

Where have we come with breeding for methane emissions – update from international collaborations

Y. de Haas¹, E. Wall², P.C. Garnsworthy³, B. Kuhla⁴, E. Negussie⁵, J. Lassen⁶

¹*Animal Breeding and Genomics, Wageningen University and Research, PO Box 338, 6700 AH Wageningen, the Netherlands*

²*SRUC, Kings Buildings, West Mains Road, Edinburgh EH9 3JG, UK*

³*The University of Nottingham, School of Biosciences, Sutton Bonington Campus, Loughborough LE12 5RD, UK*

⁴*Leibniz Institute for Farm Animal Biology, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany*

⁵*Biometrical Genetics, Natural Resources Institute, Myllytie 1, 31600 Jokioinen, Finland*

⁶*Viking Genetics, Ebeltoftevej 16, Assentoft, DK-8960 Randers, Denmark*

Summary

Climate change is a growing international concern and it is well established that release of greenhouse gases (GHG) is a contributing factor. So far, within animal production, there is little or no concerted effort on long-term breeding strategies to mitigate GHG from ruminants. In recent years, several consortia have been formed to collect and combine data for genetic evaluation. Discussion areas of these consortia focus on (1) What are genetic parameters for methane (CH₄) emissions, (2) What proxies can be used to assess CH₄ emission, and (3) What are the prospects of breeding for lower emitting animals? The estimated genetic parameters show that enteric CH₄ is a heritable trait, and that it is highly genetically correlated with DMI. So far, the most useful proxies relate to feed intake, milk mid-infrared spectral data, and fatty acid concentrations in milk. To be able to move forward with a genetic evaluation and ranking of animals for CH₄ emission, international collaboration is essential to make progress in this area. Collaboration is not only 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.

Keywords: greenhouse gas emission, enteric methane, genetic control

Introduction

Climate change is a growing international concern and it is well established that release of greenhouse gases (GHG) is a contributing factor. The European Union has committed to reduce its GHG emissions by 30% by the year 2030 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 (CH₄) is the most important contributor, with a global warming potential 28 times that of carbon dioxide (CO₂).

Reduction of enteric CH₄ from cattle is important. Studies have shown that natural variation in enteric CH₄ emission exists among animals (Grainger *et al.*, 2007). This variation can be used to breed cows with low CH₄ emission, with expected progress per generation in

terms of CH₄ reduction ranging from 10 to 20% (Waghorn & Woodward, 2006). To be able to use this potential in the long term, a database is needed with both genetic information of individual animals (pedigree, markers) and their direct individual CH₄ emission, or indirect traits based on feed intake or milk composition (Negussie *et al.*, 2017a).

So far, within animal production, there is little or no concerted effort on long-term breeding strategies to mitigate 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, reliance on 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). Another consortium 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.

An overview of progress with breeding for methane emissions will be described, related to (1) what are genetic parameters for CH₄ emissions, (2) what proxies can be used, and what is their association with CH₄ emission, and (3) what are the prospects of breeding for lower emitting animals?

Genetic parameters for enteric methane emissions

Methane phenotype

A number of CH₄ phenotypes have been defined (Herd *et al.*, 2013); the most widely used is CH₄ production (**MeP**) in litres or grams per day. The obvious problem in selecting for this trait is that it is highly correlated with feed intake and, thereby, with the ultimate breeding goal trait in dairy cattle: milk production. Alternative phenotypes are CH₄ intensity (**MeI**), which is defined as litres or grams of CH₄ per kg of energy corrected milk yield, and CH₄ yield (**MeY**), which is defined as litres or grams of CH₄ per kg of dry matter intake (**DMI**). Residual CH₄ production (**RMP**) is calculated as observed minus predicted CH₄ production (Herd *et al.*, 2014; Berry *et al.*, 2015), with predicted values based on factors such as milk production, body weight and feed intake. At the moment, it is not obvious which of these phenotypes is best to use; but it is important to monitor associations between the chosen CH₄ phenotype and the other important traits in the breeding goal (e.g. production, fertility, longevity) to avoid unfavourable consequences.

