Breeding Ruminants that Emit Less Methane – The Role of International Collaboration

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ABSTRACT: Ruminants contribute to global greenhouse gas (GHG) emissions, principally as enteric methane (CH_4) emissions. Direct selection for reduced CH_4 emissions through combined selection for both low residual feed intake and methane yield could potentially provide a long term reduction in enteric methane production of 40-45%. If a methane-related trait were to be implemented by a livestock industry it will most likely be via genomic breeding values, which demand large numbers of measured animals in the reference population. Given the size of the reference population required for methane traits, it is imperative that wherever possible groups around the world collaborate on methodologies for measurement and collection of data. This has been the primary focus of the Animal Selection Genetics and Genomics Network (ASGGN) of the Livestock Research Group of the Global Research Alliance to reduce GHG emissions from agriculture.

Keywords: Methane ; Ruminant ; asggn.org

Introduction

Ruminant livestock industries face multiple challenges of increasing edible protein production to meet anticipated demand, adapting to environmental change and at the same time reducing their impact on the environment. Ruminants have a unique ability to produce high quality protein from fibrous feeds, but in doing so they also contribute to global greenhouse gas (GHG) emissions. In extensive grazing systems this is principally as enteric methane (CH_4) production (Ripple et al. (2014)), but in intensive dairy systems nitrous oxide from effluent is also a significant contributor to GHG emissions. Although CH_4 has a global warming potential 25 times that of carbon dioxide (CO_2), CH_4 has a comparatively short lifetime in the atmosphere. Accordingly, strategies to reduce CH_4 emissions from livestock provide an opportunity to arrest the rate of anthropogenic global warming more rapidly than strategies focussed on reduction of CO_2 emissions alone.

The relative contribution of livestock to total anthropogenic GHG emissions is 9-11% (Opio et al. (2013)). On a global scale enteric emissions of CH_4 from ruminants contribute approximately half of all agricultural GHG emissions. Cattle (beef, draft and dairy) are the single largest source of enteric CH_4, followed by buffaloes, sheep and goats (Figure 1).

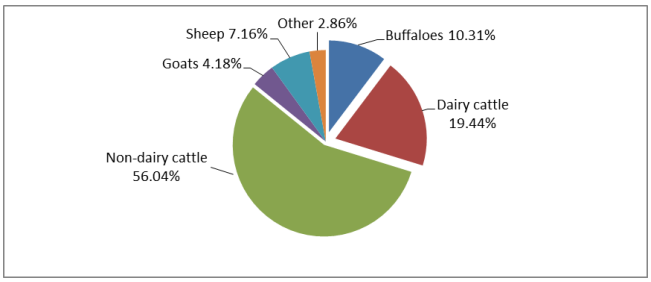

Figure 1. Contribution of different animal species and cattle types to global livestock enteric methane emission (source FAOSTAT, 2013).

There are many potential methods to reduce enteric CH_4 emissions per head and thereby intensity of CH_4 production per unit product. These include: changing feed type (for example from pasture to concentrate feed or new pasture varieties); use of supplements that reduce CH_4 emissions (fats, oils, plant extracts and nitrate); improving productivity through management change including use of growth enhancers and improved genetics; immunisation against methanogens; and selective breeding of animals with low methane emissions, through either reduced feed intake per product or reduced CH_4 production per feed consumed, without compromising production characteristics (Martin et al. (2010); Hristov et al. (2013)).

The extent to which genetic improvement can contribute to improvement in individual animal milk production and consequent impacts on GHG emissions has been highlighted by Wall et al. (2010). They describe how systematic improvement in environmental outcomes (reduced intensity of methane emissions) has resulted from productivity improvements and discuss how direct and indirect measures of emissions can be incorporated into breeding objectives to reduce emissions. However focusing on productivity improvements alone is unlikely to reduce total enteric CH_4 emissions because of the growing market demand for ruminant products, leading to increased global populations of ruminants.

