Genetic solutions for reducing enteric emissions from livestock – the Netherlands

Yvette de Haas[1], Nico Ogink[2], Jan Dijkstra[3], Jennie Pryce[4], Ron Crump[1], Roel Veerkamp[1]

[1] Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, P.O. Box 65, NL-8200 AB Lelystad;
[2] Environment Dept., Wageningen UR Livestock Research, NL-6700 WC Wageningen;
[3] Animal Nutrition Group, Wageningen University, P.O. Box 338, NL-6700 AH Wageningen;
[4] Biosciences Research Division, Department of Primary Industries Victoria, 1 Park Drive, Bundoora, VIC 3083, Australia.

Introduction

In the Netherlands, approximately 13% of the greenhouse gas (GHG) emissions (mainly methane (CH_4) and nitrous oxide) can be related to agriculture. The Dutch agricultural sector did not receive a quantitative target for the reduction of GHG emissions, but it did get a qualitative aim and must implement cost effective measures in order to reduce GHG emissions with 4 to 6Mton in 2020 compared to 1990.

The reduction of enteric CH_4 of cattle, being the major source of CH_4 emission in animal production, is therefore 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 conversion, 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 conversion, expressed as the CH_4 emission per produced unit of milk during lactation, 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)).

For all these traits individual recordings across the lactation cycle are required, but it is an utopian ideal that they could be measured daily during a whole lactation, or even across parities, under practical circumstances in each country. Therefore monitoring strategies will have to be defined for recording the traits to be able to fill a large database, and international collaborations are needed to combine data worldwide and genetic parameters have to be estimated for direct and indirect environmental phenotypes.

In this discussion paper we will describe the research we have performed so far on:

1. How accurately can daily methane emissions be predicted in several practical measuring systems, compared with respiration chamber data?
2. What are genetic parameters for environmental phenotypes such as residual feed intake and predicted methane production?
3. How can international data from both ends of the world be combined and what is additional value of this to each country?

Measurement of methane emissions from individual animals – monitoring strategies

The aim of this study was to estimate the accuracies that can be achieved with several possible measuring strategies, based on the variation characteristics derived from an analysis of available cow data from research in respiration chambers. The investigated three practical measuring systems were (1) measuring during milking (i.e. twice daily, for 15 minutes); (2) measuring in concentrate dispensers (i.e. 5 times daily, 6 minutes); and (3) measuring in the cubicles (i.e. 4 hours continuously, 10 observations of 3 minutes per hour).

The prediction of total daily CH_4 production is based on observations taken throughout the day on methane or the ratio of methane to carbon dioxide (CH_4:CO_2). Daily CH_4 (or CH_4:CO_2) production curves are described using experimental data from respiration chambers. Data on 10 pairs of cows observed for 4 days in Wageningen respiration chambers were analysed. The recording equipment alternated between the two respiration chambers and a reset period such that each observation within a trial represented a three minute yield with six minute intervals between them. Figure 1 shows the three-minute yields of CH_4 production per cow plotted against time of day (sample within day) for one of the ten trials. There are two clear events within the day that result in elevated CH_4 production, and there is a brief sequence of missed observations at each of these times on each day in each trial.

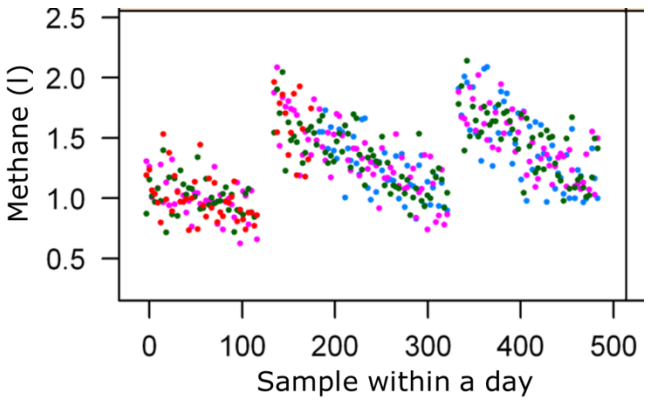

Figure 1. Three-minute methane yield against time of day within trial. Colours relate to observations on different days within the trial.

