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Workshop Report

“Livestock Breeding for Greenhouse Gas outcomes”



March 3-5 2009-05-26 Museum Hotel, Wellington New Zealand

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Executive Summary

- The 3 day workshop funded by MAF and PGgRc was held in Wellington, New Zealand on March 3-5 2009 under the auspices of LEARN.
- Twenty-nine participants from 7 countries were in attendance.
- The workshop was the first opportunity to bring together animal genetics and animal methane researchers to discuss aspects of genetic improvement for enteric emissions.
- Opportunities and constraints to reducing emissions by genetic improvement of animals were identified. The key outcomes of each of the 4 approaches to genetic improvement are summarised below:

Breeding for increased animal productivity.

Heritability of methane production and its correlation with animal production traits (meat milk wool) must be established before the impact of genetic improvement on emissions, and economic implications of doing so can be known.

Breeding specifically for reduced emissions.

While daily methane output is highly correlated with daily feed intake, there is divergence in methane production per unit feed eaten, which can be exploited and has a heritability that is comparable with a number of livestock traits.

It was concluded a two stage selection process is required to progress breeding for specific methane traits, as described:

1. Accurately measure primary traits (methane/d, intake/d, productivity, economics) and establish the genotypic correlations between them.
2. These primary traits can subsequently be combined in many secondary traits (eg. Methane/kg intake, methane/kg product) or included as separate components in a selection index as desired.

Less costly measures for determining primary traits will be required for implementing selection within industry flocks and herds.

At present it is not possible to obtain accurate independent measures of daily feed intake in grazing ruminants, but ranking of individuals for intake or measurement of their energy expenditure may be possible

Selecting more feed efficient livestock

Selecting livestock which consume less feed for a given level of production (high Net Feed Efficiency or low Net/Residual Feed intake;NFI) is a focus of research globally. This NFI trait is moderately heritable but the high cost of measurement and failure of a cheap 'proxy' test have limited selection for NFI by the ruminant industries. Industry benefits will only come with the availability of a cheap accurate test and by jointly selecting a production trait as well as NFI. NFI should only be measured on sires already selected for productivity traits.

Selection for N use efficiency

For countries with high performance (high N fertilised) pastures, genetic selection for nitrogen use efficiency is inappropriate. Only a small proportion of consumed nitrogen is retained in animal product and the remainder is excreted. Managing for reduced nitrogen intake promises an infinitely more reasonable approach to reducing nitrous oxide emissions than does genetic change in the animal.

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Introduction

Genetic improvement of livestock for ‘low methane production’ has been of growing interest as the anticipated high-impact chemical and microbiological mitigation strategies have been slow to develop. While breeding specifically for a methane trait is being considered, current breeding initiatives such as breeding for productivity and for net feed intake will indirectly affect methane output, so their potential impact and constraints also needed consideration. The definition of success in breeding low methane ruminants has been unclear, with government seeking to reduce total emissions but the farming sector preferring to consider their emission per unit product (emissions intensity). Since it is critical to define the targets in genetic improvement at the start of breeding programs, this workshop was convened to address the following objective:

“Define the most beneficial methane trait, what information we need to collect to estimate that trait, and how do we obtain that information ?”

Additionally the program sought to draw together global research on Net Feed Intake (NFI) and devise improved strategies for increasing uptake of NFI as a breeding objective.

The workshop program was developed that covered the following topics to achieve that outcome. Topics addressed were:

- Livestock greenhouse fundamentals
- Genetics of methane production in ruminants
- Defining the methane phenotype
- Individual animal feed intake estimation
- Pending research & essential tasks
- Net feed intake (possibilities and constraints)

A list of participants, workshop program and copies of summary documents from speakers are appended at the back of this report. All MS Powerpoint presentations from speakers will be submitted to PGgRc and hosted on the LEARN website.