Recording of methane emissions

Individual enteric CH₄ emissions can be recorded with several devices and techniques. The measures provided by these techniques differ with regard to unit and duration. Firstly, they provide either measures of emitted CH₄ mass per day or measures of concentration in breath. Secondly, emitted CH₄ can be recorded continuously over full circadian period or over short periods (spot samples).

The current ‘gold standard’ for measuring CH₄ emissions is respiration chambers, where continuous measurement of air flow and gas concentrations during full 24-hour periods provide complete CH₄ mass production values. In individual portable accumulation chambers (**PAC**) small ruminants can be measured for short periods (~ 1 hour), and changes in CH₄, CO₂ and O₂ concentration in the chamber’s atmosphere are extrapolated to complete days (Goopy *et al.*, 2011). The sulphur hexafluoride (**SF₆**) technique is used for measuring 24-hour CH₄ production thanks to the insertion of rumen boluses containing SF₆ as a tracer allowing quantification of CH₄ mass production from release rate of SF₆ and the CH₄/SF₆ ratio in exhaled air quantifying eructed air flow (McGinn *et al.*, 2006). The GreenFeed Emission Monitoring (**GEM**) system (C-Lock Inc, Rapid City, USA) is designed for direct measurement of air flow and CH₄ concentration, i.e. CH₄ mass production, during short-term periods of 3-5 minutes when cattle visit an automated feeder fitted with a semi-enclosed head hood in which air is continuously drawn through an air-collection pipe. Sniffer methods automatically measure CH₄ concentration in exhaled air during milking or feeding (5 to 15 minutes) either by Infrared (Garnsworthy *et al.*, 2012; Lassen *et al.*, 2012) or photo acoustic (Negussie *et al.*, 2017b) gas analysers. The laser methane detector system (**LMD**) entails directing a laser beam at a cow’s nostrils for a period of time (1 to 5 minutes), to perform highly sensitive infrared absorption measurements related to both concentration and depth of the CH₄ respiratory plume (Iseki & Miyaji, 2003; Chagunda, 2013).

Heritabilities

Genetic parameters for MeP and MeY measured in respiration chambers at fixed levels of feed intake have been estimated. Heritability (standard error in parenthesis) for MeP was 0.29 (0.05) in sheep (Pinares-Patino *et al.*, 2013) and 0.40 (0.11) in beef (Donoghue *et al.*, 2013)). Estimated heritability for MeY was 0.13 (0.03) in sheep and 0.19 (0.10) in beef cattle. Coefficient of phenotypic variation for both CH₄ traits in sheep was 0.10 to 0.13, suggesting that genetic variation does exist (Pinares-Patino *et al.*, 2013). Heritability estimates for CH₄ emissions in dairy cows measured with sniffer methods are 0.21 (0.06) for MeP and 0.16 (0.04) for MeI (Lassen & Lovendahl, 2016).

Genetic correlations with other traits

Single country dataset

A favourable association between feed efficiency and MeP is expected given that MeP represents a source of energy loss (Johnson & Johnson, 1995), and therefore inefficiency. In direct contrast however, the likely improved digestive ability of more efficient animals could result in greater MeY. Few studies, however, have enough records on both feed efficiency and MeP to perform genetic analyses. Most studies therefore focus primarily on those aspects of feed efficiency that are easy to record, such as milk yield and live weight. A Danish study with dairy cattle estimated a correlation of 0.43 (0.10) between MeP and milk yield, and a correlation of -0.18 (0.08) between MeP and live weight (Lassen & Lovendahl, 2016). The negative correlation between MeP and live weight is, however, counterintuitive, as heavier animals tend to eat more, and therefore emit more CH₄. An Australian study with growing beef cattle did estimate a strong positive correlation of 0.80 (0.06) between MeP and live weight and a correlation of 0.83 (0.05) between MeP and DMI (Manzanilla-Pech *et al.*, 2016).

