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Genetic control of greenhouse gas emissions

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Abstract

Climate change is a growing international concern and it is well established that the release of greenhouse gases (GHG) is a contributing factor. The European Union has committed itself to reduce its GHG emissions by 20% by the year 2020 relative to 1990 levels. Of the various 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). Recent studies have shown that natural variation among animals exists in enteric CH4 emission. This variation can be used to breed cows with low CH_4 emission, with expected progress per generation in terms of CH_4 reduction ranging from 10 to 20%. Successful animal breeding strategies require measurements on a large population of animals. With the recent successful incorporation of genomic information into breeding schemes the reliance on very large populations of phenotyped animals is relaxed. The rumen is the major site of methane production in which anaerobic archaeal microorganisms convert H_2 and CO_2 to CH_4. Methane is a natural by-product of anaerobic respiration, produced predominantly in the rumen (~90%), and to a small extent in the large intestine (~10%). The major factors that determine methane production include the amount of feed consumed by the ruminant, and the digestion of that feed. As more feed is ingested, more methane is produced, but the portion of methane per kg dry matter intake (DMI) decreases with increasing feed intake. International collaboration is essential to make progress in this area. This is both in terms of sharing ideas, experiences and phenotypes, but also in terms of coming to a consensus regarding what phenotype to collect and to select for.

Key words: Climate change; greenhouse gases; enteric methane.

Resumen

El cambio climático es una preocupación internacional creciente y está bien establecido que la liberación de gases de efecto invernadero (GEI) es un factor que contribuye. La Unión Europea se ha comprometido a reducir sus emisiones de GEI en un 20% para el año 2020 en relación con los niveles de 1990. De los diversos gases de efecto invernadero producidos por los rumiantes, el metano entérico (CH_4) es el contribuyente más importante, con un potencial de calentamiento global 25 veces superior al del dióxido de carbono (CO_2). Estudios recientes han demostrado que existe una variación natural entre los animales en la emisión de CH_4 entérico. Esta variación se puede utilizar para criar vacas con baja emisión de CH_4, con un progreso esperado por generación en términos de reducción de CH_4 que va del 10 al 20%. Las estrategias exitosas de reproducción animal requieren mediciones en una gran población de animales. Con la reciente incorporación exitosa de información genómica en esquemas de reproducción, se confía en la dependencia de poblaciones muy grandes de animales fenotipados. El rumen es el sitio principal de producción de metano en el que los microorganismos anaeróbicos arqueales convierten el H_2 y el CO_2 en CH_4. El metano es un subproducto natural de la respiración anaeróbica, que se produce predominantemente en el rumen (~ 90%) y, en menor medida, en el intestino grueso (~ 10%). Los principales factores que determinan la producción de metano incluyen la cantidad de alimento consumido por el rumiante y la digestión de ese alimento. A medida que se ingiere más alimento, se produce más metano, pero la porción de metano por kg de materia seca ingerida (DMI) disminuye al aumentar la ingesta de alimento. La colaboración internacional es fundamental para avanzar en esta materia. Esto es tanto en términos de compartir ideas, experiencias y fenotipos, como en términos de llegar a un consenso con respecto a qué fenotipo recopilar y seleccionar.

Palabras clave: cambio climático; gases de invernadero; metano entérico.

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Introduction

Climate change is a growing international concern and it is well established that the release of greenhouse gases (GHG) is a contributing factor. The European Union has committed itself to reduce its GHG emissions by 20% by the year 2020 relative to 1990 levels. The global livestock sector, particularly ruminants, contributes approximately 18% of total anthropogenic GHG emissions (Steinfeld et al., 2006). In the EU, the livestock sector accounts for about 13% of total GHG emissions (Leip et al., 2010). Of the various 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 reduction of enteric CH_4 of cattle is important. Recent studies have shown that natural variation among animals exists in enteric CH_4 emission (Grainger et al., 2007). This variation can be used to breed cows with low CH_4 emission, with expected progress per generation in terms of CH_4 reduction ranging from 10 to 20% (Waghorn and Woodward, 2006). To be able to use this potential in the long term, a database is needed with both genetic information of the individual animals (pedigree, markers) and their direct individual CH_4 emission, or indirect traits like (residual) feed intake, predicted CH_4 production based on IPCC (Intergovernmental Panel on Climate Change)-rules (de Haas et al., 2011), or milk composition traits (e.g., mid infrared spectra (Dehareng et al., 2012) or milk fatty acids (Dijkstra et al., 2011). So far, within animal production, there is little or no concerted effort on long-term breeding strategies to mitigate against GHG from ruminants. This is because successful animal breeding strategies require measurements on a large population of animals. With the recent successful incorporation of genomic information into breeding schemes the reliance on very large populations of phenotyped animals is relaxed. However, a reference population of several thousand animals is still required to estimate the contribution of each genomic region to expression of the phenotype under investigation (Calus et al., 2013).