Given the potential of cumulative change from genetic selection, we focus here on the evidence that direct selection for reduced CH_4 emissions may be an option for long term reduction in enteric methane production, and the means by which the necessary measurements may be implemented. This has been the primary focus of the

Animal Selection Genetics and Genomics Network (ASGGN) of the Livestock Research Group of the Global Research Alliance over the past 2 years to reduce greenhouse gases from agriculture.

Genetic selection for reduced methane emissions

There are 3 levels in which a methane trait can be defined (Figure 2).

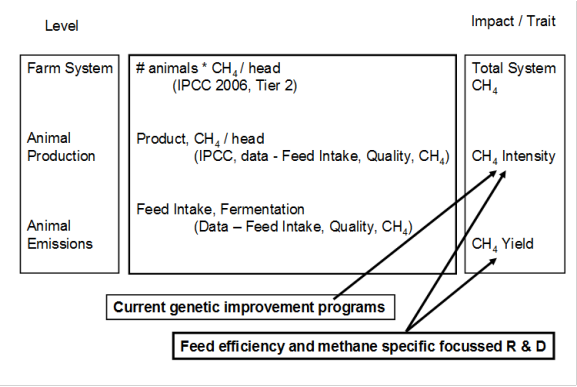

Figure 2. Levels at which a methane trait can be defined.

1. The farm system level which uses information on the number of animals present within a system boundary with a related estimate of CH_4 emissions per head, calculated using the IPCC (2006) Tier 2 calculations. These calculations have embedded within them assumptions about the factors which affect CH_4 per head, i.e. feed intake, diet quality, age at harvest and CH_4 yield.

2. The animal production level which uses information about productivity per head i.e. milk yield or kg carcass weight, from individual animals to estimate intensity of CH_4 per unit product (g CH_4/kg product).

3. In addition to improving overall productivity using current selection objectives, there are two additional complementary strategies that could be implemented to reduce methane emissions without a reduction in overall productivity.

I. Selection for reduced feed intake without affecting production e.g. selection for lower residual feed intake (RFI).

II. Selection for reduced methane production per amount of feed ingested i.e. selection for reduced methane yield (MY; g CH_4/kg feed DM eaten)

Residual Feed Intake. Selection for lower RFI in ruminants has been the subject of considerable research over the past two decades, and has been demonstrated to be possible in a range of species (see Arthur and Herd (2012) for a recent review of beef cattle). Hegarty et al. (2007) have shown that cattle selected for lower RFI have reduced daily methane production. Selection for low RFI in beef cattle is an approved practice for reducing GHG by cattle in Alberta, Canada (Alberta Environment (2012)) and has been placed on the "positive list" for development of a suitable methodology in Australia.

Selection for low RFI in beef cattle results in lower feed intake for the same level of production. There is the possibility that lower intake (of the same feed) *per se* is associated with increased MY (Blaxter and Clapperton (1965)). To explore the trade-off between the effect of reduced feed intake on methane emissions and potential effect on MY, emissions of GHGs were modelled for four western Canadian beef production systems using data outlined by Basarab et al. (2012), following IPCC Tier 2 methodology (IPCC 2006) and modified for nitrogen excretion according to NRC (2000). Farm GHG emissions included enteric CH_4, manure CH_4 and N_2O, cropping N_2O and energy-use CO_2. A baseline simulation resulted in carbon intensities of 21.09, 19.87, 22.52 and 21.21 kg CO_2e/kg carcass weight for calf-fed hormone free, calf-fed hormone implanted, yearling-fed hormone free and yearling-fed implanted beef production systems, respectively (Basarab et al. (2012)). A 10% reduction in DMI at equal productivity was simulated to reflect a 10% improvement in feed efficiency due to selection for low RFI. This scenario resulted in carbon intensities of 19.22, 18.10, 20.54 and 19.34 kg CO_2e/kg carcass weight for calf-fed hormone free, calf-fed implanted, yearling-fed hormone free and yearling-fed implanted beef production systems, respectively, or an average reduction in carbon intensity of 8.85% compared with the baseline scenario. A second scenario was simulated to reflect a 10% decrease in DMI at equal productivity and where a 10% decrease in DMI leads to a 1.4% increase in the MY following the general equations of Blaxter and Clapperton (1965). This scenario resulted in carbon intensities of 19.29, 18.16, 20.62 and 19.41 kg CO_2e/kg carcass weight for calf-fed hormone free, calf-fed implanted, yearling-fed hormone free and yearling-fed implanted beef production systems, respectively, or an average reduction in carbon intensity of 8.55% compared with the baseline scenario. The difference between the scenarios was small (0.3 percentile points), indicating that a rise in MY (g CH_4/kg DMI) associated with reduced feed intake will not offset the drop in methane production (g CH_4/day). These results support selection for low RFI as a means to reduce GHG emissions in beef cattle.

