methane production, defined as observed minus predicted CH_4 production, has also been suggested for use (Herd et al., 2014; Berry et al., 2015; Manzanilla Pech et al., 2016). Residual methane production is based on the same concept as residual feed intake (**RFI**), where the phenotype of interest is regressed for each factor that influences this phenotype. For CH_4, this could be milk production, body weight, or feed intake, for example. It is not necessarily obvious which of these phenotypes to select for, and it is indeed necessary to make sure that correlated information is available, so that decline in other traits is avoided when selecting for the CH_4 phenotype. The most correct way might be to use methane production and include the correlation structure with milk yield, milk contents, live weight, and feed intake in the selection index. Using methane yield can create problems with double counting when setting up breeding goals, because the phenotype is adjusted, rather than running a multitrait model or including the correlated traits in an index. In beef cattle, genetic correlations between the production trait (live weight) and the several CH_4 phenotypes [i.e., methane production (0.79), methane yield (0.18) and methane intensity (−0.23)] suggest that highly different responses in the production trait are possible, depending on the CH_4 phenotype selected for (Donoghue et al., 2013). The same study also reported genetic correlations between methane production, methane yield, and methane intensity of 0.87 to 0.96, using one trait or another could have a limited effect on correlated response in the production trait. However, because the study published only preliminary results, more work and collaboration is needed in this field. Also in dairy cattle, genetic correlations between the production trait (milk yield) and the CH_4 phenotypes [i.e., methane production (0.43) and methane yield (0.15)] suggest that different responses in the production trait are possible, depending on the CH_4 phenotype selected for (Lassen and Lovendahl, 2016).

To predict methane production (L/d), a suggested method has been to measure the concentration of CH_4 and CO_2 and predict daily methane production through predicted CO_2 production from the weight of the fetus, the milk, and heat production (Madsen et al., 2010). This method ignores animal variation in CO_2 production, but has been shown to create results that are just as precise as SF_6 methodology and respiration chamber techniques (Haque et al., 2014). Another way to predict methane production is using a mobile laser methane detector (Chagunda et al., 2009). A laser methane detector is a hand-held gas detector for remote measurement of column density for CH_4-containing gases. The equipment uses infrared absorption spectroscopy to establish a CH_4 concentration measurement. The integrated concentration of CH_4 between the equipment and the target point is displayed. The measured value is expressed as CH_4 concentration, accounting for the thickness of any CH_4 plume. Measurements are in parts per million-meter (**ppm-m**).

Many of the techniques to determine CH_4 phenotypes in dairy cattle are based on short-term measurements spread over the day, indicating that only a snapshot of