Genetic Opportunities to Reduce Enteric Methane Emissions from Ruminant Livestock

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Introduction

Management and mitigation of greenhouse gas (GHG) emissions from agriculture is of increasing concern with the prospect of these activities coming under regulation. Opportunities for nutritional and microbial manipulation to reduce enteric methane emissions from livestock have been extensively researched and reviewed (Beauchemin et al 2008; McAllister and Newbold 2008), but there is little information on opportunities for mitigation via animal genetics. Recent forums have begun to address the potential impact of animal genetics on emission intensity at individual animal and whole-farm levels (DEFRA 2008; LEARN 2009). This paper evaluates the capacity of animal breeding to directly and indirectly alter the emission of enteric methane from ruminant livestock, including reviewing evidence for control of enteric methane production by the host animal.

Breeding objectives for emissions management

Mitigation of enteric emissions can currently be seen as a public good breeding objective (Wall et al 2010), but may become a private breeding objective if livestock GHG emissions are included into local or global carbon economies. There has been some recognition of the opportunity for genetic improvement, but little about the correct breeding objective(s) (Jones 2008; Hegarty 2009; Arthur et al 2009; Wall et al 2010). Possible objectives include reduction in total emissions from the sector, farm or individual animal; or reduction in emissions intensity (emissions/unit animal product or profit) or methane yield (g/kg feed). Emissions intensity is currently the preferred metric for emissions in New Zealand’s emission trading scheme. Our preference is that any breeding objective is economically based and the direct costs of GHG explicitly included in the objective. Similarly, the GHG emissions metric should be expressed on a basis that is independent of other traits to aid breeder interpretation. A strong candidate is methane yield (g/kg feed) although it is recognised that the lowest methane yield will occur at highest feed intakes, at least on forages (Blaxter and Clapperton 1965). To achieve any of these objectives, estimates of the heritability of methane traits and feed intake are required, along with their repeatability at different ages and on different diets. Cottle et al (2009) evaluated the probable changes in Merino production traits and annual methane emission if methane was included in a commercial selection index. In the absence of published genetic parameters, a range of production trait : methane correlations and a range of economic values for methane were

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assumed. When a positive correlation between methane and production traits was assumed, the low economic value of methane at current carbon values (AUD4.60/year at $30/t CO₂-e) meant there was little selection pressure for methane relative to that for higher value production traits (eg. fleece = $36/year), so methane emissions increased. A 1% p.a. reduction in methane was only achievable at carbon values well over AUD400/t. While making many assumptions, this work provides a valuable indicator that inclusion of methane in selection indexes is only likely to reduce flock emissions if the economic value of methane is at least an order of magnitude higher than that currently suggested by global carbon prices.

Modifying the genotype to reduce emissions

Impact of increasing genetic potential of stock for production (liveweight or milk)

Simply increasing the daily liveweight gain of livestock for meat production by nutrition or by genetics reduces the methane per unit product (Hunter and Neithe 2009). Faster growth to slaughter, however, will mean that more feed will be available late in the growing season that can either be harvested or left standing to be used to finish additional purchased animals. Alcock (2009) simulated the impact of a range of genetic changes (10% changes in growth rate, methane yield, residual feed intake) on productivity, economics and emissions of three sheep enterprises over 37 years. The high growth genotype led to a 2% lower emission intensity in a Merino wool and hogget producing enterprise (enterprise 2) but 3% higher intensity in enterprises producing 1<sup>st</sup> or 2<sup>nd</sup> cross lambs (enterprises 1,3; Figure 1).