In recent years, several consortia have been formed to collect and combine data for genetic evaluation. One consortium is METHAGENE (COST Action FA1302) on large-scale methane measurements on individual ruminants for genetic evaluations (www.methagene.eu). The other one is the Animal Selection, Genetics and Genomics Network (ASGGN) of the Livestock Research Group of the Global Research Alliance on agricultural greenhouse gas emissions (GRA) (www.asggn.org). Several researchers of both consortia are also involved in the ICAR working group on "Feed and Gas" to set guidelines for collection and storage of data and to collate data for genetic evaluation.

In this proceeding paper, the research on genetic control of greenhouse gases will be described, related to:

1. What are methane-determining factors?
2. What are genetic parameters for methane emissions?
3. What proxies can be used, and what is their association with methane emission?
4. How to move on with breeding for lower emitting animals?

Methane-determining factors

The methane-determining factors can be divided in three groups: (1) rumen microbial population, (2) feed intake and diet composition, and (3) host genetics. The rumen is the major site of methane production in which anaerobic archaeal microorganisms convert H_2 and CO_2 to CH_4. In ruminants, methane 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 methane released by flatulence is only marginally, while eructation and air from the lungs accounts for the majority of total methane produced by a ruminant. The major factors that determine methane production include the amount of feed consumed by the ruminant, and the digestion of that feed. As more feed is ingested, more methane is produced, but the portion of methane per kg dry matter intake (DMI) decreases with increasing feed intake (Jentsch et al., 2007). Conversion of feed material to methane in the rumen involves the integrated activities of several

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different microbial species, the final step being carried out by methanogenic archaea. A recent study determined rumen and camelid foregut microbial community composition in 742 samples from 32 animal species and 35 countries, to estimate if this was influenced by diet, host species, or geography (Henderson et al., 2015). They showed that similar bacteria and archaea dominated in nearly all samples, while protozoal communities were more variable. The dominant bacteria are poorly characterised, but the methanogenic archaea are better known and

highly conserved across the world. This universality and limited diversity could make it possible to mitigate methane emissions by developing strategies that target the few dominant methanogens. Differences in microbial community compositions were predominantly attributable to diet, with the host being less influential. There were few strong co-occurrence patterns between microbes, suggesting that major metabolic interactions are non-selective rather than specific.

Genetic parameters for methane

From a recent review it has been observed that both CH4 emissions and production (g/day) are a heritable and repeatable trait (Pickering et al., 2015). Methane emissions are strongly related to feed intake both in the short term (minutes to several hours) and over the medium term (days). When measured over the medium term, CH4 yield (MY, g CH4/kg dry matter intake) is a heritable and repeatable trait albeit with less genetic variation than for CH4 emissions. Methane emissions of individual animals are moderately repeatable across diets, and across feeding levels, when measured in respiration chambers. Repeatability is lower when short term measurements are used, possibly due to variation in time and amount of feed ingested prior to the measurement.

However, while repeated measurements add value; it is preferable the measures be separated by at least 3-14 days. This temporal separation of measurements needs to be investigated further. Given the above issue can be resolved, short term

(over minutes to hours) measurements of CH4 emissions show promise, especially on systems where animals are fed ad libitum and frequency of meals is high. However, we believe that for short term measurements to be useful for genetic evaluation, a number (between 3 and 20) of measurements will be required over an extended period of time (weeks to months).