For direct CH_4 emission, calculated accuracies were 0.85, 0.89 and 0.96, respectively. However, under practical conditions full collection of CH_4 output of individual cows may be technically complicated and costly. Thus, we also investigated the accuracies that can be achieved by measuring the ratio CH_4:CO_2, which were 0.31, 0.33 and 0.39, respectively. Daily CH_4 production can be predicted reasonably accurate by collecting samples of all cows during twice daily milking. This opens up the possibility of creating a large database of individual CH_4 emission phenotypes for the identification of suitable indicator traits for the genetic merit of CH_4 production.

Estimation of genetic parameters – residual feed intake and predicted methane emission

Mitigation of enteric CH_4 emission in ruminants has become an important area of research, because accumulation of CH_4 is linked to global warming. Nutritional and microbial opportunities to reduce CH_4 emissions have been extensively researched, but little is known on using the natural variation to breed for animals with lower CH_4 yield (Wall et al., 2010). Measuring CH_4 emission rates directly from animals is difficult and hinders direct selection on reduced CH_4 emission. However, improvements can be made through selection on associated traits (e.g. residual feed intake (Verbyla et al., 2010)), or through selection on CH_4 predicted from feed intake and diet composition (de Haas et al., 2011). The objective was to establish phenotypic and genetic variation in both residual feed intake (RFI) and predicted CH_4 emission (PME) to demonstrate the genetic basis of feed efficiency and predicted CH_4 production, and the potential use of genomic selection to facilitate the inclusion of environmental phenotypes in selection programmes.

Experimental data were used, and records on daily feed intake, weekly live weights and weekly milk productions were available from 588 heifers. Residual feed intake (MJ/d) is the difference between net energy intake and calculated energy requirements for maintenance as a function of live weight and for fat and protein corrected milk production. Predicted methane emission in grams per day (PME) is 6% of gross energy intake (method of International Panel on Climate Change (IPCC)) corrected for energy content of methane (55.65 kJ/g).

Table 1. The estimated heritability (on diagonal), phenotypic correlation (above diagonal) and genetic correlation (below diagonal) for two environmental phenotypes: residual feed intake and predicted methane emission

	RFI	PME
Residual feed intake (RFI)	0.40	0.72
Predicted methane emission (PME)	0.32	0.35

The estimated heritabilities for PME and RFI were 0.35, and 0.40, respectively (Table 1). The positive genetic correlation between RFI and PME indicated that cows with lower RFI have lower PME as well. Hence, it seems possible to decrease methane production of a cow by selecting more efficient cows, and the genetic variation

suggests that reductions of the order of 11 to 26% in 10 years are theoretically possible, and in a genomic selection program even higher (de Haas et al., 2011). For both environmental phenotypes (RFI and PME) the genomic model produced breeding values with reliability double, or even triple, that of the breeding values produced by the polygenic model (Table 2).

Table 2. Reliabilities of estimated breeding values (EBV) based on pedigree information only, and direct genomic values (DGV) based on both pedigree and marker (SNP) information for two environmental phenotypes: residual feed intake (RFI) and predicted enteric methane emission (PME)

	RFI	PME
Pedigree	0.14	0.04
Pedigree + SNP	0.27	0.14

Several uncertainties still exist with these environmental phenotypes, for example related to the lack of true methane measurements. In Denmark (Lassen et al., 2012) they are measuring individual methane emissions of dairy cattle during milking, and in the Netherlands we will start collecting data with the same equipment in July 2012. However, to overcome the limitations of recording and to predict the biological consequences of selection, an international effort is required to bring together data on feed intake and CH_4 of dairy cows.

Role of genomic selection in mitigating enteric methane emissions – international collaboration

Environmental phenotypes are difficult to measure on a large scale in each country. A number of countries have started to record dry matter intake (DMI) data, but not enough records are available to get accurate breeding values for this trait to be used in their national breeding programme. One way to obtain estimated breeding values (EBVs) in a population is to use genomic selection (Meuwissen et al., 2001), where phenotypes, such as DMI, are measured in a subset of the population and genomic predictions are calculated for other animals that have genotypes, but no phenotypes. While this approach is appealing, allowing industry wide selection for improved efficiency, the size of the reference populations from which the genomic prediction equations are derived are currently too small within each country, to achieve satisfactory levels of accuracy of genomic breeding values (Verbyla et al., 2010). One way to increase the accuracy of the genomic prediction is to combine datasets from multiple populations. Challenges when combining phenotypes from several countries include genotype by environment (GxE) interactions and differences in trait definitions. A multi-trait model can handle traits that are measured in different environments as separate traits, and therefore treat both the GxE interaction and differences in trait definitions properly. The aim of this study was therefore to estimate the accuracy of genomic prediction for DMI, when analysed together in a single-trait run, or in a multi-trait run, using both Australian data on growing heifers and European data on lactating heifers.

