GENETIC SOLUTIONS TO IMPROVE RESOURCE EFFICIENCY IN DAIRY CATTLE

Y. de Haas[1], J.E. Pryce[2], J. Dijkstra[3], E. Wall[4] and R.F. Veerkamp[1]

[1]Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, P.O. Box 65, NL-8200 AB Lelystad;
[2]Biosciences Research Division, Department of Primary Industries Victoria, 5 Ring Road, Bundoora, VIC 3083, Australia;
[3]Animal Nutrition Group, Wageningen University, P.O. Box 338, NL-6700 AH Wageningen;
[4]Scottish Rural College, Animal & Veterinary Sciences Group, Roslin Institute Building, Easter Bush, Midlothian EH25 9RG, UK.

SUMMARY
Examples of traits related to feed resource efficiency are residual feed intake (RFI) and methane (CH_4) emission. In an experimental dataset of 588 heifers, we showed that it is possible to decrease CH_4 emission (predicted on dry matter intake (DMI) and ration) by selecting more efficient cows (genetic correlation of 0.3). Feed efficiency phenotypes are difficult and expensive to measure on a large scale, but genomic selection is a promising tool to make progress in breeding resource efficient cows, since it relaxes the need for information on performance of all animals. Using genomic selection, a reduction in predicted CH_4 in the order of 15% in 10 years is theoretically possible. To double this genetic gain, a large reference population is needed. Therefore, an international collaboration between 9 countries in Europe, US and Australiasia is set up to assemble data on >6,000 cows with high quality phenotypes and genotypes. The next step is to predict the genomic breeding values with this extended dataset, and report the accuracies. This way, a combined approach, including feeding, management and genetic selection, can be set up, which is likely to be the best approach to successfully improve feed resource efficiency.

OVERALL 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 general aim of the Kyoto protocol is to reduce 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). One way to reduce the environmental impact of dairy cattle is to improve their resource efficiency. Examples of traits related to feed resource efficiency are dry matter intake (DMI), residual feed intake (RFI), and methane (CH_4) emission. This paper provides genetic parameter estimates for feed resource efficiency traits, and examines the value of creating an international data set for these traits.

GENETIC PARAMETERS FOR FEED RESOURCE EFFICIENCY TRAITS
Introduction. Nutritional and microbial opportunities to reduce CH_4 emissions have been extensively researched, but there is little knowledge regarding the use of 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. RFI (Verbyla *et al.* 2010)), or through selection on CH_4 predicted from feed intake and diet composition (de Haas *et al.* 2011).

Aim. The objective of this study was to quantify phenotypic and genetic variation in RFI and predicted CH_4 emission (PME), and to examine the potential use of genomic selection to facilitate the inclusion of resource efficiency phenotypes in selection programmes (de Haas *et al.* 2011).

Material and methods. Data from previous experiments were used, and records on daily DMI, weekly live weights and weekly milk productions were available from 588 heifers (Veerkamp *et al.* 2000). RFI (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. PME (g/d) is 6% of gross energy intake (method of International Panel on Climate Change (IPCC)) corrected for energy content of methane (55.65 kJ/g). All heifers were genotyped using the Illumina 50K SNP panel (54,001 SNP in total; Illumina, San Diego, CA). Genetic parameters were determined using a random regression sire-maternal grandsire model in ASREML (Gilmour *et al.* 2009). Effects of SNPs were estimated using Bayesian stochastic search variable selection (SSVS; (George and McCulloch 1993)). Genomic breeding values were predicted for these heifers using a model that included the genotypic information. A polygenic model was used to estimate breeding values using only pedigree information. A 10 fold cross-validation approach was employed to assess the accuracies of the two sets of predicted breeding values by correlating them with the phenotypes.

Results and discussion. The estimated heritabilities for PME and RFI were 0.35, and 0.40, respectively (Table 1). Both heritability estimates fit well in the range recently reviewed by Berry and Crowley (2013). PME has not been analysed before, but it can well be compared with DMI.

Table 1. The estimated heritability (on diagonal), phenotypic (above diagonal) and genetic correlation (below diagonal) for residual feed intake (RFI) and predicted methane emission (PME). The corresponding standard errors are shown in parentheses

	RFI	PME
Residual feed intake (RFI)	$0.40_{(0.11)}$	$0.72_{(0.08)}$
Predicted methane emission (PME)	$0.32_{(0.06)}$	$0.35_{(0.12)}$

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 feed resource efficiency 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). No other studies have published accuracies of genomic predictions of these new traits, but achieved accuracies were lower than theoretically expected accuracies (Daetwyler *et al.* 2010).

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 residual feed intake (RFI) and predicted enteric methane emission (PME)

	RFI	PME
Pedigree	0.14	0.04
Pedigree + SNP	0.27	0.14

ADDED VALUE OF INTERNATIONAL COLLABORATOIN – A FIRST ATTEMPT

Introduction. A number of countries have started to record 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, where phenotypes, e.g., 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 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.

Aim. The aim of this study was 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 (de Haas *et al.* 2012).

Material and methods. In total, DMI records were available on 1801 animals; 843 Australian (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 Scottish (UK) and 588 Dutch (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.

Results and discussion. When DMI for each country was treated as the same trait (i.e., univariate analysis), using a multi-country reference set (uni-multi) increased the accuracy of genomic prediction for DMI for UK, compared to the accuracy achieved with a univariate analysis with the national reference set. The accuracy did, however, not increase for AU and NL (Table 3).

Table 3. The average of the approximated accuracy (and corresponding standard error) of genomic prediction of dry matter intake (DMI), calculated as the correlation between genomic breeding value (GEBV) and the true breeding value (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 with a national reference set. In all other analyses, a multi-country reference set was taken consisting of all data except the validation set.

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	$0.326_{(0.098)}$	$0.312_{(0.093)}$	$0.329_{(0.092)}$	$0.328_{(0.094)}$

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%.

This first attempt has shown that it is worthwhile setting up an international collaboration and sharing data, but the increase in accuracy was not enough to get accurate breeding values for this trait to be used in their national breeding programme. Therefore, an initiative has started to combine DMI data from 9 countries in Europe, US and Australiasia. Pooling DMI data across countries can establish if this is a viable way to estimate genomic prediction equations that give breeding values with sufficient accuracy, so that these can be used for demonstration by the collaborators in the project. First results of this collaboration are expected late 2013.

OVERALL CONCLUSIONS

Examples of traits related to feed resource efficiency are residual feed intake (RFI) and methane (CH_4) emission. Our studies on national data have shown that genetic solutions to improve these feed resource efficiency traits is possible. However, international collaboration to assemble data on more cows will improve the accuracy and genetic gain. A combined approach, including feeding, management and genetic selection, can then also be set up, which is likely to be the best approach to successfully improve resource efficiency.

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