There are opportunities for using short term measurements in standardised feeding situations such as breath "sniffers" attached to milking parlours or total mixed ration feeding bins, to measure CH4. Genomic selection has the potential to reduce both CH4 emissions and MY, but measurements on thousands of individuals will be required. This

includes the need for combined resources across countries in an international effort, emphasising the need to acknowledge the impact of animal and production systems on measurement of the CH4 trait during design of experiments.

Proxies for methane

Feed intake

Methane production is, in part, dependent upon the quantity of feed consumed, although this effect is moderated by feed digestibility and other feed and animal characteristics, such as composition of the diet and dietary fat (Hegarty, 2009). The feed efficiency (i.e., residual feed intake (RFI)) of the animal may also have an impact with low-RFI cattle eating less than expected in relation to their live weight and growth rate. By comparing the CH4 emissions of Angus steers chosen from breeding lines divergently selected for RFI, Hegarty et al. (2007)

found that the most efficient animals (low-RFI) had a lower CH4 production rate. The association between RFI and CH4 emission was also shown by Nkrumah at al. (2006) where CH4 production was 28% less in low-RFI animals compared to high-RFI animals. The positive genetic correlation between predicted CH4 emission and RFI (phenotypic correlation: 0.72; genetic correlation: 0.32) suggests that selection on RFI may be one strategy to reduce CH4 emissions from ruminants (de Haas et al., 2011).

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Fatty acids

Various milk fatty acids (FA) in milk may be used as markers of microbial activity. Milk fatty acid composition has therefore been suggested as a means of predicting enteric CH_4 output in lactating dairy cattle because of the common biochemical pathways among CH_4, acetate, and butyrate in the rumen (Vlaeminck et al., 2006). Some milk FA were moderately related to CH_4 production in dairy cattle (Chilliard et al., 2009, Dijkstra et al., 2011), but more data on wider ranges of diets and animals are required to further elucidate the accuracy of prediction of methane production based on milk FA profiles.

Mid-infrared

Recently, the quantification of FA contents of bovine milk by mid-infrared spectrometry (MIR) was developed (Soyeurt et al., 2011). As the FA prediction by MIR is feasible and as the CH_4 production is correlated to the milk FA profile and potentially other milk components such as lactose, there is an interest to quantify directly the CH_4 eructed by lactating cows from the milk MIR spectra. In 2012, Dehareng et al. published the first article on this topic. The equation was developed by combining 77 MIR milk spectra and their corresponding reference SF6 CH_4 data. Even if this study was based on a limited number of records, it showed the feasibility to use milk MIR spectra to evaluate the CH_4 eructed by dairy cows.

How to move on?

In order to make a genetic evaluation and ranking of animals for CH_4 emission it is crucial to make registrations in commercial farms. In order to make that possible it will be necessary to develop phenotypes that can be used by the farmer to optimize the production on farm level. Also it is crucial to develop equipment the makes it possible to make registrations without interfering with everyday routines.

International collaboration is essential to make progress in this area. This is both in terms of sharing ideas, experiences and phenotypes, but also in terms of coming to a consensus regarding what phenotype to collect and to select for. Also methods to handle this data from small scale phenotyping to large scale genomic breeding values needs to be developed even further in order to ensure that the registrations that are being made around the globe will be utilized at farm level.

Lessons can be learned from the global Dry Matter Initiative. They have shown that there is a benefit in collaboration, as phenotypic information for DMI from other countries can be used to augment the accuracy of genomic evaluations of individual countries (de Haas et al., 2015). The optimal scenario, which was sharing data, resulted in a mean prediction accuracy of 0.44, ranging from 0.37 (Denmark) to 0.54 (the Netherlands).

Assuming near unity among-country genetic correlations, the mean accuracy of prediction dropped to 0.40, and the mean within-country accuracy was 0.30. If no records were available in a country, the accuracy based on the other populations ranged from 0.23 to 0.53 for the milking cows, but were only 0.03 and 0.19 for Australian and NZ heifers; the overall mean prediction accuracy was 0.37.

Acknowledgement

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