Methane Yield. The possibility of selection for reduced MY is comparatively new (see Hegarty and M^{c}Ewan (2010)). Genetic parameters for total methane production and MY measured in respiration chambers at fixed levels of feed intake have recently been published for sheep (Pinares-Patino et al. (2013)) and beef cattle (Donoghue et al. (2013): Arthur et al. (2014)). These show heritability of CH_4 production (g/d) to be 0.29±0.05(se) and 0.4±0.11(se) and for MY (g/kg feed) 0.13±0.03(se) and 0.19±0.10(se) respectively for sheep and cattle. To date there are no reports of adverse genetic correlations between production traits and MY (Pinares-Patino et al. (2013): Donoghue et al. (2013): Arthur et al. (2014)). Selection for

divergence in MY has recently been demonstrated in sheep (Pinares-Patino et al. (2013)).

Potential for selection for both lower residual feed intake and methane yield. The potential magnitude of effect of combined selection for lower RFI and reduced MY is unknown. Hegarty et al. (2007) reported differences in feed intake of 1.17 kg/d between beef cattle selected for and against RFI after 2.4 generations of single character selection on RFI. This resulted in a difference of 18g CH_4/d around a mean 180g CH_4/d, a 10% difference in CH_4 emissions / day (Hegarty et al. (2007)). Pinares-Patino et al. (2013) report a difference of 8% in MY between sheep after one generation of selection for and against MY.

The extent to which variation in RFI and MY can be exploited depends on the stability of the underpinning relationships, and effect on other production traits. For example, selection for low RFI in beef cattle is associated with reduced fatness (r_g = 0.49 to -0.30; Arthur and Herd, 2012). The potential magnitude of differences in RFI resulting from ongoing single trait selection that can be projected into the future is unknown, but is unlikely to exceed 25% (R.M. Herd, pers. comm.).

The lower limit of MY potentially attainable by selection against MY is also unknown at present. Measurements of MY of sheep in respiration chambers indicate a between animal coefficient of variation in MY of 10.3% (Pinares-Patino et al. (2013)) and for cattle 14% (Donoghue et al. (2013)). It would be reasonable to anticipate a response to long term selection to be in the order of 2 SDs from the mean, suggesting that a reduction of from 20 to 25% in MY may be possible.

The mechanisms that contribute to genetic variation in MY of individual animals may include: reduced fermentation of organic matter in the rumen – due to shorter retention time of digesta (Pinares-Patino et al. (2011)); smaller rumen volume (Goopy et al. (2013)); instability of rumen fermentation (Faichney and Graham (1996)); different microbial population in the rumen; and potentially reductive acetogenesis (inferred from Faichney et al. (1999)). The extent to which these combine to produce natural variation in MY is unknown, as is their potential impact on production and fitness traits.

In the long term, selection for low MY, combined with selection for low RFI, may provide a reduction in total methane emissions of 40-45%. It remains to be seen if this is independent of production traits, although in practice, selection for reduced feed intake and methane emissions will be implemented through an index that includes production traits.