Multiple country dataset

A phenotypic comparison between two types of equipment used simultaneously has shown that it is possible to interchange data and analyse data from different equipment, after correction for differences in means and variances (Difford *et al.*, 2016). A first genetic comparison of several types of equipment was conducted, where we aimed to enlarge the reference population for genomic selection by combining data on methane emissions in dairy cattle using data from 5 countries (Australia, Denmark, Ireland, the Netherlands and UK). The total dataset consisted of 2,857 dairy cows, of which most were genotyped, but with various kinds of SNP chips. We ended up with a uniform set of SNPs for each cow. Even though three different types of measurement equipment (laser, sniffer and SF₆) and protocols (measuring for 3 days, 1 week, multiple weeks) were used, these data were analysed jointly to establish genetic and genomic parameters for enteric methane. Within country and within measurement method, heritabilities of CH₄ emissions, including MeY and MeI, ranged from 0 to 0.34, indicating the existence of additive genetic variation and that it is possible to breed for reduced CH₄ emissions from dairy cows. Strong positive genetic correlations were estimated between CH₄ emissions and both milk yield and live weight. The genetic correlations between populations were mainly positive and moderate to strong, and heritabilities from the combined dataset had lower standard errors than the separate datasets, indicating that it is possible to combine CH₄ data from multiple sources even though different measurement devices and protocols were used along with different production systems and feeding strategies. This enables a world-wide collaboration to produce genomic estimated breeding values for CH₄ emissions from dairy cattle, enabling selection for a reduction in emissions levels.

Best proxies for enteric methane emissions

As described above, several techniques have been developed for measurement of CH₄ emissions from ruminants (Hammond *et al.*, 2016), but routine individual measurements on a large scale (a requisite for genetic selection) have proven to be difficult and expensive (Pickering *et al.*, 2015; Negussie *et al.*, 2017a). Therefore, proxies that are correlated to CH₄ emission, but which are easy and low-cost to record on a large scale, are an alternative. Proxies might be less accurate than direct CH₄ measurement, but could be measured repeatedly to reduce random noise.

Proxies can range from simple and low-cost measurements, such as body weight or high-throughput milk mid-infrared spectroscopy (**MIR**), to more demanding measures like rumen morphology, rumen metabolites or microbiome profiling (Negussie *et al.*, 2017a). Proxies based on rumen samples are generally poor to moderately accurate predictors of CH₄, and are costly and difficult to measure routinely on-farm. Proxies related to body weight or milk yield and composition, on the other hand, are relatively simple, low-cost, high throughput, and are easier to implement in practice. In particular, milk MIR, along with covariates such as lactation stage, are a promising option for prediction of CH₄ emission in dairy cows. As reviewed by Negussie *et al.* (2017a) no single proxy can accurately predict CH₄, so combinations of two or more proxies are likely to be a better solution. Combining proxies can increase the accuracy of predictions by up to 15 - 35%, mainly because different proxies describe independent sources of variation in CH₄ and one proxy can correct for shortcomings in the other(s). The most important applications of CH₄ proxies are in dairy

cattle management and breeding for reduced environmental impact. In breeding for traits of environmental impact, single or multiple proxies can be used as indirect criteria for the breeding objective, but care should be taken to avoid unfavourable correlated responses. Finally, although combinations of proxies appear to improve estimates of CH₄, the greatest limitation today is the lack of robustness in their general applicability. Future efforts should therefore be directed towards developing combinations of proxies that are robust and applicable across diverse production systems and environments.