![Figure 1](image-url)  
**Figure 1:** Estimated emissions intensity of three enterprises using sheep of current genetics or genetics expressing 10% improvement in growth rate, methane yield (% of gross energy), residual feed intake, or all improvements together, (independence of action assumed). Enterprise 1 – 1<sup>st</sup> cross lambs from Merino ♀; Enterprise 2 – Merino hoggets from Merino ♀; Enterprise 3 – 2nd cross lamb production (Alcock 2009).
In the dairy industry in many countries, there has been a steady decline in the greenhouse gas emission per kg of milk. This may in part be ascribed to genetic improvement. Using unselected cows and cows selected for high milk fat plus protein, Wall and coworkers (Wall et al 2010), showed cows of higher genetic merit produced less methane/kg of milk on both high energy and low energy density diets. Where nutrient availability is low, however, the advantage of higher productivity genetics can be lost by reduced reproductive performance and the need to carry more replacement females (Lovett et al 2006). In Lovett’s study, a farm of cows of high genetic merit for milk production provided with a low concentrate feed, required 21 replacements per 64 cows, compared to 17.1 replacements per 52.1 cows when fed high concentrate, raising the emission intensity from 1.05 to 1.20 kg CO$_2$-e/kg milk by suboptimal nutrition.

**Reducing the number of replacement animals required**

Since maintenance may account for 59% of feed consumed by dairy herds and a greater percentage in extensive beef herds (Thompson and Barlow 1986; Fullkerson et al 1986), reducing energy utilized in maintenance and increasing expenditure in production offers a simple way to reduce emissions intensity of animal products. Animal nutrition and management offer many opportunities for this including: improving ovulation, growing animals faster, joining younger, delayed culling and removal of non- or less-productive animals (Cruickshank et al 2009; Hunter and Neithe 2009), but animal selection can also contribute as summarized below.

**Higher weaning percentage.**

The use of using environmentally appropriate genotypes is fundamental to maximizing the efficiency of converting feed to beef. In a comparison of the methane production per tonne of LW weaned from a 16,000ha farm in the Northern Territory, Bentley et al (2008) estimated that changing from Shorthorns in 1981 (mean cow liveweight 422 kg) to composite breed cattle in 2006 (mean cow liveweight 507 kg), had reduced methane production per tonne weaned weight by 31%. This was largely on account of the higher weaning rate achieved by composite breed females (80 v 55 weaners/cow joined). In a New Zealand dairy, Beukes et al (2009) calculated the use of cows of ‘above average’ reproductive rate would reduce methane emissions associated with production of a quota of milk solids by approximately 4%. The advantages of higher weaning percentage may arise from a range of points of genetic influence on ruminant prolificacy.

Prolificacy may be enhanced though increased ovulation, conception, and pre- and post-natal survival. Major genes affecting prolificacy in sheep have been reviewed (Davis 2004) and are beginning to be exploited with economic value being estimated (Amer et al 1999). Indictor traits for high post-natal survival are also being evaluated in genetic studies (Brien et al 2009). Opportunities for genetic selection of twinning in cattle have been evaluated (Rutledge 1975) with contributing genes mapped (Meuwissen et al 2002), and some commercial marketing of cattle with high twinning frequency (Miller 2009). Modeling of the effects of prolificacy in sheep by Alcock (2009) and by Cruickshank et al (2009) showed 4% and 8% improvements in emissions/LW sold per 10% increase in lambing or scanning percentage respectively. Increasing prolificacy by nutrition would not have similar advantage
due to emissions arising from extra feed required to nutritionally boost ewes prior to ovulation.

**Longer retention in the herd/flock**

There is increased interest in identifying the highest producing animals in flocks and herds and maintaining them for extended periods, while replacing the less productive animals earlier in their life. An increase in average female age reduces the need for replacement females and so reduces emission intensity. As summarised by Cruickshank et al (2009), delaying culling of ewes for 1 year could reduce emission intensity by 6.4% (Table 1). Similarly for dairy cows, Wall et al (2010) showed that increasing retention in the milking herd reduced cow numbers required to produce milk to the quota, and so reduced methane and nitrous oxide emissions associated with producing the milk quota by approximately 4%.