It should be noted that it is unlikely that the benefits of selection for MY alone could be realized without a substantial change in the way that payment for mitigation is made. Compared to the cost of measurement, current prices for CO_2-e are so low as to make it uneconomic to consider including MY in a selection index, unless there are compelling or mandated reasons to do so.

Implementation of selection for reduced methane emissions requires reliable methods for measurement of methane emissions in animals likely to contribute offspring to the future herd or flock. If the measurement procedures are too onerous to be applied widely then it may be possible to incorporate methane emission traits into genomic tools which are increasingly being used to describe other hard to measure traits.

Measuring methane emissions from individual animals

Unlike production or product quality traits where useful data can be obtained during normal management practices, measurement of methane emissions currently requires specialized equipment and facilities and generally disrupts normal management practices. Accordingly there has been a substantial focus on attempts to devise less invasive measurement systems. These invariably result in obtaining samples of expired air from animals in production systems for short periods of time. The challenge is to relate these measures to the long–term measurements required in production environments.

Methane emissions exhibit extreme short term variation, simply sampling for longer does not remove the variation. Under identical conditions (same sheep, feed and level of feeding, animal handling and 24hr respiration chamber measurement) where repeatability of MY on consecutive days is 0.89±0.005, repeatability 2 weeks and a year later is 0.26±0.02 and 0.24±0.02 respectively (Pinares-Patino et al. (2013)). There is no published data under similar conditions for cattle. Of course, it would be useful to know the genetic correlations between measurements on the same animals over time (which may be higher than the repeatability) but there is as yet insufficient data to obtain reliable estimates.

These observations indicate that repeated measures of the trait over periods of time at least 2 weeks apart are required. Moreover, it is rare that a relevant measure of both feed intake, and methane emissions will be available. A measure of feed intake is required to calculate MY, and that measurement should include information on the same time scale as measurement of CH_4 emissions. We know from studies of RFI that measures of feed intake over a period of 35 days are required to minimize the error variance in measurement of intake (Archer et al. (1997)). However, we also know that feed intake on the day of measurement and the day prior accounts for more of the variation in methane emissions than feed intake on the measurement day alone (Robinson et al. (2011)).

For measurement of CH_4 production and MY of individual animals for genetic selection, the methodology must provide a reliable measure of the CH_4 emission by the individual for the period of measurement and the targeted production system. This requires that the capture of CH_4 emissions by the measurement procedure be stable across

time. Respiration Chambers (RC), portable accumulation chambers (PACs) and the GreenFeed Emissions Monitor (GEM) all potentially meet this criteria (Table 1). Methods where capture is less than 100% might be useful if they show consistent recovery. Such methods include SF_6, and sniffers which permit losses of CH_4 between animal and sensor. Ratio methods (e.g. CH_4/CO_2) may also be useful if the ratio is able to be equated to CH_4 production rate.

Ideally the phenotypic and genetic correlations between CH_4 emissions measured by different means should be one, i.e. they measure the same trait. In practice this is unlikely to be the case. The principal reason is that the methods as currently used require knowledge of feed intake to calculate MY, and in most cases feed intake data relevant to the period of measurement is not known (with the exception of the RC technique). Uncertainty about the estimate of MY is increased when measurements of methane emissions and feed intake are made over different durations, or made up of different sampling patterns.

The period of measurement (of CH_4 and for MY, feed intake) should be sufficient to reliably rank sires for estimation of breeding values in the trait of interest. In practice, this may mean multiple measures per animal. The repeatability of CH_4 and MY measurements over periods greater than 2 weeks using RCs is shown in Table 1 (data from Pinares Patiño et al. (2013)). They indicate that at least 2 measurements at least 2 weeks apart are required to obtain reliable estimates of MY in RCs. The repeatability of measures in PACs is only slightly less than in RCs. There is limited data to reliably estimate repeatability of CH_4 emissions using the SF_6 and GEMs (Table 1), but it is anticipated that it will not be better than in RCs. There is no reliable data on repeatability of MY measures based on emissions from GEM, SF_6 and sniffer systems.