Summary of Potential Breeding Opportunities

Selective breeding of animals can be used to modify their GHG output by selection for any of four targets, and discussion on each of the four targets for genetic improvement considered by the workshop are summarised below:

Breeding for increased animal productivity

- In New Zealand, genetic improvement in the lamb industry has reduced weight for age and increased lambs per ewe.
- Genetic improvement in growth rate has a ‘very modest’ net reduction in emissions (Amer). This is because the reduced lifetime intake of the faster growing lamb is largely offset by the increased body weight and feed intake of the breeding female. An analogous situation can be expected for impact in product output in beef if maternal body weight is not held constant by applying pressure on maternal body weight in a selection index.

- Selection which will increase the number of progeny per breeding female reliably reduces emission per unit product. This may be selection for improved production within a breed (Amer) or simply changing the breed to one which has a greater reproductive output in that environment (eg. AJEA Vol 48, p60-64).
- The correlations between methane production and productivity traits are not available which would allow back-calculation to establish the changes in national GHG emissions which have resulted from genetic improvement in animal growth and production since 1990 (Cottle).
- To maximise GHG impact while selecting for production, this should be coupled with selection for methane itself so that joint selection pressure is applied to production and methane traits simultaneously.
- More modelling is required to assess if it is economically desirable to select for a methane trait.

Breeding for a methane-specific trait

- A range of methane specific traits were discussed (methane/year, methane/kg DM intake, methane/unit product).
- It was apparent that in these foundation years of relating genetics to GHG, that emphasis should be on collection of the raw data for all key traits (methane, intake, productivity, economics). This would allow a range of desired secondary traits to be calculated.
- The two reasons for focussing on the primary traits initially are:
 - Genetic improvement of secondary traits that are expressed as ratios (eg. Methane/kgDMI) may arise by changes in either the numerator or the denominator but the selector has no control over which changes.
 - Until we know the table of correlations, we are poorly placed to know if or how primary traits should be combined to maximise impact on emission from genetic selection.
- At this time, the most desirable secondary trait is methane/kg DMI (sometimes called methane yield, although this can be applied to other ratios also) and the reasons for its preference are:
 - If the assumption that DM availability for grazing will not change, then reducing methane/kg DMI is the ONLY way to reduce total emissions arising from the nutritional feed-base (Clark). Certainly in New Zealand, profitability of dairying is seeing traditional sheep and beef pastures being reallocated to more intensive grazing rather than to forestry, which is the preferred greenhouse gas management response.
 - No forecasts of future grazing area were presented
 - Methane/kg DMI has shown itself to be heritable ($h^2 \sim 0.2$), therefore amenable to genetic improvement.
 - Selecting for methane/kgDMI is completely compatible with selecting for improved net Feed Intake (kg/d) and with selecting for improved productivity.
 - Methane/kgDMI is the basic unit of inventory in New Zealand's national greenhouse gas inventory so its improvement could readily be reflected in New Zealand's national accounts.
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- Methane per unit product is widely quoted to show that reductions in emission intensity from diet (Brazil), improved NFI (Canada) improved reproductive output (Amer, NZ). It was not discussed widely at the workshop because the current need is to measure the primary traits.
- As far as making breeding decisions, using primary rather than secondary data in a breeding index maximised the possibility to affect the component of choice.
- Phenotypic and genotypic correlations between the methane trait and animal productivity (meat, milk, fibre) are URGENTLY needed to enable calculation of whether selection for a methane trait is an economically sensible decision, taking into account the relative economic value of methane and commercial products.

Selecting more feed-efficient livestock

- Research on improvement of livestock for NFI has been underway for many years in Australia, Canada and more recently Ireland and New Zealand.
- NFI is moderately heritable trait. Its measurement identifies animals that eat less but perform the same as their cohort (low NFI)
- A reduced DMI in livestock selected for low NFI has been consistently proven.
- That this reduced intake is associated with reduced methane production per day has been difficult to prove. This is mostly because of the small difference expected (Approximately 20g CH₄/d of a total emission of 200g/d in cattle) and the poor accuracy of methods mostly used (SF₆ tracer).
- There is an absolute need to use respiration chambers to quantify both the effect of NFI on daily methane production and on methane/kg DMI. Canadian studies have shown reduced methane/kg DMI which is desirable, but is contrary to the predicted increase in methane/kgDMI predicted when intake is reduced.
- Low industry adoption of NFI has been a global problem, with work to date being largely on research animals rather than industry animals.
- A 2 stage selection is suggested with only animals already identified as being elite for valuable production traits (Stage 1), to be being taken through for NFI measurement (Stage 2).
- Making research NFI facilities currently used for selection lines available to do this testing for industry should increase industry uptake of NFI in its leading animals. This is in process in Canada and Ireland.
- GHG development money could be made available to encourage producers to put their top animals through the NFI measurement system and a central progeny test may be possible.
- GHG offsets (as being developed in Canada) may provide incentive for NFI testing (information on Canada scheme is publically available).