### Table 1: Effect of altering flock performance on methane output per lamb sold (after Cruickshank et al 2009)

<table>
<thead>
<tr>
<th>Input</th>
<th>Change</th>
<th>Methane output per lamb sold</th>
</tr>
</thead>
<tbody>
<tr>
<td>Base flock</td>
<td>Base flock</td>
<td>15.99 kg CH4/kg lam</td>
</tr>
<tr>
<td>Ewe live weight (kg)</td>
<td>10% decrease</td>
<td>-3.9%</td>
</tr>
<tr>
<td>Lamb growth rate (g/d)</td>
<td>10% increase</td>
<td>-2.6%</td>
</tr>
<tr>
<td>Ewe deaths (%)</td>
<td>10% decrease</td>
<td>-0.04%</td>
</tr>
<tr>
<td>Ewe culling (%)</td>
<td>10% decrease</td>
<td>-0.03%</td>
</tr>
<tr>
<td>Cull year</td>
<td>1 year longer</td>
<td>-6.4%</td>
</tr>
<tr>
<td>Lamb mortality</td>
<td>10% decrease</td>
<td>-1.3%</td>
</tr>
<tr>
<td>Dry ewes (%)</td>
<td>8% to 6%</td>
<td>-2.7%</td>
</tr>
<tr>
<td>Scanning percentage (%)</td>
<td>10% increase</td>
<td>-7.8%</td>
</tr>
<tr>
<td>Hogget lambing (%)</td>
<td>Wean 81%</td>
<td>-13.6%</td>
</tr>
</tbody>
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**Towards a methane-specific trait**

Daily methane production (DMP) of ruminants is primarily determined by the quantity and fermentability of the diet, but sheep and cattle that produce substantially more or less methane than expected have been observed (Pinares Patino et al 2003b; Goopy et al 2006). There are a number of mechanisms by which host animal genetics may affect DMP. These include:

- **Diet selection.** Differences in diet selection between ruminant species as well as within species are known, and sire differences documented (Warren et al 1984; Brand 2000). Ingestion of forages of differing digestibility will alter methane yield (Blaxter and Clapperton 1965)

- **Eating rate.** Faster rate of eating is associated with greater feed intake and shorter mean retention time in the gut (Forbes et al 1972), Differences in eating rate between individual cattle have been observed and shorter retention time is consistent with lower DMP (Hegarty 2004).
Digesta kinetics. The retention time of digesta fluid has a strong association with methane yield, both in continuous culture studies, and in ruminants (Pinares et al 2003). In Pinares’ studies, rumen retention time explained 57% of between sheep variation in methane emissions. Smuts et al (1995) found digesta retention time (RT) to be repeatable (0.45-0.6) and within-breed differences such that “the probability of obtaining a low wool growth rate with short RT approximated zero, in the ad libitum period.”

Diet selection, eating rate and digesta kinetics can all affect the microbial species present in the digestive tract (gut microbiome), as can an animal’s internal physiology. Evidence of mammalian genetics affecting the gut microbiome by the above or other means include:

- Discovery that mice with a single gene mutation that causes obesity (ob/ob) have significantly different gut microbial populations (Ley et al 2005), with less bacteria from the Bacteroidetes division and more from Firmicutes. This differential gut microbiome has since been found in obese and non-obese humans (Ley et al 2006).

- Among humans, only 28-50% of people in western societies produce methane. Bond et al (1971) found strong correlations between an individual’s methane status (producer/non-producer) and the methane status of other family members Studies with twins showed methane production in humans has a heritability of 0.42 (Flatz et al 1985).

Recognition of genetic control over animal processes that affect methane production and the gut microbiome has accelerated recent studies to evaluate direct selection for enteric emissions and the genetic parameters for the traits. In small original studies no differences were found in emissions between breeds of sheep or between Bos taurus and Bos indicus cattle (Hungate et al 1960). Individual sheep (Pinares et al 2003) and cattle (Goopy et al 2006) have been shown to produce more or less emissions than expected, but these phenotypic differences have not always been maintained across diets. However, recent studies using more accurate methodology with larger numbers have shown more promise (C. Pinares, pers comm.). One of the critical challenges to breeding for low emissions or emissions intensity, is the lack of an accurate measurement technology to phenotype large numbers of pedigreed progeny to establish genetic parameters for a methane trait.