Table 1. Repeatability (REP) of different CH_4 traits (total daily production g CH_4/d and methane yield gCH_4/kg feed) and estimated minimum number of measurements (#Measures) required to obtain suitable data for initial research into genetic parameters for methane traits by method.

Method	REP CH_4	REP MY	#Measures
RC*	0.5	0.25	2
PAC**	0.45	0.15-0.2+	3
GreenFeed+	0.37	§	Accumulated
SF_6++	0.17-0.18	§	3
CH_4/CO_2 in breath	~0.35***	§	Accumulated

*RC = Respiration Chamber. Data from Pinares-Patino et al, 2013, **PAC = Portable Accumulation Chamber (V.H. Oddy Pers. Comm.) +Velazco et al (2013) Greenfeed data only for 18 days, ++ Grainger et al. (2007), ***CH_4/CO_2 data from Dairy cows over 3 days (Lassen et al. (2012)), no attempt to quantify CH_4 production rate, § unable to be estimated if feed intake data not available

Having more progeny per sire will increase the accuracy of the estimate of sire breeding values and having more sires will improve the accuracy of the initial estimates of heritability. For example, data from 1000 animals in a half sib design and heritability estimates higher than 0.15 would be significantly different from 0 (Falconer & Mackay, (1996)), and daughter groups larger than 40 would provide accuracies of estimated breeding values >0.6.

Constraints due to the unique characteristic of each measurement procedure affect the values obtained by each method. The fixed level of feed offered during the measurement of MY in RCs are an artificial constraint, and may not be representative of normal animal values in real production systems (Robinson et al. (2011)). PACs require the animals to be rounded up prior to measurement, disrupting the normal pattern of feed intake as does SF_6 which requires animals to be yarded daily to change canisters. The GEM requires an attractant (usually a better / different feed to that more generally available) to bring the animal to it to measure methane and CO_2 emissions, potentially affecting grazing behaviour. Perhaps the only method that does not interrupt normal feeding behaviour is the sniffer (Garnsworthy et al. (2012)) or CH_4/CO_2 methods (Lassen et al. (2012)) when applied to a dairy milking stand where animals routinely receive their feed through a robot, although this is hardly "normal" feeding behaviour especially if the results are expected to be used to rank animals grazing pasture. Robust genetic correlations between these differing methods, especially when consuming different feeds still need to be estimated, and are unlikely to be one.

Finally, the measurement must be robust over time, as low cost as possible, not unduly influence animal behavior and permit a high rate of data capture with low labour requirements. Ideally it should replicate the normal production system as far as possible. The optimal period and number of measurements will be determined by the practicalities of the measurement protocol, repeatability of the measurements, the pedigree structure of the data and the purpose of the research.

Table 2 summarizes some of the current practical concerns with each of the methods for measuring CH_4 emissions from individual animals to obtain genetic parameters.

Table 2. Comparison of methods for measuring methane traits against practical criteria likely to influence implementation of measurement for genetic evaluation

Method	Robust	Intrusive	Cost	Throughput
RC	Yes	Yes	High	Low
PAC	Yes	Yes, but easily managed with grazing animals.	Low	High
GreenFeed	?	Moderately, requires modified grazing pattern	High	Moderate
SF_6	?	Yes for sampling, less so for grazing	High	Moderate
CH_4/CO_2	?	No if implemented in Automated Milking Station	?	High

At present we believe that each method measures a different trait. Until we can obtain the genetic correlation between each measurement protocol we don't yet know the best method. To obtain such information is expensive and time consuming and to a lesser extent transient. As methods are developed they will be superseded by alternatives, and it is likely that populations in which different measurements are made will not be comparable. The ASGGN is aware of this possibility and actively working to minimize any associated risk.

Genomic Selection.