Selection for nitrogen efficiency

- The efficiency of capture of dietary nitrogen in animal product is extremely low.
- Efficiency will be highest in highly productive animals.
- An analysis of the implications of recent genetic improvement in growth traits on N use efficiency is justified.
- Lifecycle analysis on N use in the grazing system is also justified in New Zealand to evaluate the impact of industry change to larger (USA) dairy cattle genetics.

- Using genetic improvement to make small change in an already small component of the nitrogen cycle is hard to justify, when simple reductions in nitrogen intake will provide far more substantive reductions in the nitrogen economy.

The Challenge of Intake

The quantity of feed consumed (intake) is the primary determinant of daily methane production although the intake:methane relationship is moderated by feed type. Intake is also the primary determinant of animal performance, especially in New Zealand where pasture protein supply exceeds animal protein requirements.

Consequently selecting on methane production without any allowance for the intake (or perhaps productivity) of the animals is likely to be extremely counter-productive given the relative economic values of animal product and methane emission. One tonne of feed for growing cattle will generate approximately \$200 of income (100kg growth x \$2/kg) but only \$8 of methane liability (0.4t CO₂e x \$20/t).

Possibilities for measuring intake in the field were reviewed (Dove) but no cheap simple ‘farm-ready’ technology exists. An opportunity for ranking animals using alkane technology was identified and ranking animals may be all that is required in a genetic improvement program. None the less, alkane analysis is a sophisticated task. As an alternative to measuring intake, several technologies to estimate energy expenditure of the animal were reviewed with a commercial bolus (Brosh) to soon become available holding promise.

Research Needed

- Phenotypic and genotypic correlations between methane production and wool, meat and milk productivity traits to determine how selecting for a methane trait will impact on these production traits and therefore on economic output.
- Improved tools for field measurement of methane output and of feed intake or energy status of the animal.
- Coordination of gene marker studies with major experiments to maximise sample availability.
- Mechanisms for expanded NFI testing of high performance industry sires to improve industry uptake of this trait.
- There was a recognised need to keep the interaction from this meeting going to ensure global research interfaces as effectively as possible. LEARN may provide an ideal platform for connecting delegates and the task of collating and circulating a summary of progress from delegates in 12 months time was recommended.

Closing Assessment

There is no doubt that future years will see livestock producers move to minimise the impact of carbon penalties on profitability by both reducing emissions and increasing production. In so doing they will meet national objectives of reducing total emissions while optimising profitability. Genetic improvement (for NFI or a methane trait) may be one of the tools to achieve this.

A role for genetic improvement in a methane trait will be highly dependent upon the relative economic values of emissions and the animal performance traits with which emissions correlate, either positively or negatively.

Estimating the economic impact of reducing methane output is totally dependent upon knowing the correlations between methane output and productivity traits (milk, meat wool). In the event of a low carbon price, high product prices and positive correlations between methane and production, it is unlikely that inclusion of methane in a selection index would be warranted. Conversely, if methane is of high value or is negatively associated with production, it may be economically desirable to include emissions in a livestock breeding index.

Feasibility of measuring or obtaining estimates of some of the desired primary data (daily methane production, feed or energy intake) remains a major constraint to mitigation of methane by livestock improvement. Finding of gene markers for low methane/kgDMI (Berry) is a positive indication of simple genotyping in the future but recent research on gene makers for NFI suggests hundreds rather than handfuls of markers in a panel will be required.