While field measurement of enteric emission has been made on over 800 cattle in a single study using the SF$_6$ tracer method, food safety and even accuracy of the method preclude it from being used to accurately determine the phenotype of individuals. Use of respiration chambers offers higher accuracy in establishing daily methane production than does the SF$_6$ tracer, but requires extensive associated facilities to adjust and determine the intake of large numbers of animals (over 2-3 weeks) before measurement (over 2-3 days). Tracers such as the animal’s own CO$_2$ production (Madsen et al 2010), require extensive testing before use.

Recently, enclosure of sheep in respiration booths for 1-2 hours was found to be the most useful of a suite of predictors of DMP studied (Goopy et al 2009). A standardized pre-measurement protocol and recommended multistage selection (Robinson 2009) was used by Robinson et al (2010) to measure emissions from over 700 sheep. This study identified significant sire differences in methane production (both adjusted and unadjusted for LW),
and a heritability for methane production (0.13 adjusted for LW). The short-term enclosure method of Goopy could be a useful first stage selection tool as a prelude to calorimetry in identifying animals of extreme methane phenotype. If parameters are established, and found suitable for selection, industry phenotyping may be via genome-wide selection with only key animals measured.

Breeding for improved residual feed intake
Residual feed intake (RFI) is the difference between actual feed intake and the expected feed requirements for maintenance of body weight and some measure of production (such as growth in beef cattle or milk production in dairy cattle). Low RFI beef cattle eat less than expected for their LW and growth rate. RFI is moderately heritable enabling the development of estimated breeding values for RFI (Robinson and Oddy 2004). By virtue of lower energy and nitrogen intake, lower RFI cattle can be expected to have a lower daily methane and nitrous oxide output, and lower enteric emissions have been shown and related to the breeding value of the animal for RFI (Hegarty et al 2007).

The potential national emissions impact of selecting cattle for RFI in Australia was estimated by Alford et al (2006; Figure 2), assuming realistic adoption rates and ceilings and a constant herd size, and RFI being only one component in index selection. Over a 25 year horizon, enteric emissions from adopting herds would drop 15.9%, while national beef herd emissions would ultimately be 3.1% lower than the base year. This constituted a cumulative national

Figure 2: Estimated annual reduction in enteric methane produced by the Australian beef herd as a result of reduced RFI over the period 2002 to 2026 assuming a constant national herd size (Alford et al 2006).

emission reduction of 568kT of enteric methane from the beef herd over 25 years. While Alford assumed herd size remained constant, farmers may choose to increase livestock number as RFI is improved, to utilize all existing pasture grown. Economically, one tonne of feed could be expected to generate only A$4.80 worth of methane (20kg methane x 21(GWP) x $20/t CO$_2$e). The value of animal product associated with consumption of that feed for slaughter animals however could be approximately A$150 value (producing 100kg
of LW at $1.50/kg), so there is strong financial incentive to use all available feed. The emissions impact of increasing animal populations to utilize pasture in response to improved RFI was modeled by Alcock (2009). Increased feed use efficiency reduced emissions intensity by 7-10% in Merino wool/hoggett, 1st and 2nd cross lamb production systems (Figure 1). In contrast, for dairy enterprises where cow efficiency (though arguably not RFI) was increased, and farm milk solids output was held constant, the use of fewer but more efficient cows reduced farm methane production by approximately 15% (Beukes et al 2009).

Conclusion
Genetic variation is already being utilized to reduce emissions intensity of ruminant enterprises indirectly, through traits such as live weight gain, milk production and feed efficiency. Ongoing reductions in emission intensity can be expected through these processes although this could be improved further by explicitly including GHG costs in a selection index. Additionally, many nutritional and physiological traits of the animal, including the microbial species balance in the rumen, show effects of animal genotype. While animals producing less methane than expected have been identified, the usefulness of pursuing low methane animals will be dependent upon the heritability of the trait, its correlation with productivity traits and ultimately its economic value.

References