Methane emissions (as g CH_4/ day or MY) are hard to measure traits. Methods currently available are expensive and time consuming (RCs and SF_6) and subject animals to artificial environments. Those that measure animals in production situations (pasture, feedlot or dairy feeding station) sample CH_4 for only a part of a day and require repeat measurements (PACs, Sniffers or GEM) and in some cases calculation back to known standard procedures. Those methods of estimating CH_4 emissions that rely on computation of differences between feeding standards and production account for only part of the potential variation in CH_4 emissions between animals.

Genomic selection opens the possibility to efficiently select for hard to measure traits. It is progressively being used to increase rate of genetic progress for production traits that are measured late in life (e.g. fertility, longevity, meat yield and quality), expensive to measure (e.g. RFI) or are sex linked (e.g. milk production and quality). In the dairy and increasingly in the beef and sheep industries leading sires are routinely genotyped and GEBVs are used in making selection decisions. By measuring CH_4 on industry animals which have measured production traits and have already been genotyped it would be possible to estimate GEBVs for CH_4 emissions at lower cost. This is predicated on having a genotyped reference population of sufficient size, where CH_4 emission levels are measured.

The accuracy of genomic selection for selection candidates (i.e. animals with a genotype, but no measured phenotype) with increasing size of reference population is shown in Figure 3. This was derived from the estimated heritability of MY of 0.13 (Pinares-Patiño et al. (2013)) and an effective population size of 150 using the procedure described by Hayes et al. (2009). If the individuals in the reference population were progeny tested, or if repeat measurements were available, this would make the estimated heritability of the trait much higher and thus would require fewer animals be genotyped to achieve the same accuracy.

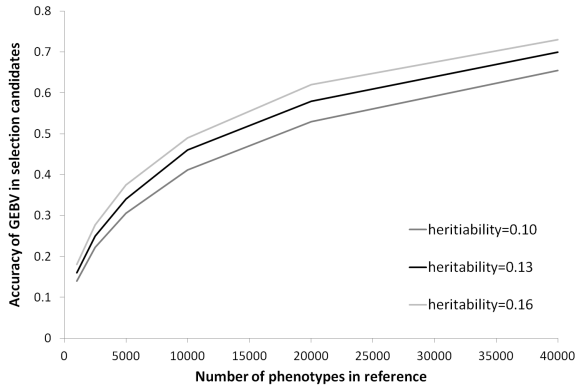

Figure 3. Accuracy of genomic estimated breeding values (GEBV) for methane yield in selection candidates as a function of heritability of the trait and number of animals with phenotypes in the reference population. Estimates of heritability of methane yield (gCH4/kg DM intake) in sheep were obtained from Pinares-Patiño et al (2013).

Because MY is a new trait, it would be anticipated that even low initial accuracy will be useful to industry. As further animals are phenotyped the GEBVs would become increasingly useful. It remains to be determined if MY is independent of other (production) traits. If it is, then adding information from the GEBVs for MY into a selection index is relatively straightforward.

The number of animals with phenotypes in the reference population required to obtain GEBVs of high accuracy for MY is large and almost certainly exceeds the resources available in any one country. To overcome these limitations an international effort is required to bring

together data on production, feed intake and CH_4 emissions of ruminants.

Role of ASGGN

It is difficult, costly and slow to develop the necessary technologies to measure methane emissions and to devise effective protocols at the scale required for establishing genetic parameters, and for industry implementation. The ASGGN provides a forum where ideas and experiences can be shared more quickly than the normal scientific process. We anticipate this will speed up, and reduce cost, of the research and development process.

Conclusion

Although ruminants have advantages in terms of being able to utilize fibrous feed otherwise unsuitable for animal production, they contribute GHG emissions due mainly to the production of enteric methane. Genetic selection is one of many strategies to maximize productivity and minimize methane production by ruminants. Selection of ruminants for low methane yield is possible. To implement that possibility requires development of low cost methods for measuring methane yield in many animals and may potentially be applied through selection using genomic breeding values. The ASGGN is helping that process by sharing experiences of groups working in different industries and countries.

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