Breeding programmes aiming for lower emitting ruminants

Although CH₄ emissions from ruminants currently do not have any direct economic value in any country, breeding is a long-term strategy and therefore must take cognisance of the potential economic incentives or penalties that may be enforced in the future (Wall *et al.*, 2010). To do so, we need to understand the genetic control of CH₄ and its relationships with production and fitness traits. As estimates of such genetic parameters become known, selection index theory can explore how to incorporate CH₄ into breeding goals. A study within METHAGENE compared three scenarios for adding CH₄ to national breeding goals of UK, Spain & Netherlands with: 1) no restriction on CH₄ emissions (i.e., current breeding goal); 2) no genetic change in CH₄, and 3) an economic value assigned to CH₄ based on the carbon price in literature. Preliminary results show that current breeding goals lead to increased MeP by between 4 and 8.5 g/d (pers. comm. Irene Breider, Sept 2017). Restricting CH₄ genetic change to zero decreases the economic gain by between 3 and 15%. Assigning an economic value to CH₄ increases CH₄, but by 11 to 15% lower than without restrictions, whilst the overall economic gain decreases by 1 to 3%.

Conclusions

To answer the question “where have we come with breeding for methane emissions?” in short: very far, but still a long way to go. Recent studies have shown that enteric methane is a heritable trait, and that it is highly genetically correlated with DMI. So far, the most useful proxies relate to feed intake, milk mid-infrared spectral data, and fatty acids in the milk. To be able to move on with a genetic evaluation and ranking of animals for methane emission, international collaboration is essential to make progress in this area. Collaboration is needed both in terms of sharing ideas, experiences, protocols and phenotypes, and in terms of coming to a consensus regarding what phenotype to collect and to select for.

List of References

- Berry, D. P., Lassen, J. & de Haas, Y., 2015. Residual feed intake and breeding approaches for enteric methane mitigation. In: *Livestock production and climate change*, Malik, P. K., Bhatta, R., Takahashi, J., Kohn, R. A. & Prasad, C. S. (editors), CABI, Oxfordshire, UK, p. 273-291.
- Calus, M. P. L., De Haas, Y., Pszczola, M. & Veerkamp, R. F., 2013. Predicted accuracy of and response to genomic selection for new traits in dairy cattle. *Anim.* 7(2): 183-191.
- Chagunda, M. G. G., 2013. Opportunities and challenges in the use of the laser methane detector to monitor enteric methane emissions from ruminants. *Anim.* 7: 394-400.
- Donoghue, K. A., Herd, R. M., Bird, S. H., Arthur, P. F. & Hegarty, R. S., 2013. Preliminary genetic parameters for methane production in Australian beef cattle. In *Proc of: AAABG*,

Napier, New Zealand.