In total, DMI records were available on 1801 animals; 843 AU growing heifers with records on DMI measured over ±70 days at 200 days of age (Williams et al., 2011; Pryce et al., 2012), 359 UK and 599 NL lactating heifers with records on DMI during the first 100 days in milk (Banos et al., 2012; Veerkamp et al., 2012). The genotypes used in this study were obtained from the Illumina Bovine 50k chip. The AU, UK and NL genomic data were matched using the SNP name. Quality controls were applied by carefully comparing the genotypes of 40 bulls that were available in each dataset. This resulted in a total of 30,949 SNPs being used in the analyses. Genomic predictions were estimated with genomic REML (G-REML), using ASReml (Gilmour et al., 2009).

The accuracy of genomic prediction was evaluated in 11 validation sets. The reference set (where animals had both DMI phenotypes and genotypes) were either within AU or Europe (UK and NL), or with a multi-country reference set consisting of all data except the validation set. When DMI for each country was treated as the same trait, using a multi-country reference set increased the accuracy of genomic prediction for DMI for UK, but not for AU and NL (Table 3). Extending the model to a bivariate (AU-EU) or trivariate (AU-UK-NL) model increased the accuracy of genomic prediction for DMI in all countries (de Haas et al., 2012). Highest accuracies were estimated for all countries when data was analysed with a trivariate model, with increases of up to 5.5%.

Table 3. The average of the approximated accuracy of genomic prediction, calculated as the correlation between genomic breeding value (GEBV) and the true breeding value (TBV) (r(GEBV,TBV)), estimated in a univariate, bivariate or trivariate run between Australia (AU), Europe (EU), United Kingdom(UK) and the Netherlands (NL), where "uni within" refers to the current situation where the reference and validation population were within AU or within EU. In all other analyses, a multi-country reference set was taken consisting of all data except the validation set. The corresponding standard errors are shown in parentheses

Country	uni within	uni multi	bi: AU-EU	tri: AU-UK-NL
AU	0.378 (0.027)	0.336 (0.046)	0.388 (0.041)	0.389 (0.042)
EU	0.313 (0.050)	0.323 (0.051)	0.322 (0.048)	0.330 (0.049)
UK	0.301 (0.042)	0.333 (0.059)	0.315 (0.048)	0.332 (0.032)
NL	0.326 (0.098)	0.312 (0.093)	0.329 (0.092)	0.328 (0.094)

This first attempt has shown that it is worthwhile setting up an international collaboration and sharing data, but that the increase in accuracy was lower than expected. Therefore, an initiative has started to combine DMI data from Australia, Canada, Denmark, Germany, Ireland, Netherlands, New Zealand, Scotland and United States to pool DMI data across countries to establish if this is a viable way to estimate genomic prediction equations that give breeding values with sufficient accuracy that these can be used for demonstration by the collaborators in the project. First results of this collaboration are expected in Summer 2012.

Conclusions

Also in the Netherlands many initiatives are running to come with genetic solutions for reducing enteric CH_4 emissions from dairy cattle. The most important ones at the moment focus on:

- Measuring individual methane emissions with Fourier Transformed Infrared Spectrometry, and to come up with the best monitoring strategy to define an environmental phenotype that is indicative for a daily CH_4 production, lactational CH_4 production or even lifetime CH_4 production.
- Estimating genetic parameters for environmental phenotypes and to demonstrate the potential use of genomic selection to facilitate the inclusion of environmental phenotypes in selection programmes.
- Setting up international collaboration to estimate genomic prediction equations for environmental phenotypes that give (genomic) breeding values with sufficient accuracy.

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