The key question of how the methane trait should be framed (methane/d; methane/kg DMI etc) was resolved by recognition that it is the primary data that should be collected for inclusion in an index. Processing of that data into secondary traits can then be done as desired.

For NFI, a move away from selection lines to testing of industry herds in research herds was the recommended way to increase producer adoption. The question of the need for methane selection lines was not resolved but key reasons for such action were (1) More divergent animals provide the surest way of establishing genetic correlations between traits. (2) Divergent animals are needed to identify the mechanisms of difference between disparate individual and so provide opportunities to establish proxy tests which may be cheaper and more widely applicable for genetic selection.

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List of Participants

Name	Company
Harry Clark	Agresearch
Ben Vlaming	Agresearch
John McEwan	Agresearch
Theresa Wilson	Agresearch
Jason Archer	Agresearch
Garry Waghorn	Dairy NZ
Kath Donoghue	NSW DPI
Dorothy Robinson	NSW DPI
Arieh Brosh	Israel
Phil Vercoe	Univ. West. Australia
Bill Montgomerie	Dairy Seedstock LIC
Roger Hegarty	NSW DPI
Eva Lewis	Teagasc
Lic. Jose Ignacio Gere	UNI ECN, Argentina
John Basarab	AGI Alberta
Dante Ianna	UNI Sao Paulo
Mark Aspin	PGgRc
Beverley Henry	MLA
Hugh Dove	CSIRO
David Kenny	Teagasc, Ireland
Peter Amer	AbacusBio
Mark Young	Sheep Improvement Ltd
Jane Kay	DairyNZ
Cesar Pinares	Agresearch
David Cottle	UNI of New England
Chris Grainger	Agresearch
Sarah Berry	ViaLactia Biosciences
Steve Davis	ViaLactia Biosciences
Gerald Rys	MAF/Learn

Program



“Livestock Breeding for GHG outcomes”

3-5 March 2009

Program for participants

Welcome:

Thanks for making the effort to attend. There have been minor program changes and some additional chairing duties, so please check your session !

We have set a relatively open program with regular discussion periods so we expect to be flexible in our timing but brilliantly successful in achieving our objectives. The ultimate objective of course is to identify and facilitate the most useful way that genetic improvement can be used to reduce GHG emission from livestock. In the process of getting there we need to come to grips with the following.

This workshop should address:

- Existing knowledge on impact of animal genetics on methane emissions (this includes the impact on emissions of selecting for production traits, selecting for efficiency, as well as selecting for a methane trait specifically).
- What is the ideal ‘methane trait’ we select for (methane/kg DMI, methane/kg product, methane/yearetc) ?
- How can we determine the ‘methane phenotype’ of large numbers of animals (and how repeatable is this phenotype) ?
- How do we correspondingly measure/estimate intake if this is required ?
- Review progress and constraints to selection for NFI globally and how NFI can be advanced as a genetic tool to reduce emissions.

FINAL PROGRAM

Day 1	Time	Time	Chair	Speaker
8.45	Introduction			Hegarty
	1. Livestock Greenhouse Fundamentals		Rys (NZ)	
9.00	<i>Livestock emissions: an overview from global to animal level and what we might breed for</i>	20+10		Hegarty (Aus:DPI)
9.30	<i>Greenhouse accounting for ruminant emissions and including animal genetic improvement in accounts</i>	20+10		Clark (NZ:AgR)
10.00	<i>Enteric methane mitigation research underway in Australia and New Zealand'</i>	20+10		Aspin/Henry (NZ/Aus)
10.30	TEA			
	2. Genetics of methane production in ruminants		Vercoe + Heg.	
10.50	<i>'Impact of genetic selection for performance on greenhouse gas emissions from Merinos'</i>	25 + 5		Cottle (AusUNE)
11.20	<i>Spin-off benefits from current genetic improvement in the NZ sheep industry and potential for enhancement.</i>	25 + 5		Amer (Abacusbio NZ)
11.50	<i>GHG changes associated with genotype changes in the NZ dairy herd</i>	15 + 5		Montgomerie LIC:NZ
12.10 – 12.45	Discussion: Are we recognising the consequences of genetic change & do we need to go to a methane specific trait?			
12.45-.30	<i>LUNCH</i>			