- Garnsworthy, P. C., Craigon, J., Hernandez-Medrano, J. H. & Saunders, N., 2012. Variation among individual dairy cows in methane measurements made on farm during milking. *J Dairy Sci.* 95(6): 3181-3189.
- Goopy, J. P., Woodgate, R., Donaldson, A., Robinson, D. L. & Hegarty, R. S., 2011. Validation of a short-term methane measurement using portable static chambers to estimate daily methane production in sheep. *Anim. Feed Sci. Techn.* 166-67: 219-226.
- Grainger, C., Clarke, T., McGinn, S. M., Auld, M. J., Beauchemin, K. A., Hannah, M. C., Waghorn, G. C., Clark, H. & Eckard, R. J., 2007. Methane emissions from dairy cows measured using the sulfur hexafluoride (SF₆) tracer and chamber techniques. *J. Dairy Sci.* 90(6): 2755-2766.
- Hammond, K., Crompton, L. A., Bannink, A., Dijkstra, J., Yanez-Ruiz, D. R., O'Kiely, P., Kebreab, E., Eugene, M. A., Yu, Z. *et al.*, 2016. Review of current in vivo measurement techniques for quantifying enteric methane emission from ruminants. *Anim. Feed Sci. Techn.* 219: 13-30.
- Herd, R. M., Arthur, P. F., Bird, S. H., Donoghue, K. A. & Hegarty, R. S., 2014. Genetic variation for methane traits in beef cattle. In Proc of: 10th World Conference on Genetics Applied to Livestock Production, Vancouver, Canada.
- Herd, R. M., Bird, S. H., Donoghue, K. A., Arthur, P. F. & Hegarty, R. F., 2013. Phenotypic associations between methane production traits, volatile fatty acids and animal breeding traits. In Proc of: AAABG, Napier, New Zealand.
- Iseki, T. & Miyaji, M., Year. A portable remote methane detector using a tunable diode laser. In Proc of: 22nd World Gas Conference, Tokyo, Japan.
- Johnson, K. A. & Johnson, D. E., 1995. Methane emissions from cattle. *J. Anim. Sci.* 73(8): 2483-2492.
- Lassen, J. & Lovendahl, P., 2016. Heritability estimates for enteric methane emissions from holstein cattle measured using noninvasive methods. *J. Dairy Sci.* 99(3): 1959-1967.
- Lassen, J., Lovendahl, P. & Madsen, J., 2012. Accuracy of noninvasive breath methane measurements using fourier transform infrared methods on individual cows. *J. Dairy Sci.* 95(2): 890-898.
- Manzanilla-Pech, C. I. V., De Haas, Y., Hayes, B. J., Veerkamp, R. F., Khansefid, M., Donoghue, K. A., Arthur, P. F. & Pryce, J. E., 2016. Genomewide association study of methane emissions in angus beef cattle with validation in dairy cattle. *J. Anim. Sci.* 94(10): 4151-4166.
- McGinn, S. M., Beauchemin, K. A., Iwaasa, A. D. & McAllister, T. A., 2006. Assessment of the sulfur hexafluoride (SF₆) tracer technique for measuring enteric methane emissions from cattle. *J. Env. Quality.* 35(5): 1686-1691.
- Negussie, E., de Haas, Y., Dehareng, F., Dewhurst, R. J., Dijkstra, J., Gengler, N., Morgavi, D. P., Soyeurt, H., van Gastelen, S. *et al.*, 2017a. Invited review: Large-scale indirect measurements for enteric methane emissions in dairy cattle: A review of proxies and their potential for use in management and breeding decisions. *J. Dairy Sci.* 100(4): 2433-2453.
- Negussie, E., Lehtinen, J., Mantysaari, P., Bayat, A. R., Liinamo, A. E., Mantysaari, E. A. & Lidauer, M. H., 2017b. Non-invasive individual methane measurement in dairy cows. *Anim.* 11(5): 890-899.
- Pickering, N. K., Oddy, V. H., Basarab, J. A., Cammack, K., Hayes, B. J., Hegarty, R. S., McEwan, J. C., Miller, S., Pinares, C. *et al.*, 2015. Invited review: Genetic possibilities to reduce enteric methane emissions from ruminants. *Anim.* 9(9): 1431-1440.
- Pinares-Patino, C. S., Hickey, S. M., Young, E. A., Dodds, K. G., MacLean, S., Molano, G.,

- Sandoval, E., Kjestrup, H., Harland, R. *et al.*, 2013. Heritability estimates of methane emissions from sheep. *Anim.* 7: 316-321.
- Steinfeld, H., Gerber, P., Wassenaar, T., Castel, V., Rosales, M. & de Haan, C., 2006. *Livestock's long shadow: Environmental issues and options.* 390 pages. Food and Agriculture Organization of the United Nations, Rome, Italy.
- Waghorn, G. C. & Woodward, S. L., 2006. Ruminant contribution to methane and global warming - a new zealand perspective. In: *Climate change and managed ecosystems*, Bhatti, J. A., Lal, R., Apps, M. J. & Price, M. A. (editors), CRC Press, New York, p. 233-260.
- Wall, E., Simm, G. & Moran, D., 2010. Developing breeding schemes to assist mitigation of greenhouse gas emissions. *Anim.* 4(3): 366-376.