1.30	<i>'New Zealand studies of low methane yield sheep'</i> .	20 + 10	O'Donoghue & Lewis	Pinares (NZ:AgR)
2.00	<i>Australian studies on "Low Methane Cattle"</i>	20 + 10		Hegarty
2.30	<i>Results of PGGRC, Vialactia, LIC dairy genomics methane study</i>	30 + 5		Berry (Vialactia)
3.05	Tea			
	3. Defining the methane phenotype			
3.20	<i>Between- and within-animal variation in methane production</i>	20 + 10	Dove & Clark	McEwan/Robinson (NZ/Aus)
3.50	<i>"Current methane measurement techniques and their errors"</i> .	20 + 10		Vlaming/Pinares (NZ)
4.20	<i>"High throughput measures and proxies for methane production from ruminants"</i> .	20 + 10		Goopy (Aus:DPI)
4.50-5.10	<i>Development and possible applications of long term slow intake breath subsamplers in identifying methane phenotype of ruminants</i>	15 + 5		Gere (Argentina)
5.10-5.40	Discussion –Measurement tools for genetic evaluation of methane trait (accuracy, ranking tools etc., marker options. include traits & type/no of samples)	20	Team	
Dinner	No formal dinner plans. We will cover dinner in Hotel, or head out on your own at will			
DAY 2	4. The intake challenge (of relevance to methane & RFI)		Young + Grainger	
9.00	<i>"Methods and possibilities for determining feed intake of grazing ruminants"</i>	20 + 10		Dove (CSIRO, Aus)
9.30	<i>"An assessment of net energy expenditure measurement in ruminants"</i>	20 + 10		Brosh (Israel)

10.00	<i>A tracer approach to measuring energy expenditure</i>	15 + 5		Lili/Hegarty
10.20	Discussion: options for estimating DMI or Energy in methane yield traits	25		
10.40	TEA			
	5. Future research & essential tasks		Aspin + Henry	
11.00	<i>“Intended Australian research for breeding low methane cattle”</i>	20+10		Donoghue (Aus:DPI)
11.30	<i>“Intended Australian research for breeding low methane sheep”</i>	15 +10		Vercoe (Aus:UWA)
11.55	<i>“New Zealand plans for sheep genetics research for GHG mitigation ”</i>	15 + 10		McEwan/Pinares (NZ)
12.20	Discussion: How do we get the most out of current & pending experiments (links, additional measures, gene markers, \$)	40		
1.00	Lunch			
1.45	Lead to resolutions/conclusions/recommendations on selection for a methane trait + ‘to do’ list (pulling lessons from day 1 & 2)	45		
	6. Net Feed Intake (possibilities and current constraints)		Cottle+ Amer	
2.30	<i>Feed Intake, residual fee intake and its implementation in Australia</i>	20 + 10		Donoghue (Aus)
3.00	<i>“Association between RFI and GHG emissions, and implementation of RFI in Canada”</i>	25 + 5		Basarab (Can)
3.30	<i>Net feed intake research initiatives for cattle in Brazil</i>	20 + 10		Lana (Braz)
4.00	<i>“Studies on breed differences in feed-use efficiency”</i>	20 + 10		Lewis (Ire)

4.30	Garry's 5 slides.... Introducing genetics & N efficiency	~5 hours		
Dinner	Arranged dinner "Mac's Brewery" – much better than it sounds !!!!!			
DAY 3				Kenny (Ire)
8.30	<i>"Irish research on Net Feed Intake for beef (and effects on GHG emissions)"</i>	20 + 10	Archer	
9.00	<i>Selection for Net Feed Intake in NZ dairy heifers</i>	20 + 10		Waghorn (NZ:DairyNZ)
9.30-	Discussion -Advancing and commercialising NFI technology as an inventory-accepted way of reducing emissions ~ how, when, what is needed	60	Archer, Hegarty & Clark +++	
10.30	TEA			
10.45-12	Recommendations on trait, measurement procedures and research needed in breeding for low GHG livestock		Team	

END